

gene_id	GO:Biological Processes	GO:Cellular Components	GO:Molecular Functions	KEGG_Ortholog	KEGG_Map	KOG_Annotation	NR_Annotation	Swissprot_Annotation
A0002	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02949 RP-S11e, RPS11; small subunit ribosomal protein S11e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1728 Hs4506681 40S ribosomal protein S11	CCE85950.1 P1so0_005592 [Milleromyces farinosa CBS 7064]	Small ribosomal subunit protein uS17 OS=Bos taurus OX=9913 GN=RPS11 PE=2 SV=3
A0003	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	-	-	KOG0634 7294778 Aromatic amino acid aminotransferase and related proteins	ORY48137.1 PLP-dependent transferase [Rhizoclostium globosum]	Aromatic-amino-acid aminotransferase 1 OS=Thermococcus litoralis (strain ATCC 51850 / DSM 5473 / JCM 8560 / NS-C) OX=523849 GN=OCC_04335 PE=1 SV=1
A0004	GO:0006914(autophagy),GO:0030242(autophagy of peroxisome)	-	-	K17906 ATG2; autophagy-related protein 2	map05014 Amyotrophic lateral sclerosis;map04140 Autophagy - animal;map04138 Autophagy - yeast;map04136 Autophagy - other;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	-	KAF9977013.1 autophagy-protein 2 [Actinomyces rella ambigua]	Autophagy-related protein 2 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=ATG2 PE=3 SV=1
A0005	-	-	-	-	-	-	-	-
A0006	-	-	-	-	-	-	-	-
A0008	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0583 Hs7661974 Serine/threonine protein kinase	OOO11155.1 protein kinase [Aspergillus oryzae]	CBL-interacting protein kinase 7 OS=Oryza sativa subsp. japonica OX=39947 GN=CIPK7 PE=2 SV=1
A0009	-	-	GO:0005515(protein binding)	K17262 TBCB, CKAP1, ALF1; tubulin-specific chaperone B	-	KOG3206 At3g10220 Alpha-tubulin folding cofactor B	TPX77231.1 hypothetical protein CcBS67573_g01466 [Chytridiomycetes confervae]	Tubulin-folding cofactor B OS=Arabidopsis thaliana OX=3702 GN=TFCB PE=1 SV=1
A0010	GO:0042254(ribosome biogenesis)	GO:0005730(nucleolus)	-	K14843 PES1, NOP7; pescadillo	-	-	RKP23563.1 Pescadillo N-terminus-domain-containing protein [Syncephala pseudoplumigaleata]	Pescadillo homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ppp1 PE=1 SV=1
A0011	-	-	-	-	-	-	-	-
A0012	-	-	-	-	-	-	-	-
A0013	-	-	-	-	-	KOG0958 Hs20560402 DNA damage-responsive repressor GIS1/RPH1, jumonji superfamily	OSD00357.1 hypothetical protein PYCCODRAFT_1437481 [Trametes coccinea BRFM310]	Probable lysine-specific demethylase 4F OS=Homo sapiens OX=9606 GN=KDM4F PE=3 SV=1

A0014	GO:0007264(small GTPase mediated signal transduction)	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K04392 RAC1; Ras-related C3 botulinum toxin substrate 1	map04360 Axon guidance;map04361 Axon regeneration;map05014 Amyotrophic lateral sclerosis;map04024 cAMP signaling pathway;map05415 Diabetic cardiomyopathy;map05417 Lipid and atherosclerosis;map05416 Viral myocarditis;map04145 Phagosome;map05135 Yersinia infection;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04810 Regulation	KOG0393 CE16833 Ras-related small GTPase, Rho type	XP_00926682.0.1 Rho-related protein rac1B [Wallemia ichthyophaga EXF-994]	Ras-related protein ced-10 OS=Caenorhabditis elegans OX=6239 GN=ced-10 PE=1 SV=2
A0015	GO:0006629(lipid metabolic process)	-	GO:0020037(heme binding),GO:0016491(oxidoreductase activity)	K13076 SLD; sphingolipid 8-(E)-desaturase [EC:1.14.19.18]	-	KOG4232 At2g46210 Delta 6-fatty acid desaturase/delta-8 sphingolipid desaturase	XP_01660558.1.1 hypothetical protein SPPG_07016 [Spizellomyces punctatus DAOM BR117]	Delta(8)-fatty-acid desaturase OS=Helianthus annuus OX=4232 GN=sld1 PE=1 SV=1
A0016	GO:0006801(superoxide metabolic process)	-	GO:0004784(superoxide dismutase activity),GO:0046872(metal ion binding)	K04564 SOD2; superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	map05417 Lipid and atherosclerosis;map04146 Peroxisome;map04211 Longevity regulating pathway;map04212 Longevity regulating pathway - worm;map04213 Longevity regulating pathway - multiple species;map05208 Chemical carcinogenesis - reactive oxygen species;map04013 MAPK signaling pathway - fly;map05016 Huntington disease;map04068 FoxO signaling pathway	KOG0876 Hs10835187 Manganese superoxide dismutase	ORZ39258.1 Manganese/superoxide dismutase [Catenaria anguillulae PL171]	Superoxide dismutase [Mn], mitochondrial OS=Mus musculus OX=10090 GN=Sod2 PE=1 SV=3
A0017	-	GO:0000124(SAGA complex)	GO:0005515(protein binding)	-	-	KOG3038 At3g27460 Histone acetyltransferase SAGA associated factor SGF29	XP_02006934.3.1 hypothetical protein CYBJADRAFT_168621 [Cyberlindnera jadinii NRRL Y-1542]	-
A0018	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs4502553 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KAG4086425.1 Pkinase-domain-containing protein [Neocallimastix sp. JGI-2020a]	Calcium/calmodulin-dependent protein kinase type 1 OS=Macrobrachium nipponense OX=159736 GN=CaMKI PE=2 SV=1

A0019	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome),GO:0140359(ABC-type transporter activity),GO:0005524(ATP binding)	-	-	KOG0061 At5g06530 Transporter, ABC superfamily (Breast cancer resistance protein)	ORX58024.1 hypothetical protein DM01DRAFT_351938 [Hesseltinella vesiculosa]	ABC transporter G family member 22 OS=Dictyostelium discoideum OX=44689 GN=abcG22 PE=2 SV=1
A0020	-	-	GO:0003723(RNA binding)	K17943 PUM; Pumilio RNA-binding family	map05017 Spinocerebellar ataxia	KOG1488 CE05044 Translational repressor Pumilio/PUF3 and related RNA-binding proteins (Puf superfamily)	XP_019023054.1 Pumilio1 in complex with Cyclinb reverse Rna [Saitoella complicata NRRL Y-17804]	Pumilio homolog 6, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=APUM6 PE=1 SV=1
A0021	-	-	-	-	-	-	-	-
A0022	-	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups),GO:0016746(acyltransferase activity)	K07508 ACAA2; acetyl-CoA acyltransferase 2 [EC:2.3.1.16]	map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map00062 Fatty acid elongation;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG1391 Hs5174429 Acetyl-CoA acetyltransferase	RKP08753.1 Thiolase, N-terminal domain-containing protein [Thamnocephalis sphaerospora]	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1 SV=2
A0023	GO:0006890(retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum)	GO:0030126(COP1 vesicle coat)	-	K20471 COPD, ARCN1, RET2; coatomer subunit delta	-	KOG2635 Hs11863154 Medium subunit of clathrin adaptor complex	ORX98913.1 clathrin adaptor, mu subunit [Basidiobolus meristosporus CBS 931.73]	Coatomer subunit delta OS=Gallus gallus OX=9031 GN=ARCN1 PE=2 SV=1
A0024	-	-	-	-	-	-	-	-
A0025	GO:1902600(proton transmembrane transport)	GO:0033179(proton-transferring V-type ATPase, V0 domain), GO:0033177(proton-transferring two-sector ATPase complex, proton-transferring domain)	GO:0046961(proton-transferring ATPase activity, rotational mechanism),GO:0015078(proton transmembrane transporter activity)	K02155 ATPeV0C, ATP6L; V-type H+-transferring ATPase 16kDa proteolipid subunit	map04145 Phagosome;map04142 Lysosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation;map05110 Vibrio cholerae infection;map05120 Epithelial cell signaling in Helicobacter pylori infection;map05152 Tuberculosis;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG0232 Hs4502313 Vacuolar H+-ATPase V0 sector, subunits c/c'	KAF1999019.1 vacuolar ATP synthase-like protein 16 kDa proteolipid subunit [Amniculicola lignicola CBS 123094]	V-type proton ATPase 16 kDa proteolipid subunit c OS=Torpedo marmorata OX=7788 PE=1 SV=1

A0026	-	-	-	K23678 PQLC2, SLC66A1, LAAT1; solute carrier family 66 (lysosomal lysine- arginine transporter), member 1	-	-	KOG2913 At4 g36850 Predicted membrane protein	KAF0392067. 1 PQ-loop- domain- containing protein [Gigaspora margarita]	Lysosomal amino acid transporter 1 homolog OS=Gallus gallus OX=9031 GN=SLC66A1 PE=2 SV=1
A0027	GO:00165 67(protein ubiquitina tion)	-	GO:0004842(ubi quitin-protein transferase activity)	-	-	-	-	CEH12291.1 hypothetical protein CBOM_00290 [Ceraceosoru s bombacis]	E3 ubiquitin-protein ligase SlrP OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=slrP PE=1 SV=1
A0028	GO:00065 08(proteo lysis)	-	GO:0008234(cys teine-type peptidase activity)	-	-	-	-	-	-
A0029	-	-	-	-	-	-	-	-	-
A0030	-	-	GO:0005515(pro tein binding)	-	-	-	-	-	-
A0031	-	-	-	-	-	-	KOG1161 YJL 012c Protein involved in vacuolar polyphosphat e accumulation , contains SPX domain	XP_00667520 0.1 uncharacteriz ed protein BATDEDRAFT _18676 [Batrachochyt rium dendrobatidi s JAM81]	Vacuolar transporter chaperone complex subunit 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VTC4 PE=1 SV=2
A0032	GO:00063 78(mRNA polyadeny lation),GO .0006379(mRNA cleavage)	GO:00058 47(mRNA cleavage and polyadeny lation specificity factor complex)	-	K14402 CPSF2, CFT2; cleavage and polyadenylati on specificity factor subunit 2	map03015 mRNA surveillance pathway	-	KOG1135 At5 g23880 mRNA cleavage and polyadenylati on factor II complex, subunit CFT2 (CPSF subunit)	KAG1174241. 1 hypothetical protein G6F71_00505 5 [Rhizopus microsporus]	Cleavage and polyadenylation specificity factor subunit 2 OS=Arabidopsis thaliana OX=3702 GN=CPSF100 PE=1 SV=2
A0033	-	-	-	-	-	-	-	-	-
A0034	-	-	GO:0003824(cat alytic activity)	K18703 SUGCT; succinate- -- hydroxymeth ylglutarate CoA- transferase [EC:2.8.3.13]	-	-	KOG3957 730 0628 Predicted L- carnitine dehydratase/ alpha- methylacyl- CoA racemase	KAF9362363. 1 hypothetical protein BGX34_00632 9 [Mortierella sp. NVP85]	Succinate- -glutarate CoA-transferase OS=Agrobacterium fabrum (strain C58 / ATCC 33970) OX=176299 GN=caiB PE=1 SV=2
A0035	-	-	-	-	-	-	-	-	-
A0036	-	-	-	-	-	-	-	ORY24608.1 hypothetical protein LY90DRAFT_7 06509 [Neocallimast ix californiae]	IQ domain-containing protein H OS=Mus musculus OX=10090 GN=lqch PE=2 SV=3
A0037	-	-	-	-	-	-	-	-	-
A0038	GO:00063 51(transcr iption, DNA- templated)	-	-	-	-	-	-	-	-
A0039	GO:00059 75(carboh ydrate metabolic process), GO:00717 04(organi c substance metabolic process)	-	GO:0016868(intr amolecular transferase activity, phosphotransfer ases)	-	-	-	KOG1220 Hs8 922804 Phosphogluc omutase/pho sphomanno mutase	CEI95986.1 hypothetical protein RMCBS34429 2_10158 [Rhizopus microsporus]	Phosphopentomutase OS=Pongo abelii OX=9601 GN=PGM2 PE=2 SV=3

A0040	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K14539 LSG1; large subunit GTPase 1 [EC:3.6.1.-]	map03008 Ribosome biogenesis in eukaryotes	KOG1424 YGL099w Predicted GTP-binding protein MMR1	RMZ83805.1 hypothetical protein DV738_g863, partial [Chaetothyrus sp. CBS 135597]	Large subunit GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LSG1 PE=1 SV=1
A0041	-	-	-	-	-	-	-	-
A0042	-	-	GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	K14411 MSI; RNA-binding protein Musashi	map03015 mRNA surveillance pathway	KOG4205 Hs4505255 RNA-binding protein musashi/mRNA cleavage and polyadenylation factor I complex, subunit HRP1	OBZ89585.1 hypothetical protein AOJ61_02367 [Choanephora cucurbitarum]	RNA-binding protein Musashi homolog 1 OS=Mus musculus OX=10090 GN=Msi1 PE=1 SV=1
A0043	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 Hs14779875 Phosphatidylinositol transfer protein SEC14 and related proteins	KAF9780209.1 CRAL-TRIO domain-containing protein [Thelephora terrestris]	SEC14-like protein 5 OS=Xenopus tropicalis OX=8364 GN=sec14l1 PE=2 SV=1
A0044	-	-	-	-	-	-	-	-
A0045	-	-	GO:0008289(lipid binding)	-	-	-	-	-
A0046	-	-	GO:0016624(oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor)	K00167 BCKDHB, bkdA2; 2-oxoisovalerate dehydrogenase E1 component subunit beta [EC:1.2.4.4]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map00640 Propionate metabolism;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0525 At1g55510 Branched chain alpha-keto acid dehydrogenase E1, beta subunit	KAG1270073.1 hypothetical protein G6F65_013398 [Rhizopus oryzae]	2-oxoisovalerate dehydrogenase subunit beta OS=Thermus thermophilus (strain ATCC BAA-163 / DSM 7039 / HB27) OX=262724 GN=TT_C1756 PE=3 SV=1
A0047	-	-	GO:0004089(carbonate dehydratase activity),GO:0008270(zinc ion binding)	K01673 cynT, can; carbonic anhydrase [EC:4.2.1.1]	map00910 Nitrogen metabolism;map01100 Metabolic pathways	-	ORY31548.1 carbonic anhydrase [Rhizoclostium globosum]	Carbonic anhydrase OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=AN1805 PE=1 SV=2
A0048	-	-	-	-	-	-	TPX67530.1 hypothetical protein SpCBS45565_g03682 [Spizellomyces sp. 'palustris']	-
A0049	-	-	GO:0003824(catalytic activity)	K12663 ECH1; Delta3,5-Delta2,4-dienoyl-CoA isomerase [EC:5.3.3.21]	map04146 Peroxisome	KOG1681 Hs1433007 Enoyl-CoA isomerase	KAG2209893.1 hypothetical protein INT46_005174 [Mucor plumbeus]	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens OX=9606 GN=ECH1 PE=1 SV=2
A0050	-	-	-	-	-	-	-	-

A0051	-	-	-	-	-	KOG2132 Hs1471442 Uncharacterized conserved protein, contains JmjC domain	PVU86257.1 hypothetical protein BB559_006586, partial [Furculomyces boomerangs]	Hypoxia-inducible factor 1-alpha inhibitor OS=Danio rerio OX=7955 GN=hif1an PE=2 SV=2
A0052	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003899(DNA-directed 5'-3' RNA polymerase activity),GO:0008270(zinc ion binding)	K03007 RPABC5, RPB10, POLR2L; DNA-directed RNA polymerases I, II, and III subunit RPABC5	map03420 Nucleotide excision repair;map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway;map05016 Huntington disease	KOG3497 At1g61700 DNA-directed RNA polymerase, subunit RPB10	ORX74955.1 DNA-directed RNA polymerase I, II, and III subunit RPABC5 [Linderina pennisporea]	DNA-directed RNA polymerases I, II, and III subunit RPABC5 OS=Brassica napus OX=3708 PE=3 SV=1
A0053	-	-	-	-	-	KOG0679 At1g18450 Actin-related protein - Arp4p/Act3p	OON03406.1 hypothetical protein BSLG_06268 [Batrachochytrium salamandrivorans]	Actin-related protein 4 OS=Oryza sativa subsp. indica OX=39946 GN=ARP4 PE=3 SV=2
A0054	GO:0016192(vesicle-mediated transport),GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	GO:0005794(Golgi apparatus),GO:000139(Golgi membrane),GO:0005801(cis-Golgi network),GO:0016021(integral component of membrane)	GO:0005484(SNAP receptor activity)	K08495 GOSR1, GOS1; golgi SNAP receptor complex member 1	map04130 SNARE interactions in vesicular transport	KOG3208 At2g45200 SNARE protein GS28	EJD54871.1 28 kda golgi snare protein [Auricularia subglabra TFB-10046 SS5]	Golgi SNAP receptor complex member 1-1 OS=Arabidopsis thaliana OX=3702 GN=GOS11 PE=2 SV=1
A0055	GO:0005975(carbohydrate metabolic process)	-	GO:0030246(carbohydrate binding)	-	-	-	CUA70386.1 putative glycosidase Rv0584 [Rhizoctonia solani]	Uncharacterized glycosidase Rv0584 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv0584 PE=3 SV=1
A0056	-	-	-	K17785 IMMT, MIC60; MICOS complex subunit MIC60	-	KOG1854 7300800 Mitochondrial inner membrane protein (mitofilin)	GAO49253.1 hypothetical protein G7K_3406-t1 [Saitoella complicata NRRL Y-17804]	MICOS complex subunit mic60 OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=mic60 PE=3 SV=1
A0057	-	-	GO:0005085(guanine nucleotide exchange factor activity),GO:0005515(protein binding)	-	-	KOG4424 Hs2047180 Predicted Rho/Rac guanine nucleotide exchange factor/facilitator protein 3	ORY56212.1 Dbl homology domain-containing protein [Neocallimastix californiae]	Myosin-M heavy chain OS=Dictyostelium discoideum OX=44689 GN=myoM PE=1 SV=1
A0058	GO:0046654(tetrahydrofolate biosynthetic process)	-	GO:0003934(GTP cyclohydrolase I activity)	K01495 GCH1, folE; GTP cyclohydrolase I [EC:3.5.4.16]	map01240 Biosynthesis of cofactors;map01100 Metabolic pathways;map00790 Folate biosynthesis	-	RKP13379.1 hypothetical protein BJ684DRAFT_20125 [Piptocephalis cylindrospora]	GTP cyclohydrolase 1 OS=Dictyostelium discoideum OX=44689 GN=gchA PE=1 SV=2

A0059	GO:0036297(interstrand cross-link repair)	GO:0043240(Fanconi anaemia nuclear complex)	GO:0004842(ubiquitin-protein transferase activity)	-	-	KOG3268 Hs8922360 Predicted E3 ubiquitin ligase	PKY44445.1 E3 ubiquitin-protein ligase [Rhizophagus irregularis]	E3 ubiquitin-protein ligase FANCL OS=Homo sapiens OX=9606 GN=FANCL PE=1 SV=2
A0060	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	KAF9904967.1 hypothetical protein BX16_001133 [Lobosporangium transversale]	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A0061	-	-	-	-	-	-	-	-
A0062	-	-	-	-	-	-	-	-
A0063	-	-	-	-	-	-	-	-
A0064	GO:0006086(acetyl-CoA biosynthetic process from pyruvate)	GO:0043231(intracellular membrane-bounded organelle)	GO:0004739(pyruvate dehydrogenase (acetyl-transferring) activity),GO:0016624(oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor)	K00161 PDHA, pdhA; pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	map05415 Diabetic cardiomyopathy; map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00620 Pyruvate metabolism;map05230 Central carbon metabolism in cancer;map01110 Metabolic	KOG0225 At1g59900 Pyruvate dehydrogenase E1, alpha subunit	KAG2200943.1 hypothetical protein [NT47_003178 [Mucor saturninus]	Pyruvate dehydrogenase E1 component subunit alpha-2, mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=Os06g0246500 PE=2 SV=1
A0065	-	GO:0031428(box C/D RNP complex), GO:0032040(small-subunit processome)	GO:0030515(snRNA binding)	K14564 NOP56; nucleolar protein 56	map05017 Spinocerebellar ataxia;map03008 Ribosome biogenesis in eukaryotes	KOG2573 At1g56110 Ribosome biogenesis protein - Nop56p/Sik1p	CDS07170.1 hypothetical protein LRAMOSA09693 [Lichtheimia ramosa]	Nucleolar protein 56 OS=Homo sapiens OX=9606 GN=NOP56 PE=1 SV=4
A0066	GO:0006470(protein dephosphorylation)	-	GO:0043169(cation binding),GO:0004722(protein serine/threonine phosphatase activity)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 At2g25070 Serine/threonine protein phosphatase	CDS12530.1 hypothetical protein LRAMOSA04724 [Lichtheimia ramosa]	Probable protein phosphatase 2C 21 OS=Arabidopsis thaliana OX=3702 GN=PPC4-2 PE=1 SV=1
A0067	-	-	-	-	-	-	-	-
A0068	-	-	GO:0008146(sulfotransferase activity)	-	-	KOG1584 Hs7657621 Sulfotransferase	ODM23809.1 hypothetical protein SI65_01398 [Aspergillus cristatus]	Sulfotransferase 1B1 OS=Homo sapiens OX=9606 GN=SULT1B1 PE=1 SV=2
A0069	GO:0071596(ubiquitin-dependent protein catabolic process via the N-end rule pathway)	-	GO:0061630(ubiquitin protein ligase activity)	K10625 UBR1; E3 ubiquitin-protein ligase UBR1 [EC:2.3.2.27]	-	-	KAF5337617.1 hypothetical protein D9758_014922 [Tetrapyrgos nigripes]	E3 ubiquitin-protein ligase ubr3 OS=Danio rerio OX=7955 GN=ubr3 PE=2 SV=2

A0070	GO:0090481(pyrimidine nucleotide-sugar transmembrane transport)	GO:0000139(Golgi membrane),GO:0016021(integral component of membrane)	GO:0015165(pyrimidine nucleotide-sugar transmembrane transporter activity)	K15272 SLC35A1_2_3; solute carrier family 35 (UDP-sugar transporter), member A1/2/3	-	KOG2234 Hs6912668 Predicted UDP-galactose transporter	GAN11710.1 UDP-N-acetylglucosamine transporter-like isoform X2 [Mucor ambiguus]	UDP-N-acetylglucosamine transporter OS=Rattus norvegicus OX=10116 GN=Slc35a3 PE=2 SV=1
A0071	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity)	-	-	KOG0698 At5g26010 Serine/threonine protein phosphatase	-	-
A0072	-	-	GO:0004518(nuclease activity)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518 YOR033c 5'-3' exonuclease	KAF8515840.1 PIN domain-like protein [Hysterangium stoloniferum]	Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EXO1 PE=1 SV=2
A0073	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding),GO:0003995(acyl-CoA dehydrogenase activity)	K00252 GCDH, gcdH; glutaryl-CoA dehydrogenase [EC:1.3.8.6]	map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map00362 Benzoate degradation;map00310 Lysine degradation;map00380 Tryptophan metabolism;map01100 Metabolic pathways;map00071 Fatty acid degradation	KOG0138 Hs4503943 Glutaryl-CoA dehydrogenase	KAG2192725.1 hypothetical protein INT47_006442 [Mucor saturninus]	Glutaryl-CoA dehydrogenase, mitochondrial OS=Bos taurus OX=9913 GN=GCDH PE=2 SV=1
A0074	GO:0006418(tRNA aminoacylation for protein translation),GO:0006436(tryptophanyl-tRNA aminoacylation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004830(tryptophan-tRNA ligase activity)	K01867 WARS, trpS; tryptophanyl-tRNA synthetase [EC:6.1.1.2]	map00970 Aminoacyl-tRNA biosynthesis	KOG2713 Hs7710154 Mitochondrial tryptophanyl-tRNA synthetase	KAG2218398.1 hypothetical protein INT45_011586 [Mucor circinatus]	Tryptophan--tRNA ligase OS=Caulobacter vibrioides (strain ATCC 19089 / CB15) OX=190650 GN=trpS PE=3 SV=1
A0075	GO:0006886(intracellular protein transport),GO:0048280(vesicle fusion with Golgi apparatus)	GO:0000139(Golgi membrane),GO:0005737(cytoplasm)	-	K20361 USO1; intracellular protein transport protein USO1	-	KOG0946 At3g27530 ER-Golgi vesicle-tethering protein p115	ORY45764.1 hypothetical protein LY90DRAFT_416458 [Neocallimastix californiae]	Golgin candidate 6 OS=Arabidopsis thaliana OX=3702 GN=GC6 PE=1 SV=2

A0076	-	-	-	K01613 psd, PISD; phosphatidylserine decarboxylase [EC:4.1.1.65]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG1032 At1g03370.2 Uncharacterized conserved protein, contains GRAM domain	KAF9938490.1 hypothetical protein BGZ67_010793 [Mortierella alpina]	C2 and GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana OX=3702 GN=At1g03370 PE=2 SV=4
A0077	-	-	-	-	-	-	-	-
A0078	GO:0046854(phosphatidylinositol phosphate biosynthetic process), GO:0048015(phosphatidylinositol-mediated signaling)	-	GO:0016301(kinase activity)	K19801 PI4KB; phosphatidylinositol 4-kinase B [EC:2.7.1.67]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0903 Hs4505809 Phosphatidylinositol 4-kinase, involved in intracellular trafficking and secretion	OBZ80960.1 Phosphatidylinositol 4-kinase PIK1 [Choanephora cucurbitarum]	Phosphatidylinositol 4-kinase beta OS=Danio rerio OX=7955 GN=pi4kb PE=2 SV=2
A0079	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	K08176 PHO84; MFS transporter, PHS family, inorganic phosphate transporter	-	KOG0253 CE06638 Synaptic vesicle transporter SV2 (major facilitator superfamily)	KFH43046.1 Inorganic phosphate transporter-like protein [Acremonium chrysogenum ATCC 11550]	Niacin transporter NiaP OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=niaP PE=1 SV=1
A0081	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003899(DNA-directed 5'-3' RNA polymerase activity)	K03006 RPB1, POLR2A; DNA-directed RNA polymerase II subunit RPB1 [EC:2.7.7.6]	map03420 Nucleotide excision repair;map03020 RNA polymerase;map05016 Huntington disease	KOG0260 Hs4505939 RNA polymerase II, large subunit	AAD12605.1 RNA polymerase II largest subunit [Antonospora locustae]	DNA-directed RNA polymerase subunit Rpo1N OS=Saccharolobus solfataricus (strain ATCC 35092 / DSM 1617 / JCM 11322 / P2) OX=273057 GN=rpo1N PE=1 SV=1
A0082	-	-	GO:0003779(activation binding)	-	-	-	-	-
A0083	GO:0046514(ceramide catabolic process)	-	GO:0017040(N-acylsphingosine amidohydrolase activity)	K12349 ASAH2; neutral ceramidase [EC:3.5.1.23]	map04071 Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG2232 At1g07380 Ceramidases	ORX89074.1 Neutral/alkaline nonlysosomal ceramidase [Basidiobolus meristosporus CBS 931.73]	Neutral ceramidase 2 OS=Arabidopsis thaliana OX=3702 GN=NCER2 PE=3 SV=1
A0084	GO:0009116(nucleoside metabolic process), GO:0009166(nucleoside catabolic process)	GO:0005737(cytoplasm)	GO:0003824(catalytic activity),GO:0004850(uridine phosphorylase activity)	-	-	KOG3728 7291505 Uridine phosphorylase	-	Uridine phosphorylase 1 OS=Mus musculus OX=10090 GN=Upp1 PE=1 SV=2
A0085	GO:0006418(tRNA aminoacylation for protein translation),GO:0006437(tyrosyl-tRNA aminoacylation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004831(tyrosine-tRNA ligase activity)	K01866 YARS, tyrS; tyrosyl-tRNA synthetase [EC:6.1.1.1]	map00970 Aminoacyl-tRNA biosynthesis	KOG2623 7291852 Tyrosyl-tRNA synthetase	EJU04247.1 hypothetical protein DACRYDRAFT_48409 [Dacryopinax primogenitus]	Tyrosine--tRNA ligase OS=Porphyromonas gingivalis (strain ATCC BAA-308 / W83) OX=242619 GN=tyrS PE=3 SV=1

A0086	-	-	-	-	-	KOG2942 At4g28020 Uncharacterized conserved protein	TPX55347.1 hypothetical protein PhCBS80983.g05391 [Powellomyces hirtus]	tRNA (adenine(37)-N6)-methyltransferase OS=Homo sapiens OX=9606 GN=TRMO PE=1 SV=2
A0087	-	-	-	K12587 MTR3, EXOSC6; exosome complex component MTR3	map03018 RNA degradation	KOG1068 Hs17402904 Exosomal 3'-5' exoribonuclease complex, subunit Rrp41 and related exoribonucleases	RKP09873.1 ribosomal protein S5 domain 2-type protein [Thamnocephalis sphaerosporalis]	Exosome complex component MTR3 OS=Homo sapiens OX=9606 GN=EXOSC6 PE=1 SV=1
A0088	-	-	-	-	-	-	-	-
A0089	-	-	-	K25877 MYG1; MYG1 exonuclease [EC:3.1.-.-]	-	KOG2948 CE18880 Predicted metal-binding protein	KAF9355024.1 hypothetical protein BGX34_010698 [Mortierella sp. NVP85]	MYG1 exonuclease OS=Homo sapiens OX=9606 GN=MYG1 PE=1 SV=4
A0090	-	-	-	-	-	KOG2545 Hs13376243 Conserved membrane protein	KAG0288451.1 hypothetical protein BGZ96_007795 [Linnemannia gamsii]	Mini-chromosome maintenance complex-binding protein OS=Xenopus tropicalis OX=8364 GN=mcmbp PE=2 SV=2
A0091	-	-	-	-	-	-	KXS08892.1 hypothetical protein M427DRAFT_50230 [Gonapodya prolifera JEL478]	-
A0092	-	-	-	-	-	-	-	-
A0093	-	GO:0016021(integral component of membrane)	-	-	-	-	TPX64807.1 hypothetical protein CcCBS67573.g08302 [Chytridiomycetes confervae]	-
A0094	-	-	-	-	-	-	ORY48980.1 DUF1697-domain-containing protein [Rhizoclostium globosum]	-
A0095	-	GO:0016020(membrane)	GO:0005227(calcium activated cation channel activity)	K21989 TMEM63, CSC1; calcium permeable stress-gated cation channel	-	KOG1134 At1g32090 Uncharacterized conserved protein	KAG0198312.1 hypothetical protein BGX28_008251 [Mortierella sp. GBA30]	CSC1-like protein At1g32090 OS=Arabidopsis thaliana OX=3702 GN=At1g32090 PE=1 SV=1
A0096	-	-	-	K20298 VPS52; vacuolar protein sorting-associated protein 52	-	KOG1961 At1g71270 Vacuolar sorting protein VPS52/suppressor of actin Sac2	RHZ76011.1 hypothetical protein Glove_208g104 [Diversispora epigaea]	Vacuolar protein sorting-associated protein 52 A OS=Arabidopsis thaliana OX=3702 GN=VPS52 PE=1 SV=1

A0097	GO:0046854(phosphatidylinositol phosphate biosynthetic process), GO:0048015(phosphatidylinositol-mediated signaling)	-	GO:0016301(kinase activity)	K19801 PI4KB; phosphatidylinositol 4-kinase B [EC:2.7.1.67]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0903 Hs4505809 Phosphatidylinositol 4-kinase, involved in intracellular trafficking and secretion	KAF2270292.1 phosphatidylinositol 4-kinase-like protein PIK1 [Didymosphaeria enalia]	Phosphatidylinositol 4-kinase OS=Dictyostelium discoideum OX=44689 GN=pikD PE=3 SV=3
A0098	-	-	GO:0005515(protein binding)	K09553 STIP1; stress-induced-phosphoprotein 1	map05020 Prion disease	KOG0548 At3g04710.2 Molecular co-chaperone ST11	OBW65472.1 General substrate transporter [Aureobasidium pullulans]	Protein STIP1 homolog OS=Dictyostelium discoideum OX=44689 GN=sti1 PE=3 SV=1
A0099	-	-	-	-	-	-	-	-
A0100	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	-	-	KOG0730 Hs20532580 AAA+-type ATPase	OAC99882.1 hypothetical protein MUCCIDRAFT_180498 [Mucor lusitanicus CBS 277.49]	ATPase family gene 2 protein homolog A OS=Mus musculus OX=10090 GN=Afg2a PE=1 SV=2
A0101	-	-	-	-	-	KOG2502 Hs19923167 Tubby family proteins	KAF7752839.1 Tubby-protein 3 [Entomophthora muscae]	Tubby protein OS=Mus musculus OX=10090 GN=Tub PE=1 SV=1
A0102	-	-	-	-	-	-	-	-
A0103	-	-	GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity)	-	-	-	XP_016608527.1 hypothetical protein SPPG_04804 [Spizellomyces punctatus DAOM BR117]	Medium chain reductase/dehydrogenase ucs1 OS=Acremonium sp. OX=2046025 GN=ucs1 PE=3 SV=1
A0104	-	-	-	K00759 APRT, apt; adenine phosphoribosyltransferase [EC:2.4.2.7]	map00230 Purine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG1712 At4g12440 Adenine phosphoribosyltransferases	RKP36904.1 adenine phosphoribosyltransferase [Dimargaris cristalligena]	Adenine phosphoribosyltransferase 4 OS=Arabidopsis thaliana OX=3702 GN=APT4 PE=1 SV=1
A0105	-	-	-	-	-	-	-	-
A0106	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A0107	-	-	-	K01897 ACSL fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04146 Peroxisome;map04216 Ferroptosis;map04714 Thermogenesis;map00061 Fatty acid biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation;map04920 Adipocytokine signaling pathway	KOG1256 Hs21359960 Long-chain acyl-CoA synthetases (AMP-forming)	KZM27732.1 hypothetical protein ST47_g1294 [Ascochyta rabiei]	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Gallus gallus OX=9031 GN=ACSBG2 PE=2 SV=2

A0108	-	-	-	K01897 ACSL fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04146 Peroxisome;map04216 Ferroptosis;map04714 Thermogenesis;map00061 Fatty acid biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation;map04920 Adipocytokine signaling pathway	KOG1256[7298130 Long-chain acyl-CoA synthetases (AMP-forming)	KZM27732.1 hypothetical protein ST47_g1294 [Ascochyta rabiei]	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Gallus gallus OX=9031 GN=ACSBG2 PE=2 SV=2
A0109	-	-	-	K01897 ACSL fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04146 Peroxisome;map04216 Ferroptosis;map04714 Thermogenesis;map00061 Fatty acid biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation;map04920 Adipocytokine signaling pathway	KOG1256[7298130 Long-chain acyl-CoA synthetases (AMP-forming)	KZM27732.1 hypothetical protein ST47_g1294 [Ascochyta rabiei]	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Gallus gallus OX=9031 GN=ACSBG2 PE=2 SV=2
A0110	-	-	-	-	-	-	KNE72792.1 phosphatidyl serine decarboxylase [Allomyces macrogynus ATCC 38327]	Multiple C2 domain and transmembrane region protein 8 OS=Arabidopsis thaliana OX=3702 GN=MCTP8 PE=2 SV=1
A0111	GO:0006364(rRNA processing)	GO:0005730(nucleolus)	GO:0034511(U3 snoRNA binding)	K14774 UTP25, DEF; U3 small nucleolar RNA-associated protein 25	-	KOG2340[Hs7657019 Uncharacterized conserved protein	PKC66581.1 DUF1253-domain-containing protein [Rhizophagus irregularis]	U3 small nucleolar RNA-associated protein 25 homolog OS=Mus musculus OX=10090 GN=Utp25 PE=1 SV=2
A0112	-	-	-	-	-	-	-	-
A0113	-	-	-	-	-	KOG2502[At2g47900 Tub family proteins	RKP03020.1 hypothetical protein CXG81DRAFT_10077 [Caulochytrium protostelioides]	Tubby-like F-box protein 3 OS=Arabidopsis thaliana OX=3702 GN=TULP3 PE=1 SV=1
A0114	-	-	GO:0016787(hydrolase activity)	K17615 PPG1; serine/threonine-protein phosphatase PPG1 [EC:3.1.3.16]	-	KOG0374[At1g03445_2 Serine/threonine specific protein phosphatase PP1, catalytic subunit	KCZ74481.1 serine/threonine-protein phosphatase, partial [Anacalia algerae PRA109]	Serine/threonine-protein phosphatase BSU1 OS=Arabidopsis thaliana OX=3702 GN=BSU1 PE=1 SV=2

A0115	GO:0008380(RNA splicing)	-	-	-	-	KOG3263 CE06242 Nucleic acid binding protein	ORX72253.1 DUF1777-domain-containing protein [Linderina pennisporea]	U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein OS=Mus musculus OX=10090 GN=Snmp27 PE=1 SV=1
A0116	GO:0006338(chromatin remodeling)	GO:0005634(nucleus)	GO:0003677(DNA binding),GO:0031491(nucleosome binding),GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K11654 SMARCA5, SNF2H, ISWI; SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 [EC:5.6.2.-]	map03082 ATP-dependent chromatin remodeling	KOG0385 At3g06400 Chromatin remodeling complex WSTF-ISWI, small subunit	OZJ01930.1 hypothetical protein BZG36_04839 [Bifiguratus adelaidae]	Probable chromatin-remodeling complex ATPase chain OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0367900 PE=2 SV=2
A0117	-	-	-	-	-	-	-	-
A0118	GO:0006357(regulation of transcription by RNA polymerase II)	GO:0016592(mediator complex)	GO:0003712(transcription coregulator activity),GO:0005509(calcium ion binding)	-	-	-	-	-
A0119	-	-	-	-	-	-	-	-
A0120	GO:0006289(nucleotide-excision repair)	GO:0000439(transcription factor TFIIH core complex),GO:0005871(kinesin complex)	GO:0001671(ATPase activator activity),GO:0005515(protein binding)	K03144 TFIIH4, GTF2H4, TFB2; transcription initiation factor TFIIH subunit 4	map03420 Nucleotide excision repair;map03022 Basal transcription factors;map05203 Viral carcinogenesis	-	KAF9978729.1 RNA polymerase II transcription factor B 52 kDa subunit [Actinomortierella ambigua]	General transcription and DNA repair factor IIH subunit TFB2 OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=TFB2 PE=3 SV=1
A0121	-	-	GO:0008887(glycerate kinase activity)	-	-	KOG3935 Hs21687104 Predicted glycerate kinase	RYO87475.1 hypothetical protein DL763_006345 [Monosporascus cannonballus]	D-glycerate 2-kinase OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=TM_1585 PE=1 SV=1
A0122	GO:0007165(signal transduction),GO:0034551(mitochondrial respiratory chain complex III assembly)	-	GO:0005515(protein binding)	-	-	-	XP_031026095.1 uncharacterized protein SmJEL517_g01946 [Synchytrium microbalum]	-
A0123	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity),GO:0004965(G protein-coupled GABA receptor activity)	-	-	KOG1056 Hs4504141 Glutamate-gated metabotropic ion channel receptor subunit GRM2 and related subunits, G-protein coupled receptor superfamily	XP_016606771.1 hypothetical protein SPPG_06409 [Spizellomyces punctatus DAOM BR117]	Metabotropic glutamate receptor-like protein J OS=Dictyostelium discoideum OX=44689 GN=grI PE=2 SV=1
A0124	-	-	-	-	-	-	-	-

A0125	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity),GO:0004965(G protein-coupled GABA receptor activity)	-	-	KOG1056 Hs4557411 Glutamate-gated metabotropic ion channel receptor subunit GRM2 and related subunits, G-protein coupled receptor superfamily	TPX72914.1 hypothetical protein SpCBS45565.g00397 [Spizellomyces sp. 'palustris']	Metabotropic glutamate receptor-like protein E OS=Dictyostelium discoideum OX=44689 GN=grlE PE=2 SV=2
A0126	-	-	-	-	-	-	-	-
A0127	-	-	GO:0005540(hyaluronic acid binding)	-	-	-	-	-
A0128	-	-	-	-	-	-	-	-
A0129	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At5g54280 Myosin class V heavy chain	KAG4083932.1 hypothetical protein H8356DRAFT_1299151 [Neocallimastix sp. JGI-2020a]	Myosin-2 OS=Arabidopsis thaliana OX=3702 GN=VIII-2 PE=2 SV=1
A0130	-	-	-	-	-	-	-	-
A0131	-	-	-	-	-	-	-	-
A0132	-	-	-	K17983 SHE9; sensitive to high expression protein 9, mitochondrial	-	-	TFK48683.1 mitochondrial distribution and morphology family 33, partial [Heliocybe sulcata]	Sensitive to high expression protein 9 homolog, mitochondrial OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) OX=510516 GN=she9 PE=3 SV=1
A0133	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005509(calcium ion binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs4502553 Ca2+ /calmodulin-dependent protein kinase, EF-Hand protein superfamily	RHZ77149.1 hypothetical protein Glove_185g63 [Diversispora epigaea]	Myosin light chain kinase A OS=Dictyostelium discoideum OX=44689 GN=mlkA PE=1 SV=2
A0134	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0135	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	-	-
A0136	-	-	-	-	-	-	-	-
A0137	-	-	-	-	-	KOG2530 At4g37190 Members of tubulin/FtsZ family	GBC05392.1 hypothetical protein RclHR1_00620032 [Rhizophagus clarus]	Protein misato homolog 1 OS=Pongo pygmaeus OX=9600 GN=MSTO1 PE=2 SV=1
A0138	-	-	GO:0005515(protein binding)	-	-	KOG2046 Hs21361120 Calponin	PIA17778.1 hypothetical protein COEREDRAFT_40274, partial [Coemansia reversa NRRL 1564]	Calponin-1 OS=Bos taurus OX=9913 GN=CNN1 PE=2 SV=1

A0139	GO:0055085(transmembrane transport)	-	-	-	-	KOG0769 At5g27520 Predicted mitochondrial carrier protein	ODV90877.1 hypothetical protein CANCADRAFT_2599 [Tortispora caseinolytica NRRL Y-17796]	Peroxisomal adenine nucleotide carrier 1 OS=Glycine max OX=3847 GN=PNC1 PE=2 SV=1
A0140	-	-	-	-	-	-	-	-
A0141	GO:0015940(pantothenate biosynthetic process)	-	GO:0016491(oxidoreductase activity),GO:0008677(2-dehydropantoate 2-reductase activity)	-	-	-	TPX45786.1 2-dehydropantoate 2-reductase [Synchytrium endobioticum]	2-dehydropantoate 2-reductase OS=Archaeoglobus fulgidus (strain ATCC 49558 / DSM 4304 / JCM 9628 / NBRC 100126 / VC-16) OX=224325 GN=AF_1695 PE=3 SV=1
A0142	-	-	GO:0016491(oxidoreductase activity)	-	-	-	TPX57805.1 2-dehydropantoate 2-reductase [Powellomyces hirtus]	2-dehydropantoate 2-reductase OS=Archaeoglobus fulgidus (strain ATCC 49558 / DSM 4304 / JCM 9628 / NBRC 100126 / VC-16) OX=224325 GN=AF_1695 PE=3 SV=1
A0143	GO:0006096(glycolytic process)	GO:000015(phosphopyruvate hydratase complex)	GO:0000287(magnesium ion binding),GO:0004634(phosphopyruvate hydratase activity)	K01689 ENO, eno; enolase [EC:4.2.1.11]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00680 Methane metabolism;map03018 RNA degradation;map01100 Metabolic pathways;map04066 HIF-1 signaling pathway	KOG2670 Hs5803011 Enolase	KAF9124481.1 hypothetical protein BGX30_000922 [Mortierella sp. GBA39]	Enolase 2 OS=Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) OX=223283 GN=eno2 PE=3 SV=1
A0144	-	-	GO:0047617(acyl-CoA hydrolase activity)	-	-	KOG3328 7292258 HGG motif-containing thioesterase	ORX55904.1 Thioesterase/thiol ester dehydratase-isomerase [Piromyces finnis]	Putative esterase F42H10.6 OS=Caenorhabditis elegans OX=6239 GN=F42H10.6 PE=1 SV=2
A0145	-	-	-	-	-	-	-	-
A0146	-	-	-	K13237 DECR2, SPS19; 2,4-dienoyl-CoA reductase [(3E)-enoyl-CoA-producing], peroxisomal [EC:1.3.1.124]	map04146 Peroxisome	KOG0725 Hs19923817 Reductases with broad range of substrate specificities	KAF9976010.1 hypothetical protein BGZ73_000124 [Actinomyces ruddii]	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens OX=9606 GN=PECR PE=1 SV=2
A0147	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0575 Hs21361433 Polo-like serine/threonine protein kinase	RKP02758.1 hypothetical protein CXG81DRAFT_10449, partial [Caulochytrium protostelioides]	Serine/threonine-protein kinase PLK4 OS=Drosophila persimilis OX=7234 GN=SAK PE=3 SV=1

A0148	GO:0006397(mRNA processing)	-	-	K12621 LSM2; U6 snRNA-associated Sm-like protein LSM2	map03040 Spliceosome;map03018 RNA degradation	KOG3448 At1g03330 Predicted snRNP core protein	TPX35835.1 hypothetical protein SeMB42_g07130 [Synchytrium endobioticum]	Sm-like protein LSM2 OS=Arabidopsis thaliana OX=3702 GN=LSM2 PE=1 SV=1
A0149	-	-	GO:0005096(GTPase activator activity)	K12492 ARFGAP1; ADP-ribosylation factor GTPase-activating protein 1	map04144 Endocytosis	KOG0704 At2g37550 ADP-ribosylation factor GTPase activator	ORY69381.1 ArfGap-domain-containing protein, partial [Neocallimastix californiae]	ADP-ribosylation factor GTPase-activating protein AGD7 OS=Arabidopsis thaliana OX=3702 GN=AGD7 PE=1 SV=1
A0150	GO:0006090(pyruvate metabolic process), GO:0006094(glucoseogenesis)	-	GO:0005524(ATP binding),GO:0003824(catalytic activity),GO:0004736(pyruvate carboxylase activity),GO:0046872(metal ion binding)	K01958 PC, pyc; pyruvate carboxylase [EC:6.4.1.1]	map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00720 Carbon fixation pathways in prokaryotes;map00020 Citrate cycle (TCA cycle);map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG0369 CE09072 Pyruvate carboxylase	KAG0239950.1 pyruvate carboxylase [Mortierella sp. GBA43]	Pyruvate carboxylase, mitochondrial OS=Bos taurus OX=9913 GN=PC PE=2 SV=2
A0151	-	-	-	-	-	-	-	-
A0152	GO:0006007(glucose catabolic process)	GO:0005737(cytoplasm)	GO:0003824(catalytic activity),GO:0046872(metal ion binding),GO:0004619(phosphoglycerate mutase activity),GO:0030145(manganese ion binding)	-	-	KOG4513 CE11302 Phosphoglycerate mutase	KDQ55721.1 hypothetical protein JAAARDRAFT_37145 [Jaapia argillacea MUCL 33604]	2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Gluconobacter oxydans (strain 621H) OX=290633 GN=gpmI PE=3 SV=1
A0153	GO:0019354(siroheme biosynthetic process)	-	GO:0008168(methyltransferase activity)	K00589 MET1; uroporphyrin-III C-methyltransferase [EC:2.1.1.107]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	-	ORX98221.1 uroporphyrin-III C-m [Basidiobolus meristosporus CBS 931.73]	Probable uroporphyrinogen-III C-methyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC1739.06c PE=2 SV=1

A0154	GO:0001522(pseudouridine synthesis), GO:0009451(RNA modification)	-	GO:0003723(RNA binding),GO:0009982(pseudouridine synthase activity),GO:0016866(intramolecular transferase activity)	-	-	-	KAF9393948.1 hypothetical protein CPC16_000660 [Podila verticillata]	Ribosomal large subunit pseudouridine synthase B OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=rluB PE=3 SV=1
A0155	-	-	-	-	-	-	-	-
A0156	GO:0006488(dolichol-linked oligosaccharide biosynthetic process)	GO:0016021(integral component of membrane)	-	K06316 RFT1; oligosaccharide translocation protein RFT1	-	KOG2864[Hs16418361 Nuclear division RFT1 protein	KAG2189450.1 hypothetical protein INT44_004592, partial [Umbelopsis vinacea]	Protein RFT1 homolog OS=Xenopus tropicalis OX=8364 GN=rft1 PE=2 SV=1
A0157	-	-	GO:0005096(GTPase activator activity)	K12486 SMAP; stromal membrane-associated protein	map04144 Endocytosis	KOG0703[At3g17660 Predicted GTPase-activating protein	XP_023469528.1 ArfGap-domain-containing protein [Rhizopus microsporus ATCC 52813]	Probable ADP-ribosylation factor GTPase-activating protein AGD15 OS=Arabidopsis thaliana OX=3702 GN=AGD15 PE=2 SV=1
A0158	-	-	-	-	-	-	-	-
A0159	GO:0006508(proteolysis)	-	GO:0008237(metallopeptidase activity),GO:0004222(metalloendopeptidase activity)	-	-	-	-	-
A0160	-	-	GO:0005515(protein binding)	K15042 KPNA5_6; importin subunit alpha-6/7	map03013 Nucleocytoplasmic transport;map05207 Chemical carcinogenesis - receptor activation;map05164 Influenza A	KOG0166[At4g02150 Karyopherin (importin) alpha	OIR57392.1 Importin alpha subunit [Amphiblyss sp. WSBS2006]	Importin subunit alpha-1b OS=Oryza sativa subsp. japonica OX=39947 GN=Os05g0155601 PE=1 SV=2
A0161	-	-	GO:0016491(oxidoreductase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	K00128 ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]	map00410 beta-Alanine metabolism;map00981 Insect hormone biosynthesis;map00770 Pantothenate and CoA biosynthesis;map00340 Histidine metabolism;map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map00903 Limonene degradation;map01240 Biosynthesis of cofactors;map00330 Arginine and proline metabolism;map01120 Microbial metabolism in	KOG2450[At3g48000 Aldehyde dehydrogenase	KAG1717079.1 hypothetical protein ID866_53 [Astraeus odoratus]	NADP/NAD-dependent aldehyde dehydrogenase PuuC OS=Escherichia coli (strain K12) OX=83333 GN=puuC PE=1 SV=2
A0162	-	-	GO:0008237(metallopeptidase activity)	-	-	-	-	-

A0163	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05643 ABCA3; ATP-binding cassette, subfamily A (ABC1), member 3	map02010 ABC transporters	KOG0059 At2g41700 Lipid exporter ABCA1 and related proteins, ABC superfamily	ORX93119.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	ABC transporter A family member 1 OS=Arabidopsis thaliana OX=3702 GN=ABCA1 PE=2 SV=2
A0164	-	-	-	-	-	KOG3309 At3g07480 Ferredoxin	-	Ferredoxin-2, mitochondrial OS=Xenopus laevis OX=8355 GN=fdx2 PE=2 SV=1
A0165	-	-	-	-	-	KOG1776 At3g02260 Zn-binding protein Push	-	Auxin transport protein BIG OS=Oryza sativa subsp. japonica OX=39947 GN=Os09g0247700 PE=2 SV=1
A0166	-	-	-	-	-	-	-	-
A0167	-	-	-	-	-	-	-	-
A0168	-	GO:0005737(cytoplasm)	-	K14801 TSR4; pre-rRNA-processing protein TSR4	-	KOG2061 7291749 Uncharacterized MYND Zn-finger protein	ORX68656.1 hypothetical protein DL89DRAFT_181495 [Linderina pennisporea]	Programmed cell death protein 2 OS=Rattus norvegicus OX=10116 GN=Pcdc2 PE=2 SV=2
A0169	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0170	-	-	-	-	-	KOG3599 CE25589 Ca2+-modulated nonselective cation channel polycystin	-	Polycystin-2 OS=Caenorhabditis elegans OX=6239 GN=pkd-2 PE=1 SV=3
A0171	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs4502553 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	RGB35544.1 kinase-like domain-containing protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Serine/threonine-protein kinase PKZ1 OS=Phytophthora infestans OX=4787 GN=PKZ1 PE=1 SV=1
A0172	-	-	-	-	-	-	-	-
A0173	GO:0032007(negative regulation of TOR signaling)	-	-	-	-	-	-	-
A0174	-	-	-	-	-	-	-	-
A0175	GO:0006629(lipid metabolic process)	GO:0016021(integral component of membrane)	GO:0008081(phosphoric diester hydrolase activity)	K18694 PGC1; phosphatidylglycerol phospholipase C [EC:3.1.4.-]	map00564 Glycerophospholipid metabolism	KOG2258 Hs13236540 Glycerophosphoryl diester phosphodiesterase	TPX58644.1 hypothetical protein SpCBS45565_g07938 [Spizellomyces sp. 'palustris']	Lysophospholipase D GPD1 OS=Homo sapiens OX=9606 GN=GDPD1 PE=1 SV=2
A0176	-	-	-	-	-	KOG3393 Hs7657595 Predicted membrane protein	KNE72169.1 hypothetical protein AMAG_16656 [Allomyces macrogynus ATCC 38327]	Transmembrane protein 50A OS=Mus musculus OX=10090 GN=Tmem50a PE=1 SV=1

A0177	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	K14830 MAK11, PAK1IP1; protein MAK11	-	KOG2106 Hs18597790 Uncharacterized conserved protein, contains HELP and WD40 domains	XP_031023021.1 uncharacterized protein SmJEL517_g05070 [Synchytrium microbalum]	Echinoderm microtubule-associated protein-like 6 OS=Homo sapiens OX=9606 GN=EML6 PE=2 SV=2
A0178	-	-	-	-	-	-	-	-
A0179	GO:0051169(nuclear transport), GO:0006886(intracellular protein transport)	-	GO:0005049(nuclear export signal receptor activity),GO:0031267(small GTPase binding)	-	-	KOG4541 Hs11967999 Nuclear transport receptor exportin 4 (importin beta superfamily)	XP_031024642.1 uncharacterized protein SmJEL517_g03402 [Synchytrium microbalum]	Exportin-4 OS=Xenopus laevis OX=8355 GN=xpo4 PE=2 SV=1
A0180	-	-	-	-	-	-	-	-
A0181	GO:0000398(mRNA splicing, via spliceosome)	GO:0005681(spliceosomal complex), GO:0005634(nucleus)	GO:0003723(RNA binding),GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	K12827 SF3A3, SAP61, PRP9; splicing factor 3A subunit 3	map03040 Spliceosome	KOG2636 At5g06160 Splicing factor 3a, subunit 3	ORY95836.1 hypothetical protein BCR43DRAFT_459761 [Syncephalastrium racemosum]	Splicing factor SF3a60 homolog OS=Arabidopsis thaliana OX=3702 GN=ATO PE=1 SV=1
A0182	GO:0009231(riboflavin biosynthetic process)	-	GO:0008531(riboflavin kinase activity)	K00861 RFK, FMN1; riboflavin kinase [EC:2.7.1.26]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00740 Riboflavin metabolism;map01100 Metabolic pathways	KOG3110 Hs19923525 Riboflavin kinase	K1Y65445.1 riboflavin kinase [Cylindrobaculum torrendii FP15055 ss-10]	Riboflavin kinase OS=Mus musculus OX=10090 GN=Rfk PE=1 SV=2
A0183	-	-	-	-	-	-	-	cGMP-dependent 3',5'-cGMP phosphodiesterase A OS=Dictyostelium discoideum OX=44689 GN=pdeD PE=1 SV=1
A0184	-	-	GO:0030170(pyridoxal phosphate binding)	K06997 yggS, PROSC; PLP dependent protein	-	KOG3157 At1g11930 Proline synthetase co-transcribed protein	ORX51813.1 hypothetical protein BCR36DRAFT_369723 [Piromyces finnis]	Pyridoxal phosphate homeostasis protein OS=Dictyostelium discoideum OX=44689 GN=prosc PE=3 SV=2
A0185	-	GO:0005730(nucleolus)	GO:0005525(GTP binding)	K14537 NUG2, GNL2; nuclear GTP-binding protein	map03008 Ribosome biogenesis in eukaryotes	KOG2423 Hs7019419 Nucleolar GTPase	EXX68242.1 Nog2p [Rhizophagus irregularis DAOM 197198w]	Nucleolar GTP-binding protein 2 OS=Homo sapiens OX=9606 GN=GNL2 PE=1 SV=1
A0186	-	-	-	-	-	-	-	-

A0187	-	-	GO:0016746(acyltransferase activity)	K13509 AGPAT1_2; lysophosphatidate acyltransferase [EC:2.3.1.51]	map01110 Biosynthesis of secondary metabolites;map04072 Phospholipase D signaling pathway;map04975 Fat digestion and absorption;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	KOG2848 At4g30580 1-acyl-sn-glycerol-3-phosphate acyltransferase	EPZ36451.1 Phospholipid/glycerol acyltransferase domain-containing protein [Rozella allomycis CSF55]	1-acyl-sn-glycerol-3-phosphate acyltransferase BAT2, chloroplastic OS=Brassica napus OX=3708 GN=BAT2 PE=1 SV=2
A0188	GO:0006413(translational initiation)	-	GO:0003743(translation initiation factor activity)	K03113 EIF1, SUI1; translation initiation factor 1	-	KOG1770 Hs5031711 Translation initiation factor 1 (eIF-1/SUI1)	OMH85690.1 Protein translation factor sui1 [Zancudomyces culisetiae]	Eukaryotic translation initiation factor 1b OS=Homo sapiens OX=9606 GN=EIF1B PE=1 SV=2
A0189	-	-	-	-	-	-	-	-
A0190	-	GO:1990879(CST complex)	GO:0003697(single-stranded DNA binding)	-	-	-	-	-
A0191	GO:0016226(iron-sulfur cluster assembly)	-	GO:0005524(ATP binding);GO:0051536(iron-sulfur cluster binding)	-	-	KOG3022 At5g50960 Predicted ATPase, nucleotide-binding	GBB99369.1 hypothetical protein RclHR1_00350025 [Rhizophagus clarus]	Cytosolic Fe-S cluster assembly factor NBP35 OS=Arabidopsis thaliana OX=3702 GN=NBP35 PE=1 SV=1
A0192	-	-	-	-	-	-	RKO87395.1 hypothetical protein BDK51DRAFT_26769 [Blyttomyces helicus]	E3 ubiquitin-protein ligase WAV3 OS=Arabidopsis thaliana OX=3702 GN=WAV3 PE=1 SV=1
A0193	GO:0044255(cellular lipid metabolic process)	-	GO:0008374(O-acyltransferase activity);GO:0016746(acyltransferase activity)	-	-	KOG1221 Hs20149657 Acyl-CoA reductase	KAG2172784.1 hypothetical protein INT43_000131, partial [Umbelopsis isabellina]	Fatty acyl-CoA reductase 2 OS=Homo sapiens OX=9606 GN=FAR2 PE=1 SV=1
A0194	-	-	GO:0005509(calcium ion binding)	-	-	-	RKO88594.1 hypothetical protein BDK51DRAFT_40064 [Blyttomyces helicus]	Sperm flagellar protein 2 OS=Sus scrofa OX=9823 GN=SPEF2 PE=2 SV=1
A0195	-	-	-	-	-	-	-	-
A0196	-	-	GO:0005515(protein binding)	-	-	-	-	-

A0197	GO:0015914(phospholipid transport)	GO:0016021(integral component of membrane)	GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0001666(nucleotide binding),GO:0000287(magnesium ion binding),GO:0140326(ATPase-coupled intramembrane lipid transporter activity)	K14802 DRS2, ATP8A; phospholipid-transporting ATPase [EC:7.6.2.1]	-	-	TFY79586.1 hypothetical protein EWM64_g4423 [Hericium alpestre]	Phospholipid-transporting ATPase C887.12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC887.12 PE=3 SV=1
A0198	GO:0015813(L-glutamate transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015501(glutamate:sodium symporter activity)	-	-	-	-	-
A0199	GO:0015813(L-glutamate transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015501(glutamate:sodium symporter activity)	-	-	-	-	-
A0200	GO:0006383(transcription by RNA polymerase III)	GO:0005666(RNA polymerase III complex)	-	K03025 RPC6, POLR3F; DNA-directed RNA polymerase III subunit RPC6	map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway	KOG3233[Hs18592434 RNA polymerase III, subunit C34	KAG2213525.1 hypothetical protein INT47_009199 [Mucor saturninus]	DNA-directed RNA polymerase III subunit RPC6 OS=Bos taurus OX=9913 GN=POLR3F PE=2 SV=1
A0201	-	-	-	K18171 CMC1; COX assembly mitochondria l protein 1	-	-	KAG2186196.1 hypothetical protein INT43_002634 [Umbelopsis isabellina]	-
A0202	GO:0006413(translational initiation)	-	GO:0003743(translation initiation factor activity),GO:0003924(GTPase activity),GO:0005525(GTP binding)	K02519 infB, MTIF2; translation initiation factor IF-2	-	KOG1145[At4g11160 Mitochondria l translation initiation factor 2 (IF-2; GTPase)	XP_016613130.1 translation initiation factor IF-2 [Spizellomyces punctatus DAOM BR117]	Translation initiation factor IF-2 OS=Acidiphilium cryptum (strain JF-5) OX=349163 GN=infB PE=3 SV=1
A0203	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	RHZ60280.1 hypothetical protein Glove_355g97 [Diversispora epigaea]	-
A0204	-	-	-	-	-	-	-	-
A0205	-	-	-	-	-	-	ORY31737.1 hypothetical protein BCR33DRAFT_771696 [Rhizoclostium globosum]	-
A0206	-	-	-	-	-	-	-	-

A0207	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A0208	GO:0043087(regulation of GTPase activity)	-	-	-	-	KOG2727 Hs19923790 Rab3 GTPase-activating protein, non-catalytic subunit	-	Rab3 GTPase-activating protein non-catalytic subunit OS=Rattus norvegicus OX=10116 GN=Rab3gap2 PE=1 SV=2
A0209	-	-	GO:0005515(protein binding)	-	-	-	-	Omega-hydroxy-beta-dihydromenaquinone-9 sulfotransferase Stf3 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=stf3 PE=3 SV=1
A0210	GO:0010390(histone monoubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	K10696 BRE1; E3 ubiquitin-protein ligase BRE1 [EC:2.3.2.27]	-	KOG0978 Hs7662230 E3 ubiquitin ligase involved in syntaxin degradation	EJD35307.1 hypothetical protein AUDEDRAFT_188795 [Auricularia subglabra TFB-10046 SS5]	Trophozoite exported protein 1 OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=TEX1 PE=1 SV=1
A0211	GO:0006351(transcription, DNA-templated)	-	-	K03016 RPABC3, RPBB, POLR2H; DNA-directed RNA polymerases I, II, and III subunit RPABC3	map03420 Nucleotide excision repair;map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway;map05016 Huntington disease	KOG3400 Hs14589953 RNA polymerase subunit 8	EPZ33273.1 Nucleic acid-binding domain-containing protein [Rozella allomycis CSF55]	DNA-directed RNA polymerases I, II, and III subunit rpabc3 OS=Dictyostelium discoideum OX=44689 GN=polr2h PE=3 SV=1
A0212	GO:0030001(metal ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	K16075 MRS2, MFM1; magnesium transporter	-	KOG2662 At5g22830 Magnesium transporters: CorA family	PVU94786.1 hypothetical protein BB561_002252 [Smittium simulii]	Magnesium transporter MRS2-11, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=MRS2-11 PE=1 SV=1
A0213	-	-	GO:0016274(protein-arginine N-methyltransferase activity),GO:0005515(protein binding)	K18477 RMT2; type IV protein arginine methyltransferase [EC:2.1.1.322]	-	KOG1709 At5g65860 Guanidinooacetate methyltransferase and related proteins	GBC07065.1 hypothetical protein RclHRI_07220007 [Rhizophagus clarus]	Protein arginine N-methyltransferase 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rmt2 PE=3 SV=2
A0214	-	-	GO:0005515(protein binding)	-	-	KOG4293 At3g07570 Predicted membrane protein, contains DoH and Cytochrome b-561/ferric reductase transmembrane domains	TPX48486.1 hypothetical protein SeMB42_g02985 [Synchytrium endobioticum]	Cytochrome b561 and DOMON domain-containing protein At3g07570 OS=Arabidopsis thaliana OX=3702 GN=At3g07570 PE=2 SV=1
A0215	-	-	-	-	-	KOG4580 ECU06g1420i_2 Component of vacuolar transporter chaperone (Vtc) involved in vacuole fusion	ORD93360.1 polyphosphate synthase put [Enterospora canceri]	Vacuolar transporter chaperone complex subunit 1 OS=Trypanosoma brucei (strain 927/4 GUTat10.1) OX=185431 GN=VTC1 PE=3 SV=1
A0216	-	-	-	-	-	-	-	-

A0217	-	-	-	K10580 UBE2N, BLU, UBC13; ubiquitin-conjugating enzyme E2 N [EC:2.3.2.23]	map05131 Shigellosis;map04624 Toll and Imd signaling pathway;map04120 Ubiquitin mediated proteolysis	KOG0417[Hs7661808 Ubiquitin-protein ligase	RKP15093.1 ubiquitin-conjugating enzyme/RWD-like protein, partial [Piptocephalis cylindrospora]	Ubiquitin-conjugating enzyme E2 T OS=Homo sapiens OX=9606 GN=UBE2T PE=1 SV=1
A0218	-	-	-	-	-	KOG2372[Hs8922241 Oxidation resistance protein	CDS09341.1 hypothetical protein LRAMOSA10701 [Lichtheimia ramosa]	Oxidation resistance protein 1 OS=Homo sapiens OX=9606 GN=OXR1 PE=1 SV=2
A0219	GO:0046856(phosphatidylinositol dephosphorylation)	-	GO:0016791(phosphatase activity),GO:0003824(catalytic activity)	-	-	KOG0565[At2g43900 Inositol polyphosphate 5-phosphatase and related proteins	XP_025354527.1 DNase I-like protein, partial [Meiramiltonrushii]	Type I inositol polyphosphate 5-phosphatase 12 OS=Arabidopsis thaliana OX=3702 GN=IP5P12 PE=1 SV=2
A0220	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0221	-	-	-	-	-	KOG2551[7300631 Phospholipase/carboxylolase	ORX49990.1 FSH1-domain-containing protein [Piromyces finnis]	Esterase CG5412 OS=Drosophila melanogaster OX=7227 GN=CG5412 PE=2 SV=1
A0222	-	-	-	-	-	-	-	-
A0223	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K16196 EIF2AK4; eukaryotic translation initiation factor 2-alpha kinase 4 [EC:2.7.11.1]	map04140 Autophagy - animal;map04138 Autophagy - yeast;map05160 Hepatitis C;map05162 Measles;map05168 Herpes simplex virus 1 infection	KOG0198[At2g40560 MEK1 and related serine/threonine protein kinases	XP_008717248.1 hypothetical protein HMPREF1541_04682 [Cyphellophora europaea CBS 101466]	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase wee-1.3 OS=Caenorhabditis elegans OX=6239 GN=wee-1.3 PE=1 SV=1
A0224	-	-	-	-	-	KOG1303[CE21306 Amino acid transporters	VDC06081.1 unnamed protein product [Peniophora sp. CBMAI 1063]	N amino acid transport system protein OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=mtr PE=3 SV=2
A0225	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0226	-	-	-	-	-	-	-	-
A0227	GO:0006325(chromatin organization),GO:0006351(transcription, DNA-templated)	GO:0005634(nucleus)	GO:0005515(protein binding)	K11293 HIRA, HIR1; protein HIRA/HIR1	-	-	KAF8678405.1 Protein HIR [Rhizoctonia solani]	Protein HIR1 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=HIR1 PE=3 SV=1
A0228	-	-	-	-	-	-	-	-
A0229	-	-	-	K22696 EEF2KMT; protein-lysine N-methyltransferase EEF2KMT [EC:2.1.1.-]	-	-	XP_013022607.1 methyltransferase [Schizosaccharomyces cryophilus OY26]	Protein-lysine N-methyltransferase efm3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC3A11.03 PE=3 SV=3

A0230	GO:0006096(glycolytic process)	-	GO:0003824(catalytic activity),GO:0004743(pyruvate kinase activity),GO:0000287(magnesium ion binding),GO:0030955(potassium ion binding)	K00873 PK, pyk; pyruvate kinase [EC:2.7.1.40]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map05203 Viral carcinogenesis; map04930 Type II diabetes mellitus;map00620 Pyruvate metabolism;map05230 Central carbon metabolism in cancer;map01100 Metabolic	KOG2323 At3g04050 Pyruvate kinase	RKP20138.1 pyruvate kinase [Rozella allomyces CSF55]	Pyruvate kinase OS=Eimeria tenella OX=5802 GN=PYK PE=2 SV=1
A0231	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08793 STK32, YANK; serine/threonine kinase 32 [EC:2.7.11.1]	-	KOG0598 At3g08720 Ribosomal protein S6 kinase and related proteins	KNE69265.1 AGC/YANK protein kinase, variant [Allomyces macrogynus ATCC 38327]	Serine/threonine-protein kinase 32C OS=Mus musculus OX=10090 GN=Stk32c PE=1 SV=1
A0232	GO:0035025(positive regulation of Rho protein signal transduction)	-	GO:0003779(activin binding)	-	-	KOG3376 CE15975 Uncharacterized conserved protein	-	Actin-binding Rho-activating protein OS=Sus scrofa OX=9823 GN=ABRA PE=2 SV=1
A0233	-	-	-	-	-	-	-	-
A0234	-	-	-	-	-	-	-	-
A0235	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A0236	-	-	-	-	-	-	-	-
A0237	GO:0006281(DNA repair),GO:0006310(DNA recombination),GO:0051103(DNA ligation involved in DNA repair),GO:0071897(DNA biosynthetic process)	-	GO:0005524(ATP binding),GO:0003910(DNA ligase (ATP) activity),GO:0003677(DNA binding)	K10777 LIG4, DNL4; DNA ligase 4 [EC:6.5.1.1]	map03450 Non-homologous end-joining	KOG0966 Hs4504997 ATP-dependent DNA ligase IV	OZJ05239.1 hypothetical protein BZG36_02293 [Bifiguratus adalaidae]	DNA ligase 4 OS=Cricetulus griseus OX=10029 GN=LIG4 PE=1 SV=1
A0238	-	-	-	-	-	-	-	-
A0239	GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	-	-	KOG2605 At2g27350 OTU (ovarian tumor)-like cysteine protease	TPX41034.1 hypothetical protein SeLEV6574_g06278 [Synchytrium endobioticum]	OVARIAN TUMOR DOMAIN-containing deubiquitinating enzyme 6 OS=Arabidopsis thaliana OX=3702 GN=OTU6 PE=1 SV=2
A0240	-	-	-	-	-	-	-	-
A0241	-	-	-	-	-	-	-	-
A0242	-	-	-	-	-	-	-	-
A0243	GO:0005975(carbohydrate metabolic process)	-	GO:0016810(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds)	-	-	-	KAF1849580.1 carbohydrate esterase family 4 protein [Cucurbitaria berberidis CBS 394.84]	Chitoooligosaccharide deacetylase OS=Mesorhizobium japonicum (strain LMG 29417 / CECT 9101 / MAFF 303099) OX=266835 GN=nodB PE=3 SV=2

A0244	GO:0006914 (autophagy); GO:0048208 (COPII vesicle coating)	-	-	K20353 SEC16; COPII coat assembly protein SEC16	-	KOG1913 At5g47490 Regucalcin gene promoter region-related protein (RGPR)	RIA82559.1 Sec23-binding domain of Sec16-domain-containing protein, partial [Glomus cerebriforme]	Protein transport protein SEC16B homolog OS=Arabidopsis thaliana OX=3702 GN=SEC16B PE=1 SV=1
A0245	GO:0006508 (proteolysis)	-	GO:0070006 (metalloaminopeptidase activity)	K01265 map; methionyl aminopeptidase [EC:3.4.11.18]	-	KOG2775 7297553 Metallopeptidase	RIA87916.1 peptidase M24, structural domain-containing protein [Glomus cerebriforme]	Methionine aminopeptidase 2B OS=Arabidopsis thaliana OX=3702 GN=MAP2B PE=2 SV=2
A0246	GO:0055085 (transmembrane transport)	-	GO:0022857 (transmembrane transporter activity)	K08192 DAL5; MFS transporter, ACS family, DAL5 transporter family protein	-	KOG2532 At2g29650 Permease of the major facilitator superfamily	PJF17131.1 MFS transporter, anion:cation symporter (ACS) family [Paramicrosporidium saccamoebae]	Ascorbate transporter, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PHT4;4 PE=1 SV=1
A0247	GO:0006508 (proteolysis)	-	GO:0070006 (metalloaminopeptidase activity)	K01265 map; methionyl aminopeptidase [EC:3.4.11.18]	-	KOG2775 7297553 Metallopeptidase	TPX61129.1 hypothetical protein SpCBS45565_g07337 [Spizellomyces sp. 'palustris']	Methionine aminopeptidase 2B OS=Arabidopsis thaliana OX=3702 GN=MAP2B PE=2 SV=2
A0248	GO:0006412 (translation)	GO:0005840 (ribosome)	GO:0003735 (structural constituent of ribosome)	-	-	-	-	-
A0249	-	-	-	K01301 NAALAD; N-acetylated-alpha-linked acidic dipeptidase [EC:3.4.17.21]	-	KOG2195 Hs20480969 Transferrin receptor and related proteins containing the protease-associated (PA) domain	ORE09673.1 Zn-dependent exopeptidase [Rhizopus microsporus var. microsporus]	Probable glutamate carboxypeptidase ARB_02390 OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) OX=663331 GN=ARB_02390 PE=1 SV=1
A0250	GO:0036211 (protein modification process)	-	GO:0008641 (ubiquitin-like modifier activating enzyme activity)	K03178 UBE1; UBA1; ubiquitin-activating enzyme E1 [EC:6.2.1.45]	map04120 Ubiquitin mediated proteolysis; map05022 Pathways of neurodegeneration - multiple diseases; map05012 Parkinson disease	KOG2012 Hs4507763 Ubiquitin activating enzyme UBA1	KAF2861759.1 E1 ubiquitin activating enzyme [Piedraia hortae CBS 480.64]	Ubiquitin-activating enzyme E1 2 OS=Triticum aestivum OX=4565 GN=UBA2 PE=2 SV=1
A0251	GO:0006281 (DNA repair)	-	-	-	-	KOG4553 Hs20551861 Uncharacterized conserved protein	KAG2203245.1 hypothetical protein INT46_000435 [Mucor plumbeus]	Fanconi anemia group I protein homolog OS=Mus musculus OX=10090 GN=Fanci PE=1 SV=2
A0252	-	-	-	-	-	-	-	14 kDa phosphohistidine phosphatase OS=Sus scrofa OX=9823
A0253	-	-	-	-	-	-	-	-
A0254	-	-	-	-	-	-	-	-

A0255	-	-	-	K17065 DNM1L; dynamin 1-like protein [EC:3.6.5.5]	map04214 Apoptosis - fly;map04217 Necroptosis;map04139 Mitophagy - yeast;map04668 TNF signaling pathway;map04621 NOD-like receptor signaling pathway	KOG0446 At2g14120 Vacuolar sorting protein VPS1, dynamin, and related proteins	KAF4952229.1 hypothetical protein FSARC_127111, partial [Fusarium sarcochrom]	-
A0256	GO:0051259(protein complex oligomerization),GO:0044571([2Fe-2S] cluster assembly)	-	GO:0001671(AT Pase activator activity),GO:0051087(chaperone binding)	K04082 hscB, HSCB, HSC20; molecular chaperone HscB	-	KOG3192 At5g06410 Mitochondria I J-type chaperone	CDS02814.1 hypothetical protein LRAMOSA00218 [Lichtheimia ramosa]	Iron-sulfur cluster co-chaperone protein HscB OS=Homo sapiens OX=9606 GN=HSCB PE=1 SV=3
A0257	-	GO:0016021(integral component of membrane)	-	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis -	-	TFK77302.1 membrane-associated proteins in eicosanoid and glutathione metabolism [Pluteus cervinus]	Glutathione S-transferase 3, mitochondrial OS=Bos taurus OX=9913 GN=MGST3 PE=2 SV=1
A0258	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0051082(unfolded protein binding)	K04043 dnaK, HSPA9; molecular chaperone DnaK	map04212 Longevity regulating pathway - worm;map03018 RNA degradation;map05152 Tuberculosis	KOG0102 Hs21314627 Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	GEM07417.1 molecular chaperone DnaK [Rhodotorula toruloides]	Chaperone protein DnaK OS=Sinorhizobium medicae (strain WSM419) OX=366394 GN=dnaK PE=3 SV=1
A0259	-	-	-	-	-	-	-	-
A0260	-	-	-	-	-	-	-	-
A0261	-	-	-	-	-	-	-	-
A0262	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	-	-	-	OLL26594.1 Telomere length regulation protein elg1, partial [Neolecta irregularis DAH-3]	Telomere length regulation protein elg1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=elg1 PE=1 SV=1
A0263	GO:0006891(intra-Golgi vesicle-mediated transport)	GO:0030173(integral component of Golgi membrane)	-	K09313 CUTL; homeobox protein cut-like	-	KOG0963 At3g18480 Transcription factor/CCAAT displacement protein CDP1	KAF8863841.1 Golgi membrane protein-like protein [Acephala macrosclerotiorum]	Protein CASP OS=Arabidopsis thaliana OX=3702 GN=CASP PE=1 SV=2
A0264	-	-	-	-	-	-	-	-

A0265	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K20872 NEK2; serine/threonine-protein kinase Nek2 [EC:2.7.11.1]	-	KOG0589[Hs4507277_1 Serine/threonine protein kinase	EPZ31422.1 Protein kinase, catalytic domain-containing protein [Rozella allomycis CSF55]	Serine/threonine-protein kinase Nek4 OS=Mus musculus OX=10090 GN=Nek4 PE=1 SV=1
A0266	-	-	GO:0005515(protein binding)	-	-	KOG0504[Hs4885087 FOG: Ankyrin repeat	PHH70989.1 hypothetical protein CDD82_6806 [Ophiocordyceps australis]	Nuclear factor NF-kappa-B p105 subunit OS=Gallus gallus OX=9031 GN=NFKB1 PE=2 SV=2
A0267	-	-	-	-	-	-	-	-
A0268	-	GO:0016021(integral component of membrane)	-	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis	-	ORY50962.1 MAPEG-domain-containing protein [Rhizoclostium globosum]	Glutathione S-transferase 3, mitochondrial OS=Bos taurus OX=9913 GN=MGST3 PE=2 SV=1
A0269	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0043565(sequence-specific DNA binding)	-	-	KOG0627[At5g45710 Heat shock transcription factor	RIA97357.1 hypothetical protein C1645_686964 [Glomus cerebriforme]	Heat stress transcription factor A-4c OS=Arabidopsis thaliana OX=3702 GN=HSFA4C PE=2 SV=1
A0270	-	-	-	-	-	-	PKC50126.1 hypothetical protein RhiirA1_487317, partial [Rhizophagus irregularis]	Gigasins-3a (Fragment) OS=Crassostrea gigas OX=29159 PE=1 SV=1
A0271	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0272	-	-	-	-	-	-	-	-
A0273	-	-	-	-	-	-	-	-
A0274	GO:0006801(superoxide metabolic process)	-	GO:0004784(superoxide dismutase activity),GO:0046872(metal ion binding)	-	-	KOG0876[Hs10835187 Manganese superoxide dismutase	KAG0956012.1 hypothetical protein G6F31_012721 [Rhizopus oryzae]	Superoxide dismutase [Mn/Fe] OS=Methylobionas sp. (strain J) OX=32038 GN=sodB PE=1 SV=1
A0275	-	-	GO:0005515(protein binding)	K13137 STRAP, UNRIP; serine-threonine kinase receptor-associated protein	-	-	EPZ35679.1 Quinonprotein alcohol dehydrogenase-like superfamily domain-containing protein [Rozella allomycis CSF55]	Cilia- and flagella-associated protein 57 OS=Mus musculus OX=10090 GN=Cfap57 PE=1 SV=3

A0276	-	-	-	-	-	-	RIB16117.1 hypothetical protein C2G38_22472 29 [Gigaspora rosea]	-
A0277	-	GO:0005869(dynactin complex)	-	-	-	-	CEJ04981.1 hypothetical protein RMCBS34429 2_18929 [Rhizopus microsporus]	Dynactin subunit 4 OS=Mus musculus OX=10090 GN=Dctn4 PE=1 SV=1
A0278	-	-	-	-	-	KOG2219[Hs2069680 Uncharacterized conserved protein]	KAF9913963.1 Protein CL16A [Lobosporangium transversale]	Protein CLEC16A homolog OS=Drosophila melanogaster OX=7227 GN=ema PE=1 SV=2
A0279	GO:0019264(glycine biosynthetic process from serine),GO:0035999(tetrahydrofolate interconversion)	-	GO:0004372(glycine hydroxymethyltransferase activity),GO:0030170(pyridoxal phosphate binding),GO:0003824(catalytic activity)	K00600 glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1]	map00670 One carbon pool by folate;map01110 Biosynthesis of secondary metabolites;map00460 Cyanoamino acid metabolism;map01200 Carbon metabolism;map01523 Antifolate resistance;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00680 Methane metabolism;map00260 Glycine, serine and threonine	KOG2467[At4g37930 Glycine/serine hydroxymethyltransferase]	KAF7724758.1 Cytochrome B translational activator protein cbs2 [Apophysomyces ossiformis]	Serine hydroxymethyltransferase 1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=SHM1 PE=1 SV=1
A0280	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	APETALA2-like protein 3 OS=Oryza sativa subsp. indica OX=39946 GN=AP2-3 PE=3 SV=1
A0281	-	-	GO:0008168(methyltransferase activity)	K22857 EEF1AKMT4; EEF1A lysine methyltransferase 4 [EC:2.1.1.-]	-	KOG2352[Hs14150112 Predicted spermine/spermidine synthase]	KAG0261296.1 hypothetical protein DFQ27_003083 [Actinomortierella ambigua]	EEF1A lysine methyltransferase 4 OS=Bos taurus OX=9913 GN=EEF1AKMT4 PE=2 SV=1
A0282	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K16196 EIF2AK4; eukaryotic translation initiation factor 2-alpha kinase 4 [EC:2.7.11.1]	map04140 Autophagy - animal;map04138 Autophagy - yeast;map05160 Hepatitis C;map05162 Measles;map05168 Herpes simplex virus 1 infection	KOG1035[YDR283c eIF-2alpha kinase GCN2]	KAG4084045.1 Serine/threonine-protein kinase [Neocallimastix sp. JGI-2020a]	eIF-2-alpha kinase GCN2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=gcn2 PE=2 SV=2

A0283	-	-	GO:0004491(methylmalonate-semialdehyde dehydrogenase (acylating) activity),GO:0016491(oxidoreductase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	K00140 mmsA, ioIA, ALDH6A1; malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]	map00410 beta-Alanine metabolism;map01200 Carbon metabolism;map00640 Propanoate metabolism;map00280 Valine, leucine and isoleucine degradation;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG2449 At2g14170 Methylmalonate semialdehyde dehydrogenase	KAF9979310.1 hypothetical protein BGZ73_000004 [Actinomortierella ambigua]	Malonate-semialdehyde dehydrogenase 2 OS=Geobacillus kaustophilus (strain HTA426) OX=235909 GN=ioIA2 PE=3 SV=2
A0284	-	GO:0000124(SAGA complex)	GO:0003712(transcription coregulator activity)	-	-	-	-	-
A0285	-	GO:0005838(proteasome regulatory particle)	GO:0005515(protein binding),GO:0008233(peptidase activity),GO:0008237(metalloproteinase activity)	K03038 PSMD7, RPN8; 26S proteasome regulatory subunit N8	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG1556 At5g05780 26S proteasome regulatory complex, subunit RPN8/PSMD7	RHZ49172.1 hypothetical protein Glove_529g40 [Diversispora epigaea]	26S proteasome non-ATPase regulatory subunit 7 homolog A OS=Arabidopsis thaliana OX=3702 GN=RPN8A PE=1 SV=1
A0286	-	-	-	-	-	-	-	-
A0287	-	-	GO:0003824(catalytic activity),GO:0016833(oxo-acid-lyase activity)	-	-	KOG2368 At2g26800 Hydroxymethylglutaryl-CoA lyase	ORX90360.1 hydroxymethylglutaryl-CoA lyase [Basidiobolus meristosporus CBS 931.73]	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Gallus gallus OX=9031 GN=HMGCL PE=1 SV=1
A0288	-	-	-	-	-	-	-	-
A0289	GO:0007010(cytoskeleton organization)	-	GO:0005515(protein binding),GO:0003779(actin binding)	-	-	KOG0445 Hs4507323 Actin regulatory protein supervillin (gelsolin/villin family)	-	-
A0290	-	-	GO:0003735(structural constituent of ribosome)	K17427 MRPL46; large subunit ribosomal protein L46	-	KOG4548 At1g14620 Mitochondrial ribosomal protein L17	KAG2177916.1 hypothetical protein INT43_003163 [Umbelopsis isabellina]	Large ribosomal subunit protein mL46 OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=mrpL17 PE=1 SV=1
A0291	-	-	-	-	-	-	-	-

A0292	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	KOG1995 At5g58470 Conserved Zn-finger protein	TPX55226.1 hypothetical protein PhCBS80983.g05495 [Powellomyces hirtus]	Transcription initiation factor TFIID subunit 15b OS=Arabidopsis thaliana OX=3702 GN=TAF15B PE=1 SV=1
A0293	GO:0006744(ubiquitination biosynthetic process), GO:0045333(cellular respiration)	-	GO:0048039(ubiquinone binding)	K18588 COQ10; coenzyme Q-binding protein COQ10	-	KOG3177 Hs21389353 Oligoketide cyclase/lipid transport protein	K1Y73761.1 hypothetical protein CYLTODRAFT_434109 [Cylindrobacterium torrendii FP15055 ss-10]	Coenzyme Q-binding protein COQ10 homolog A, mitochondrial OS=Homo sapiens OX=9606 GN=COQ10A PE=2 SV=2
A0294	-	-	GO:0005096(GTPase activator activity)	K12492 ARFGAP1; ADP-ribosylation factor GTPase-activating protein 1	map04144 Endocytosis	KOG0702 At1g08680 Predicted GTPase-activating protein	RKP38080.1 hypothetical protein BJ085DRAFT_27793 [Dimargaris cristalligena]	Probable ADP-ribosylation factor GTPase-activating protein AGD14 OS=Arabidopsis thaliana OX=3702 GN=AGD14 PE=1 SV=2
A0295	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0035091(phosphatidylinositol binding)	K04508 TBL1; transducin (beta)-like 1	map04310 Wnt signaling pathway;map04013 MAPK signaling pathway - fly	KOG0192 At3g06630 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KZO99058.1 kinase-like protein, partial [Calocera viscosa TUF12733]	Dual specificity protein kinase shkA OS=Dictyostelium discoideum OX=44689 GN=shkA PE=2 SV=1
A0297	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ12941.1 Transposon TX1 protein [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A0298	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0299	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0601 CE14884_1 Cyclin-dependent kinase WEE1	PIA15486.1 kinase-like protein, partial [Coemansia reversa NRRL1564]	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase wee-1.3 OS=Caenorhabditis briggsae OX=6238 GN=wee-1.3 PE=3 SV=1
A0300	-	-	-	-	-	-	-	-
A0301	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	KAF8726638.1 hypothetical protein AX14_007619 [Amanita brunnescens Koide BX004]	-
A0302	GO:0008299(isoprenoid biosynthetic process)	-	GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups)	K00787 FDPS; farnesyl diphosphate synthase [EC:2.5.1.1 2.5.1.10]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis;map01100 Metabolic pathways;map05164 Influenza A;map05166 Human T-cell leukemia virus 1 infection	KOG0711 YJL167w Polyprenyl synthetase	KAG4088855.1 isoprenoid synthase domain-containing protein [Neocallimastix sp. JGI-2020a]	Farnesyl pyrophosphate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG20 PE=1 SV=2

A0303	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0304	-	-	GO:0003676(nucleic acid binding)	-	-	KOG3070 At2g21060 Predicted RNA-binding protein containing PIN domain and involved in translation or RNA processing	KAG0193327.1 hypothetical protein DFQ28_005556 [Apophysomyces sp. BC1034]	Cold shock-like protein CspG OS=Escherichia coli O157:H7 OX=83334 GN=cspG PE=3 SV=1
A0305	-	-	-	K20523 SH3YL1; SH3 domain-containing YSC84-like protein 1	-	-	ORY43985.1 DUF500-domain-containing protein [Rhizoclostium globosum]	LAS seventeen-binding protein 3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=LSB3 PE=3 SV=2
A0306	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0000981(DNA-binding transcription factor activity, RNA polymerase II-specific),GO:0008270(zinc ion binding)	-	-	-	-	-
A0307	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A0308	GO:005085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG2533 Hs4503847 Permease of the major facilitator superfamily	KGO13517.1 Regulatory protein uhpC [Beauveria bassiana D1-5]	Probable hexose phosphate transport protein OS=Chlamydia pneumoniae OX=83558 GN=uhpC PE=3 SV=1
A0309	-	-	-	-	-	-	-	-
A0310	-	-	GO:0003676(nucleic acid binding),GO:0004523(RNA-DNA hybrid ribonuclease activity)	K03469 rnhA, RNASEH1; ribonuclease HI [EC:3.1.26.4]	map03030 DNA replication	-	XP_014566508.1 hypothetical protein [L969DRAFT_95765 [Mixia osmundae IAM 14324]	Ribonuclease H OS=Phenylobacterium zucineum (strain HLK1) OX=450851 GN=rnhA PE=3 SV=1
A0311	GO:005085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05662 ABCB7, ATM; ATP-binding cassette, subfamily B (MDR/TAP), member 7	map02010 ABC transporters	KOG0057 Hs22058461 Mitochondrial Fe/S cluster exporter, ABC superfamily	XP_025595377.1 P-loop containing nucleoside triphosphate hydrolase protein [Tilletiopsis washingtonensis]	Iron-sulfur clusters transporter ABCB7, mitochondrial OS=Oryzias latipes OX=8090 GN=abcb7 PE=1 SV=2
A0312	-	-	-	-	-	-	-	-
A0313	-	-	-	-	-	-	-	-
A0314	-	-	-	-	-	-	-	-
A0315	-	-	-	-	-	-	-	-
A0316	GO:0036211(protein modification process)	-	-	-	-	-	-	Protein polyglycolase TTLL10 OS=Macaca fascicularis OX=9541 GN=TTLL10 PE=2 SV=1
A0317	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	KOG1516 At3g02410 Carboxylesterase and related proteins	XP_031027373.1 uncharacterized protein SmJEL517_g00765 [Synchytrium microbalum]	Esterase LipQ OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=lipQ PE=1 SV=1

A0318	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07893 RAB6A; Ras-related protein Rab-6A	-	KOG0094 At5g10260 GTPase Rab6/YPT6/Ryh1, small G protein superfamily	KAF7750497.1 Ras-protein Rab-6A [Entomophthora muscae]	Intraflagellar transport protein 27 homolog OS=Mus musculus OX=10090 GN=Ift27 PE=1 SV=1
A0319	-	-	GO:0018580(nitronate monooxygenase activity)	K23948 E1.6.5.9; NADH:quinone reductase (non-electrogenic) [EC:1.6.5.9]	-	-	KHJ34144.1 putative 2-nitropropane dioxygenase [Erysiphe necator]	NADH:quinone reductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA1024 PE=1 SV=1
A0320	GO:0051016(barbed-end actin filament capping)	GO:0008290(F-actin capping protein complex)	-	K10365 CAPZB; F-actin-capping protein subunit beta	map04144 Endocytosis;map04814 Motor proteins	KOG3174 7296053 F-actin capping protein, beta subunit	KXS17917.1 F-actin capping protein, beta subunit [Gonapodya prolifera JEL478]	F-actin-capping protein subunit beta OS=Drosophila melanogaster OX=7227 GN=cgb PE=2 SV=1
A0321	-	GO:0008537(proteasome activator complex)	-	K06698 PSME3; proteasome activator subunit 3 (PA28 gamma)	map04612 Antigen processing and presentation;map03050 Proteasome;map05160 Hepatitis C	KOG4470 Hs5453990 Proteasome activator subunit	EJT99932.1 proteasome activator pa28 REG alpha/beta subunit, partial [Dacryopinax primogenitus]	Proteasome activator complex subunit 1 OS=Bos taurus OX=9913 GN=PSME1 PE=1 SV=1
A0322	GO:0032259(methylation)	-	GO:0008168(methyltransferase activity)	K18203 LCMT1; [phosphatase 2A protein]-leucine-carboxy methyltransferase [EC:2.1.1.233]	-	-	XP_003191172.1 C-terminal protein carboxyl methyltransferase, putative [Cryptococcus gattii WM276]	Putative S-adenosyl-L-methionine-dependent methyltransferase MAB_4328c OS=Mycobacteroides abscessus (strain ATCC 19977 / DSM 44196 / CCUG 20993 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543 / L948) OX=561007 GN=MAB_4328c PE=3 SV=1
A0323	-	-	-	-	-	-	-	-
A0324	-	-	-	-	-	-	-	-
A0325	-	-	-	-	-	-	-	-
A0326	-	-	-	-	-	-	ORY44819.1 hypothetical protein BCR33DRAFT_716768 [Rhizoclostium globosum]	-
A0327	-	-	GO:0005096(GTPase activator activity)	-	-	KOG2998 7298852 Uncharacterized conserved protein	RKP16772.1 hypothetical protein ROZALSC1DRAFT_31364, partial [Rozella allomyces CSF55]	ELMO domain-containing protein C OS=Dictyostelium discoideum OX=44689 GN=elmoC PE=4 SV=1

A0328	GO:0015986(ATP synthesis coupled proton transport), GO:0046034(ATP metabolic process), GO:1902600(proton transmembrane transport)	GO:0045261(proton-transporting ATP synthase complex, catalytic core F(1))	GO:0046933(proton-transporting ATP synthase activity, rotational mechanism),GO:0005524(ATP binding)	K02132 ATPeF1A, ATP5A1, ATP1; F-type H+-transporting ATPase subunit alpha	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05008 Chemical carcinogenesis - reactive oxygen species;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease;map01100 Metabolic pathways	KOG1353 YBL099w FOF1-type ATP synthase, alpha subunit	RKP39020.1 P-loop containing nucleoside triphosphate hydrolase protein [Dimargaris cristalligena]	ATP synthase subunit alpha OS=Novosphingobium aromaticivorans (strain ATCC 700278 / DSM 12444 / CCUG 56034 / CIP 105152 / NBRC 16084 / F199) OX=279238 GN=atpA PE=3 SV=1
A0329	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	KOG1754 Hs14165469 40S ribosomal protein S15/S22	TPX40759.1 hypothetical protein SeMB42_g05894 [Synchytrium endobioticum]	Small ribosomal subunit protein uS8 OS=Bos taurus OX=9913 GN=RPS15A PE=2 SV=1
A0330	-	-	GO:0005515(protein binding)	K17804 TIM44; mitochondria l import inner membrane translocase subunit TIM44	-	KOG2580 At2g20510 Mitochondria l import inner membrane translocase, subunit TIM44	XP_018296305.1 hypothetical protein PHYBLDRAFT_99338, partial [Phycomyces blakesleeanus NRRL 1555(-)]	Mitochondrial import inner membrane translocase subunit TIM44-2 OS=Arabidopsis thaliana OX=3702 GN=TIM44-2 PE=1 SV=1
A0331	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K14811 DBP3; ATP-dependent RNA helicase DBP3 [EC:3.6.4.13]	-	KOG0331 At1g31970 ATP-dependent RNA helicase	KAG1470811.1 hypothetical protein G6F56_002467 [Rhizopus delemar]	ATP-dependent RNA helicase DBP3 OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=DBP3 PE=3 SV=1
A0332	GO:0006412(translation)	GO:0005840(ribosome),GO:0015935(small ribosomal subunit)	GO:0003735(structural constituent of ribosome),GO:003723(RNA binding)	K02958 RP-S15e, RPS15; small subunit ribosomal protein S15e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0898 7302912 40S ribosomal protein S15	KAF9978989.1 ribosomal protein S15 [Actinomyces rella ambigua]	Small ribosomal subunit protein uS19 OS=Podospora anserina OX=2587412 GN=RPS15 PE=3 SV=1
A0333	GO:0051315(attachment of mitotic spindle microtubules to kinetochore)	GO:0031262(Ndc80 complex)	-	K11547 NDC80, HEC1, TID3; kinetochore protein NDC80	map04110 Cell cycle	KOG0995 Hs5174457 Centromere-associated protein HEC1	CCJ29005.1 unnamed protein product [Pneumocystis jirovecii]	Kinetochore protein NDC80 homolog OS=Macaca fascicularis OX=9541 GN=NDC80 PE=2 SV=1
A0334	GO:0006003(fructose 2,6-bisphosphate metabolic process), GO:0032259(methylation),GO:0006000(fructose metabolic process)	-	GO:0003824(catalytic activity),GO:0005524(ATP binding),GO:0003676(nucleic acid binding),GO:0008168(methyltransferase activity),GO:0003873(6-phosphofructose-2-kinase activity)	K19029 PFKFB2; 6-phosphofructose-2-kinase / fructose-2,6-bisphosphatase 2 [EC:2.7.1.105 3.1.3.46]	map04919 Thyroid hormone signaling pathway;map00051 Fructose and mannose metabolism;map04152 AMPK signaling pathway;map01100 Metabolic pathways	KOG0234 Hs4758900 Fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase	KAF3391705.1 Fructose-2,6-bisphosphatase [Penicillium rolsii]	6-phosphofructose-2-kinase/fructose-2,6-bisphosphatase 2 OS=Bos taurus OX=9913 GN=PFKFB2 PE=1 SV=2

A0335	-	-	-	-	-	KOG2080 Hs20558056 Uncharacterized conserved protein, contains DENN and RUN domains	OAJ44264.1 hypothetical protein, variant 1 [Batrachomyxolabium dendrobatidis JEL423]	DENN domain-containing protein 5A OS=Homo sapiens OX=9606 GN=DENND5A PE=1 SV=2
A0336	-	-	-	-	-	-	-	-
A0337	GO:0051169(nuclear transport)	-	GO:0005049(nuclear export signal receptor activity)	-	-	KOG1410 At5g06120 Nuclear transport receptor RanBP16 (importin beta superfamily)	XP_025168880.1 armadillo-type protein [Rhizophagus irregularis DAOM181602=DAOM197198]	Exportin-7 -A OS=Xenopus laevis OX=8355 GN=xpo7-a PE=1 SV=1
A0338	-	-	-	-	-	-	-	-
A0339	-	-	-	K22721 CSG1, SUR1, CSH1; inositol phosphorylceramide mannosyltransferase catalytic subunit [EC:2.4.1.370]	-	-	XP_025354713.1 glycosyltransferase family 32 protein, partial [Meirionia miltorushii]	Inositol phosphoceramide mannosyltransferase 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC4F11.04c PE=3 SV=1
A0340	-	-	-	-	-	-	TPX75825.1 hypothetical protein CcCBS67573_g02885 [Chytridiomycota confervae]	Spermatogenesis-associated protein 4 OS=Homo sapiens OX=9606 GN=SPATA4 PE=1 SV=1
A0341	-	-	GO:0016491(oxidoreductase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	-	-	KOG2450 YOR374w Aldehyde dehydrogenase	KAF4910003.1 putative aldehyde dehydrogenase FUS7, partial [Colletotrichum viniferum]	Putative aldehyde dehydrogenase DhaS OS=Bacillus subtilis (strain 168) OX=224308 GN=dhaS PE=3 SV=1
A0342	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	TPX76668.1 hypothetical protein CcCBS67573_g02078 [Chytridiomycota confervae]	-
A0343	-	-	-	K17818 ARD1; D-arabinitol dehydrogenase (NADP+) [EC:1.1.1.287]	map00040 Pentose and glucuronate interconversions; map01100 Metabolic pathways	-	KAF5345350.1 hypothetical protein D9758_008466 [Tetrapyrgos nigripes]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A0344	-	-	-	-	-	-	TPX56409.1 hypothetical protein PhCBS80983_g04545 [Powellomyces hirtus]	-

A0345	GO:0006400(tRNA modification)	-	GO:0000287(magnesium ion binding),GO:0008193(tRNA guanylyltransferase activity)	K10761 THG1; tRNA(His) guanylyltransferase [EC:2.7.7.79]	-	KOG2721 Hs8923514 Uncharacterized conserved protein	CAE6410190.1 unnamed protein product [Rhizoctonia solani]	Probable tRNA(His) guanylyltransferase OS=Mus musculus OX=10090 GN=Thg1l PE=1 SV=1
A0346	-	-	-	-	-	-	-	-
A0347	-	-	-	-	-	-	-	-
A0348	-	-	-	-	-	-	-	-
A0349	-	-	-	-	-	-	-	-
A0350	-	-	GO:0016491(oxidoreductase activity)	-	-	-	KAF7748600.1 hypothetical protein DSO57_015414 [Entomophthora muscae]	Rubber oxygenase OS=Streptomyces sp. (strain K30) OX=256642 GN=lcp PE=1 SV=2
A0351	-	-	-	-	-	-	-	-
A0352	-	-	-	-	-	-	-	-
A0353	-	-	GO:0005515(protein binding)	K14556 DIP2, UTP12, WDR3; U3 small nucleolar RNA-associated protein 12	map03008 Ribosome biogenesis in eukaryotes	KOG0306 YLR129w WD40-repeat-containing subunit of the 18S rRNA processing complex	KAF9975830.1 hypothetical protein BGZ73_000371 [Actinomyces rella ambigua]	U3 small nucleolar RNA-associated protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DIP2 PE=1 SV=1
A0354	-	-	GO:0046872(metal ion binding),GO:0005515(protein binding)	K12182 HGS, HRS, VPS27; hepatocyte growth factor-regulated tyrosine kinase substrate	map04144 Endocytosis;map04145 Phagosome;map03250 Viral life cycle - HIV-1	KOG1818 7295922 Membrane trafficking and cell signaling protein HRS, contains VHS and FYVE domains	KXS12132.1 ubiquitin binding protein [Gonapodya prolifera JEL478]	Vacuolar protein sorting-associated protein 27 OS=Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) OX=321614 GN=VPS27 PE=3 SV=1
A0355	-	GO:0005856(cytoskeleton),GO:0016459(myosin complex)	GO:0005515(protein binding),GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At3g19960 Myosin class V heavy chain	RKO94560.1 myosin VIIA, isoform CRA_d, partial [Blyttomyces helicus]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1
A0356	GO:0010960(magnesium ion homeostasis)	-	-	K16302 CNNM; metal transporter CNNM	-	KOG2118 Hs19923808 Predicted membrane protein, contains two CBS domains	ORX88610.1 DUF21-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Metal transporter CNNM2 OS=Homo sapiens OX=9606 GN=CNNM2 PE=1 SV=2
A0357	-	-	-	-	-	-	-	-
A0358	-	GO:0016020(membrane)	GO:0005227(calcium activated cation channel activity)	K21989 TMEM63, CSC1; calcium permeable stress-gated cation channel	-	KOG1134 At3g21620 Uncharacterized conserved protein	ORX53130.1 DUF221-domain-containing protein [Hesseltinella vesiculosa]	CSC1-like protein At3g21620 OS=Arabidopsis thaliana OX=3702 GN=At3g21620 PE=2 SV=1
A0359	GO:0006457(protein folding)	-	GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding),GO:0001671(ATPase activator activity),GO:0051087(chaperone binding),GO:0005515(protein binding)	K09553 STIP1; stress-induced-phosphoprotein 1	map05020 Prion disease	KOG0548 YOR027w Molecular co-chaperone STI1	KAG0656584.1 Hsp90 cochaperone [Kazachstania unispora]	Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STI1 PE=1 SV=1

A0360	GO:0006355(regulation of transcription, DNA-templated)	GO:0016602(CCAAT-binding factor complex)	GO:0046982(protein heterodimerization activity),GO:0003700(DNA-binding transcription factor activity)	K08066 NFYC, HAP5; nuclear transcription factor Y, gamma	map04612 Antigen processing and presentation;map05152 Tuberculosis	KOG1657 At3g48590 CCAAT-binding factor, subunit C (HAP5)	SCU84338.1 LANO_0C01090g1_1 [Lachancea nothofagi CBS 11611]	Nuclear transcription factor Y subunit C-2 OS=Oryza sativa subsp. japonica OX=39947 GN=NFYC2 PE=1 SV=1
A0361	GO:1901135(carbohydrate derivative metabolic process), GO:1901137(carbohydrate derivative biosynthetic process)	-	GO:0097367(carbohydrate derivative binding),GO:0004360(glutamine-fructose-6-phosphate transaminase (isomerizing) activity)	-	-	KOG1268 7289004 Glucosamine 6-phosphate synthetases, contain amidotransferase and phosphosugar isomerase domains	CAE6521419.1 unnamed protein product [Rhizoctonia solani]	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Chlorobaculum tepidum (strain ATCC 49652 / DSM 12025 / NBRC 103806 / TLS) OX=194439 GN=glmS PE=3 SV=3
A0362	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0030130(clathrin coat of trans-Golgi network vesicle),GO:0030132(clathrin coat of coated pit)	GO:0005096(GTPase activator activity),GO:0005198(structural molecule activity)	-	-	KOG2512 7295735 Beta-tubulin folding cofactor C	OON00687.1 hypothetical protein, variant [Batrachochytrium salamandrivorans]	Tubulin-specific chaperone C OS=Mus musculus OX=10090 GN=Tbccc PE=1 SV=1
A0363	-	GO:0016021(integral component of membrane)	GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0001666(nucleotide binding)	K01537 ATP2C; P-type Ca2+ transporter type 2C [EC:7.2.2.10]	-	KOG0204 CE28372 Calcium transporting ATPase	RIA95340.1 PMCA-type calcium-translocating P-type ATPase [Glomus cerebriforme]	Plasma membrane calcium-transporting ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2B3 PE=1 SV=3
A0364	GO:0016052(carbohydrate catabolic process)	-	GO:0004557(alpha-galactosidase activity)	-	-	-	OBZ84874.1 Alpha-galactosidase 1 [Choanephora cucurbitarum]	Alpha-galactosidase OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=galA PE=1 SV=1
A0365	-	-	-	K24781 BPH1; beige protein homolog 1	-	KOG1786 7292461 Lysosomal trafficking regulator LYST and related BEACH and WD40 repeat proteins	EXX77184.1 Bph1p [Rhizophagus irregularis DAOM 197198w]	Neurobeachin-like protein 2 OS=Danio rerio OX=7955 GN=nbeal2 PE=1 SV=1

A0366	GO:0046416(D-amino acid metabolic process)	-	GO:0003884(D-amino-acid oxidase activity),GO:0071949(FAD binding),GO:0016491(oxidoreductase activity)	K00273 DAO; aao; D-amino-acid oxidase [EC:1.4.3.3]	map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map00330 Arginine and proline metabolism;map00470 D-Amino acid metabolism;map00260 Glycine, serine and threonine metabolism;map00311 Penicillin and cephalosporin biosynthesis;map01100 Metabolic pathways	KOG3923 7297177 D-aspartate oxidase	KAF2795579.1 nucleotide-binding domain-containing protein [Melanomma pulvis-pyrius CBS 109.77]	D-aspartate oxidase OS=Mus musculus OX=10090 GN=DDO PE=1 SV=1
A0367	-	-	-	-	-	-	TPX77043.1 hypothetical protein CcCBS67573_g01690 [Chytridiomycetes confervae]	Protein rliB OS=Dictyostelium discoideum OX=44689 GN=rliB PE=3 SV=2
A0368	-	-	GO:0016491(oxidoreductase activity),GO:0020037(heme binding),GO:0051536(iron-sulfur cluster binding),GO:0010181(FMN binding),GO:0003824(catalytic activity)	K00381 cysI; sulfite reductase (NADPH) hemoprotein beta-component [EC:1.8.1.2]	map01120 Microbial metabolism in diverse environments;map00920 Sulfur metabolism;map01100 Metabolic pathways	-	ORX99594.1 sulphite reductase hemo protein, beta subunit [Basidiobolus meristosporus CBS 931.73]	Sulfite reductase [NADPH] subunit beta OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=sir1 PE=3 SV=1
A0369	-	-	GO:0016491(oxidoreductase activity),GO:0003824(catalytic activity)	K00380 cysJ; sulfite reductase (NADPH) flavoprotein alpha-component [EC:1.8.1.2]	map01120 Microbial metabolism in diverse environments;map00920 Sulfur metabolism;map01100 Metabolic pathways	KOG1158 YFR030w NADP/FAD dependent oxidoreductase	OBZ89030.1 putative sulfite reductase [NADPH] flavoprotein component, partial [Choanephora cucurbitarum]	Sulfite reductase [NADPH] flavoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET10 PE=1 SV=2
A0370	-	-	GO:0016491(oxidoreductase activity)	K00344 qor, CRYZ; NADPH:quinone reductase [EC:1.6.5.5]	-	KOG1198 At3g56460 Zinc-binding oxidoreductase	PVU89327.1 hypothetical protein BB561_005430 [Smittium simulii]	Quinone oxidoreductase-like protein 2 homolog OS=Nematostella vectensis OX=45351 GN=v1g238856 PE=3 SV=1

A0371	-	-	GO:0003860(3-hydroxyisobutyryl-CoA hydrolase activity)	K05605 HIBCH; 3-hydroxyisobutyryl-CoA hydrolase [EC:3.1.2.4]	map00410 beta-Alanine metabolism;map01200 Carbon metabolism;map00640 Propanoate metabolism;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG1684 CE00689 Enoyl-CoA hydratase	KAG0262023.1 hypothetical protein DFAQ27_002578 [Actinomortierella ambigua]	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Xenopus tropicalis OX=8364 GN=hibch PE=2 SV=1
A0372	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors);GO:0050660(flavin adenine dinucleotide binding)	K00249 ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map03320 PPAR signaling pathway;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map04936 Alcoholic liver disease;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG1469 At3g06810 Predicted acyl-CoA dehydrogenase	ORX60581.1 acyl-CoA dehydrogenase NM domain-like protein [Hesseltinella vesiculosa]	Acyl-CoA dehydrogenase family member 10 OS=Mus musculus OX=10090 GN=Acad10 PE=1 SV=1
A0373	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors);GO:0050660(flavin adenine dinucleotide binding)	K00249 ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map03320 PPAR signaling pathway;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map04936 Alcoholic liver disease;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG1469 At3g06810 Predicted acyl-CoA dehydrogenase	KAF7730200.1 hypothetical protein EC973_002808 [Apophysomyces ossiformis]	Acyl-CoA dehydrogenase family member 10 OS=Mus musculus OX=10090 GN=Acad10 PE=1 SV=1
A0374	-	-	-	-	-	-	-	-
A0375	GO:0006508(proteolysis)	GO:0016021(integral component of membrane)	GO:0004252(serine-type endopeptidase activity)	-	-	KOG2289 At3g53780 Rhomboid family proteins	KAG4090541.1 rhomboid-domain-containing protein [Neocallimastix sp. JGI-2020a]	RHOMBOLD-like protein 4 OS=Arabidopsis thaliana OX=3702 GN=RBL4 PE=2 SV=1

A0376	GO:0071985(multivesicular body sorting pathway)	-	GO:0005515(protein binding);GO:0016491(oxidoreductase activity)	K12200 PDCD6IP, ALIX, RIM20; programmed cell death 6-interacting protein	map04144 Endocytosis;map03250 Viral life cycle - HIV-1	KOG2220 At1g15130 Predicted signal transduction protein	XP_016604539.1 hypothetical protein SPPG_08088 [Spizellomyces punctatus DAOM BR117]	Vacuolar-sorting protein BRO1 OS=Arabidopsis thaliana OX=3702 GN=BRO1 PE=1 SV=1
A0377	-	-	-	-	-	-	KAF9117359.1 hypothetical protein BGX30_005554 [Mortierella sp. GBA39]	tRNA (guanine(6)-N2)-methyltransferase THUMP3 OS=Bos taurus OX=9913 GN=THUMP3 PE=2 SV=1
A0378	GO:0006096(glycolytic process)	-	GO:0004332(fructose-bisphosphate aldolase activity)	K01623 ALDO; fructose-bisphosphate aldolase, class I [EC:4.1.2.13]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00051 Fructose and mannose metabolism;map00680 Methane metabolism;map00710 Carbon fixation in photosynthetic organisms;map00030 Pentose phosphate pathway;map01	KOG1557 At4g26530 Fructose-bisphosphate aldolase	XP_006679107.1 uncharacterized protein BATDEDRAFT_35107 [Batrachochytrium dendrobatidis JAM81]	Fructose-bisphosphate aldolase, cytoplasmic isozyme OS=Spinacia oleracea OX=3562 PE=2 SV=1
A0379	-	-	-	-	-	-	-	-
A0380	-	-	GO:0005515(protein binding)	-	-	-	KAG0747887.1 hypothetical protein G6F23_002363 [Rhizopus oryzae]	-
A0381	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A0382	-	-	GO:0005515(protein binding)	K17662 CBP3, UQC; cytochrome b pre-mRNA-processing protein 3	-	KOG2873 At5g51220 Ubiquinol cytochrome c reductase assembly protein CBP3	KAG0736343.1 hypothetical protein G6F23_011004 [Rhizopus oryzae]	-
A0383	-	-	-	-	-	KOG2585 At5g49970_1 Uncharacterized conserved protein	KAF0521751.1 NADPH-hydrate epimerase [Gigaspora margarita]	NAD(P)H-hydrate epimerase OS=Danio rerio OX=7955 GN=naxe PE=1 SV=1
A0384	-	-	-	-	-	KOG0048 Hs4505293_1 Transcription factor, Myb superfamily	XP_007869587.1 hypothetical protein GLOTRDRAFT_48219 [Gloeophyllum trabeum ATCC 11539]	Myb-related protein B OS=Xenopus laevis OX=8355 GN=mybl2 PE=2 SV=2

A0385	GO:0032958(inositol phosphate biosynthetic process)	-	GO:0016301(kinase activity)	K07756 IP6K, IHPK; inositol-hexakisphosphate 5-kinase [EC:2.7.4.21]	map04070 Phosphatidylinositol signaling system;map04138 Autophagy - yeast	KOG1620 7296185 Inositol polyphosphate multikinase, component of the ARGR transcription regulatory complex	ODV92205.1 hypothetical protein CANCEADRAFT_13522, partial [Tortispora caseinolytica NRRL Y-17796]	Inositol polyphosphate multikinase OS=Homo sapiens OX=9606 GN=IPMK PE=1 SV=1
A0386	GO:0006561(proline biosynthetic process)	GO:0005737(cytoplasm)	GO:0004349(glutamate 5-kinase activity),GO:0003723(RNA binding),GO:0005524(ATP binding),GO:0016301(kinase activity)	K00931 proB; glutamate 5-kinase [EC:2.7.2.11]	map01110 Biosynthesis of secondary metabolites;map00332 Carbapenem biosynthesis;map00330 Arginine and proline metabolism;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways	KOG1154 YDR300c Gamma-glutamyl kinase	KHJ34816.1 putative glutamate 5-kinase [Erysiphe necator]	Glutamate 5-kinase OS=Synechococcus elongatus (strain ATCC 33912 / PCC 7942 / FACHB-805) OX=1140 GN=proB PE=3 SV=1
A0387	-	-	-	K25866 NUDC; nuclear migration protein NudC	-	KOG2265 At5g53400 Nuclear distribution protein NUDC	XP_025361423.1 CS-domain-containing protein [Jaminaea rosea]	Protein BOBBER 1 OS=Arabidopsis thaliana OX=3702 GN=BOB1 PE=1 SV=1
A0388	-	-	-	-	-	-	-	-
A0389	GO:0006744(ubiquinone biosynthetic process)	-	GO:0008289(lipid binding)	K18587 COQ9; ubiquinone biosynthesis protein COQ9	-	KOG2969 7304168 Uncharacterized conserved protein	GBC01707.1 hypothetical protein RclHR1_00430024 [Rhizophagus clarus]	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Coq9 PE=2 SV=1
A0390	-	-	-	-	-	-	RPB12450.1 periplasmic binding protein-like II [Morchella conica CCBA5932]	-
A0391	-	-	-	-	-	-	-	-
A0392	-	GO:0031932(TORC2 complex)	-	-	-	-	-	-
A0393	-	-	-	-	-	KOG0381 7293212 HMG box-containing protein	CRK35341.1 hypothetical protein BN1708_006693, partial [Verticillium longisporum]	High mobility group-T protein OS=Oncorhynchus mykiss OX=8022 PE=2 SV=2
A0394	-	-	GO:0016491(oxidoreductase activity),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG1336 At3g27820 Monodehydroascorbate/ferredoxin reductase	KKY19845.1 putative rubredoxin-nad(+) reductase [Diplodia seriata]	Monodehydroascorbate reductase OS=Solanum lycopersicum OX=4081 GN=AFRR PE=1 SV=1
A0395	-	-	-	K24104 GPN; GPN-loop GTPase	-	KOG1534 CE23026 Putative transcription factor FET5	ORZ24370.1 GPN-loop GTPase 3 [Absidia repens]	GPN-loop GTPase 3 OS=Danio rerio OX=7955 GN=gpn3 PE=2 SV=2

A0396	-	-	-	-	-	-	OKP10088.1 hypothetical protein PENSUB_455 3 [Penicillium subrubescens]	-
A0397	GO:0042254(ribosome biogenesis)	GO:1990904(ribonucleoprotein complex), GO:0005730(nucleolus)	GO:0003723(RNA binding)	K11129 NHP2, NOLA2; H/ACA ribonucleoprotein complex subunit 2	map03008 Ribosome biogenesis in eukaryotes	KOG3167 At5g08180 Box H/ACA snoRNP component, involved in ribosomal RNA pseudouridylation	XP_018987567.1 uncharacterized protein BABINDRAFT_158875 [Babjeviella inositovora NRRL Y-12698]	H/ACA ribonucleoprotein complex subunit 2-like protein OS=Arabidopsis thaliana OX=3702 GN=At5g08180 PE=1 SV=1
A0398	-	-	-	-	-	-	-	-
A0399	-	GO:0016020(membrane)	GO:0005227(calcium activated cation channel activity)	K21989 TMEM63, CSC1; calcium permeable stress-gated cation channel	-	KOG1134 At1g30360 Uncharacterized conserved protein	RUS20123.1 hypothetical protein BC937DRAFT_86311 [Endogone sp. FLAS-F59071]	CSC1-like protein ERD4 OS=Brassica juncea OX=3707 GN=ERD4 PE=3 SV=2
A0400	-	-	-	-	-	-	-	-
A0401	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K11838 USP7, UBP15; ubiquitin carboxyl-terminal hydrolase 7 [EC:3.4.19.12]	map03083 Polycomb repressive complex;map05203 Viral carcinogenesis; map04068 FoxO signaling pathway;map05169 Epstein-Barr virus infection	KOG1863 At3g11910 Ubiquitin carboxyl-terminal hydrolase	KAG0168450.1 hypothetical protein DFQ30_004753 [Apophysomyces sp. BC1015]	Ubiquitin C-terminal hydrolase 13 OS=Arabidopsis thaliana OX=3702 GN=UBP13 PE=1 SV=1
A0402	-	-	-	-	-	KOG1502 At1g09490 Flavonol reductase/cinnamoyl-CoA reductase	KAE8161376.1 hypothetical protein BDV40DRAFT_313128 [Aspergillus tamarii]	Cinnamoyl-CoA reductase 1 OS=Petunia hybrida OX=4102 GN=CCR1 PE=1 SV=1
A0403	-	-	-	-	-	KOG4033 Hs2045268 Uncharacterized conserved protein	ORY28665.1 hypothetical protein LY90DRAFT_89083 [Neocallimastix californiae]	Protein OSCP1 OS=Bos taurus OX=9913 GN=OSCP1 PE=2 SV=1
A0404	-	-	-	-	-	KOG0231 Hs2045068 Junctional membrane complex protein Junctophilin and related MORN repeat proteins	RKO86588.1 hypothetical protein BDK51DRAFT_35997 [Blyttiomycetes helicus]	MORN repeat-containing protein 5 OS=Danio rerio OX=7955 GN=morn5 PE=2 SV=1
A0405	-	-	GO:0005515(protein binding)	K24348 UBXN1_4; UBX domain-containing protein 1/4	map04141 Protein processing in endoplasmic reticulum	KOG2689 CE20713 Predicted ubiquitin regulatory protein	KAF7939756.1 hypothetical protein EAE99_001561 [Botrytis elliptica]	UBX domain-containing protein 1 OS=Caenorhabditis elegans OX=6239 GN=ubxn-1 PE=1 SV=1

A0406	-	-	-	-	-	KOG2992 At5g57120 Nucleolar GTPase/ATPase p130	RKO98513.1 hypothetical protein CXG81DRAFT_5735, partial [Caulochytrium protostelioides]	Nucleolar protein dao-5 OS=Caenorhabditis elegans OX=6239 GN=dao-5 PE=1 SV=1
A0407	-	-	-	-	-	-	-	Cilia- and flagella-associated protein 161 OS=Danio rerio OX=7955
A0408	-	-	-	-	-	-	-	-
A0409	-	GO:0016021(integral component of membrane)	-	K19525 VPS13A_C; vacuolar protein sorting-associated protein 13A/C	-	-	-	-
A0410	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity),GO:0004672(protein kinase activity)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0598 CE14798 Ribosomal protein S6 kinase and related proteins	ORX65635.1 Pkinase-domain-containing protein [Linderina pennisporea]	Serine/threonine-protein kinase sgk-1 OS=Caenorhabditis elegans OX=6239 GN=sgk-1 PE=1 SV=1
A0411	-	-	GO:0035091(phosphatidylinositol binding)	-	-	-	XP_013025199.1 retromer complex subunit Vps5 [Schizosaccharomyces cryophilus OY26]	Autophagy-related protein 20 OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294 / BCRC 21397 / CBS 2163 / NBRC 10782 / NRRL Y-8283 / UCD 57-17) OX=436907 GN=ATG20 PE=3 SV=1
A0412	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0725 7290108 Reductases with broad range of substrate specificities	OQE27470.1 hypothetical protein PENSTE_c004G06373 [Penicillium steckii]	Uncharacterized short-chain type dehydrogenase/reductase y4eL OS=Sinorhizobium fredii (strain NBRC 101917 / NGR234) OX=394 GN=NGR_a03830 PE=3 SV=1
A0413	-	-	-	-	-	-	-	-
A0414	-	-	-	-	-	-	-	-
A0415	-	-	-	-	-	-	-	Inactive serine/threonine-protein kinase 19 OS=Homo sapiens
A0416	-	-	-	-	-	-	-	-
A0417	-	-	-	K19838 SST2; GTPase-activating protein SST2	map04011 MAPK signaling pathway - yeast	KOG3589 CE29404 G protein signaling regulators	ORX71762.1 regulator of G protein signaling superfamily [Basidiobolus meristosporus CBS 931.73]	Developmental regulator flbA OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=flbA PE=2 SV=1
A0418	-	-	-	-	-	-	TPX64676.1 hypothetical protein SpCBS45565_g05698 [Spizellomyces sp. 'palustris']	18 kDa heat shock protein OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) OX=272562 GN=hsp18 PE=2 SV=1
A0419	-	-	-	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0697 Hs18589868 Protein phosphatase 1B (formerly 2C)	ORX79408.1 protein serine/threonine phosphatase 2C, partial [Anaeromyces robustus]	Probable protein phosphatase 1N OS=Homo sapiens OX=9606 GN=PPM1N PE=2 SV=2

A0420	GO:0006364(rRNA processing)	GO:0016020(membrane)	GO:0016740(transferase activity)	K26392 STOML2, SLP2; stomatin-like protein 2	-	KOG2620 At4g27580 Prohibitins and stomatins of the PID superfamily	KAF8978288.1 hypothetical protein BGZ46_006630 [Entomortiera lignicola]	Stomatin-like protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=STOML2 PE=1 SV=1
A0421	-	GO:0000776(kinetochore);GO:0031262(Ndc80 complex)	-	K11548 NUF2, CDCA1; kinetochore protein Nuf2	-	-	RUS27142.1 hypothetical protein BC938DRAFT_483658 [Jimgerdennia flammicorona]	Probable kinetochore protein NUF2 OS=Cryptococcus neoformans var. neoformans serotype D (strain B-3501A) OX=283643 GN=NUF2 PE=3 SV=1
A0422	-	-	-	K15340 DCLRE1A, SNM1A, PSO2; DNA cross-link repair 1A protein	-	KOG1361 Hs12383082 Predicted hydrolase involved in interstrand cross-link repair	KAG1137128.1 hypothetical protein G6F38_011540 [Rhizopus oryzae]	5' exonuclease Apollo OS=Rattus norvegicus OX=10116 GN=Dclre1b PE=1 SV=2
A0423	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding);GO:0004674(protein serine/threonine kinase activity);GO:0004672(protein kinase activity)	K13303 SGK2;serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	-	XP_037218368.1 Non-specific serine/threonine protein kinase [Mycena indigotica]	RAC family serine/threonine-protein kinase homolog OS=Dictyostelium discoideum OX=44689 GN=pkbA PE=1 SV=1
A0424	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K19800 SCH9;serine/threonine protein kinase SCH9 [EC:2.7.11.1]	map04213 Longevity regulating pathway - multiple species;map04138 Autophagy - yeast	KOG0614 CE19898 cGMP-dependent protein kinase	KNE68995.1 AGC protein kinase [Allomyces macrogynus ATCC 38327]	cGMP-dependent protein kinase egl-4 OS=Caenorhabditis elegans OX=6239 GN=egl-4 PE=1 SV=2
A0425	-	-	-	-	-	-	ORZ14799.1 NAD(P)-binding protein, partial [Absidia repens]	-
A0426	GO:003129(TOR signaling)	GO:003131(TORC1 complex)	GO:0005515(protein binding)	K07204 RAPTOR; regulatory associated protein of mTOR	map04140 Autophagy - animal;map05131 Shigellosis;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map04910 Insulin signaling pathway;map04138 Autophagy - yeast;map04136 Autophagy - other;map04714 Thermogenesis; map05206 MicroRNAs in cancer;map04152 AMPK signaling pathway;map04151 PI3K-Akt signaling	KOG1517 At3g08850 Guanine nucleotide binding protein MIP1	ORY51824.1 hypothetical protein BCR33DRAFT_712020 [Rhizoclostium globosum]	Regulatory-associated protein of mTOR OS=Homo sapiens OX=9606 GN=RPTOR PE=1 SV=1
A0427	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding);GO:0004672(protein kinase activity)	-	-	KOG0198 At3g13530 MEKK and related serine/threonine protein kinases	XP_031027699.1 uncharacterized protein SmJEL517_g0405 [Synchytrium microbalum]	Serine/threonine-protein kinase sepA OS=Dictyostelium discoideum OX=44689 GN=sepA PE=2 SV=1

A0428	-	-	-	-	-	-	-	-
A0429	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	OUM60759.1 hypothetical protein PIROE2DRAFT_45959 [Piromyces sp. E2]	Adenylate cyclase type 10 OS=Homo sapiens OX=9606 GN=ADCY10 PE=1 SV=3
A0430	GO:0007165(signal transduction),GO:007186(G protein-coupled receptor signaling pathway)	-	GO:0003924(GTPase activity),GO:0019001(guanylate binding),GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04730 Long-term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082[Hs20542545 G-protein alpha subunit (small G protein superfamily)]	KAF8310845.1 guanine nucleotide binding protein, alpha subunit [Clavulina sp. PMI_390]	Guanine nucleotide-binding protein subunit alpha-15 OS=Mus musculus OX=10090 GN=Gna15 PE=2 SV=1
A0431	GO:0006099(tricarboxylic acid cycle)	GO:0005829(cytosol)	GO:0003994(aconitate hydratase activity),GO:0051539(4 iron, 4 sulfur cluster binding)	-	-	KOG0454[At4g13430 3-isopropylmalate dehydratase (aconitase superfamily)]	KAG1716593.1 hypothetical protein ID866_554 [Astraeus odoratus]	Aconitate hydratase B OS=Escherichia coli (strain K12) OX=83333 GN=acnB PE=1 SV=3
A0432	-	-	-	-	-	-	-	-
A0433	-	-	-	-	-	-	XP_007913568.1 putative set domain-containing protein [Phaeoacremonium minimum UCRPA7]	-
A0434	GO:0006457(protein folding)	GO:0005829(cytosol),GO:0005832(chaperonin-containing T-complex)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0051082(unfolded protein binding)	K09494 CCT2; T-complex protein 1 subunit beta	-	KOG0363[Hs5453603 Chaperonin complex component, TCP-1 beta subunit (CCT2)]	XP_016610562.1 T-complex protein 1 subunit beta [Spizellomyces punctatus DAOM BR117]	T-complex protein 1 subunit beta OS=Dictyostelium discoideum OX=44689 GN=cct2 PE=1 SV=1
A0435	-	-	GO:0005515(protein binding)	-	-	-	-	Rho GTPase-activating protein 27 OS=Mus musculus OX=10090 GN=Arhgap27 PE=1 SV=1
A0436	GO:1902600(proton transmembrane transport)	GO:0005887(integral component of plasma membrane)	GO:0030171(voltage-gated proton channel activity)	-	-	-	XP_009156598.1 hypothetical protein HMPREF1120_04234 [Exophiala dermatitidis NIH/UT8656]	Voltage-gated hydrogen channel 1 OS=Danio rerio OX=7955 GN=hvcn1 PE=2 SV=1
A0437	-	-	GO:0003950(NAD+ ADP-ribosyltransferase activity)	-	-	-	-	Protein mono-ADP-ribosyltransferase PARP12 OS=Mus musculus OX=10090 GN=Parp12 PE=1 SV=3

A0438	GO:0007017(microtubule-based process)	GO:0030286(dynein complex)	-	K10418 DYNLL1; dynein light chain LC8-type	map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3430 Hs20542486 Dynein light chain type 1	KAF3764557.1 hypothetical protein M406DRAFT_291669 [Cryphonectria parasitica EP155]	Dynein light chain 1, cytoplasmic OS=Bos taurus OX=9913 GN=DYNLL1 PE=1 SV=1
A0439	-	-	GO:0008270(zinc ion binding);GO:0005515(protein binding)	-	-	-	-	-
A0440	-	-	-	-	-	-	-	-
A0441	GO:0006260(DNA replication);GO:0006281(DNA repair);GO:0006310(DNA recombination)	GO:0005634(nucleus)	GO:0003676(nucleic acid binding);GO:0003677(DNA binding)	K10739 RFA2; RPA2; replication factor A2	map03420 Nucleotide excision repair;map03030 DNA replication;map03440 Homologous recombination;map03430 Mismatch repair;map03460 Fanconi anemia pathway	KOG3108 Hs4506585 Single-stranded DNA-binding replication protein A (RPA), medium (30 kD) subunit	TPX61573.1 hypothetical protein SpCBS45565.g07240 [Spizellomyces sp. 'palustris']	Replication protein A 32 kDa subunit B OS=Oryza sativa subsp. japonica OX=39947 GN=RPA2B PE=1 SV=1
A0442	-	-	GO:0005515(protein binding)	-	-	-	XP_025572736.1 CBS and PB1 domain protein [Aspergillus ibericus CBS 121593]	CBS domain-containing protein CBSCBSPB2 OS=Arabidopsis thaliana OX=3702 GN=CBSCBSPB2 PE=2 SV=1
A0443	-	-	GO:0016798(hydrolase activity, acting on glycosyl bonds);GO:0004730(pseudouridylate synthase activity)	K16330 K16330; pseudouridylate synthase / pseudouridine kinase [EC:4.2.1.70 2.7.1.83]	map00240 Pyrimidine metabolism;map01100 Metabolic pathways	KOG3009 7296188 Predicted carbohydrate kinase, contains PfkB domain	XP_016606624.1 hypothetical protein SPPG_06269 [Spizellomyces punctatus DAOM BR117]	Pseudouridine-5'-phosphate glycosidase OS=Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) OX=273068 GN=psuG PE=3 SV=1
A0444	-	-	-	K17279 REEP5_6; receptor expression-enhancing protein 5/6	-	KOG1725 Hs19923919 Protein involved in membrane traffic (YOP1/TB2/DPI1/HVA22 family)	ORY05602.1 hypothetical protein K493DRAFT_274828 [Basidiobolus meristosporus CBS 931.73]	Receptor expression-enhancing protein 5 OS=Homo sapiens OX=9606 GN=REEP5 PE=1 SV=3
A0445	GO:0017196(N-terminal peptidyl-methionine acetylation)	-	GO:0004596(peptide alpha-N-acetyltransferase activity);GO:0016407(acetyltransferase activity)	-	-	KOG3139 Hs18596951 N-acetyltransferase	RKO84113.1 N-acetyltransferase 12, isoform CRA_a [Blytiomyces helicus]	N-alpha-acetyltransferase 30 OS=Xenopus laevis OX=8355 GN=naa30 PE=2 SV=1
A0446	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 At4g36490 Phosphatidylinositol transfer protein SEC14 and related proteins	XP_001841214.1 SEC14 cytosolic factor [Coprinopsis cinerea okayama7#130]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH12 OS=Arabidopsis thaliana OX=3702 GN=SFH12 PE=2 SV=1
A0447	-	-	-	-	-	-	-	-

A0448	-	-	-	-	-	KOG1269 At5g13710 SAM-dependent methyltransferases	TDZ35242.1 Phosphoethanolamine N-methyltransferase 3 [Colletotrichum spinosum]	-
A0449	-	-	GO:0016491(oxidoreductase activity)	K03934 NDUFS1; NADH dehydrogenase (ubiquinone) Fe-S protein 1 [EC:7.1.1.2]	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG2282 Hs13637608 NADH-ubiquinone oxidoreductase, NDUFS1/75 kDa subunit	KXN71541.1 putative NADH dehydrogenase 78K chain precursor [Conidiobolus coronatus NRRL 28638]	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Pan troglodytes OX=9598 GN=NDUFS1 PE=2 SV=1
A0450	-	-	-	-	-	-	-	-
A0451	GO:0006811(ion transport); GO:0055085(transmembrane transport)	GO:0016020(membrane); GO:0005886(plasma membrane)	GO:0005509(calcium ion binding); GO:0005216(ion channel activity); GO:0005261(cation channel activity)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG2301 Hs13386500 Voltage-gated Ca2+ channels, alpha1 subunits	P41041.1 RecName: Full=Calmodulin; Short=CaM [Pneumocystis carinii]	Voltage-dependent P/Q-type calcium channel subunit alpha-1A OS=Rattus norvegicus OX=10116 GN=Cacna1a PE=1 SV=1
A0452	GO:0006261(DNA-dependent DNA replication); GO:0006260(DNA replication)	GO:0008622(epsilon DNA polymerase complex)	GO:0003677(DNA binding)	K02325 POLE2; DNA polymerase epsilon subunit 2 [EC:2.7.7.7]	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair	KOG3818 Hs4505935 DNA polymerase epsilon, subunit B	ORY88361.1 DNA polymerase alpha/epsilon subunit B-domain-containing protein [Leucosporidium creatinivorum]	DNA polymerase epsilon subunit B OS=Arabidopsis thaliana OX=3702 GN=DPB2 PE=1 SV=1
A0453	-	-	-	-	-	-	-	-
A0454	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0455	-	-	-	-	-	KOG1700 At1g01780 Regulatory protein MLP and related LIM proteins	KAG2175331.1 hypothetical protein INT44_007819 [Umbelopsis vinacea]	LIM domain-containing protein PLIM2b OS=Arabidopsis thaliana OX=3702 GN=PLIM2B PE=1 SV=1

A0456	GO:0033617(mitochondrial cytochrome c oxidase assembly)	GO:0005743(mitochondrial inner membrane)	GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0003724(RNA helicase activity)	K12823 DDX5, DBP2; ATP-dependent RNA helicase DDX5/DBP2 [EC:3.6.4.13]	map03040 Spliceosome;map05202 Transcriptional misregulation in cancer;map05205 Proteoglycans in cancer	KOG0331 At4g09730 ATP-dependent RNA helicase	CEG82740.1 hypothetical protein RMA1CC62417_16764 [Rhizopus microsporus]	DEAD-box ATP-dependent RNA helicase 39 OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0184500 PE=2 SV=1
A0457	-	-	GO:0005525(GTP binding)	K03650 mnmE, trmE, MSS1; tRNA modification GTPase [EC:3.6.-.-]	-	KOG1191 At5g39960 Mitochondrial GTPase	KAG0322460.1 hypothetical protein BGZ97_006314 [Linnemania gamsii]	GTPase Der OS=Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966) OX=402881 GN=der PE=3 SV=1
A0458	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A0459	-	GO:0016021(integral component of membrane)	-	K17086 TM9SF2_4; transmembrane 9 superfamily member 2/4	-	KOG1277 At1g10950 Endosomal membrane proteins, EMP70	KAG2175877.1 hypothetical protein INT44_000355 [Umbelopsis vinacea]	Transmembrane 9 superfamily member 1 OS=Arabidopsis thaliana OX=3702 GN=TMN1 PE=1 SV=1
A0460	-	-	-	-	-	KOG2417 Hs7706704 Predicted G-protein coupled receptor	RKP16513.1 G protein-coupled receptor 89C [Rozella allomyces CSF55]	Golgi pH regulator OS=Mus musculus OX=10090 GN=Gpr89 PE=1 SV=2
A0461	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG0637 At1g71890 Sucrose transporter and related proteins	XP_016608745.1 hypothetical protein SPPG_09148 [Spizellomyces punctatus DAOM BR117]	-
A0462	-	-	-	K09602 OTUB1; ubiquitin thioesterase protein OTUB1 [EC:3.4.19.12]	-	KOG3991 Hs8923114 Uncharacterized conserved protein	RKP18627.1 cysteine proteinase, partial [Rozella allomyces CSF55]	Ubiquitin thioesterase OTUB1 OS=Mus musculus OX=10090 GN=Otub1 PE=1 SV=2
A0463	GO:0042254(ribosome biogenesis)	GO:1990904(ribonucleoprotein complex)	-	K02936 RPL7Ae, RPL7A; large subunit ribosomal protein L7Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3166 At2g47610 60S ribosomal protein L7A	PIA17434.1 L30e-like protein [Coemansia reversa NRRL 1564]	Large ribosomal subunit protein eL8z OS=Arabidopsis thaliana OX=3702 GN=RPL7AA PE=2 SV=2

A0464	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0051603(proteolysis involved in cellular protein catabolic process), GO:0043161(proteasome-mediated ubiquitin-dependent protein catabolic process)	GO:0019773(proteasome complex, alpha-subunit complex), GO:0005839(proteasome complex)	-	K02729 PSMA5; 20S proteasome subunit alpha 5 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	-	XP_002837618.1 hypothetical protein [Tuber melanosporum Mel28]	Proteasome subunit alpha type-5 OS=Oryza sativa subsp. japonica OX=39947 GN=PAE1 PE=2 SV=1
A0465	-	-	-	-	-	-	-	-
A0466	-	-	GO:0005509(calcium ion binding),GO:0008597(calcium-dependent protein serine/threonine phosphatase activity)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	KOG0027ICE27325 Calmodulin and related proteins (EF-Hand superfamily)	OLY85483.1 Calcineurin subunit B [Smittium mucronatum]	Calcineurin subunit B OS=Naegleria gruberi OX=5762 GN=CNB1 PE=3 SV=1
A0467	-	GO:0016021(integral component of membrane)	-	-	-	-	XP_007263836.1 DUF887-domain-containing protein [Fomitiporia mediterranea MF3/22]	-
A0468	-	-	GO:0005515(protein binding),GO:0016787(hydrolase activity),GO:0003824(catalytic activity)	-	-	KOG1939 At5g37830 Oxoprolinase	XP_016610489.1 hypothetical protein SPPG_02915 [Spizellomyces punctatus DAOM BR117]	5-oxoprolinase OS=Mus musculus OX=10090 GN=Oplah PE=1 SV=1
A0469	-	-	-	-	-	-	-	-
A0470	-	-	-	-	-	-	-	-
A0471	GO:0017121(plasma membrane phospholipid scrambling)	-	GO:0017128(phospholipid scrambling activity)	-	-	KOG0621 CE16440 Phospholipid scrambling	-	Phospholipid scrambling 3 OS=Rattus norvegicus OX=10116 GN=Plscr3 PE=1 SV=1
A0472	-	-	-	-	-	-	-	-
A0473	-	-	-	K14834 NOC3; nucleolar complex protein 3	-	KOG2153 Hs20806097 Protein involved in the nuclear export of pre-ribosomes	XP_031026983.1 uncharacterized protein SmJEL517_g00999 [Synchytrium microbalum]	Nucleolar complex protein 3 homolog OS=Pongo abelii OX=9601 GN=NOC3L PE=2 SV=1

A0474	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10398 KIF11, EG5; kinesin family member 11	map04814 Motor proteins	KOG4280[Hs6857804 Kinesin-like protein	RKO97108.1 kinesin-domain-containing protein, partial [Caulochytrium protostelioides]	Kinesin-like protein KIF3A OS=Mus musculus OX=10090 GN=Kif3a PE=1 SV=2
A0475	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0030131(clathrin adaptor complex)	-	K12398 AP3M; AP-3 complex subunit mu	map04142 Lysosome	KOG2740[Hs6912240 Clathrin-associated protein medium chain	GBC09140.1 hypothetical protein RclHR1_08620016 [Rhizophagus clarus]	AP-3 complex subunit mu OS=Dictyostelium discoideum OX=44689 GN=apm3 PE=2 SV=1
A0476	-	-	-	-	-	-	-	-
A0477	-	GO:0016021(integral component of membrane)	-	-	-	-	-	CD82 antigen OS=Mus musculus OX=10090 GN=Cd82 PE=1 SV=1
A0478	GO:0006996(organelle organization)	-	GO:0005515(protein binding)	-	-	-	ORY53414.1 hypothetical protein BCR33DRAFT_760871 [Rhizoclosmatium globosum]	-
A0479	-	-	-	-	-	-	-	-
A0480	GO:0006629(lipid metabolic process)	-	GO:0008081(phosphoric diester hydrolase activity)	-	-	-	-	-
A0481	-	-	-	-	-	KOG3595[Hs22067157 Dyneins, heavy chain	EPZ36260.1 Dynein heavy chain-2 domain-containing protein [Rozella allomycis CSF55]	Dynein axonemal heavy chain 1 OS=Mus musculus OX=10090 GN=Dnah1 PE=1 SV=1
A0482	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0008569(minus-end-directed microtubule motor activity),GO:0005524(ATP binding)	-	-	KOG3595[Hs17864092 Dyneins, heavy chain	XP_016613230.1 hypothetical protein SPPG_00852 [Spizellomyces punctatus DAOM BR117]	Dynein axonemal heavy chain 1 OS=Mus musculus OX=10090 GN=Dnah1 PE=1 SV=1
A0483	-	-	GO:0008168(methyltransferase activity)	-	-	-	XP_024664677.1 hypothetical protein B9G98_02352 [Wickerhamia sorbophila]	Ubiquinone biosynthesis O-methyltransferase OS=Chelativorans sp. (strain BNC1) OX=266779 GN=ubiG PE=3 SV=1
A0484	-	-	GO:0005515(protein binding)	-	-	-	-	-

A0485	GO:0043039(tRNA aminoacylation),GO:0006432(phenylalanyl-tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0000049(tRNA binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0005515(protein binding),GO:0000166(nucleotide binding),GO:0004826(phenylalanine-tRNA ligase activity)	K01889 FARS, pheS; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]	map00970 Aminoacyl-tRNA biosynthesis	KOG2783 At3g58140 Phenylalanyl-tRNA synthetase	CDS03604.1 hypothetical protein LRAMOSA01006 [Lichtheimia ramosa]	Phenylalanine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At3g58140 PE=1 SV=1
A0486	-	-	-	K06688 UBE2C, UBC11; ubiquitin-conjugating enzyme E2 C [EC:2.3.2.23]	map04120 Ubiquitin mediated proteolysis	KOG0421 Hs5902146 Ubiquitin-protein ligase	KAG4101510.1 ubiquitin-conjugating enzyme [Neocallimastix sp. JGI-2020a]	Ubiquitin-conjugating enzyme E2 C OS=Xenopus laevis OX=8355 GN=ube2c PE=1 SV=1
A0487	-	GO:0016020(membrane)	GO:0005509(calcium ion binding)	-	-	KOG3599 Hs7706639 Ca2+-modulated nonselective cation channel polycystin	-	Polycystin-2-like protein 1 OS=Homo sapiens OX=9606 GN=PKD2L1 PE=1 SV=1
A0488	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07889 RAB5C; Ras-related protein Rab-5C	map04144 Endocytosis;map04145 Phagosome;map05132 Salmonella infection;map05146 Amoebiasis;map04014 Ras signaling pathway;map05152 Tuberculosis;map04962 Vasopressin-regulated water reabsorption	KOG0092 Hs4506371 GTPase Rab5/YPT51 and related small G protein superfamily GTPases	RIA93522.1 ras protein [Glomus cerebriforme]	Ras-related protein Rab-5B OS=Gallus gallus OX=9031 GN=RAB5B PE=2 SV=1
A0489	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11254 H4; histone H4	map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG3467 At1g07660 Histone H4	XP_025187259.1 histone-fold-containing protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Histone H4 variant TH011 OS=Triticum aestivum OX=4565 PE=3 SV=2

A0490	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005509(calcium ion binding),GO:0008273(calcium, potassium:sodium antiporter activity)	K13754 SLC24A6, NCKX6; solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	-	KOG1307 Hs9966787 K+-dependent Ca2+/Na+ exchanger NCKX1 and related proteins	EIE76366.1 hypothetical protein RO3G_01070 [Rhizopus delemar RA 99-880]	Sodium/potassium/calcium exchanger 2 OS=Mus musculus OX=10090 GN=Slc24a2 PE=1 SV=1
A0491	GO:0001522(pseudouridine synthesis),GO:0009451(RNA modification)	-	GO:0003723(RNA binding),GO:0009982(pseudouridine synthase activity)	K06176 truD, PUS7; tRNA pseudouridine synthase [EC:5.4.99.27]	-	KOG2339 7295083 Uncharacterized conserved protein	KAG0958815.1 hypothetical protein G6F31_012275 [Rhizopus oryzae]	tRNA pseudouridine synthase D OS=Syntrophotalea carbinolica (strain DSM 2380 / NBRC 103641 / GraBd1) OX=338963 GN=truD PE=3 SV=1
A0492	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0157 At2g45510 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	XP_025174876.1 cytochrome P450 [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Cytochrome P450 86B1 OS=Arabidopsis thaliana OX=3702 GN=CYP86B1 PE=2 SV=1
A0493	-	GO:0016021(integral component of membrane)	-	K12385 NPC1; Niemann-Pick C1 protein	map04142 Lysosome;map04979 Cholesterol metabolism	KOG1933 Hs4557803 Cholesterol transport protein (Niemann-Pick C disease protein)	RIB17063.1 patched family-domain-containing protein [Gigaspora rosea]	NPC intracellular cholesterol transporter 1 OS=Homo sapiens OX=9606 GN=NPC1 PE=1 SV=2
A0494	-	GO:0016021(integral component of membrane)	-	K12385 NPC1; Niemann-Pick C1 protein	map04142 Lysosome;map04979 Cholesterol metabolism	KOG1934 7302178 Predicted membrane protein (patched superfamily)	TPX49954.1 hypothetical protein SeMB42_g02416 [Synchronytrium endobioticum]	Patched domain-containing protein 3 OS=Mus musculus OX=10090 GN=Ptchd3 PE=1 SV=1
A0495	-	GO:0005737(cytoplasm),GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0003723(RNA binding),GO:0003743(translation initiation factor activity),GO:0003676(nucleic acid binding)	K03248 EIF3G; translation initiation factor 3 subunit G	-	KOG0122 Hs4503517 Translation initiation factor 3, subunit g (eIF-3g)	KAF6741058.1 eukaryotic translation initiation factor 3 subunit G-domain-containing protein [Coprinellus angulatus]	Eukaryotic translation initiation factor 3 subunit G OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) OX=341663 GN=tif35 PE=3 SV=1
A0496	GO:0006233(dTDP biosynthetic process)	-	GO:0004798(thymidylate kinase activity),GO:0005524(ATP binding)	K00943 tmk, DTYMK; dTMP kinase [EC:2.7.4.9]	map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3327 Hs2042064 Thymidylate kinase/adenylate kinase	ORE22844.1 putative thymidylate kinase [Rhizopus microsporus]	Thymidylate kinase OS=Homo sapiens OX=9606 GN=DTYMK PE=1 SV=4
A0497	-	-	-	-	-	-	-	-

A0498	GO:000972(aromatic amino acid family metabolic process)	-	GO:0003824(catalytic activity),GO:0004334(fumarylacetoacetase activity)	K01555 FAH, fahA; fumarylacetoacetase [EC:3.7.1.2]	map01120 Microbial metabolism in diverse environments;map00643 Styrene degradation;map00350 Tyrosine metabolism;map01100 Metabolic pathways	KOG2843 Hs4557587 Fumarylacetoacetase	KNE68811.1 fumarylacetoacetase [Allomyces macrogynus ATCC 38327]	Fumarylacetoacetase OS=Bos taurus OX=9913 GN=FAH PE=2 SV=1
A0499	-	-	GO:0016787(hydrolase activity)	-	-	KOG1432 At5g63140 Predicted DNA repair exonuclease SIA1	KAG2175084.1 hypothetical protein INT44_007562 [Umbelopsis vinacea]	Probable inactive purple acid phosphatase 29 OS=Arabidopsis thaliana OX=3702 GN=PAP29 PE=2 SV=1
A0500	-	-	GO:0005515(protein binding)	K26797 GORASP, GRASP65_55; golgi reassembly-stacking protein	map04140 Autophagy - animal	KOG3834 CE25278 Golgi reassembly stacking protein GRASP65, contains PDZ domain	KAF9359572.1 hypothetical protein BGX26_012016 [Mortierella sp. AD094]	Golgi reassembly-stacking protein 1 OS=Homo sapiens OX=9606 GN=GORASP1 PE=1 SV=3
A0501	-	-	-	-	-	-	-	-
A0502	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0503	GO:0015937(coenzyme A biosynthetic process)	-	GO:0004140(dephospho-CoA kinase activity),GO:0005524(ATP binding)	K00859 coaE; dephospho-CoA kinase [EC:2.7.1.24]	map00770 Pantothenate and CoA biosynthesis;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG3220 Hs21489977_2 Similar to bacterial dephospho-CoA kinase	ORX41384.1 dephospho-CoA kinase [Piromyces finnis]	Dephospho-CoA kinase OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) OX=243231 GN=coaE PE=3 SV=1
A0504	GO:0043161(proteasome-mediated ubiquitin-dependent protein catabolic process), GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0019774(proteasome core complex, beta-subunit complex), GO:0005839(proteasome core complex)	-	K02735 PSMB3; 20S proteasome subunit beta 3 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0180 At1g21720 20S proteasome, regulatory subunit beta type PSMB3/PUP3	KAF7747676.1 Proteasome subunit beta type-3 [Entomophthora muscae]	Proteasome subunit beta type-3 OS=Dictyostelium discoideum OX=44689 GN=psmB3 PE=3 SV=1
A0505	-	-	-	-	-	-	-	-
A0506	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1235 At5g24810 Predicted unusual protein kinase	ORY42369.1 ABC1-domain-containing protein [Rhizoclostium globosum]	AarF domain-containing protein kinase 1 OS=Gallus gallus OX=9031 GN=ADCK1 PE=2 SV=1

A0507	GO:0006351(transcription, DNA-templated),GO:0006352(DNA-templated transcription, initiation)	-	-	K03022 RPC8, POLR3H; DNA-directed RNA polymerase III subunit RPC8	map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway	KOG3297 Hs2068810 DNA-directed RNA polymerase subunit E'	ORX55784.1 hypothetical protein DM01DRAFT_1321129 [Hesseltinella vesiculosa]	DNA-directed RNA polymerase III subunit RPC8 OS=Homo sapiens OX=9606 GN=POLR3H PE=1 SV=1
A0508	-	-	-	-	-	-	-	-
A0509	-	-	GO:0016787(hydrolase activity)	-	-	KOG0648 Hs20149583 Predicted NUDIX hydrolase FGF-2 and related proteins	-	Nucleoside diphosphate-linked moiety X motif 6 OS=Homo sapiens OX=9606 GN=NUDT6 PE=1 SV=2
A0510	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239 At1g73860 Kinesin (KAR3 subfamily)	RKO98564.1 hypothetical protein CXG81DRAFT_6275, partial [Caulochytrium protostelioides]	Kinesin-like protein KIN-14P OS=Arabidopsis thaliana OX=3702 GN=KIN14P PE=2 SV=1
A0511	GO:0006415(translational termination)	GO:0005737(cytoplasm)	GO:0003747(translation release factor activity),GO:0016149(translation release factor activity, codon specific)	-	-	KOG2726 At1g56350 Mitochondrial polypeptide chain release factor	TPX57180.1 hypothetical protein SpCBS45565_g08254 [Spizellomyces sp. 'palustris']	Peptide chain release factor 2 OS=Kosmotoga olearia (strain ATCC BAA-1733 / DSM 21960 / TBF 19.5.1) OX=521045 GN=prfB PE=3 SV=1
A0512	GO:0006979(response to oxidative stress)	-	GO:0004601(peroxidase activity),GO:0020037(heme binding)	-	-	-	PHH91479.1 hypothetical protein CDD83_262 [Cordyceps sp. RAO-2017]	Inosine/xanthosine triphosphatase OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) OX=243277 GN=VC_0702 PE=1 SV=1
A0513	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K20872 NEK2; serine/threonine-protein kinase Nek2 [EC:2.7.11.1]	-	KOG0591 Hs19424132 NIMA (never in mitosis)-related G2-specific serine/threonine protein kinase	RKP02987.1 hypothetical protein CXG81DRAFT_4810, partial [Caulochytrium protostelioides]	Serine/threonine-protein kinase Nek7 OS=Homo sapiens OX=9606 GN=NEK7 PE=1 SV=1
A0514	-	-	-	-	-	KOG2502 CE29091 Tub family proteins	KAG0166070.1 hypothetical protein DFQ30_007627 [Apophysomyces sp. BC1015]	Tubby protein homolog 1 OS=Caenorhabditis elegans OX=6239 GN=tub-1 PE=1 SV=3
A0515	-	-	-	-	-	-	-	-
A0516	-	-	-	-	-	-	-	Protein ENHANCED DISEASE RESISTANCE 2-like OS=Arabidopsis
A0517	GO:0007018(microtubule-based movement)	-	GO:0005515(protein binding),GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10392 KIF1; kinesin family member 1	map04814 Motor proteins	KOG0245 CE02031 Kinesin-like protein	KAF7330877.1 Kinesin-like protein [Mycena venus]	Kinesin-like protein unc-104 OS=Aedes aegypti OX=7159 GN=unc-104 PE=3 SV=1
A0518	-	-	-	-	-	-	-	-

A0519	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10398 KIF11, EG5; kinesin family member 11	map04814 Motor proteins	KOG4280 Hs6857804 Kinesin-like protein	KAG4099845.1 kinesin-domain-containing protein [Neocallimastix sp. JGI-2020a]	Kinesin-like protein KIF3A OS=Mus musculus OX=10090 GN=Kif3a PE=1 SV=2
A0520	-	-	-	-	-	-	ORY42201.1 DUF455-domain-containing protein [Rhizoclostium globosum]	Uncharacterized protein HI_0077 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_0077 PE=4 SV=1
A0521	GO:0006508(proteolysis)	-	GO:0008236(serine-type peptidase activity),GO:0004252(serine-type endopeptidase activity)	-	-	KOG2237 7297690 Predicted serine protease	KXS12888.1 putative exported oligopeptidase [Gonapodya prolifera JEL478]	Uncharacterized peptidase y4nA OS=Sinorhizobium fredii (strain NBRC 101917 / NGR234) OX=394 GN=NGR_a02410 PE=3 SV=1
A0522	-	-	-	K22149 SID1; mevalonyl-CoA ligase	-	KOG1179 Hs4826722 Very long-chain acyl-CoA synthetase/fatty acid transporter	CEJ56598.1 hypothetical protein PMG11_02800 [Penicillium brasilianum]	Acyl-CoA ligase SID4 OS=Ajellomyces capsulatus OX=5037 GN=SID4 PE=2 SV=1
A0523	-	-	-	-	-	-	-	-
A0524	-	-	GO:0005515(protein binding)	-	-	-	KAG0956339.1 hypothetical protein G6F31_012650 [Rhizopus oryzae]	NHL repeat-containing protein 2 OS=Gallus gallus OX=9031 GN=NHLRC2 PE=2 SV=1
A0525	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0526	-	-	GO:0016787(hydrolase activity)	-	-	-	RHZ89985.1 hypothetical protein Glove_9g353 [Diversispora epigaea]	Acyl-protein thioesterase 1 OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=B2J23.070 PE=3 SV=2
A0527	-	-	-	-	-	-	-	-
A0528	GO:0006364(rRNA processing),GO:0006396(rRNA processing)	-	GO:0003676(nucleic acid binding),GO:0005515(protein binding)	K14792 RRP5, PDCD11; rRNA biogenesis protein RRP5	-	KOG1070 YMR229c rRNA processing protein Rrp5	KAG0047226.1 rRNA biogenesis protein rrp5 [Gryganskiella cystojenkini]	rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP5 PE=1 SV=1
A0529	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	TPX62680.1 hypothetical protein PhCBS80983_g00365 [Powellomyces hirtus]	-
A0530	GO:0005975(carbohydrate metabolic process)	-	-	-	-	-	-	-
A0531	-	-	-	-	-	-	-	-

A0532	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K22399 TRIP13; pachytene checkpoint protein 2	map04110 Cell cycle	KOG0744 At4g24710 AAA+ -type ATPase	ORX98587.1 pachytene checkpoint protein 2 [Basidiobolus meristosporus CBS 931.73]	Pachytene checkpoint protein 2 homolog OS=Oryza sativa subsp. indica OX=39946 GN=OsI_16324 PE=3 SV=2
A0533	-	-	GO:0016491(oxidoreductase activity)	K06123 AYR1; 1-acylglycerone phosphate reductase [EC:1.1.1.101]	map00564 Glycerophospholipid metabolism;map00565 Ether lipid metabolism;map01100 Metabolic pathways	KOG1610 Hs19743808 Corticosteroid 11-beta-dehydrogenase and related short chain-type dehydrogenases	KAF9126507.1 Retinol dehydrogenase 5 [Mortierella sp. 14UC]	17-beta-hydroxysteroid dehydrogenase type 6 OS=Bos taurus OX=9913 GN=HSD17B6 PE=2 SV=1
A0534	-	GO:0016459(myosin complex)	GO:0005515(protein binding),GO:0003774(motor activity),GO:0005524(ATP binding)	-	-	KOG0160 At5g43900 Myosin class V heavy chain	GAN04656.1 conserved hypothetical protein [Mucor ambiguus]	Myosin-17 OS=Arabidopsis thaliana OX=3702 GN=XI-K PE=1 SV=2
A0535	-	-	GO:0005515(protein binding)	-	-	KOG0503 7290456 Asparaginase	KAF2871447.1 ankyrin repeat-containing domain protein [Massariosphaeria phaeospora]	Ankyrin repeat domain-containing protein 55 OS=Mus musculus OX=10090 GN=Ankrd55 PE=1 SV=2
A0536	-	-	-	K20352 TMED10, ERV25; p24 family protein delta-1	map05130 Pathogenic Escherichia coli infection	KOG1691 CE05883 emp24/gp25 L/p24 family of membrane trafficking proteins	KXS18126.1 endoplasmic reticulum vesicle protein 25, partial [Gonapodya prolifera JEL478]	Endoplasmic reticulum vesicle protein 25 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / BCRC 21394 / JCM 1990 / NBRC 0083 / IGC 2968) OX=284592 GN=ERV25 PE=3 SV=2
A0537	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08838 STK24_25_MST4; serine/threonine-protein kinase 24/25/MST4 [EC:2.7.11.1]	-	KOG0582 Hs7019543 Ste20-like serine/threonine protein kinase	XP_021884729.1 kinase-like domain-containing protein [Lobosporangium transversale]	Serine/threonine-protein kinase OSR1 OS=Rattus norvegicus OX=10116 GN=Oxsr1 PE=1 SV=1
A0538	GO:0006886(intracellular protein transport),GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport),GO:0090114(COPII-coated vesicle budding)	GO:0030127(COPII vesicle coat)	GO:0008270(zinc ion binding)	K14006 SEC23; protein transport protein SEC23	map04141 Protein processing in endoplasmic reticulum	KOG1986 Hs5454042 Vesicle coat complex COPII, subunit SEC23	KAG0021695.1 GTPase-activating protein S23 [Podila clonocystis]	Protein transport protein SEC23 OS=Cryptococcus neoformans var. neoformans serotype D (strain B-3501A) OX=283643 GN=SEC23 PE=3 SV=1

A0539	-	-	-	K11353 NDUFA13; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 13	map05014 Amyotrophic lateral sclerosis;map054 15 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04 714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map050 22 Pathways of neurodegenerati on - multiple diseases;map052 08 Chemical carcinogenesis - reactive oxygen species;map049 32 Non- alcoholic fatty liver disease;map050	KOG3300 At2 g33220 NADH:ubiqui none oxidoreducta se, B16.6 subunit/cell death- regulatory protein	TBU33119.1 GRIM-19 [Dichomitus squalens]	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-B OS=Arabidopsis thaliana OX=3702 GN=At2g33220 PE=2 SV=1
A0540	GO:0033567(DNA replication, Okazaki fragment processing)	-	GO:0003677(DNA binding);GO:0003824(catalytic activity);GO:0017108(5'-flap endonuclease activity)	-	-	-	KAG0773360.1 hypothetical protein G6F22_014938 [Rhizopus oryzae]	DNA polymerase I, thermostable OS=Thermus thermophilus OX=274 GN=polA PE=1 SV=1
A0541	GO:0006913(nucleocytoplasmic transport)	-	-	-	-	-	XP_007004979.1 uncharacterized protein TREMEDRAFT_39381 [Tremella mesenterica DSM 1558]	Nuclear transport factor 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ntf2 PE=3 SV=2
A0542	-	-	-	-	-	-	OA139082.1 hypothetical protein BDEG_22956 [Batrachochytrium dendrobatidis JEL423]	-
A0543	-	-	-	-	-	-	-	-
A0544	GO:0006479(protein methylation)	-	GO:0008276(protein methyltransferase activity)	K21804 METTL21A; protein N-lysine methyltransferase METTL21A [EC:2.1.1.-]	-	KOG2793 CE26910 Putative N2,N2-dimethylguanosine tRNA methyltransferase	GAO51010.1 hypothetical protein G7K_5122-t1 [Saitoella complicata NRRL Y-17804]	Methyltransferase-like protein 22 OS=Mus musculus OX=10090 GN=Mettl22 PE=2 SV=1
A0545	-	-	-	-	-	-	-	-
A0546	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity);GO:0030170(pyridoxal phosphate binding)	K00654 SPT; serine palmitoyltransferase [EC:2.3.1.50]	map04071. Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map04138 Autophagy - yeast;map01100 Metabolic pathways	KOG1357 At3g48780 Serine palmitoyltransferase	KAF0427522.1 Serine palmitoyltransferase [Gigaspora margarita]	Long chain base biosynthesis protein 2a OS=Arabidopsis thaliana OX=3702 GN=LCB2a PE=1 SV=1

A0547	GO:0009058(biosynthetic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0003824(catalytic activity)	K00654 SPT; serine palmitoyltransferase [EC:2.3.1.50]	map04071 Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map04138 Autophagy - yeast;map01100 Metabolic pathways	KOG1357 At3g48780 Serine palmitoyltransferase	KAF0427522.1 Serine palmitoyltransferase [Gigaspora margarita]	Long chain base biosynthesis protein 2a OS=Arabidopsis thaliana OX=3702 GN=LCB2a PE=1 SV=1
A0548	-	-	-	-	-	-	-	-
A0549	-	-	-	K06630 YWHAE; 14-3-3 protein epsilon	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04722 Neurotrophin signaling pathway;map04621 NOD-like receptor signaling pathway;map05203 Viral carcinogenesis; map04151 PI3K-Akt signaling pathway;map04011 MAPK signaling pathway - yeast;map04114 Oocyte meiosis;map04110 Cell cycle;map05160 Hepatitis C	-	ORX70169.1 14-3-3 family protein epsilon [Linderina pennisporea]	Checkpoint signal transducer rad24 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rad24 PE=1 SV=2
A0550	GO:0006368(transcription elongation from RNA polymerase II promoter),GO:0016570(histone modification)	GO:0016593(Cdc73/Paf1 complex)	-	-	-	KOG2478 Hs9506583 Putative RNA polymerase II regulator	OON05141.1 hypothetical protein BSLG_04911 [Batrachochytrium salamandrivorans]	Protein PAF1 homolog OS=Arabidopsis thaliana OX=3702 GN=VIP2 PE=1 SV=1
A0551	GO:0000469(cleavage involved in rRNA processing)	-	-	K14795 RRP36; ribosomal RNA-processing protein 36	-	-	PQE11952.1 hypothetical protein CJF31_00000095 [Rutstroemia sp. NJR-2017a BVV2]	rRNA biogenesis protein RRP36 OS=Pyricularia oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) OX=242507 GN=RRP36 PE=3 SV=1
A0552	-	-	GO:0005515(protein binding)	-	-	-	RKO93747.1 hypothetical protein BDK51DRAFT_29285 [Blyttomyces helicus]	-
A0553	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome),GO:0008097(5S rRNA binding)	-	-	-	-	Large ribosomal subunit protein bL25 OS=Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) OX=246200 GN=rpLY PE=3 SV=1

A0554	-	-	GO:0003924(GTase activity),GO:0005525(GTP binding)	K03234 EF2; elongation factor 2	map04152 AMPK signaling pathway;map04921 Oxytocin signaling pathway	KOG0469 CE15900 Elongation factor 2	XP_007860345.1 P-loop containing nucleoside triphosphate hydrolase protein [Gloeophyllum trabeum ATCC 11539]	Elongation factor 2 OS=Caenorhabditis elegans OX=6239 GN=eef-2 PE=1 SV=4
A0555	-	-	-	-	-	-	-	-
A0556	GO:0008643(carbohydrate transport)	GO:0016021(integral component of membrane)	GO:0015293(symporter activity)	-	-	-	-	Inner membrane symporter YicJ OS=Escherichia coli (strain K12) OX=83333 GN=yicJ PE=1 SV=2
A0557	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0003724(RNA helicase activity)	K11594 DDX3X, bel; ATP-dependent RNA helicase DDX3X [EC:3.6.4.13]	map04622 RIG-I-like receptor signaling pathway;map05203 Viral carcinogenesis; map05161 Hepatitis B	KOG0335 At2g42520 ATP-dependent RNA helicase	XP_037137574.1 uncharacterized protein HG536_0A07140 [Torulaspora globosa]	DEAD-box ATP-dependent RNA helicase 37 OS=Arabidopsis thaliana OX=3702 GN=RH37 PE=2 SV=2
A0558	-	-	GO:0008483(transaminase activity),GO:0030170(pyridoxal phosphate binding),GO:0004587(ornithine-oxo-acid transaminase activity),GO:0003824(catalytic activity)	K00819 rocD; OAT; ornithine--oxo-acid transaminase [EC:2.6.1.13]	map01110 Biosynthesis of secondary metabolites;map00330 Arginine and proline metabolism;map01100 Metabolic pathways	KOG1402 Hs4557809 Ornithine aminotransferase	CDH55574.1 ornithine aminotransferase [Lichtheimia corymbifera JMRc:FSU:9682]	Ornithine aminotransferase, mitochondrial OS=Bos taurus OX=9913 GN=OAT PE=2 SV=1
A0559	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015297(antiporter activity),GO:0042910(xenobiotic transmembrane transporter activity)	K03327 TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family	-	KOG1347 At5g38030 Uncharacterized membrane protein, predicted efflux pump	XP_013019562.1 MatE family transporter [Schizosaccharomyces octosporus yFS286]	Protein DETOXIFICATION 30 OS=Arabidopsis thaliana OX=3702 GN=DTX30 PE=2 SV=1
A0560	-	-	GO:0070569(uridylyltransferase activity)	K00972 UAP1; UDP-N-acetylglucosamine/UDP-N-acetylgalactosamine diphosphorylase [EC:2.7.7.23 2.7.7.83]	map01250 Biosynthesis of nucleotide sugars;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG2388 Hs19923739 UDP-N-acetylglucosamine pyrophosphorylase	VDC05798.1 unnamed protein product [Peniophora sp. CBMAI 1063]	UDP-N-acetylhexosamine pyrophosphorylase OS=Mus musculus OX=10090 GN=Uap1 PE=1 SV=1
A0561	-	-	GO:0005515(protein binding)	K05841 E2.4.1.173; sterol 3beta-glucosyltransferase [EC:2.4.1.173]	-	-	KAF8270552.1 hypothetical protein E194DRAFT_1570923 [Lactarius quietus]	Sterol 3-beta-glucosyltransferase OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) OX=341663 GN=atg26 PE=3 SV=1
A0562	-	-	GO:0005515(protein binding)	-	-	-	-	-

A0563	GO:0006413(translation initiation)	-	GO:0003743(translation initiation factor activity)	K24272 DENR, TMA22; density-regulated protein	-	KOG3239 At5g11900 Density-regulated protein related to translation initiation factor 1 (eIF-1/SUI1)	PSR99377.1 translation initiation factor SUI1 [Coniella lustricola]	Translation machinery-associated protein 22 OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=tma-22 PE=3 SV=1
A0564	GO:0008033(tRNA processing),GO:0032259(methylation),GO:0001510(RNA methylation)	-	GO:0008175(tRNA methyltransferase activity),GO:0008168(methyltransferase activity)	K14864 FTSJ1, TRM7; tRNA (cytidine32/guanosine34-2'-O)-methyltransferase [EC:2.1.1.205]	-	KOG1099 Hs7110661 SAM-dependent methyltransferase/cell division protein FtsJ	TPX66942.1 hypothetical protein SpCBS45565_g04122 [Spizellomyces sp. 'palustris']	tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase OS=Homo sapiens OX=9606 GN=FTSJ1 PE=1 SV=2
A0565	-	-	-	-	-	-	-	-
A0566	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs4557511 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	XP_024666951.1 Calcium/calmodulin-dependent protein kinase [Wickerhamiella sorbophila]	Death-associated protein kinase 3 OS=Homo sapiens OX=9606 GN=DAPK3 PE=1 SV=1
A0567	-	-	-	-	-	-	ORY39534.1 hypothetical protein BCR33DRAFT_853320, partial [Rhizoclostium globosum]	Hydrocephalus-inducing protein homolog OS=Homo sapiens OX=9606 GN=HYDIN PE=1 SV=3
A0568	-	-	-	-	-	-	CEP17780.1 hypothetical protein [Parasitella parasitica]	-
A0569	-	-	GO:0016788(hydrolase activity, acting on ester bonds)	-	-	-	ORX73691.1 hypothetical protein DL89DRAFT_263710 [Linderina pennisporea]	N-alpha-acetyl-L-2,4-diaminobutyric acid deacetylase OS=Halomonas elongata (strain ATCC 33173 / DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9) OX=768066 GN=doeB PE=1 SV=1
A0570	GO:0006397(mRNA processing)	-	-	-	-	-	TPX71758.1 hypothetical protein SpCBS45565_g00811 [Spizellomyces sp. 'palustris']	-
A0571	GO:0006099(tricarboxylic acid cycle),GO:0015977(carbon fixation)	-	GO:0008964(phosphoenolpyruvate carboxylase activity),GO:0003824(catalytic activity)	-	-	-	TPX68375.1 phosphoenolpyruvate carboxylase [Spizellomyces sp. 'palustris']	Phosphoenolpyruvate carboxylase OS=Pectobacterium carotovorum subsp. carotovorum (strain PC1) OX=561230 GN=ppc PE=3 SV=1

A0572	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	-	-	KOG0032 CE25046 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORY52947.1 Pkinase-domain-containing protein [Rhizoclostium globosum]	Calcium/calmodulin-dependent protein kinase type 1 OS=Caenorhabditis elegans OX=6239 GN=cmk-1 PE=1 SV=1
A0573	-	-	-	-	-	-	-	Protein polyglycolase TTL10 OS=Rattus norvegicus OX=10116
A0574	GO:0009062(fatty acid catabolic process)	-	GO:0008670(2,4-dienoyl-CoA reductase (NADPH) activity)	K13237 DEC2, SPS19; 2,4-dienoyl-CoA reductase [(3E)-enoyl-CoA-producing], peroxisomal [EC:1.3.1.124]	map04146 Peroxisome	KOG0725 Hs10190704 Reductases with broad range of substrate specificities	RCH89820.1 hypothetical protein CU097_00961.1 [Rhizopus azygosporus]	Peroxisomal 2,4-dienoyl-CoA reductase [(3E)-enoyl-CoA-producing] OS=Arabidopsis thaliana OX=3702 GN=At3g12800 PE=2 SV=1
A0575	-	-	GO:0005515(protein binding)	-	-	KOG0440 At5g45550 Cell cycle-associated protein Mob1-1	KXS17134.1 mps one binder kinase activator-like 1 protein [Gonapodya prolifera JEL478]	MOB kinase activator-like 1A OS=Arabidopsis thaliana OX=3702 GN=MOB1A PE=1 SV=1
A0576	-	-	GO:0017056(structural constituent of nuclear pore)	-	-	-	PHH63841.1 hypothetical protein CDD81_5398 [Ophiocordyceps australis]	Acyl-protein thioesterase 1 OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=FGRAMPH1_01T20223 PE=3 SV=1
A0577	-	-	-	-	-	-	-	-
A0578	GO:0019408(dolichol biosynthetic process)	GO:1904423(dehydrodolichol diphosphate synthase complex)	GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups)	K19177 NUS1; dehydrodolichol diphosphate synthase complex subunit NUS1 [EC:2.5.1.87]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis	-	KAF1347021.1 Decaprenyl diphosphate synthase-like protein [Delphinella strobiligena]	-
A0579	-	-	-	-	-	-	-	-
A0580	-	-	GO:0016972(thiol oxidase activity),GO:0016971(flavin-linked sulfhydryl oxidase activity)	-	-	KOG1731 Hs13325075 FAD-dependent sulfhydryl oxidase/quiescin and related proteins	-	Sulfhydryl oxidase 1 OS=Homo sapiens OX=9606 GN=QSOX1 PE=1 SV=3
A0581	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 At5g47730 Phosphatidylinositol transfer protein SEC14 and related proteins	XP_018294266.1 hypothetical protein PHYBLDRAFT_143210 [Phycomyces blakesleeana NRRL 1555(-)]	CRAL-TRIO domain-containing protein T23G5.2 OS=Caenorhabditis elegans OX=6239 GN=T23G5.2 PE=4 SV=3
A0582	-	-	-	-	-	-	-	-
A0583	-	-	GO:0005515(protein binding)	-	-	-	-	-

A0584	GO:0006474(N-terminal protein amino acid acetylation)	GO:0031415(NatA complex)	GO:0016407(acetyltransferase activity),GO:0004596(peptide alpha-N-acetyltransferase activity)	K20791 NAA10_11, ARD1_2; N-alpha-acetyltransferase 10/11 [EC:2.3.1.255]	-	KOG3235 At5g13780 Subunit of the major N-alpha-acetyltransferase	POY73573.1 GNAT family acetyltransferase [Rhodotorula taiwanensis]	N-terminal acetyltransferase A complex catalytic subunit NAA10 OS=Arabidopsis thaliana OX=3702 GN=NAA10 PE=1 SV=1
A0585	-	-	-	-	-	-	-	-
A0586	GO:0006913(nucleocytoplasmic transport)	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07936 RAN; GTP-binding nuclear protein Ran	map03250 Viral life cycle - HIV-1;map03013 Nucleocytoplasmic transport;map03008 Ribosome biogenesis in eukaryotes;map05166 Human T-cell leukemia virus 1 infection	KOG0096 7292609 GTPase Ran/TC4/GSP1 (nuclear protein transport pathway), small G protein superfamily	RUO96643.1 GTP-binding nuclear protein GSP1/Ran, partial [Jimgerdennia flammicorona]	GTP-binding nuclear protein GSP1/Ran OS=Candida albicans (strain WO-1) OX=294748 GN=GSP1 PE=3 SV=2
A0587	GO:0043631(RNA polyadenylation)	GO:0031499(TRAMP complex)	GO:0003723(RNA binding),GO:0004652(polynucleotide adenylyltransferase activity),GO:0003676(nucleic acid binding)	K03514 PAPD5_7, TRF4; non-canonical poly(A) RNA polymerase PAPD5/7 [EC:2.7.7.19]	map03018 RNA degradation	KOG1906 At5g53770 DNA polymerase sigma	TPX63764.1 hypothetical protein SpCBS45565_g06412 [Spizellomyces sp. 'palustris']	Terminal nucleotidyltransferase 4B OS=Homo sapiens OX=9606 GN=TENT4B PE=1 SV=2
A0588	-	-	-	-	-	-	-	-
A0589	GO:0006468(protein phosphorylation),GO:0009058(biosynthetic process)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	K14264 BNA3; kynurenine aminotransferase [EC:2.6.1.7]	map00380 Tryptophan metabolism;map01100 Metabolic pathways	KOG0257 7299520 Kynurenine aminotransferase, glutamine transaminase K	KAG0280132.1 hypothetical protein BGZ95_011207 [Linnemannia exigua]	Kynurenine--oxoglutarate transaminase OS=Dictyostelium discoideum OX=44689 GN=ccbl PE=3 SV=1
A0590	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0592	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0593	-	-	-	-	-	KOG0725 At3g03980 Reductases with broad range of substrate specificities	XP_024664204.1 Short chain dehydrogenase mdpC [Wickerhamia sorbophila]	Short-chain type dehydrogenase/reductase OS=Picea abies OX=3329 PE=2 SV=1
A0594	-	-	-	-	-	-	-	Uncharacterized protein PP_0002 OS=Pseudomonas putida (strain ATCC 47054 / DSM 6125 / CFBP 8728 / NCIMB 11950 / KT2440) OX=160488
A0595	-	-	-	K10704 UBE2V; ubiquitin-conjugating enzyme E2 variant	map05131 Shigellosis;map04624 Toll and lmd signaling pathway	KOG0896 YG_L087c Ubiquitin-conjugating enzyme E2	KAG0151669.1 hypothetical protein CROQUODRAFT_86283 [Cronartium quercuum f. sp. fusiforme G11]	Probable ubiquitin-conjugating enzyme E2 variant OS=Dictyostelium discoideum OX=44689 GN=ube2v PE=3 SV=1
A0596	-	-	-	-	-	-	-	-

A0597	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs9966875 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	XP_018984791.1 uncharacterized protein BABINDRAFT_161859 [Babjeviella inositovora NRRL Y-12698]	Calcium and calcium/calmodulin-dependent serine/threonine-protein kinase OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CCAMK PE=2 SV=1
A0598	-	-	-	K15117 SLC25A34_35, OAC1; solute carrier family 25, member 34/35	-	KOG0759 At2g22500 Mitochondrial oxoglutarate/malate carrier proteins	KNE67875.1 hypothetical protein AMAG_12592 [Allomyces macrogynus ATCC 38327]	Probable mitochondrial 2-oxoglutarate/malate carrier protein OS= <i>Dictyostelium discoideum</i> OX=44689 GN=ucpC PE=3 SV=1
A0599	-	-	GO:0005515(protein binding),GO:0004842(ubiquitin-protein transferase activity)	-	-	-	KZZ92650.1 HECT domain-containing protein [Ascosphaera apis ARSEF 7405]	E3 ubiquitin-protein ligase ptr1 OS= <i>Schizosaccharomyces pombe</i> (strain 972 / ATCC 24843) OX=284812 GN=ptr1 PE=1 SV=1
A0600	-	-	-	-	-	-	-	-
A0601	-	-	GO:0005515(protein binding)	K17821 RNF165; E3 ubiquitin-protein ligase RNF165 [EC:2.3.2.27]	-	KOG0800 Hs20485138 FOG: Predicted E3 ubiquitin ligase	KAF2738158.1 hypothetical protein EJ04DRAFT_71245 [Polyposphaeria fusca]	E3 ubiquitin-protein ligase RNF181 OS= <i>Xenopus tropicalis</i> OX=8364 GN=rnf181 PE=2 SV=1
A0602	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K14536 RIA1; ribosome assembly protein 1 [EC:3.6.5.-]	map03008 Ribosome biogenesis in eukaryotes	KOG0467 At3g22980 Translation elongation factor 2/ribosome biogenesis protein RIA1 and related proteins	OZJ03843.1 hypothetical protein BZG36_04304 [Bifiguratus adelaidae]	Elongation factor-like GTPase 1 OS= <i>Homo sapiens</i> OX=9606 GN=EFL1 PE=1 SV=2
A0603	-	-	-	-	-	KOG2605 At5g03330 OTU (ovarian tumor)-like cysteine protease	SPO41243.1 uncharacterized protein PSFLO_06725 [Anthracoystis flocculosa]	OVARIAN TUMOR DOMAIN-containing deubiquitinating enzyme 10 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=OTU10 PE=1 SV=1
A0604	GO:0032006(regulation of TOR signaling)	-	-	-	-	-	-	-
A0605	-	-	-	K14002 SCJ1; DnaJ-related protein SCJ1	map04141 Protein processing in endoplasmic reticulum	KOG0715 At1g80030 Molecular chaperone (DnaJ superfamily)	OCH95395.1 DnaJ-domain-containing protein [Obba rivulosa]	Chaperone protein DnaJ OS= <i>Mycoplasmoides gallisepticum</i> (strain R(low / passage 15 / clone 2)) OX=710127 GN=dnaJ PE=3 SV=2
A0606	-	-	-	-	-	-	ORZ35457.1 hypothetical protein BCR44DRAFT_1499651 [Catenaria anguillulae PL171]	Protein psiC OS= <i>Dictyostelium discoideum</i> OX=44689 GN=psiC PE=3 SV=1

A0607	-	-	-	-	-	KOG3589 Hs M4506515 G protein signaling regulators	ORX96773.1 hypothetical protein K493DRAFT_ 370509 [Basidiobolus meristosporu s CBS 931.73]	Regulator of G-protein signaling 1 OS=Mus musculus OX=10090 GN=Rgs1 PE=2 SV=2
A0608	-	-	-	-	-	-	XP_01660408 8.1 hypothetical protein, variant [Spizellomyces punctatus DAOM BR117]	UPF0652 protein C22H10.08 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC22H10.08 PE=3 SV=1
A0609	GO:00229 00(electro n transport chain)	-	GO:0004174(ele ctron- transferring- flavoprotein dehydrogenase activity)	K00311 ETFDH; electron- transferring- flavoprotein dehydrogena se [EC:1.5.5.1]	-	KOG2415 730 3826 Electron transfer flavoprotein ubiquinone oxidoreducta se	KAF9969121. 1 hypothetical protein BGZ73_00868 2 [Actinomortie rella ambigua]	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Mus musculus OX=10090 GN=Etfdh PE=1 SV=1
A0610	-	-	-	-	-	-	-	-
A0611	-	GO:00160 21(integra l compone nt of membra ne)	-	K13348 MPV17; protein Mpv17	map04146 Peroxisome	KOG1944 Hs8 923892 Peroxisomal membrane protein MPV17 and related proteins	XP_00804039 4.1 hypothetical protein TRAVEDRAFT_ 150763 [Trametes versicolor FP- 101664 SS1]	Mpv17-like protein OS=Mus musculus OX=10090 GN=Mpv17I PE=1 SV=2
A0612	-	-	-	-	-	-	-	-
A0613	-	GO:00712 03(WASH complex), GO:00160 20(membr ane)	GO:0140359(AB C-type transporter activity),GO:000 5524(ATP binding)	K05681 ABCG2, CD338; ATP- binding cassette, subfamily G (WHITE), member 2	map01523 Antifolate resistance;map0 4976 Bile secretion;map02 010 ABC transporters	KOG3666 Hs7 661988 Uncharacteriz ed conserved protein	KAG2228680. 1 hypothetical protein INT48_00482 3 [Thamnidium elegans]	WASH complex subunit 5 OS=Dictyostelium discoideum OX=44689 GN=washc5 PE=1 SV=1
A0614	GO:00092 64(deoxyri bonucleo tide catabolic process)	GO:00057 37(cytopl asm)	GO:0004139(de oxyribose- phosphate aldolase activity),GO:001 6829(lyase activity)	-	-	KOG3981 730 3455 Deoxyribose- phosphate aldolase	KAF9778701. 1 deoxyribose- phosphate aldolase [Thelephora terrestris]	Deoxyribose-phosphate aldolase OS=Geobacillus sp. (strain WCH70) OX=471223 GN=deoC PE=3 SV=1
A0615	GO:00065 08(proteo lysis),GO:0 007155(ce ll adhesion)	GO:00160 20(membr ane)	GO:0004222(me talloendopeptid ase activity),GO:000 8237(metallope ptidase activity)	-	-	-	-	-
A0616	-	-	-	-	-	-	-	-
A0617	GO:00071 65(signal transducti on)	-	GO:0005515(pro tein binding)	-	-	-	PCH43318.1 WD40 repeat-like protein, partial [Wolfiporia cocos MD- 104 SS10]	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A0618	GO:00071 31(recipro cal meiotic recombination)	-	GO:0003690(do uble-stranded DNA binding)	-	-	KOG3433 Hs1 4149769 Protein involved in meiotic recombination/ predicted coiled-coil protein	KAF8070154. 1 meiotic nuclear division protein 1 [Lyophyllum atratum]	Meiotic nuclear division protein 1 homolog OS=Xenopus laevis OX=8355 GN=mnd1 PE=2 SV=1

A0619	GO:0030071(regulation of mitotic metaphase/anaphase transition)	GO:0005680(anaphase-promoting complex)	GO:0005515(protein binding)	K03355 APC8, CDC23; anaphase-promoting complex subunit 8	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG1155 At3g48150 Anaphase-promoting complex (APC), Cdc23 subunit	KAF9965046.1 Anaphase-promoting complex subunit 23 [Mortierella alpina]	Anaphase-promoting complex subunit 8 OS=Arabidopsis thaliana OX=3702 GN=APC8 PE=1 SV=1
A0620	-	-	-	-	-	-	RCH89104.1 hypothetical protein CU097_009207 [Rhizopus azygosporus]	-
A0621	-	-	GO:0051879(Hsp90 protein binding)	-	-	-	CDS14405.1 hypothetical protein LRAMOSA6574 [Lichtheimia ramosa]	Protein wos2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=wos2 PE=2 SV=1
A0622	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity),GO:0005515(protein binding)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	KNE72038.1 hypothetical protein AMAG_15981 [Allomyces macrogynus ATCC 38327]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A0623	-	-	GO:0005200(structural constituent of cytoskeleton)	-	-	-	-	-
A0624	-	-	-	K15117 SLC25A34_35, OAC1; solute carrier family 25, member 34/35	-	KOG0755 YKL120w Mitochondrial oxaloacetate carrier protein	KAG0373359.1 Mitochondrial oxaloacetate carrier protein [Mortierella sp. AD032]	Mitochondrial substrate carrier family protein ucpA OS=Dictyostelium discoideum OX=44689 GN=ucpA PE=3 SV=1
A0625	-	-	-	-	-	-	-	-
A0626	-	-	-	K09958 K09958; uncharacterized protein	-	-	GBC03252.1 hypothetical protein RclHR1_05030009 [Rhizophagus clarus]	-
A0627	-	-	-	-	-	KOG1675 Hs21450735 Predicted cyclin	TPX56447.1 hypothetical protein PhCBS80983_g04537 [Powellomyces hirtus]	Cyclin-Y OS=Homo sapiens OX=9606 GN=CCNY PE=1 SV=2

A0628	-	-	-	-	-	-	RUS19665.1 hypothetical protein BC937DRAFT_87135 [Endogone sp. FLAS-F59071]	-
A0629	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0690[Hs4502023 Serine/threonine protein kinase	RKP33203.1 kinase-like domain-containing protein, partial [Dimargaris cristalligena]	RAC-alpha serine/threonine-protein kinase OS=Xenopus laevis OX=8355 GN=akt1 PE=2 SV=1
A0630	-	-	GO:0005515(protein binding)	K20792 NAA15_16; N-alpha-acetyltransferase 15/16, NatA auxiliary subunit	-	KOG1156[At1g80410 N-terminal acetyltransferase	KAF9208298.1 N-alpha-acetyltransferase 16, NatA auxiliary subunit [Haplosporangium sp. Z27]	N-terminal acetyltransferase A complex auxiliary subunit NAA15 OS=Arabidopsis thaliana OX=3702 GN=NAA15 PE=1 SV=1
A0631	GO:0006821(chloride transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005247(voltage-gated chloride channel activity)	K05012 CLCN3_4_5; chloride channel 3/4/5	map04613 Neutrophil extracellular trap formation	KOG0474[Hs14149607 Cl-channel CLC-7 and related proteins (CLC superfamily)	ORY06278.1 voltage-gated chloride channel [Basidiobolus meristosporus CBS 931.73]	H(+)/Cl(-) exchange transporter 7 OS=Rattus norvegicus OX=10116 GN=Clcn7 PE=2 SV=1
A0632	GO:0007264(small GTPase mediated signal transduction)	-	GO:0005085(guanine nucleotide exchange factor activity)	K03099 SOS; son of sevenless	map04810 Regulation of actin cytoskeleton;map05223 Non-small cell lung cancer;map04722 Neurotrophin signaling pathway;map04320 Dorsal-ventral axis formation;map044510 Focal adhesion;map04072 Phospholipase D signaling pathway;map01521 EGFR tyrosine kinase inhibitor resistance;map01522 Endocrine resistance;map04917 Prolactin signaling pathway;map04915 Estrogen signaling	KOG3417[Hs8922307 Ras1 guanine nucleotide exchange factor	XP_026606425.1 Uncharacterized protein DSM5745_03543 [Aspergillus mulundensis]	Ras guanine nucleotide exchange factor L OS=Dictyostelium discoideum OX=44689 GN=gefL PE=2 SV=1
A0633	-	-	-	-	-	-	-	-
A0634	-	-	-	-	-	-	-	-
A0635	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	-	PVU92546.1 hypothetical protein BB559_003678 [Furculomyces boomerangs]	Large ribosomal subunit protein bL34 OS=Colwellia psychrerythraea (strain 34H / ATCC BAA-681) OX=167879 GN=rpH PE=3 SV=1
A0636	-	-	-	-	-	-	-	-
A0637	-	-	-	-	-	-	-	-

A0638	GO:0007018(microtubule-based movement),GO:0060285(ciliium-dependent cell motility)	GO:0030286(dynein complex),GO:0005858(axonemal dynein complex)	GO:0008569(minus-end-directed microtubule motor activity),GO:0003777(microtubule motor activity),GO:0016887(ATP hydrolysis activity),GO:0005524(ATP binding)	K10413 DYNC1H1; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595 7293415 Dyneins, heavy chain	EPZ34616.1 Dynein heavy chain-2 domain-containing protein [Rozella allomycis CSF55]	Dynein axonemal heavy chain 6 OS=Homo sapiens OX=9606 GN=DNAH6 PE=1 SV=3
A0639	-	-	GO:0016491(oxidoreductase activity)	K00344 qor, CRYZ; NADPH:quinone reductase [EC:1.6.5.5]	-	-	KAG0650197.1 Zinc-type alcohol dehydrogenase [Hyphodiscus hymeniophilus]	Zinc-type alcohol dehydrogenase-like protein C337.11 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC337.11 PE=3 SV=1
A0640	-	-	-	-	-	-	KAE8235634.1 hypothetical protein A4X03_0g9707, partial [Tilletia caries]	-
A0641	GO:0032508(DNA duplex unwinding),GO:0006270(DNA replication initiation),GO:1905775(negative regulation of DNA helicase activity),GO:0006260(DNA replication)	GO:0005634(nucleus),GO:0042555(MCM complex)	GO:0003677(DNA binding),GO:0005524(ATP binding)	K02540 MCM2; DNA replication licensing factor MCM2 [EC:5.6.2.3]	map03030 DNA replication;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0477 At1g44900 DNA replication licensing factor, MCM2 component	EPZ37085.1 DNA replication licensing factor Mcm2 domain-containing protein [Rozella allomycis CSF55]	DNA replication licensing factor MCM2 OS=Arabidopsis thaliana OX=3702 GN=MCM2 PE=1 SV=1
A0642	-	-	-	-	-	-	-	-
A0643	-	-	-	-	-	-	-	-
A0644	-	-	-	-	-	-	-	-
A0645	-	-	GO:0005515(protein binding)	-	-	-	TPX67920.1 hypothetical protein SpCBS45565_g03474 [Spizellomyces sp. 'palustris']	Cilia- and flagella-associated protein 70 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP70 PE=1 SV=1
A0646	GO:0006777(Molybdopterins cofactor biosynthetic process)	GO:0005829(cytosol)	-	K21232 MOCS2A, CNXG; molybdopterins synthase sulfur carrier subunit	map04122 Sulfur relay system	KOG3474 At4g10100 Molybdopterins converting factor, small subunit	ORX46343.1 Molybdopterins converting factor, subunit 1 [Hesseltinella vesiculosa]	Molybdopterins synthase sulfur carrier subunit OS=Chlamydomonas reinhardtii OX=3055 GN=CHLREDRAFT_109356 PE=3 SV=1
A0647	-	-	GO:0035091(phosphatidylinositol binding),GO:0005515(protein binding)	K20520 DBNL, ABP1; drebrin-like protein	-	KOG1118 Hs4506929 Lysophosphatidic acid acyltransferase endophilin/S H3GL, involved in synaptic vesicle formation	RVX74543.1 hypothetical protein B0A52_01669 [Exophiala mesophila]	Endophilin-A2 OS=Bos taurus OX=9913 GN=SH3GL1 PE=2 SV=1

A0648	-	-	-	K11493 RCC1; regulator of chromosome condensation	-	KOG1426 At5 g63860 FOG: RCC1 domain	PHH51076.1 Protein pim1 [Ceratocystis fimbriata CBS 114723]	E3 ubiquitin-protein ligase HERC2 OS=Mus musculus OX=10090 GN=Herc2 PE=1 SV=3
A0649	-	-	GO:0003824(cat alytic activity)	K07511 ECHS1; enoyl-CoA hydratase [EC:4.2.1.17]	map00410 beta- Alanine metabolism;map 01110 Biosynthesis of secondary metabolites;map 01200 Carbon metabolism;map 01120 Microbial metabolism in diverse environments;m ap00640 Propanoate metabolism;map 00930 Caprolactam degradation;ma p00280 Valine, leucine and isoleucine degradation;ma p00650 Butanoate metabolism;map 00062 Fatty acid elongation;map 00627 Aminobenzoate	KOG1682 Hs2 0471188 Enoyl-CoA isomerase	RYP55482.1 hypothetical protein DL771_01250 0 [Monosporas cus sp. 5C6A]	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial OS=Rattus norvegicus OX=10116 GN=Echdc3 PE=2 SV=1
A0650	-	-	-	K13346 PEX10; peroxin-10	map04146 Peroxisome	KOG0317 Hs4 505715 Predicted E3 ubiquitin ligase, integral peroxisomal membrane protein	KAF3213071. 1 peroxisome bioproteins factor 10 [Orbilina oligospora]	Peroxisome biogenesis factor 10 OS=Arabidopsis thaliana OX=3702 GN=PEX10 PE=1 SV=1
A0651	-	-	-	-	-	-	-	-
A0652	GO:00068 11(ion transport), GO:00550 85(transm embrane transport)	GO:00160 20(memb rane),GO: 0016021(i ntegral compone nt of membra ne)	GO:0005216(ion channel activity)	K13754 SLC24A6, NCKX6; solute carrier family 24 (sodium/pota ssium/calciu m exchanger), member 6	-	KOG1307 Hs1 0190740 K+- dependent Ca2+/Na+ exchanger NCKX1 and related proteins	XP_02536107 3.1 hypothetical protein BDZ90DRAFT _39546 [Jaminaea rosea]	Sodium/potassium/calcium exchanger 1 OS=Gallus gallus OX=9031 GN=SLC24A1 PE=2 SV=1
A0653	-	-	-	K15436 TRPO3, MTR10; transportin-3	map03250 Viral life cycle - HIV- 1;map03013 Nucleocytoplas mic transport	KOG2081 At5 g62600 Nuclear transport regulator	KAF9581145. 1 Nuclear import receptor, partial [Lunasporang iospora selenospora]	Transportin MOS14 OS=Arabidopsis thaliana OX=3702 GN=MOS14 PE=1 SV=1
A0654	-	-	-	-	-	-	-	-
A0655	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	K04563 CDC28, CDC2; cyclin- dependent kinase [EC:2.7.11.22]	map04011 MAPK signaling pathway - yeast;map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0594 Hs4 557439 Protein kinase PCTAIRE and related kinases	ORX96878.1 Pkinase- domain- containing protein [Basidiobolus meristosporu s CBS 931.73]	Cell division control protein 2 homolog A OS=Antirrhinum majus OX=4151 GN=CDC2A PE=2 SV=2

A0656	-	-	GO:0016491(oxidoreductase activity)	K13299 GSTK1; glutathione S-transferase kappa 1 [EC:2.5.1.18]	map04146 Peroxisome;map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00480 Glutathione metabolism;map05204 Chemical carcinogenesis - DNA adducts;map01100 Metabolic pathways	-	RKO88189.1 thioredoxin-like protein [Blyttomyces helicus]	Glutathione S-transferase kappa 1 OS=Mus musculus OX=10090 GN=Gstk1 PE=1 SV=3
A0657	-	-	-	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 At3g62260 Serine/threonine protein phosphatase	SAM07630.1 hypothetical protein [Absidia glauca]	Probable protein phosphatase 2C 49 OS=Arabidopsis thaliana OX=3702 GN=At3g62260 PE=2 SV=1
A0658	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG0139 CE24778 Short-chain acyl-CoA dehydrogenase	CDS12487.1 hypothetical protein LRAMOSA04681 [Lichtheimia ramosa]	Acyl-CoA dehydrogenase apdG OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=apdG PE=2 SV=1
A0659	-	-	-	-	-	-	-	-
A0660	-	-	-	-	-	-	-	-
A0661	-	-	GO:0005515(protein binding)	-	-	KOG2505 At1g01930 Ankyrin repeat protein	RKO84866.1 hypothetical protein BDK51DRAFT_43923 [Blyttomyces helicus]	tRNA endonuclease ANKZF1 OS=Homo sapiens OX=9606 GN=ANKZF1 PE=1 SV=1
A0662	-	-	-	-	-	-	-	-
A0663	GO:1902600(proton transmembrane transport)	GO:0033177(proton - transporting two-sector ATPase complex, proton-transporting domain), GO:0033179(proton - transporting V-type ATPase, V0 domain)	GO:0015078(proton transmembrane transporter activity),GO:0046961(proton-transporting ATPase activity, rotational mechanism)	K03661 ATPeV0B, ATP6F; V-type H+ - transporting ATPase 21kDa proteolipid subunit	map04145 Phagosome;map04142 Lysosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation;map05110 Vibrio cholerae infection;map05120 Epithelial cell signaling in Helicobacter pylori infection;map05152 Tuberculosis;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG0233 Hs4757816 Vacuolar H+-ATPase V0 sector, subunit c''	KAF7543517.1 hypothetical protein G7Z17_g10673 [Cylindrodendrum hubeiense]	V-type proton ATPase 21 kDa proteolipid subunit c'' OS=Bos taurus OX=9913 GN=ATP6V0B PE=1 SV=1

A0664	GO:0046488(phosphatidylinositol metabolic process)	-	GO:0005509(calcium ion binding),GO:0016307(phosphatidylinositol phosphate kinase activity)	K00889 PIP5K; 1-phosphatidylinositol-4-phosphate 5-kinase [EC:2.7.1.68]	map04144 Endocytosis;map05135 Yersinia infection;map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04070 Phosphatidylinositol signaling system;map04072 Phospholipase D signaling pathway;map04139 Mitophagy - yeast;map04666 Fc gamma R-mediated phagocytosis;map00562 Inositol phosphate metabolism;map04011 MAPK signaling pathway - yeast;map05231 Choline metabolism in	KOG0229 YDR208w Phosphatidylinositol-4-phosphate 5-kinase	KAF9513798.1 hypothetical protein BS47DRAFT_1295750 [Hydnum rufescens UP504]	Phosphatidylinositol 4-phosphate 5-kinase OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=PIP5K PE=1 SV=1
A0665	-	-	-	-	-	KOG2563 Hs14249552 Permease of the major facilitator superfamily	-	-
A0666	-	-	-	K01684 dgoD; galactonate dehydratase [EC:4.2.1.6]	map01120 Microbial metabolism in diverse environments;map00052 Galactose metabolism;map01100 Metabolic pathways	-	RSH80103.1 hypothetical protein EHS25_007305 [Saitozyma podzolica]	D-galactarolactone cycloisomerase OS=Agrobacterium fabrum (strain C58 / ATCC 33970) OX=176299 GN=gci PE=1 SV=1
A0667	-	-	-	-	-	-	-	-
A0668	-	GO:0016021(integral component of membrane)	-	-	-	-	TDL25040.1 DUF887-domain-containing protein [Rickenella mellea]	Uncharacterized TLC domain-containing protein C17A2.02c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC17A2.02c PE=4 SV=1
A0669	-	-	GO:0008146(sulfotransferase activity)	-	-	KOG1584 Hs7657633 Sulfotransferase	ORY00775.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	Cytosolic sulfotransferase 3 OS=Danio rerio OX=7955 GN=sult1st3 PE=1 SV=1
A0670	-	-	GO:0043169(cation binding)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0697 Hs10337595 Protein phosphatase 1B (formerly 2C)	CDS10693.1 hypothetical protein LRAMOSA1179 [Lichtheimia ramosa]	Protein phosphatase 1B OS=Mus musculus OX=10090 GN=Ppm1b PE=1 SV=1
A0671	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0603 CE13014 Ribosomal protein S6 kinase	OZJ05863.1 hypothetical protein BZG36_00869 [Bifiguratus adelaidae]	Putative ribosomal protein S6 kinase alpha-1 OS=Caenorhabditis elegans OX=6239 GN=rskn-1 PE=3 SV=4

A0672	GO:0006139(nucleobase-containing compound metabolic process), GO:0006289(nucleotide-excision repair)	GO:0005634(nucleus)	GO:0003676(nucleic acid binding),GO:0004386(helicase activity),GO:0005524(ATP binding),GO:0016818(hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides),GO:0003677(DNA binding),GO:0003678(DNA helicase activity)	K10844 ERCC2, XPD; DNA excision repair protein ERCC-2 [EC:5.6.2.3]	map03420 Nucleotide excision repair;map03022 Basal transcription factors	KOG1131 At1g03190 RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH, 5'-3' helicase subunit RAD3	RKP35763.1 hypothetical protein BJ085DRAFT_37046 [Dimargaris cristalligena]	General transcription and DNA repair factor IIH helicase subunit XPD OS=Arabidopsis thaliana OX=3702 GN=XPD PE=1 SV=1
A0673	GO:0006406(mRNA export from nucleus), GO:0043248(proteasome assembly)	GO:0008541(proteasome regulatory particle, lid subcomplex)	-	-	-	KOG4764 Hs5453640 Uncharacterized conserved protein	OMJ26505.1 26S proteasome complex subunit DSS1 [Smittium culicis]	26S proteasome complex subunit SEM1 OS=Bos taurus OX=9913 GN=SEM1 PE=3 SV=1
A0674	GO:0000160(phosphorelay signal transduction system)	-	GO:0005515(protein binding)	K19691 NIK1, TCSC; osomolarity two-component system, sensor histidine kinase NIK1 [EC:2.7.13.3]	map02020 Two-component system	-	XP_01829621.8.1 SSK1 signal transduction response regulator [Phycomyces blakesleeanus NRRL 1555(-)]	Response regulator ArlR OS=Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229 / NCIMB 8711 / NCTC 7292 / S-41) OX=342451 GN=arlR PE=3 SV=1
A0675	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG4280 Hs4758646 Kinesin-like protein	RKO90944.1 P-loop containing nucleoside triphosphate hydrolase protein, partial [Blyttiomycetes helicus]	Kinesin-II 95 kDa subunit OS=Strongylocentrotus purpuratus OX=7668 GN=KRP95 PE=1 SV=1
A0676	GO:0015671(oxygen transport)	-	GO:0019825(oxygen binding),GO:0020037(heme binding),GO:0005344(oxygen carrier activity)	-	-	-	KXS19376.1 hypothetical protein M427DRAFT_52814 [Gonapodya prolifera JEL478]	Two-on-two hemoglobin-3 OS=Arabidopsis thaliana OX=3702 GN=GLB3 PE=1 SV=1
A0677	-	-	GO:0046872(metal ion binding)	K07213 ATOX1, ATX1, copZ, golB; copper chaperone	map04978 Mineral absorption	KOG1603 7296474_2 Copper chaperone	KAF2833620.1 hypothetical protein CC86DRAFT_12299 [Ophiobolus disseminans]	Copper transport protein ATOX1 homolog OS=Dictyostelium discoideum OX=44689 GN=atox1 PE=3 SV=2
A0678	-	-	-	-	-	-	-	-

A0679	-	-	GO:0003824(catalytic activity)	-	-	KOG1211 At5g64440 Amidases	TPX62935.1 glutaminyl-tRNA synthase (glutamine- hydrolysing) [Powellomyces hirtus]	Fatty acid amide hydrolase OS=Medicago truncatula OX=3880 GN=FAAH PE=1 SV=1
A0680	GO:000629(lipid metabolic process)	-	-	K14674 TGL4; TAG lipase / steryl ester hydrolase / phospholipase A2 / LPA acyltransferase [EC:3.1.1.3 3.1.1.13 3.1.1.4 2.3.1.51]	map01110 Biosynthesis of secondary metabolites;map 00590 Arachidonic acid metabolism;map 00100 Steroid biosynthesis;map 00564 Glycerophospho- lipid metabolism;map 00565 Ether lipid metabolism;map 00561 Glycerolipid metabolism;map 00592 alpha- linolenic acid metabolism;map 00591 Linoleic acid metabolism;map 01100 Metabolic pathways	KOG2214 At5g04040 Predicted esterase of the alpha- beta hydrolase superfamily	KAF0501202. 1 patatin- domain- containing protein [Gigaspora margarita]	Triacylglycerol lipase SDP1 OS=Arabidopsis thaliana OX=3702 GN=SDP1 PE=1 SV=1
A0681	-	-	GO:0005509(cal- cium ion binding)	-	-	-	-	-
A0682	-	-	-	K15728 LPIN; phosphatidate phosphatase LPIN [EC:3.1.3.4]	map01110 Biosynthesis of secondary metabolites;map 04936 Alcoholic liver disease;map005 64 Glycerophospho- lipid metabolism;map 00561 Glycerolipid metabolism;map 04150 mTOR signaling pathway;map01 100 Metabolic pathways	-	TNY21643.1 Lipin/Ned1/S mp2- domain- containing protein [Rhodotorula diobovata]	-
A0683	GO:0055085(transm- embrane transport)	-	GO:0005509(cal- cium ion binding)	K14684 SLC25A23S; solute carrier family 25 (mitochondrial phosphate transporter), member 23/24/25/41	-	KOG0036 Hs2 2046149 Predicted mitochondria l carrier protein	ORX88868.1 mitochondria l carrier [Basidiobolus meristosporus CBS 931.73]	Mitochondrial adenyl nucleotide antiporter SLC25A24-B OS=Xenopus laevis OX=8355 GN=slc25a24-b PE=2 SV=1
A0684	-	-	-	-	-	KOG1502 CE 04390 Flavonol reductase/cin- namoyl-CoA reductase	OQO28868.1 hypothetical protein B0A51_03450 [Rachicladospo- rium sp. CCFEE 5018]	Cinnamoyl-CoA reductase 1 OS=Arabidopsis thaliana OX=3702 GN=CCR1 PE=1 SV=1
A0685	-	-	-	-	-	-	-	-
A0686	-	-	-	-	-	-	-	-

A0687	-	GO:0016021(integral component of membrane)	-	K03321 TC.SULP; sulfate permease, SulP family	-	-	ORY40905.1 hypothetical protein BCR33DRAFT_699149 [Rhizoclostium globosum]	Uncharacterized protein C24H6.11c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC24H6.11c PE=4 SV=1
A0688	GO:0006139(nucleobase-containing compound metabolic process), GO:0009116(nucleoside metabolic process)	-	GO:0004731(purine-nucleoside phosphorylase activity),GO:0003824(catalytic activity)	K03783 punA, PNP; purine-nucleoside phosphorylase [EC:2.4.2.1]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01232 Nucleotide metabolism;map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	KOG3984[Hs4557801 Purine nucleoside phosphorylase	KAF9320631.1 hypothetical protein BG003_005380 [Podila horticola]	Purine nucleoside phosphorylase OS=Bos taurus OX=9913 GN=PNP PE=1 SV=3
A0689	GO:0006629(lipid metabolic process)	-	-	K04712 DEGS; sphingolipid 4-desaturase/C4-monooxygenase [EC:1.14.19.17 1.14.18.5]	map04071 Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG2987[7297049 Fatty acid desaturase	XP_016270924.1 sphingolipid delta-4 desaturase [Rhodotorula toruloides NP11]	Sphingolipid delta(4)-desaturase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=DES1 PE=1 SV=1
A0690	-	-	GO:0005515(protein binding)	K10520 ABTB1, BPOZ; ankyrin repeat and BTB/POZ domain-containing protein 1	-	KOG0511[YIL001w Ankyrin repeat protein	ORY98900.1 BTB/POZ protein [Syncephalaster racemosus]	Ankyrin repeat and BTB/POZ domain-containing protein 1 OS=Mus musculus OX=10090 GN=Abtb1 PE=2 SV=1
A0691	-	-	-	-	-	-	-	-
A0692	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192[At3g01490 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAG0262956.1 hypothetical protein DFQ27_002023 [Actinomortierella ambigua]	Probable serine/threonine-protein kinase SIS8 OS=Arabidopsis thaliana OX=3702 GN=SIS8 PE=1 SV=1
A0693	-	-	GO:0003723(RNA binding),GO:0033897(ribonuclease T2 activity)	-	-	-	-	Intracellular ribonuclease LX OS=Solanum lycopersicum OX=4081 GN=RNALX PE=1 SV=2
A0694	-	-	-	-	-	-	-	Ankyrin repeat and ELMO domain-containing protein D OS=Dictyostelium discoideum OX=44689 GN=elmoD PE=4 SV=1
A0695	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K14778 DDX49, DBP8; ATP-dependent RNA helicase DDX49/DBP8 [EC:3.6.4.13]	-	KOG0340[At1g16280 ATP-dependent RNA helicase	TPX61013.1 hypothetical protein SpCBS45565_g07358 [Spizellomyces sp. 'palustris']	DEAD-box ATP-dependent RNA helicase 36 OS=Arabidopsis thaliana OX=3702 GN=RH36 PE=2 SV=1
A0696	-	-	-	-	-	-	-	-

A0697	GO:0019915(lipid storage)	GO:0005811(lipid droplet)	GO:0016298(lipase activity)	-	-	KOG3975 Hs11345458 Uncharacterized conserved protein	OBZ86713.1 hypothetical protein A0J61_05246 [Choanephora cucurbitarum]	Lipid droplet-associated hydrolase OS=Pongo abelii OX=9601 GN=LDAH PE=2 SV=1
A0698	GO:0016226(iron-sulfur cluster assembly)	-	GO:0005506(iron ion binding),GO:0051536(iron-sulfur cluster binding)	K22074 NFU1, HIRIP5; NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	-	KOG2358 CE06292 NifU-like domain-containing proteins	TGZ85258.1 HIRA-interacting protein 5 [Ascodesmis nigricans]	NifU-like protein C1709.19c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC1709.19c PE=3 SV=1
A0699	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4503899 Sulfatase	XP_024663337.1 Arylsulfatase [Wickerhamia sorbophila]	N-acetylglactosamine-6-sulfatase OS=Canis lupus familiaris OX=9615 GN=GALNS PE=2 SV=1
A0700	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs6005990 Sulfatase	XP_007828072.1 hypothetical protein PFIC1_01300 [Pestalotiopsis fici W106-1]	Arylsulfatase OS=Strongylocentrotus purpuratus OX=7668 PE=2 SV=1
A0701	GO:0007017(microtubule-based process)	GO:0005874(microtubule)	GO:0003924(GTPase activity),GO:0005200(structural constituent of cytoskeleton),GO:0005525(GTP binding)	K07375 TUBB; tubulin beta	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins;map04540 Gap junction;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG1375 Hs5174735 Beta tubulin	XP_006680448.1 Alpha-Beta tubulin [Batrachochytrium dendrobatidis JAM81]	Tubulin beta chain OS=Tetrahymena thermophila OX=5911 GN=BTU1 PE=1 SV=1
A0702	-	-	-	-	-	-	-	-
A0703	-	-	GO:0005515(protein binding)	-	-	KOG0613 Hs20143914 Projectin/twintchin and related proteins	-	Titin OS=Homo sapiens OX=9606 GN=TTN PE=1 SV=4

A0704	GO:0007017(microtubule-based process)	GO:0005874(microtubule)	GO:0003924(GTPase activity),GO:0005200(structural constituent of cytoskeleton),GO:0005525(GTP binding)	K07375 TUBB; tubulin beta	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins;map04540 Gap junction;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG1375 Hs5174735 Beta tubulin	XP_006680448.1 Alpha-Beta tubulin [Batrachochytrium dendrobatidis JAM81]	Tubulin beta chain OS=Tetrahymena thermophila OX=5911 GN=BTU1 PE=1 SV=1
A0705	-	-	-	-	-	KOG3376 Hs2054484 Uncharacterized conserved protein	XP_006680866.1 uncharacterized protein BATDEDRAFT_90678 [Batrachochytrium dendrobatidis JAM81]	Costars family protein OS=Oryza sativa subsp. indica OX=39946 GN=Osl_012692 PE=3 SV=1
A0706	-	-	-	-	-	-	-	-
A0707	-	-	-	-	-	-	-	-
A0708	-	-	-	-	-	-	XP_018283782.1 hypothetical protein PHYBLDRAFT_119920 [Phycomyces blakesleeanus NRRL 1555(-)]	Glycerophosphocholine acyltransferase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=gpc1 PE=3 SV=2
A0709	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07893 RAB6A; Ras-related protein Rab-6A	-	KOG0078 Hs4758994 GTP-binding protein SEC4, small G protein superfamily, and related Ras family GTP-binding proteins	ORX54803.1 P-loop containing nucleoside triphosphate hydrolase protein [Piromyces finnis]	Ras-related protein Rab-28 OS=Bos taurus OX=9913 GN=RAB28 PE=2 SV=1
A0710	-	-	-	-	-	-	-	-
A0711	-	-	GO:0016874(ligase activity),GO:0005524(ATP binding),GO:0046872(metal ion binding)	-	-	KOG0369 7303838 Pyruvate carboxylase	XP_031024206.1 acetyl-CoA carboxylase [Synchytrium microbalum]	Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=accA3 PE=1 SV=2
A0712	-	-	-	-	-	-	-	-
A0713	-	-	-	-	-	-	-	Phosphate acetyltransferase OS=Desulfovibrio vulgaris (strain ATCC 29579 / DSM 644 / NCIMB 8303 / VKM B-1760 / Hildenborough)
A0714	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	-	-	KOG0319 CE14894 WD40-repeat-containing subunit of the 18S rRNA processing complex	-	-

A0715	-	-	GO:0005515(protein binding)	K24927 TTC4, CNS1; tetratricopeptide repeat protein 4	-	KOG0550 Hs4507713 Molecular chaperone (DnaJ superfamily)	KKY33988.1 putative chip protein (carboxyl terminus of hsc70-interacting protein) [Diaporthe ampelina]	DnaJ homolog subfamily C member 7 OS=Homo sapiens OX=9606 GN=DNAJC7 PE=1 SV=2
A0716	GO:0042254(ribosome biogenesis)	-	GO:0005515(protein binding)	K14863 WDR12, YTM1; ribosome biogenesis protein	-	KOG0313 Hs16445424 Microtubule binding protein YTM1 (contains WD40 repeats)	KAF7732740.1 WD repeat-containing protein 12 [Apophysomyces ossiformis]	Ribosome biogenesis protein WDR12 homolog OS=Chlamydomonas reinhardtii OX=3055 GN=CHLREDRAFT_128420 PE=3 SV=2
A0717	-	-	-	-	-	-	KXS13265.1 hypothetical protein M427DRAFT_125218 [Gonapodya prolifera] JEL478]	-
A0719	GO:0006457(protein folding)	-	-	K14002 SCJ1; DnaJ-related protein SCJ1	map04141 Protein processing in endoplasmic reticulum	KOG0724 Hs21361912 Zuotin and related molecular chaperones (DnaJ superfamily), contains DNA-binding domains	CCG84480.1 protein of unknown function [Taphrina deformans PYCC 5710]	Chaperone protein DnaJ 2 OS=Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10) OX=262316 GN=dnaJ2 PE=3 SV=1
A0720	-	-	GO:0005515(protein binding);GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0310 7290304 Conserved WD40 repeat-containing protein	ORY42797.1 WD40 repeat-like protein [Rhizoclostium globosum]	WD repeat-containing protein 49 OS=Homo sapiens OX=9606 GN=WDR49 PE=2 SV=1
A0721	-	GO:0008180(COP9 signalosome)	-	K12177 COPS3, CSN3; COP9 signalosome complex subunit 3	-	KOG2582 Hs4502975 COP9 signalosome, subunit CSN3	CDS03619.1 hypothetical protein [RAMOSA01021 [Lichtheimia ramosa]	COP9 signalosome complex subunit 3 OS=Xenopus tropicalis OX=8364 GN=cops3 PE=2 SV=1
A0722	-	-	GO:0003950(NAD+ ADP-ribosyltransferase activity)	K15258 PARP6.8; poly [ADP-ribose] polymerase 6/8 [EC:2.4.2.30]	-	-	TXTO6009.1 hypothetical protein VHUM_03770 [Vanrija humicola]	Protein mono-ADP-ribosyltransferase PARP8 OS=Mus musculus OX=10090 GN=Parp8 PE=2 SV=1

A0723	-	-	GO:0016787(hydrolase activity)	K15423 PPP4C; serine/threonine-protein phosphatase 4 catalytic subunit [EC:3.1.3.16]	map04922 Glucagon signaling pathway	KOG0372 At5g55260 Serine/threonine specific protein phosphatase involved in glycogen accumulation, PP2A-related	ORX96373.1 Metallo-dependent phosphatase [Basidiobolus meristosporus CBS 931.73]	Serine/threonine-protein phosphatase PP-X isozyme 2 OS=Arabidopsis thaliana OX=3702 GN=PPX2 PE=2 SV=2
A0724	-	-	-	-	-	KOG1471 Hs18571255 Phosphatidylinositol transfer protein SEC14 and related proteins	RKP34094.1 CRAL-TRIO domain-containing protein [Dimargaris cristalligena]	Clavesin-2 OS=Danio rerio OX=7955 GN=clvs2 PE=2 SV=1
A0725	GO:0006508(proteolysis)	-	GO:0004222(metalloendopeptidase activity),GO:0008237(metalloprotease activity),GO:0008270(zinc ion binding)	-	-	KOG3714 7300984 Meprin A metalloprotease	KAF8931219.1 hypothetical protein BGZ47_000190 [Haplosporangium gracile]	High choriolytic enzyme 1 OS=Oryzias latipes OX=8090 GN=hcea PE=1 SV=1
A0726	GO:0030833(regulation of actin filament polymerization),GO:0034314(Arp2/3 complex-mediated actin nucleation)	GO:0005885(Arp2/3 protein complex),GO:0015629(actin cytoskeleton)	-	K05754 ARPC5; actin related protein 2/3 complex, subunit 5	map04144 Endocytosis;map05135 Yersinia infection;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04810 Regulation of actin cytoskeleton;map04138 Autophagy - yeast;map05100 Bacterial invasion of epithelial cells;map04666 Fc gamma R-mediated phagocytosis;map04530 Tight junction	KOG3380 Hs031593 Actin-related protein Arp2/3 complex, subunit ARPC5	KAF5102982.1 hypothetical protein DV451_001682 [Geotrichum candidum]	Actin-related protein 2/3 complex subunit 5 OS=Dictyostelium discoideum OX=44689 GN=arcE PE=1 SV=1
A0727	-	-	-	-	-	KOG3780 Hs20543322 Thioredoxin binding protein TBP-2/VDUP1	PJF17204.1 hypothetical protein PSACC_03008 [Paramicrosporidium saccamoebae]	Arrestin domain-containing protein 3 OS=Bos taurus OX=9913 GN=ARRDC3 PE=2 SV=1

A0728	-	-	GO:0003824(catalytic activity)	K01899 LSC1; succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00020 Citrate cycle (TCA cycle);map01100 Metabolic pathways	KOG1255[Hs1321581 Succinyl-CoA synthetase, alpha subunit	KNE58305.1 succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondria I [Allomyces macrogynus ATCC 38327]	Succinate--CoA ligase [ADP-forming] subunit alpha OS=Blastocystis sp. subtype 1 (strain ATCC 50177 / Nandli) OX=478820 GN=SCSa PE=1 SV=1
A0729	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0730	-	-	GO:0004386(helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K12820 DHX15, PRP43; pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15/PRP43 [EC:3.6.4.13]	map03040 Spliceosome	KOG0925[At3g62310 mRNA splicing factor ATP-dependent RNA helicase	TPX62246.1 hypothetical protein PhCBS80983_g00454 [Powellomyces hirtus]	Probable pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH2 OS=Arabidopsis thaliana OX=3702 GN=At3g62310 PE=2 SV=1
A0731	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0589[At1g54510 Serine/threonine protein kinase	OJT05228.1 MAP kinase kinase kinase mkh1 [Trametes pubescens]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei brucei OX=5702 GN=CRK2 PE=3 SV=1
A0732	-	-	-	-	-	-	-	-
A0733	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity)	-	-	-	KAG0253177.1 hypothetical protein DFQ27_007628 [Actinomortierella ambigua]	-
A0734	-	-	-	-	-	-	-	-
A0735	-	-	GO:0003824(catalytic activity)	-	-	KOG1075[CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A0736	-	-	GO:0016746(acyltransferase activity)	K13507 GAT; glycerol-3-phosphate O-acyltransferase / dihydroxyacetone phosphate acyltransferase [EC:2.3.1.15 2.3.1.42]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	-	KAF9144939.1 hypothetical protein BG015_012054 [Linnemannia schmuckeri]	Glycerol-3-phosphate O-acyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPT2 PE=1 SV=1

A0737	GO:0009058(biosynthetic process), GO:0000162(tryptophan biosynthetic process)	-	GO:0004049(anthranilate synthase activity)	K01657 trpE; anthranilate synthase component I [EC:4.1.3.27]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map00405 Phenazine biosynthesis;map02025 Biofilm formation - Pseudomonas aeruginosa;map02024 Quorum sensing;map01100 Metabolic pathways	KOG0026 YKL211c.1 Anthranilate synthase, beta chain	TPX67207.1 hypothetical protein SpCBS45565.g03912 [Spizellomyces sp. 'palustris']	Anthranilate synthase OS=Rhizobium meliloti (strain 1021) OX=266834 GN=trpE(G) PE=4 SV=1
A0738	-	-	GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	-	CEJ54662.1 hypothetical protein PMG11_00962 [Penicillium brasilianum]	N-acetylglucosamine-1-phosphotransferase subunits alpha/beta OS=Homo sapiens OX=9606 GN=GNPTAB PE=1 SV=1
A0739	-	-	GO:0005509(calcium ion binding)	-	-	-	OQD67598.1 hypothetical protein PENPOL_c003G04888 [Penicillium polonicum]	N-acetylglucosamine-1-phosphotransferase subunits alpha/beta OS=Homo sapiens OX=9606 GN=GNPTAB PE=1 SV=1
A0740	GO:0035556(intracellular signal transduction),GO:006629(lipid metabolic process), GO:0007165(signal transduction)	-	GO:0008081(phosphoric diester hydrolase activity),GO:0004435(phosphatidylinositol phospholipase C activity)	K05857 PLCD; phosphatidylinositol phospholipase C, delta [EC:3.1.4.11]	map04020 Calcium signaling pathway;map05131 Shigellosis;map04933 AGE-RAGE signaling pathway in diabetic complications;map04070 Phosphatidylinositol signaling system;map04919 Thyroid hormone signaling pathway;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0169 Hs20475709 Phosphoinositide-specific phospholipase C	ORX89142.1 PLC-like phosphodiesterase [Basidiobolus meristosporus CBS 931.73]	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase OS=Dictyostelium discoideum OX=44689 GN=plc PE=2 SV=1
A0741	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3731 7292365 Sulfatases	KLU88009.1 choline-sulfatase [Magnaporthe oryzae ATCC 64411]	Iduronate 2-sulfatase OS=Homo sapiens OX=9606 GN=IDS PE=1 SV=1
A0742	-	-	-	-	-	-	-	-

A0743	GO:0006807(nitrogen compound metabolic process), GO:0006207('de novo' pyrimidine nucleobase biosynthetic process), GO:0006541(glutamine metabolic process)	-	GO:0005524(ATP binding),GO:0046872(metal ion binding),GO:0004088(carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity)	K11541 URA2; carbamoyl-phosphate synthase / aspartate carbamoyltransferase [EC:6.3.5.5 2.1.3.2]	map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG0370 Hs21361331 Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phosphate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)	KMU90562.1 pyrABCN [Coccidioides immitis H538.4]	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens OX=9606 GN=CPS1 PE=1 SV=2
A0744	-	-	-	-	-	-	RYP14605.1 hypothetical protein DL765_006276 [Monosporascus sp. GIB2]	-
A0745	-	-	-	-	-	-	-	-
A0746	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K11839 USP8, UBP5; ubiquitin carboxyl-terminal hydrolase 8 [EC:3.4.19.12]	map04144 Endocytosis;map04137 Mitophagy - animal;map04934 Cushing syndrome	KOG1870 Hs21489975 Ubiquitin C-terminal hydrolase	GBB85144.1 hypothetical protein RclHR1_01170028 [Rhizophagus clarus]	Ubiquitin carboxyl-terminal hydrolase 33 OS=Danio rerio OX=7955 GN=usp33 PE=2 SV=1
A0747	-	-	-	-	-	-	KNE59105.1 hypothetical protein AMAG_18099 [Allomyces macrogynus ATCC 38327]	Leucine-rich repeat-containing protein 45 OS=Gallus gallus OX=9031 GN=LRRC45 PE=2 SV=1
A0748	GO:0006526(arginine biosynthetic process)	GO:0005737(cytoplasm),GO:0005739(mitochondrion)	GO:0003942(N-acetyl-gamma-glutamyl-phosphate reductase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor),GO:0051287(NAD binding),GO:0003991(acetylglutamate kinase activity)	-	-	-	CDH48582.1 arginine biosynthetic enzyme activities [Lichtheimia corymbifera JMRC:FSU:9682]	Protein ARG5,6, mitochondrial OS=Candida albicans OX=5476 GN=ARG5,6 PE=3 SV=1
A0749	GO:0070940(dephosphorylation of RNA polymerase II C-terminal domain)	-	GO:0008420(RNA polymerase II CTD heptapeptide repeat phosphatase activity),GO:0043175(RNA polymerase core enzyme binding)	K20827 RPAP2; RNA polymerase II-associated protein 2 [EC:3.1.3.16]	-	-	ORY91914.1 Rtr1/RPAP2 family-domain-containing protein [Syncephalaster racemosus]	Putative RNA polymerase II subunit B1 CTD phosphatase RPAP2 homolog OS=Drosophila melanogaster OX=7227 GN=CG34183 PE=2 SV=1

A0750	-	-	GO:0005515(protein binding)	K24781 BPH1; beige protein homolog 1	-	KOG1786 At1g03060.2 Lysosomal trafficking regulator LYST and related BEACH and WD40 repeat proteins	KXS11307.1 beach-domain-containing protein [Gonapodya prolifera JEL478]	BEACH domain-containing protein A2 OS=Arabidopsis thaliana OX=3702 GN=BCHA2 PE=4 SV=1
A0751	GO:0031087(deadenylation-independent decapping of nuclear-transcribed mRNA)	-	GO:0005515(protein binding)	-	-	KOG1916 HsM7657510 Nuclear protein, contains WD40 repeats	RHZ75827.1 hypothetical protein Glove_209g95 [Diversispora epigaea]	Enhancer of mRNA-decapping protein 4 OS=Homo sapiens OX=9606 GN=EDC4 PE=1 SV=1
A0752	GO:0006913(nuclear cytoplasmic transport)	GO:0031965(nuclear membrane)	GO:0017056(structural constituent of nuclear pore),GO:0003676(nucleic acid binding)	-	-	KOG4285 Hs19923074 Mitotic phosphoprotein	ORX91049.1 MPPN-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Nucleoporin NUP35 OS=Homo sapiens OX=9606 GN=NUP35 PE=1 SV=1
A0753	-	-	GO:0005515(protein binding)	-	-	KOG0550 Hs4507713 Molecular chaperone (DnaJ superfamily)	PY128781.1 DnaJ and TPR domain protein [Aspergillus nidulogenus CBS 114.80]	DnaJ homolog subfamily C member 7 homolog OS=Dictyostelium discoideum OX=44689 GN=dnajc7 PE=1 SV=1
A0754	-	-	-	-	-	-	RUS18963.1 hypothetical protein BC938DRAFT_475855 [Jimgerdeman nia flammicorona]	-
A0755	-	-	GO:0016846(carbon-sulfur lyase activity)	-	-	-	GFZ44469.1 hypothetical protein JCM24511_02191 [Saitozyma sp. JCM 24511]	-
A0756	-	-	-	-	-	-	-	-
A0757	GO:0007064(mitotic sister chromatid cohesion)	-	-	K11267 PDS5; sister chromatid cohesion protein PDS5	map04110 Cell cycle	KOG1525 Hs7657269 Sister chromatid cohesion complex Cohesin, subunit PDS5	ORX94611.1 ARM repeat-containing protein [Basidiobolus meristosporus CBS 931.73]	Sister chromatid cohesion protein PDS5 homolog B OS=Gallus gallus OX=9031 GN=PDS5B PE=2 SV=3
A0758	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	-	-	KOG0240 At1g01950 Kinesin (SMY1 subfamily)	KAF5105450.1 hypothetical protein DV453_004811 [Geotrichum candidum]	Kinesin-related protein 5 OS=Dictyostelium discoideum OX=44689 GN=kif5 PE=1 SV=1
A0759	-	-	-	K00894 ETNK, EKI; ethanolamine kinase [EC:2.7.1.82]	map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG4720 At2g26830 Ethanolamine kinase	PIA16085.1 choline/ethanolamine kinase [Coemansia reversa NRRL 1564]	Probable ethanolamine kinase OS=Arabidopsis thaliana OX=3702 GN=EMB1187 PE=2 SV=1

A0760	GO:000958(biosynthetic process), GO:0009396(folic acid-containing compound biosynthetic process)	-	GO:0005524(ATP binding),GO:0016881(acid-amino acid ligase activity),GO:0004326(tetrahydrofolylpolyglutamate synthase activity)	K20457 DHFS; dihydrofolate synthase [EC:6.3.2.12]	map01240 Biosynthesis of cofactors;map01100 Metabolic pathways;map00790 Folate biosynthesis	-	PUU84363.1 Mur ligase [Tuberculosis]	Probable dihydrofolate synthetase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=fol3 PE=3 SV=1
A0761	-	-	-	-	-	-	TPX73454.1 hypothetical protein CcCBS67573_g05284 [Chytridiomycota]	Lipase OS=Bacillus sp. OX=1409 PE=1 SV=3
A0762	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0763	GO:0030837(negative regulation of actin filament polymerization)	-	GO:0003779(actin binding)	K08870 TWF; twinfilin	-	KOG1747[Hs6005846 Protein tyrosine kinase 9/actin monomer-binding protein	XP_016609854.1 hypothetical protein SPPG_03606 [Spizellomyces punctatus DAOM BR117]	Twinfilin-2 OS=Mus musculus OX=10090 GN=Twf2 PE=1 SV=1
A0764	GO:0055085(transmembrane transport)	-	-	K15275 SLC35B1; solute carrier family 35 (UDP-galactose transporter), member B1	-	KOG1582[Hs21361503 UDP-galactose transporter related protein	KNZ78281.1 UDP-galactose transporter like protein [Termitomyces sp. J132]	Adenosine 3'-phospho 5'-phosphosulfate transporter 2 OS=Mus musculus OX=10090 GN=Slc35b3 PE=2 SV=1
A0765	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07910 RAB18; Ras-related protein Rab-18	-	KOG0080[At1g43890 GTPase Rab18, small G protein superfamily	KXN73795.1 hypothetical protein CONCODRAFT_77179 [Conidiobolus coronatus NRRL 28638]	GTP-binding protein yptV3 OS=Volvox carteri OX=3067 GN=YPTV3 PE=3 SV=1
A0766	-	-	-	-	-	-	-	-
A0767	GO:0006470(protein dephosphorylation)	-	GO:0043169(cation binding),GO:0004722(protein serine/threonine phosphatase activity)	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698[At1g43900 Serine/threonine protein phosphatase	KAF7731553.1 Protein phosphatase 2C 1 [Apophysomycetes]	Probable protein phosphatase 2C 59 OS=Arabidopsis thaliana OX=3702 GN=WIN2 PE=1 SV=1
A0768	-	-	-	-	-	-	OON08238.1 hypothetical protein BSLG_02445 [Batrachochytrium salamandrivorans]	-
A0769	GO:0006368(transcription elongation from RNA polymerase II promoter),GO:0016570(histone modification)	GO:0016593(Cdc73/Paf1 complex)	-	K15175 CDC73; parafibromin	-	KOG3786[CE24942 RNA polymerase II accessory factor Cdc73p	ORY61992.1 CDC73-domain-containing protein [Neocallimastix californiae]	Cell division cycle protein 73 OS=Caenorhabditis elegans OX=6239 GN=cdc-73 PE=3 SV=4
A0770	-	-	-	-	-	-	-	-

A0771	-	-	GO:0003824(catalytic activity)	-	-	KOG1260 At1g77060 Isocitrate lyase	KXS21146.1 putative carboxyvinyl-carboxyphosphonate phosphorylmutase [Gonapodya prolifera JEL478]	2,3-dimethylmalate lyase OS=Eubacterium barkeri OX=1528 GN=Dml PE=1 SV=1
A0772	-	-	-	-	-	-	-	-
A0773	-	-	-	-	-	-	-	-
A0774	-	-	-	-	-	KOG0763 Hs7657585 Mitochondrial ornithine transporter	XP_016607099.1 hypothetical protein SPPG_06008 [Spizellomyces punctatus DAOM BR117]	Mitochondrial substrate carrier family protein S OS=Dictyostelium discoideum OX=44689 GN=mcfs PE=3 SV=1
A0775	-	-	-	-	-	-	-	-
A0776	-	-	-	-	-	-	-	-
A0777	GO:0006508(proteolysis)	-	GO:0046872(metal ion binding),GO:0004222(metalloendopeptidase activity)	K01408 IDE, ide; insulin [EC:3.4.24.56]	map05010 Alzheimer disease;map03266 Virion - Herpesvirus	KOG0959 Hs4505453 N-arginine dibasic convertase NRD1 and related Zn2+-dependent endopeptidases, insulinase superfamily	SAM82685.1 related to STE23-Metalloprotease involved in a-factor processing [Ustilago bromivora]	Nardilysin OS=Rattus norvegicus OX=10116 GN=Nrdc PE=1 SV=1
A0778	GO:0055085(transmembrane transport)	GO:0016020(membrane),GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	K08150 SLC2A13, ITR; MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	-	KOG0254 At2g16120 Predicted transporter (major facilitator superfamily)	ORE21562.1 general substrate transporter [Rhizopus microsporus]	Glucose transporter GlcP OS=Staphylococcus epidermidis (strain ATCC 12228 / FDA PCI 1200) OX=176280 GN=glcP PE=1 SV=2
A0779	-	-	-	-	-	-	-	-
A0780	GO:0006606(protein import into nucleus)	-	-	K20222 IPO5, KPNB3, RANBP5; importin-5	map03013 Nucleocytoplasmic transport	KOG2171 At5g19820 Karyopherin (importin) beta 3	XP_031022518.1 uncharacterized protein SmJEL517_g05575 [Synchytrium microbalum]	Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4
A0781	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0782	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding),GO:0016491(oxidoreductase activity)	K00227 SC5DL, ERG3; Delta7-sterol 5-desaturase [EC:1.14.19.20]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG0872 Hs20558831 Sterol C5 desaturase	XP_035319582.1 Delta7-sterol 5-desaturase [Geosmithia morbida]	Delta(7)-sterol 5(6)-desaturase ERG3A OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=ERG3A PE=3 SV=1
A0783	GO:0006506(GPI anchor biosynthetic process)	-	GO:0051377(mannose-ethanolamine phosphotransferase activity)	K05310 PIGG, GPI7; ethanolamine phosphate transferase 2 subunit G [EC:2.7.-.-]	map00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis;map01100 Metabolic pathways	-	ODM20475.1 hypothetical protein SI65_03528 [Aspergillus cristatus]	GPI ethanolamine phosphate transferase 2 OS=Homo sapiens OX=9606 GN=PIGG PE=1 SV=1

A0784	-	-	GO:0016787(hydrolase activity)	-	-	-	XP_007919262.1 putative lipase esterase protein [Phaeoacremonium minimum UCRPA7]	Acetyl-hydrolase OS=Streptomyces hygroscopicus OX=1912 GN=bah PE=3 SV=3
A0785	GO:0055085(transmembrane transport), GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0005509(calcium ion binding),GO:0008324(cation transmembrane transporter activity)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	-	GAN06810.1 calmodulin [Mucor ambiguus]	Sodium/calcium exchanger NCL1 OS=Oryza sativa subsp. japonica OX=39947 GN=NCL1 PE=2 SV=1
A0786	GO:0006887(exocytosis)	GO:0000145(exocyst)	-	K19983 EXOC1, SEC3; exocyst complex component 1	-	-	KAG2186053.1 hypothetical protein INT43_002491 [Umbelopsis isabellina]	-
A0787	-	-	-	-	-	-	-	-
A0788	-	-	-	-	-	-	-	-
A0789	GO:0033567(DNA replication, Okazaki fragment processing)	-	GO:0017108(5'-flap endonuclease activity),GO:0017116(single-stranded DNA helicase activity),GO:0004386(helicase activity)	K10742 DNA2; DNA replication ATP-dependent helicase/nuclease Dna2 [EC:5.6.2.3 3.1.-.-]	map03030 DNA replication	KOG1805[Hs20470741 DNA replication helicase	KAG2173226.1 hypothetical protein INT43_004600, partial [Umbelopsis isabellina]	DNA replication ATP-dependent helicase/nuclease DNA2 OS=Xenopus laevis OX=8355 GN=dna2 PE=1 SV=1
A0790	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0791	GO:0006996(organelle organization)	-	GO:0005515(protein binding)	-	-	-	KAG4093546.1 PH-domain-containing protein [Neocallimastix sp. JGI-2020a]	-
A0792	-	-	-	-	-	KOG0725[CE12990 Reductases with broad range of substrate specificities	XP_007813233.1 short-chain dehydrogenase/reductase [Metarhizium acridum CQMa 102]	Benzil reductase ((S)-benzoin forming) OS=Bacillus cereus OX=1396 GN=yueD PE=1 SV=1

A0793	GO:0015031(protein transport), GO:0006605(protein targeting), GO:0006886(intracellular protein transport)	GO:0016020(membrane)	GO:0008320(protein transmembrane transporter activity)	K07342 SEC61G, SSS1, secE; protein transport protein SEC61 subunit gamma and related proteins	map04145 Phagosome;map04141 Protein processing in endoplasmic reticulum;map03060 Protein export;map05110 Vibrio cholerae infection	KOG3498 CE05785 Preprotein translocase, gamma subunit	ORX87545.1 SecE-domain-containing protein [Anaeromyces robustus]	Protein transport protein Sec61 subunit gamma OS=Branchiostoma belcheri OX=7741 GN=SEC61G PE=3 SV=1
A0794	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K12599 SKI2, SKIV2L; antiviral helicase SKI2 [EC:3.6.4.13]	map03018 RNA degradation	-	XP_007298282.1 antiviral helicase [Stereum hirsutum FP-91666 SS1]	Putative ATP-dependent RNA helicase C550.03c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC550.03c PE=3 SV=1
A0795	-	-	-	-	-	-	-	-
A0796	-	-	GO:0005515(protein binding)	K20520 DBNL, ABP1; drebrin-like protein	-	KOG4225 Hs2043851 Sorbin and SH3 domain-containing protein	SGZ57452.1 CIC11C0000002547 [[Candida] intermedia]	SH3 domain-containing protein 19 OS=Homo sapiens OX=9606 GN=SH3D19 PE=1 SV=2
A0797	-	-	-	-	-	-	-	-
A0798	-	-	GO:0005525(GTP binding)	-	-	-	-	-
A0799	-	-	-	-	-	KOG0714 7296101 Molecular chaperone (DnaJ superfamily)	KAG1444585.1 hypothetical protein G6F56_010242 [Rhizopus deleamar]	DnaJ homolog subfamily B member 9 OS=Mus musculus OX=10090 GN=Dnajb9 PE=1 SV=2
A0800	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K08956 AFG3, AFG3 family protein [EC:3.4.24.-]	map05017 Spinocerebellar ataxia	KOG0731 At3g47060 AAA+-type ATPase containing the peptidase M41 domain	KAG0754271.1 hypothetical protein G6F24_012533 [Rhizopus oryzae]	ATP-dependent zinc metalloprotease FtsH OS=Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10) OX=518766 GN=ftsH PE=3 SV=1
A0801	-	-	GO:0005515(protein binding)	K12857 SNRNP40, PRP8BP; Prp8 binding protein	map03040 Spliceosome	-	RKO94023.1 WD repeat-containing protein 92-like protein [Blyttomyces helicus]	Dynein axonemal assembly factor 10 OS=Mus musculus OX=10090 GN=Dnaaf10 PE=1 SV=1
A0802	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG4686 Hs12232393 Predicted sugar transporter	XP_031026851.1 uncharacterized protein SmJEL517_g01304 [Synchytrium microbalum]	Major facilitator superfamily domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MFS1 PE=2 SV=2
A0803	-	-	GO:0016787(hydrolase activity)	-	-	KOG3947 Hs7427509 Phosphoesterases	RKP27380.1 Metallo-dependent phosphatase-like protein, partial [Syncephalis pseudoplumi galeata]	Metallophosphoesterase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=MPPED1 PE=1 SV=3
A0804	-	-	-	-	-	-	-	-

A0805	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	-	-	KOG0239 At4g05190 Kinesin (KAR3 subfamily)	KXS14690.1 kinesin-domain-containing protein [Gonapodya prolifera JEL478]	Kinesin-like protein KIN-14H OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14H PE=2 SV=1
A0806	-	-	-	-	-	-	-	-
A0807	-	-	-	-	-	-	-	-
A0808	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0809	-	-	GO:0005515(protein binding),GO:0001671(ATPase activator activity),GO:0051087(chaperone binding)	K05864 PPID; CYPD; peptidyl-prolyl isomerase D [EC:5.2.1.8]	map05131 Shigellosis;map04217 Necroptosis;map04218 Cellular senescence;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease	KOG0543 At5g48570 FKBP-type peptidyl-prolyl cis-trans isomerase	KFH45056.1 41 kDa peptidyl-prolyl cis-trans isomerase-like protein [Acremonium chrysogenum ATCC 11550]	Peptidyl-prolyl cis-trans isomerase FKBP65 OS=Arabidopsis thaliana OX=3702 GN=FKBP65 PE=1 SV=1
A0810	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0811	-	-	GO:0046872(metal ion binding),GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	K13195 CIRBP; cold-inducible RNA-binding protein	-	KOG0118 At4g13850 FOG:RRM domain	PTD08829.1 Glycine-rich RNA-binding protein 4, mitochondria I [Fusarium culmorum]	Glycine-rich RNA-binding protein 1 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=GRP1 PE=1 SV=1
A0812	-	-	-	-	-	-	-	-
A0813	GO:0009073(aromatic amino acid family biosynthetic process), GO:0009058(biosynthetic process)	-	GO:0003849(3-deoxy-7-phosphoheptulonate synthase activity)	K01626 E2.5.1.54, aroF, aroG, aroH; 3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways	-	TPX69845.1 hypothetical protein SpCBS45565_g02235 [Spizellomyces sp. 'palustris']	Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=aro4 PE=3 SV=1
A0814	-	-	-	-	-	-	-	-
A0815	-	-	-	-	-	-	XP_013319205.1 hypothetical protein PV05_03122 [Exophiala xenobiotica]	-
A0816	-	-	-	-	-	-	-	-

A0817	-	-	GO:0008237(metallopeptidase activity)	-	-	-	KAF8499119.1 Metallo-peptidase family M12-domain-containing protein [Russula emetica]	-
A0818	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	-	-	KOG0054 Hs5032101 Multidrug resistance-associated protein/mitochondrion resistance protein, ABC superfamily	OON11123.1 hypothetical protein BSLG_00236 [Batrachochytrium salamandrivorans]	ATP-binding cassette sub-family C member 5 OS=Rattus norvegicus OX=10116 GN=Abcc5 PE=2 SV=2
A0819	-	-	-	-	-	-	-	-
A0820	-	-	-	-	-	-	-	-
A0821	GO:0006081(cellular aldehyde metabolic process)	-	GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor);GO:0016491(oxidoreductase activity)	K00128 ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]	map00410 beta-Alanine metabolism;map00981 Insect hormone biosynthesis;map00770 Pantothenate and CoA biosynthesis;map00340 Histidine metabolism;map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map00903 Limonene degradation;map01240 Biosynthesis of cofactors;map00330 Arginine and proline metabolism;map01120 Microbial metabolism in	KOG2456 Hs21359829 Aldehyde dehydrogenase	KAG0245400.1 hypothetical protein BGW41_000027 [Actinomortella wolfii]	Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens OX=9606 GN=ALDH3A1 PE=1 SV=3
A0822	-	-	-	-	-	KOG1109 Hs20070349 Vacuole membrane protein VMP1	KAG4100933.1 hypothetical protein H8356DRAFT_933847 [Neocallimastix sp. JGI-2020a]	Vacuole membrane protein KMS1 OS=Arabidopsis thaliana OX=3702 GN=KMS1 PE=1 SV=1
A0823	GO:0046488(phosphatidylinositol metabolic process)	-	GO:0016307(phosphatidylinositol phosphate kinase activity)	K00889 PIP5K; 1-phosphatidylinositol-4-phosphate 5-kinase [EC:2.7.1.68]	map04144 Endocytosis;map05135 Yersinia infection;map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04070 Phosphatidylinositol signaling system;map04072 Phospholipase D signaling pathway;map04139 Mitophagy - yeast;map04666 Fc gamma R-mediated phagocytosis;map00562 Inositol phosphate metabolism;map04011 MAPK signaling pathway - yeast;map05231 Choline metabolism in	KOG0229 YDR208w Phosphatidylinositol-4-phosphate 5-kinase	SCU96670.1 LAFA_0G07492g1_1 [Lachancea sp. CBS 6924]	Phosphatidylinositol 4-phosphate 5-kinase MSS4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MSS4 PE=1 SV=2

A0824	GO:0006325(chromatin organization)	-	GO:0003677(DNA binding)	-	-	KOG2266 At4g26630 Chromatin-associated protein Dek and related proteins, contains SAP DNA binding domain	KAG4107762.1 hypothetical protein H8356DRAFT_1417119 [Neocallimastix sp. JGI-2020a]	DEK domain-containing chromatin-associated protein 3 OS=Arabidopsis thaliana OX=3702 GN=DEK3 PE=1 SV=1
A0825	-	-	-	-	-	-	-	-
A0826	-	-	-	-	-	-	-	-
A0827	GO:0006357(regulation of transcription by RNA polymerase II)	GO:0016592(mediator complex)	GO:0003712(transcription coregulator activity)	-	-	-	-	-
A0828	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0829	-	-	-	-	-	-	XP_031027090.1 uncharacterized protein SmJEL517_g00804 [Synchytrium microbalum]	Cilia- and flagella-associated protein 45 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP45 PE=1 SV=1
A0830	-	GO:0016020(membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	K05681 ABCG2, CD338; ATP-binding cassette, subfamily G (WHITE), member 2	map01523 Antifolate resistance;map04976 Bile secretion;map02010 ABC transporters	KOG0061 Hs20143975 Transporter, ABC superfamily (Breast cancer resistance protein)	PJF18591.1 ABC-2 type transporter domain-containing protein [Paramicrosporidium saccamoebae]	ATP-binding cassette subfamily G member 4 OS=Mus musculus OX=10090 GN=Abcg4 PE=1 SV=2
A0831	-	-	-	-	-	-	-	-
A0832	-	-	-	-	-	-	-	-
A0833	GO:0005975(carbohydrate metabolic process), GO:0030259(lipid glycosylation)	-	GO:0016758(hexosyltransferase activity)	K05841 E2.4.1.173; sterol 3beta-glucosyltransferase [EC:2.4.1.173]	-	KOG1192 At1g43620 UDP-glucuronosyl and UDP-glucosyl transferase	KLO14794.1 UDP-Glycosyltransferase/glycogen phosphorylase [Schizopora paradoxa]	Sterol 3-beta-glucosyltransferase OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1 / QM 1276 / 107) OX=344612 GN=atg26 PE=3 SV=1
A0834	GO:0006783(heme biosynthetic process)	GO:0016021(integral component of membrane)	GO:0008495(protoheme IX farnesyltransferase activity);GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups)	K02257 COX10, ctaB, cyoE; heme oxygenase [EC:2.5.1.141]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map01100 Metabolic pathways	KOG1380 Z797663 Heme A farnesyltransferase	KU51336.1 hypothetical protein M422DRAFT_26753 [Sphaerobolus stellatus SS14]	Protoheme IX farnesyltransferase, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=COX10 PE=2 SV=4
A0835	GO:0016192(vesicle-mediated transport)	GO:0016021(integral component of membrane)	-	-	-	-	-	-

A0836	GO:0080162(intracellular auxin transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A0837	-	-	-	-	-	-	-	-
A0838	-	-	-	-	-	-	KAG0163436.1 hypothetical protein DFQ30_000172 [Apophysomyces sp. BC1015]	CBS domain-containing protein CBSX3, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=CBSX3 PE=1 SV=1
A0839	-	-	GO:0071949(FAD binding)	-	-	KOG2614 At2g35660 Kynurenine 3-monooxygenase and related flavoprotein monooxygenases	TPX59863.1 hypothetical protein SpCBS45565.g07640 [Spizellomyces sp. 'palustris']	FAD-dependent urate hydroxylase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=hpxO PE=1 SV=1
A0840	GO:0000256(allantoic catabolic process),GO:0006097(glyoxylate cycle)	-	GO:0003824(catalytic activity),GO:0004037(allantoicase activity),GO:0004474(malate synthase activity)	K01477 alc, ALLC; allantoicase [EC:3.5.3.4]	map00230 Purine metabolism;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG1261 At5g03860 Malate synthase	KAF9946699.1 Allantoicase, partial [Mortierella alpina]	Probable allantoicase 1 OS=Burkholderia mallei (strain ATCC 23344) OX=243160 GN=alc1 PE=3 SV=1
A0841	GO:0006357(regulation of transcription by RNA polymerase II)	GO:0016592(mediator complex)	GO:0016538(cyclin-dependent protein serine/threonine kinase regulator activity)	K15161 CCNC, SSN8; cyclin-C	-	KOG0794 Hs4885119 CDK8 kinase-activating protein cyclin C	XP_031024041.1 uncharacterized protein SmJEL517_g04080 [Synchytrium microbalum]	Cyclin-C OS=Bos taurus OX=9913 GN=CCNC PE=2 SV=1
A0842	GO:0030041(actin filament polymerization),GO:0030833(regulation of actin filament polymerization),GO:0034314(Arp2/3 complex-mediated actin nucleation)	GO:0005885(Arp2/3 protein complex),GO:0015629(actin cytoskeleton)	-	K05758 ARPC2; actin related protein 2/3 complex, subunit 2	map04144 Endocytosis;map05135 Yersinia infection;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04810 Regulation of actin cytoskeleton;map04138 Autophagy - yeast;map05100 Bacterial invasion of epithelial cells;map04666 Fc gamma R-mediated phagocytosis;map04530 Tight junction	KOG2826 7298678 Actin-related protein Arp2/3 complex, subunit ARPC2	TPX46511.1 hypothetical protein SeLEV6574.g03201 [Synchytrium endobioticum]	Actin-related protein 2/3 complex subunit 2 OS=Drosophila melanogaster OX=7227 GN=Arpc2 PE=2 SV=2
A0843	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0140359(ABC-type transporter activity),GO:0005524(ATP binding)	K05643 ABCA3; ATP-binding cassette, subfamily A (ABC1), member 3	map02010 ABC transporters	KOG0059 At2g41700 Lipid exporter ABCA1 and related proteins, ABC superfamily	TPX71151.1 hypothetical protein SpCBS45565.g01187 [Spizellomyces sp. 'palustris']	ABC transporter A family member 1 OS=Arabidopsis thaliana OX=3702 GN=ABCA1 PE=2 SV=2

A0844	-	-	GO:0003824(catalytic activity)	K12603 CNOT6, CCR4; CCR4-NOT transcription complex subunit 6 [EC:3.1.13.4]	map03018 RNA degradation	KOG0620 At3g58560 Glucose-repressible alcohol dehydrogenase transcriptional effector CCR4 and related proteins	KAA1122437.1 Glucose-repressible alcohol dehydrogenase transcriptional effector [Puccinia graminis f. sp. tritici]	Carbon catabolite repressor protein 4 homolog 1 OS=Arabidopsis thaliana OX=3702 GN=CCR4-1 PE=2 SV=1
A0845	-	GO:0005643(nuclear pore)	GO:0017056(structural constituent of nuclear pore)	K14306 NUP62, NSP1; nuclear pore complex protein Nup62	map05014 Amyotrophic lateral sclerosis;map03013 Nucleocytoplasmic transport	KOG2196 Hs6912544 Nuclear porin	XP_006695774.1 hypothetical protein CHTT_0054390 [Chaetomium thermophilum var. thermophilum DSM 1495]	Nucleoporin NSP1 OS=Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719) OX=759272 GN=NSP1 PE=1 SV=1
A0846	-	-	-	-	-	-	KAF8273130.1 NADP+-dependent D-mannitol dehydrogenase [Lactarius quietus]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces ribosidificus OX=80859 GN=rbcM PE=3 SV=1
A0847	-	-	-	-	-	-	-	-
A0848	-	-	-	-	-	-	QRW12765.1 short chain dehydrogenase [Ceratobasidium sp. AG-Ba]	Very-long-chain 3-oxoacyl-CoA reductase 1 OS=Arabidopsis thaliana OX=3702 GN=KCR1 PE=1 SV=1
A0849	-	-	GO:0003824(catalytic activity)	K01557 FAHD1; acylpyruvate hydrolase [EC:3.7.1.5]	map01120 Microbial metabolism in diverse environments;map00350 Tyrosine metabolism;map01100 Metabolic pathways	KOG1535 At4g15940 Predicted fumarylacetoacetate hydrolase	PIA14433.1 hypothetical protein COEREDRAFT_46926 [Coemansia reversa NRRL 1564]	Acylpyruvase FAHD1, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=fahd1 PE=3 SV=1
A0850	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1543 CE14682 Cysteine proteinase Cathepsin L	OAL44930.1 cysteine proteinase [Pyrenochaeta sp. DS3sAY3a]	Cathepsin B-like cysteine proteinase 5 OS=Caenorhabditis elegans OX=6239 GN=cpr-5 PE=2 SV=1
A0851	GO:0055085(transmembrane transport)	-	-	K15108 SLC25A19, DNC, TPC1; solute carrier family 25 (mitochondrial thiamine pyrophosphate transporter), member 19	-	KOG0752 CE29222 Mitochondrial solute carrier protein	OAL07508.1 mitochondrial thiamine pyrophosphate carrier 1 [Stagonospora sp. SRC1IsM3a]	Mitochondrial thiamine pyrophosphate carrier 1 OS=Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) OX=321614 GN=TPC1 PE=3 SV=3
A0852	-	-	-	-	-	-	-	-
A0853	-	-	-	-	-	-	-	-
A0854	GO:0016579(protein ubiquitination),GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase)	K11855 USP36_42; ubiquitin carboxyl-terminal hydrolase 36/42 [EC:3.4.19.12]	-	KOG1868 HsM19923759 Ubiquitin C-terminal hydrolase	TPX43046.1 hypothetical protein SeMB42_g04876 [Synchytrium endobioticum]	Ubiquitin carboxyl-terminal hydrolase 2 OS=Mus musculus OX=10090 GN=Usp2 PE=1 SV=3
A0855	-	-	-	-	-	-	-	-

A0856	-	-	-	-	-	-	KNE66443.1 PAS domain S-box protein [Allomyces macrogynus ATCC 38327]	-
A0857	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0198 At1g54960 MEKK and related serine/threonine protein kinases	KDQ33324.1 hypothetical protein PLEOSDRAFT_1060999 [Pleurotus ostreatus PC15]	Mitogen-activated protein kinase kinase kinase NPK1 OS=Nicotiana tabacum OX=4097 GN=NPK1 PE=1 SV=1
A0858	-	-	GO:0016407(acyltransferase activity)	-	-	-	KAG0731861.1 hypothetical protein G6F23_014888 [Rhizopus oryzae]	N-acetyltransferase aca1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=aca1 PE=1 SV=1
A0859	-	-	-	-	-	-	-	-
A0860	-	-	-	-	-	-	-	-
A0861	GO:0018216(peptidyl-arginine methylation)	-	GO:0016274(protein-arginine N-methyltransferase activity)	K11434 PRMT1; type I protein arginine methyltransferase [EC:2.1.1.319]	map04068 FoxO signaling pathway;map04922 Glucagon signaling pathway	KOG1499 7299364 Protein arginine N-methyltransferase PRMT1 and related enzymes	KAF0514311.1 S-adenosyl-L-methionine-dependent methyltransferase [Gigaspora margarita]	Protein arginine N-methyltransferase 8 OS=Mus musculus OX=10090 GN=Prmt8 PE=1 SV=2
A0862	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0051082(unfolded protein binding)	K09495 CCT3, TRIC5; T-complex protein 1 subunit gamma	-	KOG0364 Hs20539011 Chaperonin complex component, TCP-1 gamma subunit (CCT3)	KXN72827.1 T-complex protein 1 subunit gamma [Conidiobolus coronatus NRRL 28638]	T-complex protein 1 subunit gamma OS=Thalassiosira weissflogii OX=1577725 PE=2 SV=1
A0863	-	-	-	-	-	KOG1039 At5g01520 Predicted E3 ubiquitin ligase	XP_016758329.1 uncharacterized protein SEP_MUDRAFT_119925 [Sphaerulina musiva SO2202]	E3 ubiquitin-protein ligase AIRP2 OS=Arabidopsis thaliana OX=3702 GN=AIRP2 PE=1 SV=1
A0864	-	-	-	-	-	-	-	-
A0865	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	KOG0118 At1g47500 FOG; RRM domain	XP_013021240.1 RNA-binding protein [Schizosaccharomyces cryophilus OY26]	Polyadenylate-binding protein RBP47C' OS=Arabidopsis thaliana OX=3702 GN=RBP47C' PE=2 SV=1

A0866	GO:0007264(small GTPase mediated signal transduction)	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K04393 CDC42; cell division control protein 42	map04360 Axon guidance;map05417 Lipid and atherosclerosis;map04144 Endocytosis;map05135 Yersinia infection;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04810 Regulation of actin cytoskeleton;map04722 Neurotrophin signaling pathway;map04510 Focal adhesion;map04933 AGE-RAGE signaling pathway in diabetic complications;map04912 GnRH	KOG0393[Hs16357472 Ras-related small GTPase, Rho type	XP_03338381.2.1 cell division control protein [Aaospheria arxii CBS 175.79]	Rho-related protein racB OS=Dictyostelium discoideum OX=44689 GN=racB PE=1 SV=1
A0867	-	-	-	-	-	-	-	-
A0868	-	-	-	K11493 RCC1; regulator of chromosome condensation	-	KOG1426[Hs4557026 FOG:RCC1 domain	KAF8724692.1 chromosome condensation (RCC1) repeat, partial [Rhizoctonia solani]	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens OX=9606 GN=HERC1 PE=1 SV=2
A0869	GO:0006974(cellular response to DNA damage stimulus),GO:0018142(protein-DNA covalent cross-linking)	-	GO:0003697(single-stranded DNA binding)	-	-	KOG2618[At2g26470 Uncharacterized conserved protein	XP_03102802.1.1 uncharacterized protein SmJEL517_g0134 [Synchytrium microbalum]	Abasic site processing protein HMCES OS=Gallus gallus OX=9031 GN=HMCES PE=2 SV=1
A0870	-	-	-	-	-	-	-	-
A0871	-	-	-	-	-	-	TPX34426.1 hypothetical protein SeMB42_g07324 [Synchytrium endobioticum]	-
A0872	-	-	GO:0005509(calcium ion binding)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	KOG4666[Hs8923446 Predicted phosphate acyltransferase, contains PlsC domain	EDV12918.1 calcineurin regulatory B subunit [Saccharomyces cerevisiae RM11-1a]	Lysophosphatidylcholine acyltransferase 2 OS=Mus musculus OX=10090 GN=Lpcat2 PE=1 SV=1

A0873	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG0239 At5g65930.2 Kinesin (KAR3 subfamily)	XP_022459332.1 uncharacterized protein KUCA_T00003315001 [Kuraishia capsulata CBS 1993]	Kinesin-like protein KIN-14E OS=Arabidopsis thaliana OX=3702 GN=KIN14E PE=1 SV=1
A0874	GO:0006996(organelle organization)	-	-	K03255 TIF31, CLU1; protein TIF31	-	-	KAG2188485.1 hypothetical protein INT44_001239 [Umbelopsis vinacea]	-
A0875	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG0240 7302958 Kinesin (SMY1 subfamily)	KXN72330.1 kinesin-domain-containing protein [Conidiobolus coronatus NRRL 28638]	Kinesin heavy chain OS=Drosophila melanogaster OX=7227 GN=Khc PE=1 SV=2
A0876	GO:1901642(nucleoside transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005337(nucleoside transmembrane transporter activity)	-	-	KOG1479 Hs10835019 Nucleoside transporter	RKO99029.1 hypothetical protein CXG81DRAFT_28181 [Caulochytrium protostelioides]	-
A0877	-	-	-	-	-	-	-	-
A0878	GO:0008610(lipid biosynthetic process)	-	-	-	-	KOG3628 Hs2067353 Predicted AMP-binding protein	TPX56549.1 hypothetical protein PhCBS80983_g04458 [Powellomyces hirtus]	Long-chain-fatty-acid--AMP ligase FadD32 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=fadD32 PE=3 SV=1

A0879	GO:0006397(mRNA processing)	GO:0005634(nucleus)	GO:0004721(phosphoprotein phosphatase activity)	-	-	KOG2424 At1g73820 Protein involved in transcription start site selection	KAG0092673.1 RNA polymerase II subunit A C-terminal domain phosphatase [Podila epiciadia]	RNA polymerase II subunit A C-terminal domain phosphatase SSU72 OS=Danio rerio OX=7955 GN=ssu72 PE=2 SV=1
A0880	-	-	GO:0005509(calcium ion binding)	-	-	-	XP_018291688.1 hypothetical protein PHYBLDRAFT_177506 [Phycomyces blakesleeanus NRRL 1555(-)]	Membrane-bound O-acyltransferase gup1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=gup1 PE=3 SV=4
A0881	-	-	-	-	-	-	-	-
A0882	-	-	GO:0005515(protein binding)	K04649 UBE2K, HIP2, UBC1; ubiquitin-conjugating enzyme (huntingtin interacting protein 2) [EC:2.3.2.23]	map04120 Ubiquitin mediated proteolysis	KOG0418 At5g50870 Ubiquitin-protein ligase	CCE72456.1 PISO0_000027 [Milleriozyma farinosa CBS 7064]	Ubiquitin-conjugating enzyme E2 27 OS=Arabidopsis thaliana OX=3702 GN=UBC27 PE=2 SV=1
A0883	-	-	-	-	-	-	-	-
A0884	-	-	-	-	-	-	-	-
A0885	-	-	-	-	-	-	-	-
A0886	-	-	-	-	-	-	-	-
A0887	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K14545 RRP7; ribosomal RNA-processing protein 7	map03008 Ribosome biogenesis in eukaryotes	KOG4008 At5g38720 rRNA processing protein RRP7	PKK79274.1 hypothetical protein RhiirC2_769282 [Rhizophagus irregularis]	Ribosomal RNA-processing protein 7 homolog A OS=Homo sapiens OX=9606 GN=RRP7A PE=1 SV=2
A0888	GO:0006508(proteolysis),GO:0036211(protein modification process)	-	GO:0004177(aminopeptidase activity),GO:0008270(zinc ion binding)	-	-	KOG2596 At5g60160 Aminopeptidase I zinc metalloprotease (M18)	KAG0274812.1 hypothetical protein BGZ95_009435 [Linnemannia exigua]	Probable aspartyl aminopeptidase OS=Ricinus communis OX=3988 GN=RCOM_1506700 PE=2 SV=2
A0889	-	-	-	-	-	-	-	-
A0890	-	-	-	-	-	-	-	-
A0891	-	-	-	-	-	KOG4099 Hs20533122 Predicted membrane protein	XP_018291183.1 hypothetical protein PHYBLDRAFT_78171 [Phycomyces blakesleeanus NRRL 1555(-)]	FUN14 domain-containing protein 1 OS=Tetraodon nigroviridis OX=99883 GN=fundc1 PE=3 SV=1
A0892	-	-	-	-	-	-	-	-
A0893	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0894	-	-	-	-	-	KOG3861 Hs7705769 Sensory cilia assembly protein	TPX66906.1 hypothetical protein CcCBS67573_g07676 [Chytridiomycetes confervae]	Intraflagellar transport protein 52 homolog OS=Mus musculus OX=10090 GN=ift52 PE=1 SV=2
A0895	-	-	-	-	-	-	-	-

A0896	GO:0006281(DNA repair)	-	GO:0004518(nuclease activity),GO:0003824(catalytic activity)	K10771 APEX1; AP endonuclease 1 [EC:3.1.11.2]	map03410 Base excision repair	KOG1294 At2g41460 Apurinic/apyrimidinic endonuclease and related enzymes	RKP10385.1 Endonuclease/exonuclease/phosphatase [Thamnocephalis sphaerospora]	DNA-(apurinic or apyrimidinic site) endonuclease, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ARP PE=1 SV=2
A0897	-	-	-	-	-	-	KAG0775949.1 hypothetical protein G6F22_012931 [Rhizopus oryzae]	-
A0898	-	-	GO:0004364(glutathione transferase activity)	-	-	KOG2903 At5g45020 Predicted glutathione S-transferase	OBZ90567.1 Glutathione S-transferase omega-like 2 [Choanephora cucurbitarum]	Glutathionyl-hydroquinone reductase YqjG OS=Escherichia coli (strain K12) OX=83333 GN=yqjG PE=1 SV=1
A0899	GO:0016560(protein import into peroxisome matrix, docking)	GO:0005778(peroxisomal membrane)	GO:0005515(protein binding)	K13343 PEX14; peroxin-14	map04146 Peroxisome	-	-	-
A0900	-	-	-	-	-	-	-	-
A0901	GO:0035434(copper ion transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005375(copper ion transmembrane transporter activity)	-	-	KOG3386 Hs4507015 Copper transporter	-	High affinity copper uptake protein 1 OS=Rattus norvegicus OX=10116 GN=Slc31a1 PE=2 SV=1
A0902	-	-	GO:0005515(protein binding)	K20526 TAGLN; transgelin	-	KOG2046 7303337 Calponin	KXS15507.1 hypothetical protein M427DRAFT_56613 [Gonapodya prolifera JEL478]	Myophilin OS=Echinococcus granulosus OX=6210 PE=2 SV=1
A0903	GO:0055085(transmembrane transport),GO:1990547(mitochondrial phosphate ion transmembrane transport)	-	GO:0005315(organic phosphate transmembrane transporter activity)	K15102 SLC25A3, PHC, PIC; solute carrier family 25 (mitochondrial phosphate transporter), member 3	-	KOG0767 YJR077c Mitochondrial phosphate carrier protein	RKO88852.1 mitochondrial carrier family [Blytiomyces helicus]	Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIR1 PE=1 SV=1
A0904	-	GO:0005740(mitochondrial envelope),GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0005515(protein binding)	-	-	-	-	-
A0905	GO:0070475(rRNA base methylation)	-	GO:0070042(rRNA (uridine-N3-)-methyltransferase activity)	K19307 BMT5; 25S rRNA (uracil2634-N3)-methyltransferase [EC:2.1.1.313]	-	KOG4174 Hs14770439_1 Uncharacterized conserved protein	KAF2418669.1 hypothetical protein EJ08DRAFT_572444, partial [Tothia fuscilla]	Ferredoxin-fold anticodon-binding domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FDXACB1 PE=1 SV=3
A0906	-	-	GO:0005515(protein binding)	-	-	-	-	-

A0907	GO:0006508(proteolysis)	-	GO:0005515(protein binding),GO:0004252(serine-type endopeptidase activity)	K22686 NMA111; pro-apoptotic serine protease NMA111 [EC:3.4.21.-]	-	-	XP_01660658.7.1 hypothetical protein SPPG_06237 [Spizellomyces punctatus DAOM BR117]	Protease Do-like 7 OS=Arabidopsis thaliana OX=3702 GN=DEGP7 PE=2 SV=1
A0908	GO:0007015(actin filament organization)	-	-	-	-	-	-	-
A0909	-	-	GO:0005515(protein binding)	K24752 WDR70; WD repeat-containing protein 70	-	KOG0772 7291643 Uncharacterized conserved protein, contains WD40 repeat	KAF9329258.1 hypothetical protein BG006_007643 [Podila minutissima]	Gastrulation defective protein 1 homolog OS=Drosophila melanogaster OX=7227 GN=CG5543 PE=2 SV=1
A0910	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	K14265 Tam1; tryptophan aminotransferase [EC:2.6.1.27]	map00380 Tryptophan metabolism;map01100 Metabolic pathways	KOG0634 Hs7705897 Aromatic amino acid aminotransferase and related proteins	TPX40790.1 hypothetical protein SeLEV6574_g06410 [Synchytrium endobioticum]	Aromatic amino acid aminotransferase DDB_G0287711 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0287711 PE=3 SV=1
A0911	-	-	-	-	-	-	-	-
A0912	GO:0018193(peptidyl-amino acid modification)	-	-	-	-	KOG3696 Hs14589866 Aspartyl beta-hydroxylase	KGQ02391.1 Aspartyl/asparaginyl beta-hydroxylase [Beauveria bassiana D1-5]	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens OX=9606 GN=ASPH PE=1 SV=3
A0913	-	-	-	-	-	-	-	-
A0914	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0008569(minus-end-directed microtubule motor activity)	K10413 DYNC1H1; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595 Hs19115954 Dyneins, heavy chain	XP_016610510.1 hypothetical protein SPPG_02933 [Spizellomyces punctatus DAOM BR117]	Dynein gamma chain, flagellar outer arm OS=Chlamydomonas reinhardtii OX=3055 GN=ODA2 PE=1 SV=1
A0915	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	-	-	-	-	-
A0916	GO:0016042(lipid catabolic process)	-	GO:0016787(hydrolase activity)	-	-	-	TPX36103.1 hypothetical protein SeMB42_g07103 [Synchytrium endobioticum]	-
A0917	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	-	-	KOG3627 7295687 Trypsin	OJ 99917.1 hypothetical protein ASPVEDRAFT_90323, partial [Aspergillus versicolor CBS 583.65]	Trypsin 5G1 OS=Aedes aegypti OX=7159 GN=AAEL013712 PE=2 SV=2

A0918	GO:0006384(transcription initiation from RNA polymerase III promoter)	GO:0000127(transcription factor TFIIC complex)	GO:0003677(DNA binding)	-	-	-	-	-
A0919	-	-	GO:0016780(phosphotransferase activity, for other substituted phosphate groups)	-	-	-	KAF9093880.1 hypothetical protein BGX23_002772 [Mortierella sp. AD031]	-
A0920	-	-	GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG1198 At1g23740 Zinc-binding oxidoreductase	KAG2177387.1 hypothetical protein INT44_007898 [Umbelopsis vinacea]	2-methylene-furan-3-one reductase OS=Fragaria ananassa OX=3747 GN=EO PE=1 SV=2
A0921	GO:0032012(regulation of ARF protein signal transduction)	-	GO:0005085(guananyl-nucleotide exchange factor activity)	K18442 ARFGEF, BIG; brefeldin A-inhibited guanine nucleotide-exchange protein	map04144 Endocytosis	KOG0930 Hs4758964 Guanine nucleotide exchange factor Cytohesin, contains PH and Sec7 domains	ORX56493.1 Sec7-domain-containing protein [Piromyces finnis]	Cytohesin-1 OS=Chlorocebus aethiops OX=9534 GN=CYTH1 PE=2 SV=1
A0922	-	-	-	-	-	-	-	-
A0923	GO:0090090(negative regulation of canonical Wnt signaling pathway)	GO:0005856(cytoskeleton),GO:0097730(non-motile cilium)	GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	-	OON07509.1 hypothetical protein BSLG_03031 [Batrachochytrium salamandrivorans]	Nephrocystin-4 OS=Homo sapiens OX=9606 GN=NPHP4 PE=1 SV=2
A0924	-	-	-	-	-	-	PRQ78083.1 hypothetical protein AAT19DRAFT_9151 [Rhodotorula toruloides]	Protein ENHANCED DISEASE RESISTANCE 2 OS=Arabidopsis thaliana OX=3702 GN=EDR2 PE=2 SV=1
A0925	-	-	-	-	-	-	-	-
A0926	GO:0006851(mitochondrial calcium ion transmembrane transport)	-	GO:0005509(calcium ion binding)	-	-	KOG2643 Hs20548380 Ca2+ binding protein, contains EF-hand motifs	TPX68867.1 hypothetical protein SpCBS45565_g02827 [Spizellomyces sp. 'palustris']	Calcium uptake protein 2, mitochondrial OS=Homo sapiens OX=9606 GN=MICU2 PE=1 SV=2
A0927	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	K06902 UMF1; MFS transporter, UMF1 family	map04138 Autophagy - yeast	-	PKY50729.1 MFS general substrate transporter [Rhizophagus irregularis]	Autophagy-related protein 22 OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294 / BCRC 21397 / CBS 2163 / NBRC 10782 / NRRL Y-8283 / UCD 57-17) OX=436907 GN=ATG22 PE=3 SV=1

A0928	-	-	-	K06902 UMF1; MFS transporter, UMF1 family	map04138 Autophagy - yeast	-	XP_02267359 2.1 autophagy- related protein 22 [Kluyveromyc es marxianus DMKU3- 1042]	-
A0929	-	-	-	-	-	-	-	-
A0930	-	-	-	-	-	-	-	-
A0931	-	-	-	-	-	-	-	-
A0932	-	-	-	K13120 FAM32A; protein FAM32A	-	KOG3410 Hs7 661696 Conserved alpha-helical protein	KAF9513592. 1 hypothetical protein BS47DRAFT_ 1344070 [Hydnum rufescens UP504]	Protein FAM32A OS=Xenopus tropicalis OX=8364 GN=fam32a PE=3 SV=1
A0933	GO:00704 75(rRNA base methylation)	-	GO:0070042(rR NA (uridine- N3-)- methyltransferas e activity)	K19307 BMT5; 25S rRNA (uracil2634- N3)- methyltransfe rase [EC:2.1.1.313]	-	KOG4174 At5 g56060 Uncharacteriz ed conserved protein	ORZ37636.1 hypothetical protein BCR44DRAFT_ 39563 [Catenaria anguillulae PL171]	Uncharacterized protein At4g26485 OS=Arabidopsis thaliana OX=3702 GN=At4g26485 PE=4 SV=1
A0934	-	-	-	-	-	-	-	-
A0935	-	-	-	-	-	-	-	-
A0936	-	-	-	-	-	-	-	-
A0937	-	-	-	-	-	KOG3599 Hs7 706639 Ca2+- modulated nonselective cation channel polycystin	-	Polycystin-2 OS=Bos taurus OX=9913 GN=PKD2 PE=2 SV=1
A0938	-	-	GO:0005515(pro tein binding),GO:000 3824(catalytic activity),GO:001 6715(oxidoredu ctase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced ascorbate as one donor, and incorporation of one atom of oxygen)	-	-	KOG3567 Hs2 1070980 Peptidylglycin e alpha- amidating monooxygen ase	-	Peptidyl-glycine alpha-amidating monooxygenase B OS=Xenopus laevis OX=8355 GN=pam-b PE=2 SV=1
A0939	-	-	GO:0003724(RN A helicase activity),GO:000 5524(ATP binding),GO:000 3676(nucleic acid binding)	K11594 DDX3X, bel; ATP- dependent RNA helicase DDX3X [EC:3.6.4.13]	map04622 RIG- I-like receptor signaling pathway;map05 203 Viral carcinogenesis; map05161 Hepatitis B	KOG0335 Hs1 3514813 ATP- dependent RNA helicase	EJU03568.1 DEAD- domain- containing protein [Dacryopinax primogenitus]	ATP-dependent RNA helicase DED1 OS=Coccidioides immitis (strain RS) OX=246410 GN=DED1 PE=3 SV=2
A0940	-	-	-	K25866 NUDC; nuclear migration protein NudC	-	KOG2265 CE 16096 Nuclear distribution protein NUDC	XP_02346491 9.1 CS- domain- containing protein [Rhizopus microsporus ATCC 52813]	Protein BOBBER 1 OS=Arabidopsis thaliana OX=3702 GN=BOB1 PE=1 SV=1

A0941	GO:0009396(folic acid-containing compound biosynthetic process), GO:000958(biosynthetic process)	-	GO:0004326(tetrahydrofolylpolyglutamate synthase activity),GO:0005524(ATP binding),GO:0016881(acid-amino acid ligase activity)	-	-	-	RUS18238.1 Mur ligase [Endogone sp. FLAS-F59071]	Probable bifunctional folylpolyglutamate synthase/dihydropteroate synthase OS=Haloflex volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) OX=309800 GN=folCP PE=3 SV=1
A0942	-	-	-	-	-	-	ORY38847.1 hypothetical protein BCR33DRAFT_700354 [Rhizoclostium globosum]	Coiled-coil domain-containing protein 113 OS=Homo sapiens OX=9606 GN=CCDC113 PE=1 SV=1
A0943	-	-	-	-	-	-	-	-
A0944	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07937 ARF1_2; ADP-ribosylation factor 1/2	map04144 Endocytosis;map05134 Legionellosis;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04072 Phospholipase D signaling pathway;map05110 Vibrio cholerae infection	KOG0070[Hs14149815 GTP-binding ADP-ribosylation factor Arf1	XP_006682559.1 uncharacterized protein BATDEDRAFT_14608 [Batrachochytrium dendrobatidis JAM81]	ADP-ribosylation factor-like protein 6 OS=Homo sapiens OX=9606 GN=ARL6 PE=1 SV=1
A0945	-	-	-	-	-	KOG2205[At1g58350 Uncharacterized conserved protein	TPX75904.1 hypothetical protein CcCBS67573_g02815 [Chytridiomycetes confervae]	Protein FAM135A OS=Mus musculus OX=10090 GN=Fam135a PE=1 SV=2
A0946	GO:0007010(cytoskeleton organization)	-	GO:0005515(protein binding),GO:0003779(actin binding),GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K09568 FKBP1; FK506-binding protein 1 [EC:5.2.1.8]	-	KOG0543[At5g48570 FKBP-type peptidyl-prolyl cis-trans isomerase	KEY81875.1 peptidyl prolyl isomerase FKBP type [Aspergillus fumigatus var. RP-2014]	FK506-binding protein 1B OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=fpr1B PE=3 SV=1
A0947	-	-	-	-	-	-	-	-

A0948	GO:0008652 (cellular amino acid biosynthetic process), GO:0009086 (methionine biosynthetic process), GO:0009088 (threonine biosynthetic process), GO:0009089 (lysine biosynthetic process via diaminopimelate), GO:0009097 (isoleucine biosynthetic process)	-	GO:0016620 (oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor), GO:0051287 (NAD binding), GO:0046983 (protein dimerization activity), GO:004073 (aspartate-semialdehyde dehydrogenase activity), GO:0050661 (NADP binding)	K00133 asd; aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	map00300 Lysine biosynthesis; map01110 Biosynthesis of secondary metabolites; map01120 Microbial metabolism in diverse environments; map01230 Biosynthesis of amino acids; map00261 Monobactam biosynthesis; map00260 Glycine, serine and threonine metabolism; map01100 Metabolic pathways; map01210 2-Oxocarboxylic acid metabolism; map00270 Cysteine and methionine metabolism	KOG4777 At1g14810 Aspartate-semialdehyde dehydrogenase	KAG1453884.1 hypothetical protein G6F57_015629 [Rhizopus oryzae]	Aspartate-semialdehyde dehydrogenase OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=asd PE=3 SV=2
A0949	-	-	GO:0005515 (protein binding)	-	-	-	-	Leucine-rich repeat-containing protein 36 OS=Mus musculus OX=10090 GN=Lrrc36 PE=1 SV=2
A0950	GO:0000413 (protein peptidyl-prolyl isomerization)	-	GO:0003755 (peptidyl-prolyl cis-trans isomerase activity)	-	-	-	-	-
A0951	-	-	-	-	-	-	EPZ33996.1 NAD(P)-binding domain-containing protein [Rozella allomycis CSF55]	1-hydroxy-2-glutathionyl-2-methyl-3-butene dehydrogenase OS=Rhodococcus sp. (strain AD45) OX=103808 GN=isoH PE=1 SV=1
A0952	GO:0006412 (translation)	GO:0015935 (small ribosomal subunit)	GO:0003735 (structural constituent of ribosome), GO:0003723 (RNA binding)	K02989 RP-S5e, RPS5; small subunit ribosomal protein S5e	map05171 Coronavirus disease - COVID-19; map03010 Ribosome	KOG3291 Hs13904870 Ribosomal protein S7	XP_006678213.1 uncharacterized protein BATDEDRAFT_87732 [Batrachochytrium dendrobatidis JAM81]	Small ribosomal subunit protein uS7 (Fragment) OS=Cicer arietinum OX=3827 GN=RPS5 PE=2 SV=1
A0953	GO:0006468 (protein phosphorylation)	-	GO:0004672 (protein kinase activity), GO:0005524 (ATP binding)	-	-	KOG0661 Hs7662388 MAPK related serine/threonine protein kinase	RKO86701.1 kinase-like domain-containing protein, partial [Blyttiomycetes helicus]	Serine/threonine-protein kinase ICK OS=Mus musculus OX=10090 GN=Cilk1 PE=1 SV=2
A0954	-	-	GO:0005515 (protein binding)	-	-	KOG1769 At5g55160 Ubiquitin-like proteins	KAF8198199.1 small ubiquitin-related modifier [Mycena galopus ATCC 62051]	Small ubiquitin-related modifier 3-like OS=Danio rerio OX=7955 GN=sumo3l PE=3 SV=1

A0955	GO:0019722(calci m- mediated signaling)	-	GO:0005509(cal cium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04 022 cGMP-PKG signaling pathway;map04 020 Calcium signaling pathway;map05 417 Lipid and atherosclerosis; map05133 Pertussis;map04 722 Neurotrophin signaling pathway;map04 218 Cellular senescence;map 04070 Phosphatidyli nitol signaling system;map0491 5 Estrogen signaling pathway;map04 912 GnRH signaling pathway;map04 910 Insulin	KOG0027 At1 g66410 Calmodulin and related proteins (EF- Hand superfamily)	XP_01661105 0.1 calmodulin [Spizellomyces punctatus DAOM BR117]	Calmodulin OS=Globisporangium splendens OX=82926 PE=2 SV=1
A0956	GO:0006470(protein dephosph orylation)	-	GO:0004722(pro tein serine/threonine phosphatase activity)	-	-	-	-	-
A0957	-	-	GO:0004518(nu clease activity),GO:000 5515(protein binding)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518 YO R033c 5'-3' exonuclease	KAF8515840. 1 PIN domain-like protein [Hysterangium stoloniferum]	Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EXO1 PE=1 SV=2
A0958	-	-	-	-	-	-	-	-
A0959	-	-	GO:0005515(pro tein binding)	-	-	-	-	-
A0960	GO:0051276(chrom osome organizati on)	GO:0005694(chrom osome)	GO:0005515(pro tein binding),GO:000 5524(ATP binding),GO:001 6887(ATP hydrolysis activity)	-	-	KOG0996 At5 g48600 Structural maintenance of chromosome protein 4 (chromosom e condensation complex Condensin, subunit C)	RKP39574.1 RecF/RecN/S MC [Dimargaris crystalligena]	Structural maintenance of chromosomes protein 4 OS=Arabidopsis thaliana OX=3702 GN=SMC4 PE=1 SV=1
A0961	-	-	-	-	-	-	-	-
A0962	GO:0030163(protein catabolic process), GO:0006811(ion transport), GO:0055085(transm embrane transport)	GO:0005737(cytopl asm),GO: 0016020(membran e)	GO:0005524(AT P binding),GO:001 6887(ATP hydrolysis activity),GO:003 6402(proteasom e-activating activity),GO:000 5216(ion channel activity)	K03061 PSMC2, RPT1; 26S proteasome regulatory subunit T1	map05014 Amyotrophic lateral sclerosis;map050 20 Prion disease;map050 22 Pathways of neurodegenerati on - multiple diseases;map030 50 Proteasome;ma p05010 Alzheimer disease;map050 12 Parkinson disease;map050 17 Spinocerebellar ataxia;map05016 Huntington disease;map051 69 Epstein-Barr virus infection	KOG0729 At1 g53750 26S proteasome regulatory complex, ATPase RPT1	KXN71323.1 26S protease regulatory subunit 7 [Conidiobolus coronatus NRRL 28638]	26S proteasome regulatory subunit 7A OS=Oryza sativa subsp. japonica OX=39947 GN=RPT1A PE=2 SV=1

A0963	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity);GO:0005524(ATP binding);GO:0008017(microtubule binding)	K10398 KIF11, EG5; kinesin family member 11	map04814 Motor proteins	KOG0243[At2g28620 Kinesin-like protein	ORX77302.1 kinesin-domain-containing protein, partial [Basidiobolus meristosporus CBS 931.73]	Kinesin-like protein KIF11-B OS=Xenopus laevis OX=8355 GN=kif11-b PE=1 SV=2
A0964	GO:0000413(protein peptidyl-prolyl isomerization)	-	GO:0003723(RNA binding);GO:0003755(peptidyl-prolyl cis-trans isomerase activity);GO:0003676(nucleic acid binding)	K12735 PPIL4; peptidyl-prolyl cis-trans isomerase-like 4 [EC:5.2.1.8]	-	KOG0415[Hs20911035 Predicted peptidyl-prolyl cis-trans isomerase	RKP07448.1 cyclophilin-like domain-containing protein, partial [Thamnocephalus sphaerospora]	Peptidyl-prolyl cis-trans isomerase-like 4 OS=Homo sapiens OX=9606 GN=PPIL4 PE=1 SV=1
A0965	-	-	-	-	-	-	-	-
A0966	-	-	-	-	-	-	-	-
A0967	GO:0007017(microtubule-based process)	GO:0005874(microtubule)	GO:0005525(GTP binding);GO:0003924(GTPase activity);GO:0005200(structural constituent of cytoskeleton)	K07375 TUBB; tubulin beta	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins;map04540 Gap junction;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG1375[Hs5174735 Beta tubulin	XP_006680448.1 Alpha-Beta tubulin [Batrachochytrium dendrobatidis JAM81]	Tubulin beta chain OS=Tetrahymena thermophila OX=5911 GN=BTU1 PE=1 SV=1
A0968	-	-	-	-	-	-	-	-
A0969	-	-	GO:0005515(protein binding)	-	-	-	-	-
A0970	GO:0036211(protein modification process)	-	-	-	-	KOG2157[7301272 Predicted tubulin-tyrosine ligase	OON10004.1 hypothetical protein BSLG_01082 [Batrachochytrium salamandrivorans]	Tubulin polyglutamylase TTL5 OS=Homo sapiens OX=9606 GN=TTL5 PE=1 SV=3
A0971	GO:0043622(cortical microtubule organization)	-	-	-	-	-	-	Protein SPIRAL1-like 1 OS=Arabidopsis thaliana OX=3702 GN=SP1L1 PE=2 SV=1
A0972	-	-	-	K01514 PRUNE, PPX1; exopolyphosphatase [EC:3.6.1.11]	map00230 Purine metabolism;map01100 Metabolic pathways	-	KAF9114746.1 hypothetical protein BGX30_006509 [Mortierella sp. GBA39]	Probable manganese-dependent inorganic pyrophosphatase OS=Staphylococcus epidermidis (strain ATCC 12228 / FDA PCI 1200) OX=176280 GN=ppaC PE=3 SV=1

A0973	-	-	-	K01904 4CL; 4-coumarate--CoA ligase [EC:6.2.1.12]	map01110 Biosynthesis of secondary metabolites;map00940 Phenylpropanoid biosynthesis;map00130 Ubiquinone and other terpenoid-quinone biosynthesis;map01100 Metabolic pathways	KOG1176 At1g51680 Acyl-CoA synthetase	XP_016606865.1 hypothetical protein SPPG_05802 [Spizellomyces punctatus DAOM BR117]	4-coumarate--CoA ligase 1 OS=Petroselinum crispum OX=4043 GN=4CL1 PE=2 SV=1
A0974	-	-	-	-	-	-	KAG2178951.1 hypothetical protein INT43_001798 [Umbelopsis isabellina]	Beta-lactamase domain-containing protein 2 OS=Caenorhabditis elegans OX=6239 GN=lact-2 PE=4 SV=1
A0975	-	-	-	-	-	-	-	-
A0976	-	-	GO:0005515(protein binding)	K14829 IPI3; pre-rRNA-processing protein IPI3	-	KOG0646 At3g49180 WD40 repeat protein	-	Protein ROOT INITIATION DEFECTIVE 3 OS=Arabidopsis thaliana OX=3702 GN=RID3 PE=1 SV=1
A0977	-	-	-	-	-	-	XP_031026482.1 uncharacterized protein SmJEL517_g01438 [Synchytrium microbalum]	Beta-lactamase domain-containing protein 2 OS=Caenorhabditis elegans OX=6239 GN=lact-2 PE=4 SV=1
A0978	GO:0006631(fatty acid metabolic process)	-	GO:0004467(long-chain fatty acid-CoA ligase activity)	K01897 ACSL; fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04146 Peroxisome;map04216 Ferroptosis;map04714 Thermogenesis;map00061 Fatty acid biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation;map04920 Adipocytokine signaling pathway	KOG1256 At5g27600 Long-chain acyl-CoA synthetases (AMP-forming)	RKP19201.1 acetyl-CoA synthetase-like protein [Rozella allomyces CSF55]	Long chain acyl-CoA synthetase 7, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=LACS7 PE=1 SV=2
A0979	-	-	-	-	-	KOG2621 7293554 Prohibitins and stomatins of the PID superfamily	ORX76090.1 hypothetical protein BCR32DRAFT_329524 [Anaeromyces robustus]	Stomatin OS=Homo sapiens OX=9606 GN=STOM PE=1 SV=3
A0980	GO:0006821(chloride transport) GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005247(voltage-gated chloride channel activity)	-	-	-	-	Putative ion-transport protein YfeO OS=Salmonella schwarzengrund (strain CVM19633) OX=439843 GN=yfeO PE=3 SV=1

A0981	-	-	-	K17286 STOM; stomatin	-	KOG2621 729 3554 Prohibitins and stomatins of the PID superfamily	KAG4092517. 1 hypothetical protein H8356DRAFT _1702108 [Neocallimast ix sp. JGI- 2020a]	Stomatin OS=Homo sapiens OX=9606 GN=STOM PE=1 SV=3
A0982	GO:00004 13(protein peptidyl- prolyl isomerizat ion),GO:0 006457(pr otein folding)	-	GO:0003755(pe ptidyl-prolyl cis-trans isomerase activity),GO:000 5515(protein binding)	K01802 E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]	-	KOG0865 At5 g58710 Cyclophilin type peptidyl- prolyl cis- trans isomerase	KAG2192848. 1 hypothetical protein INT46_01087 5 [Mucor plumbeus]	Peptidyl-prolyl cis-trans isomerase CYP20-1 OS=Arabidopsis thaliana OX=3702 GN=CYP20-1 PE=1 SV=1
A0983	-	-	GO:0008418(pro tein-N-terminal asparagine amidohydrolase activity)	-	-	-	-	-
A0984	GO:00516 03(proteo lysis involved in cellular protein catabolic process), GO:00104 98(protea somal protein catabolic process)	GO:00058 39(protea some core complex)	-	K02734 PSMB2; 20S proteasome subunit beta 4 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map050 20 Prion disease;map050 22 Pathways of neurodegenerati on - multiple diseases;map030 50 Proteasome;ma p05010 Alzheimer disease;map050 12 Parkinson disease;map050 17 Spinocerebellar ataxia;map05016 Huntington disease	KOG0177 At4 g14800 20S proteasome, regulatory subunit beta type PSMB2/PRE1	EPZ31979.1 Proteasome, beta-type subunit domain- containing protein [Rozella allomycis CSF55]	Proteasome subunit beta type-2-B OS=Arabidopsis thaliana OX=3702 GN=PBD2 PE=1 SV=1
A0985	-	-	-	-	-	KOG1011 730 4376 Neurotransmi tter release regulator, UNC-13	KAF9948731. 1 hypothetical protein BGZ72_00941 0, partial [Mortierella alpina]	Fer-1-like protein 6 OS=Homo sapiens OX=9606 GN=FER1L6 PE=2 SV=2
A0986	-	-	-	K07018 K07018; uncharacteriz ed protein	-	-	SAL96903.1 hypothetical protein [Absidia glauca]	Uncharacterized protein RP471 OS=Rickettsia prowazekii (strain Madrid E) OX=272947 GN=RP471 PE=4 SV=1
A0987	GO:00090 58(biosyn thetic process)	-	GO:0030170(pyr idoxal phosphate binding),GO:000 3824(catalytic activity)	K00654 SPT; serine palmitoyltran sferase [EC:2.3.1.50]	map04071 Sphingolipid signaling pathway;map00 600 Sphingolipid metabolism;map 04138 Autophagy - yeast;map01100 Metabolic pathways	KOG1358 Hs5 454084 Serine palmitoyltran sferase	KAG0176138. 1 serine palmitoyltran sferase component [Apophysom yces sp. BC1021]	Serine palmitoyltransferase 1 OS=Mus musculus OX=10090 GN=Sptlc1 PE=1 SV=2

A0988	GO:0035522(monoubiquitinated histone H2A deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase), GO:0005515(protein binding),GO:0008233(peptidase activity),GO:0008237(metalloproteinase activity),GO:0003677(DNA binding)	-	-	KOG1555 Hs16158201_2265 proteasome regulatory complex, subunit RPN11	KAF7728178.1 hypothetical protein EC973_006572 [Apophysomyces ossiformis]	Histone H2A deubiquitinase MYSM1 OS=Branchiostoma floridae OX=7739 GN=MYSM1 PE=3 SV=1
A0989	-	-	GO:0003824(catalytic activity)	-	-	KOG1680 At4g16210 Enoyl-CoA hydratase	KXS19600.1 ClpP/crotonase [Gonapodya prolifera JEL478]	1,2-epoxyphenylacetyl-CoA isomerase OS=Escherichia coli (strain K12) OX=83333 GN=paaG PE=1 SV=1
A0990	-	-	-	-	-	-	-	-
A0991	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity)	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698 Hs21245120 Serine/threonine protein phosphatase	KAG4087228.1 protein serine/threonine phosphatase 2C [Neocallimastix sp. JGI-2020a]	Protein phosphatase 1L OS=Mus musculus OX=10090 GN=Ppm1l PE=1 SV=1
A0992	GO:0006886(intracellular protein transport), GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	GO:0030127(COPII vesicle coat)	GO:0008270(zinc ion binding)	K14007 SEC24; protein transport protein SEC24	map04141 Protein processing in endoplasmic reticulum;map05130 Pathogenic Escherichia coli infection	KOG1985 At3g07100 Vesicle coat complex COPII, subunit SEC24/subunit SFB2	RKO90883.1 hypothetical protein BDK51DRAFT_15521 [Blytiomyces helicus]	Protein transport protein SEC24 A OS=Arabidopsis thaliana OX=3702 GN=SEC24A PE=1 SV=2
A0993	-	-	-	-	-	KOG3978 Hs2048211 Predicted membrane protein	-	Transmembrane protein 161B OS=Danio rerio OX=7955 GN=tmem161b PE=2 SV=1
A0994	-	-	GO:0005515(protein binding)	K25164 WRAP73, WDR8; WD repeat-containing protein WRAP73	-	KOG4497 Hs16445434 Uncharacterized conserved protein WDR8, contains WD repeats	XP_031027652.1 uncharacterized protein SmJEL517_g00601 [Synchytrium microbalum]	WD repeat-containing protein WRAP73 OS=Homo sapiens OX=9606 GN=WRAP73 PE=1 SV=1
A0995	-	-	GO:0005515(protein binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K14575 AFG2, DRG1, SPATA5; AAA family ATPase	map03008 Ribosome biogenesis in eukaryotes	KOG0730 Hs21624654 AAA+ -type ATPase	PJF16525.1 hypothetical protein PSACC_03712 [Paramicrosporidium saccamoebae]	ATPase family gene 2 protein homolog B OS=Homo sapiens OX=9606 GN=AFG2B PE=1 SV=2
A0996	GO:0015940(pantothenate biosynthetic process)	-	GO:0003864(3-methyl-2-oxobutanoate hydroxymethyltransferase activity),GO:0003824(catalytic activity)	K00606 panB; 3-methyl-2-oxobutanoate hydroxymethyltransferase [EC:2.1.2.11]	map00770 Pantothenate and CoA biosynthesis;map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG2949 At3g61530 Ketopantoate hydroxymethyltransferase	OZI04053.1 hypothetical protein BZG36_03561 [Bifiguratus adalaidae]	3-methyl-2-oxobutanoate hydroxymethyltransferase 2, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=KPHMT2 PE=1 SV=1

A0997	-	-	-	-	-	KOG3407 Hs21389497 Uncharacterized conserved protein	-	Coiled-coil domain-containing protein 12 OS=Homo sapiens OX=9606 GN=CCDC12 PE=1 SV=1
A0998	-	-	-	K08726 EPHX2; soluble epoxide hydrolase / lipid- phosphate phosphatase [EC:3.3.2.10 3.1.3.76]	map04146 Peroxisome;map 01120 Microbial metabolism in diverse environments;map 00590 Arachidonic acid metabolism;map 05207 Chemical carcinogenesis - receptor activation;map0 5208 Chemical carcinogenesis - reactive oxygen species;map006 25 Chloroalkane and chloroalkene degradation;map 01100 Metabolic pathways	KOG4178 CE28941 Soluble epoxide hydrolase	KAF9692835.1 hypothetical protein EKO04_008998 [Ascochyta lentis]	Epoxide hydrolase 1 OS=Caenorhabditis elegans OX=6239 GN=ceeh-1 PE=1 SV=1
A0999	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding),GO:0016491(oxidoreductase activity)	-	-	-	-	-
A1000	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG0873 7292910 C-4 sterol methyl oxidase	-	-
A1001	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding),GO:0016491(oxidoreductase activity)	-	-	-	-	-
A1002	-	GO:0016021(integral component of membrane)	-	K14708 SLC26A11; solute carrier family 26 (sodium-independent sulfate anion transporter), member 11	-	KOG0236 At5g13550 Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family)	KAG0781603.1 hypothetical protein G6F22_009489 [Rhizopus oryzae]	Putative sulfate transporter YbaR OS=Bacillus subtilis (strain 168) OX=224308 GN=ybaR PE=3 SV=2
A1003	-	-	-	-	-	-	RYO87457.1 hypothetical protein DL763_006327 [Monosporascus cannonballus]	Uncharacterized protein MT1414 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=MT1414 PE=4 SV=2

A1004	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG4280 CE27986 Kinesin-like protein	ORZ36448.1 P-loop containing nucleoside triphosphate hydrolase protein [Catenaria anguillulae PL171]	Osmotic avoidance abnormal protein 3 OS=Caenorhabditis elegans OX=6239 GN=osm-3 PE=1 SV=4
A1005	GO:0018193(peptidyl-amino acid modification)	-	GO:0005515(protein binding)	K24750 WDR55, JIP5; WD repeat-containing protein 55	-	KOG2444 7299504 WD40 repeat protein	ORX77069.1 WD40 repeat-like protein [Basidiobolus meristosporus CBS 931.73]	WD repeat-containing protein 55 OS=Homo sapiens OX=9606 GN=WDR55 PE=1 SV=2
A1006	GO:0006629(lipid metabolic process)	-	GO:0046872(metal ion binding),GO:0003676(nucleic acid binding),GO:0005515(protein binding),GO:0003723(RNA binding)	-	-	KOG2191 At5g04430 RNA-binding protein NOVA1/PASILLA and related KH domain proteins	KAG2181034.1 hypothetical protein INT43_008616 [Umbelopsis isabellina]	Protein BTR1 OS=Arabidopsis thaliana OX=3702 GN=BTR1 PE=1 SV=1
A1007	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1008	-	-	GO:0003677(DNA binding)	-	-	-	-	Transcription factor MYB1R1 OS=Solanum tuberosum OX=4113 PE=2 SV=1
A1009	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity)	-	-	-	ORX97933.1 phosphatases II [Basidiobolus meristosporus CBS 931.73]	-
A1010	-	-	-	-	-	-	-	-
A1011	-	-	GO:0005515(protein binding),GO:0016409(palmitoyltransferase activity)	-	-	KOG0509 7294202 Ankyrin repeat and DHHC-type Zn-finger domain containing proteins	EPZ34150.1 hypothetical protein O9G_003749, partial [Rozella allomycis CSF55]	Palmitoyltransferase Hip14 OS=Drosophila melanogaster OX=7227 GN=Hip14 PE=1 SV=1
A1012	GO:0016226(iron-sulfur cluster assembly)	-	GO:0008199(ferrous iron binding)	K19054 FXN; frataxin [EC:1.16.3.1]	map00860 Porphyrin metabolism	KOG3413 Hs4503785 Mitochondrial matrix protein frataxin, involved in Fe/S protein biosynthesis	OON05848.1 iron donor protein CyaY [Batrachomyxium salamandrivorans]	Frataxin, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=fxn PE=3 SV=1
A1013	GO:0140647(P450-containing electron transport chain)	-	GO:0051536(iron-sulfur cluster binding),GO:0051537(2 iron, 2 sulfur cluster binding)	K22071 FDX2; ferredoxin-2, mitochondrial	-	-	GBC00687.1 hypothetical protein RclHRI_03940013 [Rhizophagus clarus]	Ferredoxin-2, mitochondrial OS=Bos taurus OX=9913 GN=FDX2 PE=2 SV=2

A1014	-	-	-	-	-	-	-	-
A1015	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	KZO94955.1 hypothetical protein CALVIDRAFT_565074 [Calocera viscosa TUFC12733]	-
A1016	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A1017	-	-	-	-	-	-	GFZ51951.1 hypothetical protein JCM24511_09721 [Saitozyma sp. JCM 24511]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A1018	-	-	-	K01613 psd, PISD; phosphatidylserine decarboxylase [EC:4.1.1.65]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG1030 At1g73580 Predicted Ca2+-dependent phospholipid-binding protein	RKP10449.1 C2 domain-containing protein [Thamnocephalis sphaerospora]	Protein C2-DOMAIN ABA-RELATED 3 OS=Arabidopsis thaliana OX=3702 GN=CAR3 PE=3 SV=1
A1019	GO:0009058(biosynthetic process), GO:0009396(folic acid-containing compound biosynthetic process)	-	GO:0005524(ATP binding),GO:0004326(tetrahydrofolylpolyglutamate synthase activity),GO:0016881(acid-amino acid ligase activity)	-	-	KOG2525 At3g55630 Folylpolyglutamate synthase	KAF8935694.1 Folylpolyglutamate synthetase [Haplosporangium bisporale]	Folylpolyglutamate synthase OS=Arabidopsis thaliana OX=3702 GN=FPGS3 PE=1 SV=1
A1020	-	-	GO:0016787(hydrolase activity)	K06269 PPP1C; serine/threonine-protein phosphatase PP1 catalytic subunit [EC:3.1.3.16]	map04390 Hippo signaling pathway;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05415 Diabetic cardiomyopathy;map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04218 Cellular senescence;map04910 Insulin signaling pathway;map04728 Dopaminergic synapse;map04720 Long-term potentiation;map05031 Amphetamine addiction;map04	KOG0374 At1g03445_2 Serine/threonine specific protein phosphatase PP1, catalytic subunit	ORX97883.1 Metallo-dependent phosphatase, partial [Basidiobolus meristosporus CBS 931.73]	Serine/threonine-protein phosphatase BSL1 OS=Arabidopsis thaliana OX=3702 GN=BSL1 PE=1 SV=2

A1021	GO:1905515(non-motile cilium assembly)	GO:0034464(BBSome)	GO:0005515(protein binding)	-	-	-	KAG4086548.1 hypothetical protein H8356DRAFT_1734355 [Neocallimastix sp. JGI-2020a]	Bardet-Biedl syndrome 1 protein homolog OS=Mus musculus OX=10090 GN=Bbs1 PE=1 SV=1
A1022	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity)	-	-	-	KAF9373141.1 hypothetical protein CPB97_000774 [Podila verticillata]	-
A1023	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02903 RP-L28e, RPL28; large subunit ribosomal protein L28e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3412 At2g19730 60S ribosomal protein L28	RGB43940.1 ribosomal protein L28 [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Large ribosomal subunit protein eL28 OS=Spodoptera frugiperda OX=7108 GN=RpL28 PE=2 SV=1
A1024	-	GO:0016021(integral component of membrane)	-	-	-	-	KXN68221.1 DUF887-domain-containing protein [Conidiobolus coronatus NRRL 28638]	Uncharacterized TLC domain-containing protein C17A2.02c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC17A2.02c PE=4 SV=1
A1025	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K20989 DUR3; urea-proton symporter	-	KOG2349 Hs17941285 Na+iodide/myo-inositol/multi vitamin symporters	ORX85711.1 solute:sodium symporter family transporter [Anaeromyces robustus]	Sodium/myo-inositol cotransporter 2 OS=Oryctolagus cuniculus OX=9986 GN=SLC5A11 PE=1 SV=2
A1026	-	-	GO:0005515(protein binding)	K04523 UBQLN, DSK2; ubiquitin	map05014 Amyotrophic lateral sclerosis;map04141 Protein processing in endoplasmic reticulum	KOG0010 At2g17200 Ubiquitin-like protein	RIA92766.1 hypothetical protein C1645_763979 [Glomus cerebiforme]	Ubiquitin domain-containing protein DSK2b OS=Arabidopsis thaliana OX=3702 GN=DSK2B PE=1 SV=1
A1027	-	-	-	-	-	-	-	-
A1028	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity);GO:0005524(ATP binding);GO:0008017(microtubule binding)	K10392 KIF1; kinesin family member 1	map04814 Motor proteins	KOG4280 7302758_1 Kinesin-like protein	TPX59559.1 hypothetical protein PhCBS80983_g02408 [Powellomyces hirtus]	Kinesin-like protein KIF12 OS=Mus musculus OX=10090 GN=Kif12 PE=1 SV=1
A1029	GO:0006811(ion transport);GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005216(ion channel activity)	-	-	KOG0498 7291726 K+-channel ERG and related proteins, contain PAS/PAC sensor domain	XP_016612440.1 hypothetical protein SPPG_00132 [Spizellomyces punctatus DAOM BR117]	Potassium voltage-gated channel subfamily H member 8 OS=Mus musculus OX=10090 GN=Kcnh8 PE=2 SV=2
A1030	-	-	-	-	-	-	-	-

A1031	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02963 RP-S18, MRPS18, rpsR; small subunit ribosomal protein S18	map03010 Ribosome	-	XP_031022215.1 uncharacterized protein SmJEL517_g05885 [Synchytrium microbalum]	Small ribosomal subunit protein bS18 OS=Synechococcus sp. (strain JA-2-3B'a(2-13)) OX=321332 GN=rpsR PE=3 SV=1
A1032	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity)	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698 At5g24940 Serine/threonine protein phosphatase	KXS21091.1 NAD(P)-binding protein [Gonapodya prolifera JEL478]	Probable protein phosphatase 2C 52 OS=Oryza sativa subsp. japonica OX=39947 GN=Os05g0587100 PE=2 SV=1
A1033	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors);GO:0050660(flavin adenine dinucleotide binding)	K00249 ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map03320 PPAR signaling pathway;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map04936 Alcoholic liver disease;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG1469 At3g06810 Predicted acyl-CoA dehydrogenase	XP_013286104.1 hypothetical protein Z517_05323 [Fonsecaea pedrosoi CBS 271.37]	Acyl-CoA dehydrogenase family member 11 OS=Gallus gallus OX=9031 GN=ACAD11 PE=2 SV=1
A1034	GO:0009117(nucleotide metabolic process)	GO:1902560(GMP reductase complex)	GO:0003824(catalytic activity);GO:0003920(GMP reductase activity);GO:0016491(oxidoreductase activity)	K00088 IMPDH, guaB; IMP dehydrogenase [EC:1.1.1.205]	map00983 Drug metabolism - other enzymes;map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG2550 Hs7706109 IMP dehydrogenase/GMP reductase	TPX66330.1 GMP reductase [Chytridiomycetes confervae]	GMP reductase OS=Phytophthora infestans OX=4787 PE=2 SV=1
A1035	-	-	-	-	-	-	-	-
A1036	-	-	-	-	-	-	-	-
A1037	-	-	GO:0000062(fatty-acyl-CoA binding)	K08762 DBI, ACBP; diazepam-binding inhibitor (GABA receptor modulator, acyl-CoA-binding protein)	map03320 PPAR signaling pathway	KOG0817 7295286 Acyl-CoA-binding protein	XP_025363646.1 acyl-CoA-binding protein [Jaminia rosea]	Acyl-CoA-binding protein OS=Ricinus communis OX=3988 PE=3 SV=1
A1038	-	-	-	-	-	-	-	-

A1039	GO:000629(lipid metabolic process)	-	-	K14676 NTE, NRE; lysophospholipid hydrolase [EC:3.1.1.5]	map00564 Glycerophospholipid metabolism	KOG2968 Hs5729951 Predicted esterase of the alpha-beta hydrolase superfamily (Neuropathy target esterase), contains cAMP-binding domains	KAF0463560.1 patatin-domain-containing protein [Gigaspora margarita]	Patatin-like phospholipase domain-containing protein 6 OS=Homo sapiens OX=9606 GN=PNPLA6 PE=1 SV=3
A1040	-	-	GO:0004329(formate-tetrahydrofolate ligase activity),GO:0005524(ATP binding)	K00288 MTHFD; methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase [EC:1.5.1.5 3.5.4.9 6.3.4.3]	map00670 One carbon pool by folate;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	-	KAG1049555.1 hypothetical protein G6F43_008120 [Rhizopus deleamar]	Formate--tetrahydrofolate ligase OS=Spinacia oleracea OX=3562 PE=1 SV=3
A1041	-	-	-	-	-	KOG2983 Hs5174423 Uncharacterized conserved protein	KAG2192383.1 hypothetical protein INT46_008208 [Mucor plumbeus]	Cell division cycle protein 123 homolog OS=Nematostella vectensis OX=45351 GN=cdc123 PE=3 SV=1
A1042	-	-	GO:0016787(hydrolase activity),GO:0008242(omega peptidase activity)	-	-	KOG1559 Hs4503987 Gamma-glutamyl hydrolase	-	Gamma-glutamyl hydrolase A OS=Dictyostelium discoideum OX=44689 GN=gghA PE=3 SV=1
A1043	GO:0006520(cellular amino acid metabolic process)	-	GO:0016491(oxidoreductase activity)	K00262 E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	map00910 Nitrogen metabolism;map01120 Microbial metabolism in diverse environments;map00250 Alanine, aspartate and glutamate metabolism;map00220 Arginine biosynthesis;map01100 Metabolic pathways	KOG2250 At1g51720 Glutamate/leucine/phenylalanine/valine dehydrogenases	OMJ13082.1 NADP-specific glutamate dehydrogenase [Smittium culicis]	NADP-specific glutamate dehydrogenase (Fragment) OS=Chlorella sorokiniana OX=3076 PE=2 SV=1
A1044	GO:0070475(rRNA base methylation)	-	GO:0008649(rRNA methyltransferase activity)	-	-	-	KAG0190448.1 hypothetical protein DFQ28_002020 [Apophysomyces sp. BC1034]	Ribosomal RNA large subunit methyltransferase J OS=Escherichia coli (strain K12) OX=83333 GN=rlmJ PE=1 SV=1

A1045	GO:0006629(lipid metabolic process)	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors)	K12343 SRD5A1; 3-oxo-5-alpha-steroid 4-dehydrogenase 1 [EC:1.3.1.22]	map00140 Steroid hormone biosynthesis;map01100 Metabolic pathways	KOG1638 CE03314 Steroid reductase	KAF7729419.1 hypothetical protein EC973_004398 [Apophysomyces ossiformis]	Steroid 5-alpha-reductase DET2 OS=Solanum lycopersicum OX=4081 GN=DET2 PE=1 SV=1
A1046	GO:0015986(ATP synthesis coupled proton transport)	-	GO:0046933(proton-transporting ATP synthase activity, rotational mechanism)	-	-	KOG1662 7299984 Mitochondrial F1F0-ATP synthase, subunit OSCP/ATP5	RAO66791.1 hypothetical protein BHQ10_002803 [Talaromyces amestolkiae]	ATP synthase subunit O, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPsynO PE=2 SV=2
A1047	GO:0006796(phosphate-containing compound metabolic process)	GO:0005737(cytoplasm)	GO:0000287(magnesium ion binding),GO:0004427(inorganic diphosphatase activity)	K01507 ppa; inorganic pyrophosphatase [EC:3.6.1.1]	map00190 Oxidative phosphorylation	KOG1626 7291807 Inorganic pyrophosphatase/Nucleosome remodeling factor, subunit NURF38	KAG2224601.1 hypothetical protein INT45_003741 [Mucor circinatus]	Inorganic pyrophosphatase OS=Bos taurus OX=9913 GN=PPA1 PE=1 SV=2
A1048	GO:0035082(axoneme assembly)	GO:0005879(axonemal microtubule)	-	-	-	-	-	-
A1049	-	-	-	-	-	-	-	-
A1050	GO:0019722(calcium-mediated signaling),GO:0006281(DNA repair)	-	GO:0005509(calcium ion binding),GO:0019900(kinase binding),GO:0003677(DNA binding)	K19932 NCS1; neuronal calcium sensor	-	KOG0044 7301392 Ca2+ sensor (EF-Hand superfamily)	CRK36449.1 hypothetical protein BN1708_007048, partial [Verticillium longisporum]	Neuron-specific calcium-binding protein hippocalcin OS=Bos taurus OX=9913 GN=HPCA PE=2 SV=3
A1051	GO:0006260(DNA replication)	-	GO:0003677(DNA binding)	K10756 RFC3_5; replication factor C subunit 3/5	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03430 Mismatch repair	KOG2035 Hs4506489 Replication factor C, subunit RFC3	ORX97418.1 replication factor C subunit 3 [Basidiobolus meristosporus CBS 931.73]	Replication factor C subunit 3 OS=Mus musculus OX=10090 GN=Rfc3 PE=1 SV=1
A1052	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0003682(chromatin binding)	K02603 ORC1; origin recognition complex subunit 1	map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG1514 Hs4758850 Origin recognition complex, subunit 1, and related proteins	ORX83257.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	Origin recognition complex subunit 1 OS=Mus musculus OX=10090 GN=Orc1 PE=1 SV=2
A1053	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	-	KAF8474920.1 phosphatase 2C-domain-containing protein [Kalahariturber pfeili]	Protein phosphatase 2C homolog 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ptc2 PE=3 SV=1
A1054	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08793 STK32, YANK; serine/threonine kinase 32 [EC:2.7.11.1]	-	KOG0603 Hs19923570 Ribosomal protein S6 kinase	KAF2858655.1 kinase-like protein [Piedraia hortae CBS 480.64]	Ribosomal protein S6 kinase alpha-2 OS=Homo sapiens OX=9606 GN=RPS6KA2 PE=1 SV=2
A1055	-	-	-	-	-	-	-	-

A1056	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K08838 STK24_25_MS T4; serine/threonine-protein kinase 24/25/MST4 [EC:2.7.11.1]	-	KOG0574 Hs5454096 STE20-like serine/threonine kinase MST	KXS17677.1 Pkinase-domain-containing protein [Gonapodya prolifera JEL478]	Serine/threonine-protein kinase 3 OS=Mus musculus OX=10090 GN=Stk3 PE=1 SV=1
A1057	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport),GO:0015031(protein transport)	GO:0030117(membrane coat),GO:0030123(AP-3 adaptor complex)	-	K12396 AP3D; AP-3 complex subunit delta	map04142 Lysosome	KOG1059 Hs20127438 Vesicle coat complex AP-3, delta subunit	RIB12840.1 adaptin N terminal region-domain-containing protein [Gigaspora rosea]	AP-3 complex subunit delta-1 OS=Homo sapiens OX=9606 GN=AP3D1 PE=1 SV=1
A1058	-	-	-	-	-	-	-	-
A1059	GO:0030001(metal ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	K14709 SLC39A1_2_3, ZIP1_2_3; solute carrier family 39 (zinc transporter), member 1/2/3	map05010 Alzheimer disease;map05012 Parkinson disease	KOG1558 At2g30080 Fe2+/Zn2+ regulated transporter	ORZ25032.1 Zinc/iron permease [Absidia repens]	Zinc-regulated transporter 1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ZRT101 PE=1 SV=1
A1060	-	-	-	-	-	-	-	-
A1061	-	-	-	-	-	-	-	-
A1062	-	GO:0009376(HslUV protease complex)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0008233(peptidase activity)	K03544 clpX, CLPX; ATP-dependent Clp protease ATP-binding subunit ClpX	map04112 Cell cycle - Caulobacter	KOG0745 At5g49840 Putative ATP-dependent Clp-type protease (AAA+ ATPase superfamily)	KAG0776627.1 hypothetical protein G6F22_012438 [Rhizopus oryzae]	ATP-dependent protease ATPase subunit HslU OS=Methylobacterium populi (strain ATCC BAA-705 / NCIMB 13946 / BJ001) OX=441620 GN=hslU PE=3 SV=1
A1063	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1064	GO:0006629(lipid metabolic process)	-	-	-	-	KOG4569 CE13898 Predicted lipase	ORZ37865.1 class 3-domain-containing protein [Catenaria anguillulae PL171]	Secreted mono- and diacylglycerol lipase 1 OS=Fusarium solani OX=169388 GN=NHL1 PE=1 SV=1
A1065	-	-	GO:0005515(protein binding)	K10415 DYNC11, DNCL; dynein cytoplasmic 1 intermediate chain	map04145 Phagosome;map05132 Salmonella infection;map041814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG1587 Hs2042593 Cytoplasmic dynein intermediate chain	TPX42236.1 hypothetical protein SeLEV6574_g05700 [Synchytrium endobioticum]	Dynein intermediate chain 3, ciliary OS=Helicoidaris crassispina OX=1043166 PE=2 SV=1
A1066	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	-	-	-	KOG1307 Hs4759128 K+-dependent Ca2+/Na+ exchanger NCKX1 and related proteins	CEQ41917.1 SPOSA6832_03684, partial [Sporidiobolus salmonicolor]	Sodium/potassium/calcium exchanger 1 OS=Homo sapiens OX=9606 GN=SLC24A1 PE=1 SV=1

A1067	-	-	-	-	-	-	KNE69191.1 hypothetical protein AMAG_13583 [Allomyces macrogynus ATCC 38327]	Outer dynein arm protein 1 OS=Chlamydomonas reinhardtii OX=3055 GN=ODA1 PE=1 SV=1
A1068	GO:0006325(chromatin organization)	GO:0005634(nucleus)	-	K10753 ASF1; histone chaperone ASF1	-	KOG3265 YJL115w Histone chaperone involved in gene silencing	OZJ02041.1 hypothetical protein BZG36_05081 [Bifiguratus adalaidae]	Histone chaperone ASF1 OS=Coccidioides immitis (strain RS) OX=246410 GN=ASF1 PE=3 SV=1
A1069	-	-	GO:0016787(hydrolase activity),GO:0003993(acid phosphatase activity)	-	-	-	OAJ35821.1 hypothetical protein BDEG_20054 [Batrachochytrium dendrobatidis JEL423]	-
A1070	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG2844 Hs7019365 Dimethylglycine dehydrogenase precursor	-	Glycine oxidase OS=Geobacillus kaustophilus (strain HTA426) OX=235909 GN=thiO PE=1 SV=1
A1071	-	-	-	K11397 EAF1, VID21; chromatin modification-related protein VID21	-	KOG0391 CE25717 SNF2 family DNA-dependent ATPase	SJX65922.1 uncharacterized protein SRS1_16475 [Sporisorium reilianum f. sp. reilianum]	Helicase ssl-1 OS=Caenorhabditis elegans OX=6239 GN=ssl-1 PE=2 SV=4
A1072	-	-	-	-	-	-	-	-
A1073	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02935 RP-L7, MRPL12, rplL; large subunit ribosomal protein L7/L12	map03010 Ribosome	KOG1715 YGL068w Mitochondrial/chloroplast ribosomal protein L12	EPS27503.1 hypothetical protein PDE_02446 [Penicillium oxalicum 114-2]	Large ribosomal subunit protein bL12m OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=mrpl12 PE=1 SV=1
A1074	-	-	-	-	-	-	-	-
A1075	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0003724(RNA helicase activity)	K14777 DDX47, RRP3; ATP-dependent RNA helicase DDX47/RRP3 [EC:3.6.4.13]	-	KOG0330 Hs20149629 ATP-dependent RNA helicase	OBZ90399.1 ATP-dependent rRNA helicase RRP3 [Choanephora cucurbitarum]	Probable ATP-dependent RNA helicase DDX47 OS=Homo sapiens OX=9606 GN=DDX47 PE=1 SV=1
A1076	GO:0016311(dephosphorylation),GO:0006470(protein dephosphorylation)	-	GO:0016791(phosphatase activity),GO:0008138(protein tyrosine/serine/threonine phosphatase activity)	K18045 SIW14, OCA3; tyrosine-protein phosphatase SIW14 [EC:3.1.3.48]	-	KOG1572 At1g05000 Predicted protein tyrosine phosphatase	KAF0421287.1 protein-tyrosine phosphatase [Gigaspora margarita]	Tyrosine-protein phosphatase DSP1 OS=Arabidopsis thaliana OX=3702 GN=DSP1 PE=1 SV=1

A1077	GO:0006508(proteolysis)	-	GO:0016491(oxidoreductase activity),GO:0008237(metalloproteinase activity),GO:0004222(metalloendopeptidase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	K01415 ECE: endothelin-converting enzyme [EC:3.4.24.71]	-	KOG3624 Hs7662200 M13 family peptidase	KAG4098912.1 Metalloproteinases [Neocallimastix sp. JGI-2020a]	Endothelin-converting enzyme homolog OS=Locusta migratoria OX=7004 PE=2 SV=1
A1078	-	-	-	-	-	-	ORY37959.1 hypothetical protein BCR33DRAFT_854415 [Rhizoclostium globosum]	-
A1079	-	-	-	-	-	-	-	-
A1080	GO:0070476(rRNA (guanine-N7)-methylation)	-	GO:0016435(rRNA (guanine) methyltransferase activity)	K19306 BUD23; 18S rRNA (guanine1575-N7)-methyltransferase [EC:2.1.1.309]	-	KOG1541 7298980 Predicted protein carboxyl methylase	KAG4107587.1 S-adenosyl-L-methionine-dependent methyltransferase [Neocallimastix sp. JGI-2020a]	Probable 18S rRNA (guanine-N(7))-methyltransferase OS=Mus musculus OX=10090 GN=Bud23 PE=1 SV=1
A1081	-	-	GO:0010181(FMN binding),GO:0016491(oxidoreductase activity)	K00354 E1.6.99.1; NADPH2 dehydrogenase [EC:1.6.99.1]	-	KOG0134 At1g76680 NADH:flavin oxidoreductase/12-oxophytodienoate reductase	KZV75200.1 FMN-linked oxidoreductase [Peniophora sp. CONT]	Putative 12-oxophytodienoate reductase 11 OS=Oryza sativa subsp. japonica OX=39947 GN=OPR11 PE=2 SV=1
A1082	GO:0016192(vesicle-mediated transport),GO:0006886(intracellular protein transport)	GO:0030117(membrane coat),GO:0030123(AP-3 adaptor complex)	-	K12397 AP3B; AP-3 complex subunit beta	map04142 Lysosome	KOG1060 Hs4758760 Vesicle coat complex AP-3, beta subunit	GES86703.1 AP-3 complex subunit beta-1 isoform X2 [Rhizophagus clarus]	AP-3 complex subunit beta-2 OS=Homo sapiens OX=9606 GN=AP3B2 PE=1 SV=2
A1083	-	-	-	-	-	-	-	-
A1084	GO:0016575(histone deacetylation)	-	GO:0004407(histone deacetylase activity)	-	-	KOG1342 Hs20551695 Histone deacetylase complex, catalytic component RPD3	KAG5365530.1 Histone deacetylase RPD3 [Yarrowia sp. C11]	Histone deacetylase 1 OS=Gallus gallus OX=9031 GN=HDAC1 PE=2 SV=1
A1085	GO:0006508(proteolysis)	-	GO:0005515(protein binding),GO:0004252(serine-type endopeptidase activity)	K22686 NMA111; pro-apoptotic serine protease NMA111 [EC:3.4.21.-]	-	KOG1421 YNL123w Predicted signaling-associated protein (contains a PDZ domain)	ORX94491.1 trypsin-like serine protease [Basidiobolus meristosporus CBS 931.73]	Protease Do-like 7 OS=Arabidopsis thaliana OX=3702 GN=DEGP7 PE=2 SV=1
A1086	-	-	-	-	-	-	-	-

A1087	-	-	-	-	-	-	OZJ03957.1 hypothetical protein B2G36_03249 [Bifiguratus adelaidae]	Nucleoside diphosphate-linked moiety X motif 17 OS=Xenopus tropicalis OX=8364 GN=nudt17 PE=2 SV=2
A1088	-	-	-	-	-	-	-	-
A1089	-	-	-	-	-	-	-	-
A1090	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	K16196 EIF2AK4; eukaryotic translation initiation factor 2- alpha kinase 4 [EC:2.7.11.1]	map04140 Autophagy - animal;map0413 8 Autophagy - yeast;map05160 Hepatitis C;map05162 Measles;map051 68 Herpes simplex virus 1 infection	KOG0198 At2 g40560 MEKK and related serine/threon ine protein kinases	XP_00871724 8.1 hypothetical protein HMPREF1541 _04682 [Cyphellopho ra europaea CBS 101466]	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase wee-1.3 OS=Caenorhabditis elegans OX=6239 GN=wee-1.3 PE=1 SV=1
A1091	GO:00071 65(signal transducti on)	-	GO:0005515(pro tein binding)	-	-	-	KAF8726638. 1 hypothetical protein AX14_007619 [Amanita brunnescens Koide BX004]	-
A1092	-	-	-	-	-	-	-	-
A1093	GO:00064 68(protein phosphor ylation)	-	GO:0005515(pro tein binding),GO:000 4672(protein kinase activity),GO:000 5524(ATP binding)	K08286 E2.7.11.-; protein- serine/threon ine kinase [EC:2.7.11.-]	-	KOG0589 At1 g54510 Serine/threon ine protein kinase	OJT05228.1 MAP kinase kinase mkh1 [Trametes pubescens]	Serine/threonine-protein kinase Nek1 OS=Arabidopsis thaliana OX=3702 GN=NEK1 PE=2 SV=2
A1094	-	-	GO:0046872(me tal ion binding)	-	-	-	TPX77043.1 hypothetical protein CcCBS67573. g01690 [Chytriomyc s confervae]	G8 domain-containing protein DDB_G0286897 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0286897 PE=3 SV=1
A1095	GO:00362 11(protein modificati on process)	-	GO:0005524(AT P binding),GO:004 6872(metal ion binding)	K06047 TTL; tubulin--- tyrosine ligase [EC:6.3.2.25]	-	KOG2157 Hs7 661564 Predicted tubulin- tyrosine ligase	TPX59531.1 hypothetical protein PhCBS80983. g02429 [Powellomyce s hirtus]	Protein polyglycylase TTLL10 OS=Macaca fascicularis OX=9541 GN=TTLL10 PE=2 SV=1
A1096	-	GO:00160 20(membr ane)	GO:0140359(AB C-type transporter activity),GO:000 5524(ATP binding)	K05681 ABCG2, CD338; ATP- binding cassette, subfamily G (WHITE), member 2	map01523 Antifolate resistance;map0 4976 Bile secretion;map02 010 ABC transporters	KOG0061 At3 g21090 Transporter, ABC superfamily (Breast cancer resistance protein)	EOD44580.1 putative abc transporter protein [Neofusicocc um parvum UCRNP2]	ABC transporter G family member 11 OS=Arabidopsis thaliana OX=3702 GN=ABCG11 PE=1 SV=1

A1097	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0003924(GTPase activity),GO:0019001(guanylnucleotide binding),GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04730 Long-term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082 Hs10567816 G-protein alpha subunit (small G protein superfamily)	RPA85620.1 guanine nucleotide binding protein, alpha subunit [Ascobolus immersus RN42]	Guanine nucleotide-binding protein G(o) subunit alpha OS=Homo sapiens OX=9606 GN=GNAO1 PE=1 SV=4
A1098	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0003924(GTPase activity),GO:0019001(guanylnucleotide binding),GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04730 Long-term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082 Hs4504041 G-protein alpha subunit (small G protein superfamily)	EIE76416.1 hypothetical protein RO3G_01120 [Rhizopus delemar RA 99-880]	Guanine nucleotide-binding protein subunit alpha OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=fadA PE=1 SV=3
A1099	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0003924(GTPase activity),GO:0019001(guanylnucleotide binding),GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04730 Long-term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082 HsM20149537 G-protein alpha subunit (small G protein superfamily)	RKO84365.1 guanine nucleotide binding protein, alpha subunit [Blyttiomycetes helicus]	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Xenopus laevis OX=8355 GN=gna1 PE=2 SV=3
A1100	-	GO:0005634(nucleus)	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	-	-	KOG0227 At2g32600 Splicing factor 3a, subunit 2	PKK78372.1 hypothetical protein RhiirC2_729994, partial [Rhizophagus irregularis]	Splicing factor 3A subunit 2 OS=Homo sapiens OX=9606 GN=SF3A2 PE=1 SV=2

A1101	-	-	-	-	-	-	PIA16436.1 NADH:ubiquinone oxidoreductase 11.6kD subunit [Coemansia reversa NRRL 1564]	-
A1102	-	-	-	-	-	KOG1667 CE23244 Zn2+-binding protein Melusin/RAR1, contains CHORD domain	KAF8516925.1 chord-domain-containing protein [Hysterangium stoloniferum]	Cysteine and histidine-rich domain-containing protein RAR1 OS=Arabidopsis thaliana OX=3702 GN=RAR1 PE=1 SV=1
A1103	GO:0016480(negative regulation of transcription by RNA polymerase III)	-	-	K25817 MAF1; repressor of RNA polymerase III transcription MAF1	-	KOG3104 Hs14150013 Mod5 protein sorting/negative effector of RNA Pol III synthesis	KAG0263728.1 RNA polymerase III-inhibiting protein maf1 [Linnemannia exigua]	Repressor of RNA polymerase III transcription MAF1 homolog OS=Bos taurus OX=9913 GN=MAF1 PE=2 SV=1
A1104	GO:0043631(RNA polyadenylation)	GO:0031499(TRANM complex)	GO:0004652(polynucleotide adenylyltransferase activity),GO:0005515(protein binding),GO:0016779(nucleotidyltransferase activity)	K03514 PAPD5_7, TRF4; non-canonical poly(A) RNA polymerase PAPD5/7 [EC:2.7.7.19]	map03018 RNA degradation	KOG1906 At5g53770 DNA polymerase sigma	XP_019024883.1 Nucleotidyltransferase, partial [Saitoella complicata NRRL Y-17804]	Non-canonical poly(A) RNA polymerase protein Trf4-1 OS=Drosophila melanogaster OX=7227 GN=Trf4-1 PE=1 SV=1
A1105	-	-	GO:0005515(protein binding)	K03130 TAF5; transcription initiation factor TFIID subunit 5	map03022 Basal transcription factors	KOG0263 At5g25150 Transcription initiation factor TFIID, subunit TAF5 (also component of histone acetyltransferase SAGA)	TID29879.1 hypothetical protein CANINC_001517 [[Candida] inconspicua]	Transcription initiation factor TFIID subunit 5 OS=Arabidopsis thaliana OX=3702 GN=TAF5 PE=1 SV=1
A1106	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0005886(plasma membrane),GO:0016020(membrane)	GO:0005261(cation channel activity),GO:0005216(ion channel activity)	K21864 CCH1; voltage-dependent calcium channel	-	KOG2301 Hs20536765 Voltage-gated Ca2+ channels, alpha1 subunits	RKP08010.1 Ion transport protein-domain-containing protein [Thamnocephalus sphaerosporus]	Sodium channel protein type 1 subunit alpha OS=Homo sapiens OX=9606 GN=SCN1A PE=1 SV=2
A1107	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	-
A1108	-	-	-	-	-	-	-	-
A1109	-	-	-	-	-	-	TPX76846.1 hypothetical protein CcCBS67573_g01871 [Chytridiomycota confervae]	Lipase OS=Bacillus sp. OX=1409 PE=1 SV=3
A1110	-	-	-	-	-	-	-	-
A1111	-	-	-	-	-	-	-	-
A1112	-	-	-	-	-	-	-	-
A1113	-	-	-	-	-	-	-	-
A1114	-	-	-	-	-	KOG1100 At1g68820.2 Predicted E3 ubiquitin ligase	-	Baculoviral IAP repeat-containing protein 7-B OS=Xenopus laevis OX=8355 GN=birc7-b PE=2 SV=2

A1115	GO:0006123(mitochondrial electron transport, cytochrome c to oxygen)	GO:0005740(mitochondrial envelope), GO:0005751(mitochondrial respiratory chain complex IV)	-	K02265 COX5B; cytochrome c oxidase subunit 5b	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04260 Cardiac muscle contraction;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map05010 Alzheimer disease;map050	-	RKP07925.1 cytochrome c oxidase, partial [Thamnocephalis sphaerospora]	Cytochrome c oxidase subunit 4, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=cox4 PE=1 SV=1
A1116	-	-	-	-	-	-	-	-
A1117	GO:0006633(fatty acid biosynthetic process)	GO:0005737(cytoplasm)	GO:0008693(3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase activity)	-	-	-	KAF9395587.1 hypothetical protein CPC16_007748 [Podila verticillata]	Polyunsaturated fatty acid synthase subunit C OS=Thraustochytrium sp. (strain ATCC 26185 / S-3) OX=672127 GN=ORF-C PE=1 SV=1
A1118	-	-	-	-	-	-	-	-
A1119	-	-	GO:0005515(protein binding)	K24935 TTC27; tetratricopeptide repeat protein 27	-	KOG1128[Hs21361761 Uncharacterized conserved protein, contains TPR repeats	ORY01097.1 TPR-like protein [Basidiobolus meristosporus CBS 931.73]	Tetratricopeptide repeat protein 27 homolog OS=Dictyostelium discoideum OX=44689 GN=ttc27 PE=3 SV=1
A1120	GO:0016575(histone deacetylation)	-	GO:0004407(histone deacetylase activity)	-	-	KOG1342[7292522 Histone deacetylase complex, catalytic component RPD3	XP_504286.1 YALIOE22935p [Yarrowia lipolytica CLIB122]	Histone deacetylase HDAC1 OS=Drosophila melanogaster OX=7227 GN=HDAC1 PE=1 SV=2
A1121	GO:1904668(positive regulation of ubiquitin protein ligase activity)	-	GO:0005515(protein binding),GO:0010997(anaphase-promoting complex binding),GO:0097027(ubiquitin-protein transferase activator activity)	K03363 CDC20; cell division cycle 20, cofactor of APC complex	map04120 Ubiquitin mediated proteolysis;map05203 Viral carcinogenesis; map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG0305[Hs4557437 Anaphase promoting complex, Cdc20, Cdh1, and Aml1 subunits	EPZ33907.1 hypothetical protein O9G_002470 [Rozella allomycis CSF55]	Cell division cycle protein 20 homolog OS=Sus scrofa OX=9823 GN=CDC20 PE=2 SV=1
A1122	-	-	-	-	-	KOG1426[At5g63860 FOG: RCC1 domain	KAF8196812.1 regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II [Mycena galopus ATCC 62051]	Ultraviolet-B receptor UVR8 OS=Arabidopsis thaliana OX=3702 GN=UVR8 PE=1 SV=1

A1123	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K18655 DDX19, DBP5; ATP-dependent RNA helicase DDX19/DBP5 [EC:3.6.4.13]	map03013 Nucleocytoplasmic transport;map03015 mRNA surveillance pathway	-	XP_025356006.1 ATP-dependent RNA helicase DBP5 [Meira miltonrushii]	ATP-dependent RNA helicase DBP5 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=DBP5 PE=3 SV=1
A1124	GO:0000105(histidine biosynthetic process)	-	GO:0004636(phosphoribosyl-ATP diphosphatase activity),GO:0004635(phosphoribosyl-AMP cyclohydrolase activity)	K14152 HIS4; phosphoribosyl-ATP pyrophosphohydrolase / phosphoribosyl-AMP cyclohydrolase / histidinol dehydrogenase [EC:3.6.1.31 3.5.4.19 1.1.1.23]	map00340 Histidine metabolism;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways	-	KAF3939147.1 hypothetical protein ABW19_dt0205158 [Dactylella cylindrospora]	Histidine biosynthesis bifunctional protein his7 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=his7 PE=3 SV=1
A1125	GO:0035721(intracellular retrograde transport)	-	GO:0005515(protein binding)	-	-	KOG2247 7302460 WD40 repeat-containing protein	TPX57607.1 hypothetical protein PhCBS80983_g03741 [Powellomyces hirtus]	WD repeat-containing protein 19 OS=Mus musculus OX=10090 GN=Wdr19 PE=1 SV=1
A1126	-	-	-	-	-	-	-	-
A1127	-	-	-	-	-	-	-	-
A1128	GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015299(solute:proton antiporter activity)	K12041 SLC9A6_7, NHE6_7; solute carrier family 9 (sodium/hydrogen exchanger), member 6/7	map04260 Cardiac muscle contraction	KOG1965 At2g01980 Sodium/hydrogen exchanger protein	RYO79157.1 hypothetical protein DL763_009381 [Monosporascus cannonballus]	Sodium/hydrogen exchanger 7 OS=Arabidopsis thaliana OX=3702 GN=NHX7 PE=1 SV=1
A1129	-	-	-	-	-	-	-	-
A1130	-	-	-	K22696 EEF2KMT; protein-lysine N-methyltransferase EEF2KMT [EC:2.1.1.-]	-	-	TPX63630.1 hypothetical protein SpCBS45565_g06479 [Spizellomyces sp. 'palustris']	Electron transfer flavoprotein beta subunit lysine methyltransferase OS=Rattus norvegicus OX=10116 GN=Etfbkmt PE=2 SV=1
A1131	-	-	-	-	-	-	-	-
A1132	GO:0005975(carbohydrate metabolic process),GO:0030259(lipid glycosylation)	-	GO:0016758(hexosyltransferase activity),GO:0008194(UDP-glycosyltransferase activity)	K05841 E2.4.1.173; sterol 3beta-glucosyltransferase [EC:2.4.1.173]	-	KOG1192 At3g07020 UDP-glucuronosyl and UDP-glucosyl transferase	RDW85836.1 hypothetical protein BP5796_04161 [Coleophoma crateriformis]	Sterol 3-beta-glucosyltransferase UGT80A2 OS=Arabidopsis thaliana OX=3702 GN=UGT80A2 PE=1 SV=1
A1133	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	K15361 WDR48, UAF1; WD repeat-containing protein 48	map03460 Fanconi anemia pathway	-	TPX58932.1 hypothetical protein SpCBS45565_g07880 [Spizellomyces sp. 'palustris']	WD repeat-containing protein 64 OS=Homo sapiens OX=9606 GN=WDR64 PE=2 SV=1
A1134	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome),GO:0003723(RNA binding)	-	-	KOG1708 Hs16161712 Mitochondrial/chloroplast ribosomal protein L24	PVU95948.1 hypothetical protein BB561_001489 [Smittium simulii]	Large ribosomal subunit protein uL24 OS=Rickettsia prowazekii (strain Madrid E) OX=272947 GN=rpIX PE=3 SV=1

A1135	GO:0006418(tRNA aminoacylation for protein translation),GO:0006438(valyl-tRNA aminoacylation)	-	GO:0002161(aminoacyl-tRNA editing activity),GO:0004812(aminoacyl-tRNA ligase activity),GO:0000166(nucleotide binding),GO:0005524(ATP binding),GO:0004832(valine-tRNA ligase activity)	K01873 VARS, valS; valyl-tRNA synthetase [EC:6.1.1.9]	map00970 Aminoacyl-tRNA biosynthesis	KOG0432 Hs5454158_2 Valyl-tRNA synthetase	ORX89339.1 hypothetical protein K493DRAFT_318758 [Basidiobolus meristosporus CBS 931.73]	Valine--tRNA ligase OS=Mus musculus OX=10090 GN=Vars1 PE=1 SV=1
A1136	-	-	GO:0005515(protein binding)	K14855 RSA4, NLE1; ribosome assembly protein 4	-	KOG0271 7296187 Notchless-like WD40 repeat-containing protein	TPX71315.1 hypothetical protein CcCBS67573_g06229 [Chytridiomycota confervae]	Notchless protein homolog 1 OS=Xenopus laevis OX=8355 GN=nle1 PE=2 SV=1
A1137	-	-	GO:0005515(protein binding)	K06867 K06867; uncharacterized protein	-	-	KXX76427.1 Ankyrin-3 [Madurella mycetomatis]	Putative ankyrin repeat domain-containing protein 26-like protein OS=Homo sapiens OX=9606 GN=ANKRD26P1 PE=5 SV=2
A1138	GO:0006147(guanine catabolic process)	-	GO:0016810(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds),GO:0016787(hydrolase activity),GO:0008270(zinc ion binding),GO:0008892(guanine deaminase activity)	K01487 guaD, GDA; guanine deaminase [EC:3.5.4.3]	map00230 Purine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3968 Hs4758426 Atrazine chlorohydrolase/guanine deaminase	RUP50184.1 hypothetical protein BC936DRAFT_140037 [Jimgerdeman nia flammicorona]	Guanine deaminase OS=Rattus norvegicus OX=10116 GN=Gda PE=1 SV=1
A1139	-	-	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	-	-	-	TPX65563.1 hypothetical protein SpCBS45565_g05067 [Spizellomyces sp. 'palustris']	-
A1140	GO:0000387(spliceosomal snRNP assembly)	-	-	-	-	-	-	-
A1141	GO:0006122(mitochondrial electron transport, ubiquinol to cytochrome c)	GO:0005750(mitochondrial respiratory chain complex III)	-	-	-	-	-	-
A1142	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	K11801 DCAF11; DDB1- and CUL4-associated factor 11	-	KOG0619 7300644_2 FOG: Leucine rich repeat	OON09397.1 hypothetical protein, variant 1 [Batrachochytrium salamandrivorans]	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1

A1143	-	-	-	K11493 RCC1; regulator of chromosome condensation	-	-	KOG1426 At5 g3860 FOG: RCC1 domain	KAF9391798. 1 hypothetical protein CPB97_00543 5 [Podila verticillata]	Ultraviolet-B receptor UVR8 OS=Arabidopsis thaliana OX=3702 GN=UVR8 PE=1 SV=1
A1144	GO:00550 85(transm embrane transport)	GO:00160 21(integra l compone nt of membran e),GO:001 6020(me mbrane)	GO:0022857(tra nsmembrane transporter activity)	-	-	-	KOG0569 Hs5 730051 Permease of the major facilitator superfamily	RKP08472.1 sugar transporter [Thamnoceph alis sphaerospora]	D-xylose transporter OS=Levilactobacillus brevis OX=1580 GN=xyIT PE=1 SV=1
A1145	-	-	-	K19327 ANO10, TMEM16K; anoctamin- 10	-	-	KOG2513 Hs8 922384 Protein required for meiotic chromosome segregation	KAF9363255. 1 Anoctamin-7 [Mortierella sp. NVP85]	Anoctamin-10 OS=Homo sapiens OX=9606 GN=ANO10 PE=1 SV=2
A1146	-	-	-	-	-	-	-	-	-
A1147	-	-	-	-	-	-	-	-	-
A1148	GO:00550 85(transm embrane transport)	GO:00160 20(memb rane),GO: 0016021(i ntegral compone nt of membran e)	GO:0015301(ani on:anion antiporter activity)	K14708 SLC26A11; solute carrier family 26 (sodium- independent sulfate anion transporter), member 11	-	-	KOG0236 At3 g12520 Sulfate/bicar bonate/oxala te exchanger SAT-1 and related transporters (SLC26 family)	RKP26025.1 sulfate transporter family- domain- containing protein, partial [Syncephalis pseudoplumi galeata]	Probable sulfate transporter 4.2 OS=Arabidopsis thaliana OX=3702 GN=SULTR4;2 PE=2 SV=2
A1149	-	GO:00056 34(nucleu s)	GO:0018024(hist one-lysine N- methyltransferas e activity),GO:000 5515(protein binding)	K23700 SET2; [histone H3]- lysine36 N- trimethyltrans ferase [EC:2.1.1.359]	map00310 Lysine degradation;ma p01100 Metabolic pathways	-	KOG4442 Hs7 661774 Clathrin coat binding protein/Hunti ngtin interacting protein HIP1, involved in regulation of endocytosis	ORX73884.1 SET domain- containing protein, partial [Linderina pennisporea]	Histone-lysine N-methyltransferase SETD2 OS=Mus musculus OX=10090 GN=Setd2 PE=1 SV=1
A1150	-	-	-	-	-	-	-	XP_02188185 3.1 kinase- like domain- containing protein [Lobosporan gium transversale]	Acyl-CoA dehydrogenase family member 11 OS=Pongo abelii OX=9601 GN=ACAD11 PE=2 SV=2
A1151	-	-	-	-	-	-	-	-	-
A1152	-	-	-	K18159 NDUFAF1, CIA30; NADH dehydrogena se [ubiquinone] 1 alpha subcomplex assembly factor 1	map04714 Thermogenesis	-	-	KAG2185215. 1 hypothetical protein INT44_00200 5 [Umbelopsis vinacea]	Complex I intermediate-associated protein 30, mitochondrial OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=cia30 PE=1 SV=1
A1153	GO:00070 20(microt ubule nucleatio n),GO:003 1122(cyto plasmic microtubu le organizati on),GO:00 07017(mic rotubule- based process)	GO:00009 30(gamm a-tubulin complex), GO:00058 74(microt ubule)	GO:0005525(GT P binding)	K10389 TUBG; tubulin gamma	map04814 Motor proteins;map051 65 Human papillomavirus infection	-	KOG1374 Hs1 4785923 Gamma tubulin	XP_03102572 5.1 uncharacteriz ed protein SmJEL517_g0 2387 [Synchytrium microbalum]	Tubulin gamma-1 chain OS=Homo sapiens OX=9606 GN=TUBG1 PE=1 SV=2

A1154	-	-	-	-	-	-	KUM66011.1 hypothetical protein ACN42_g106 1 [Penicillium freii]	Epoxide hydrolase 3 OS=Mus musculus OX=10090 GN=Ephx3 PE=2 SV=2
A1155	GO:0009058(biosynthetic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0016740(transferase activity),GO:0003824(catalytic activity)	K00654 SPT; serine palmitoyltransferase [EC:2.3.1.50]	map04071 Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map04138 Autophagy - yeast;map01100 Metabolic pathways	KOG1357 At3g48780 Serine palmitoyltransferase	KAF0427522.1 Serine palmitoyltransferase [Gigaspora margarita]	Long chain base biosynthesis protein 2b OS=Arabidopsis thaliana OX=3702 GN=LCB2b PE=1 SV=1
A1156	-	-	-	-	-	-	-	-
A1157	-	-	-	-	-	KOG1502 At1g76470 Flavonol reductase/cinnamoyl-CoA reductase	KAA1477491.1 D-lactaldehyde dehydrogenase [Dentipellis sp. KUC8613]	Cinnamoyl-CoA reductase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=CCR1 PE=1 SV=1
A1158	-	-	GO:0005515(protein binding)	K14552 NAN1, UTP17, WDR75; NET1-associated nuclear protein 1 (U3 small nucleolar RNA-associated protein 17)	map03008 Ribosome biogenesis in eukaryotes	KOG1963 Hs17439994 WD40 repeat protein	KAG0046776.1 hypothetical protein BGZ83_008059 [Gryganskiella cystojenkini]	WD repeat-containing protein 75 OS=Mus musculus OX=10090 GN=Wdr75 PE=1 SV=1
A1159	-	-	-	-	-	-	-	-
A1160	-	-	GO:0005515(protein binding)	-	-	KOG2046 7303337 Calponin	XP_031027124.1 uncharacterized protein SmJEL517_g00866 [Synchytrium microbalum]	Myophilin OS=Echinococcus granulosus OX=6210 PE=2 SV=1
A1161	-	-	-	-	-	-	-	-
A1162	-	-	-	-	-	-	-	-
A1163	-	-	-	-	-	KOG2743 At1g80480 Cobalamin synthesis protein	KAA8617635.1 Cobalamin synthesis protein [Pyrenophora tritici-repentis]	Zinc chaperone P47K OS=Pseudomonas chlororaphis OX=333 PE=3 SV=1
A1164	-	-	-	K11407 HDAC6; histone deacetylase 6 [EC:3.5.1.98]	map05014 Amyotrophic lateral sclerosis;map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG1343 CE20772 Histone deacetylase complex, catalytic component HDA1	KAG1188132.1 hypothetical protein G6F35_014320 [Rhizopus oryzae]	Type-2 histone deacetylase 2 OS=Dictyostelium discoideum OX=44689 GN=hdaC PE=2 SV=1

A1165	-	GO:0016021(integral component of membrane)	-	-	-	-	KDQ08628.1 hypothetical protein BOTBODRAFT_37777 [Botryobasidium botryosum FD-172 SS1]	-
A1166	-	-	GO:0005524(ATP binding)	K02147 ATPeV1B, ATP6B; V-type H ⁺ -transporting ATPase subunit B	map04145 Phagosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation;map05110 Vibrio cholerae infection;map04150 mTOR signaling pathway;map05120 Epithelial cell signaling in Helicobacter pylori infection;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG1351 At1g76030 Vacuolar H ⁺ -ATPase V1 sector, subunit B	CDS05377.1 Putative ZYROOC16984p [Lichtheimia ramosa]	V-type proton ATPase subunit B 2 (Fragment) OS=Gossypium hirsutum OX=3635 PE=2 SV=1
A1167	GO:0046034(ATP metabolic process), GO:1902600(proton transmembrane transport)	-	-	K02147 ATPeV1B, ATP6B; V-type H ⁺ -transporting ATPase subunit B	map04145 Phagosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation;map05110 Vibrio cholerae infection;map04150 mTOR signaling pathway;map05120 Epithelial cell signaling in Helicobacter pylori infection;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG1351 YBR127c Vacuolar H ⁺ -ATPase V1 sector, subunit B	KAE8231432.1 hypothetical protein CF326_g3554, partial [Tilletia indica]	V-type proton ATPase subunit B OS=Dictyostelium discoideum OX=44689 GN=vatB PE=1 SV=1
A1168	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	-	PFH63313.1 hypothetical protein XA68_13770 [Ophiocordyceps unilateralis]	Glycerophosphoinositol permease 1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GIT1 PE=1 SV=1
A1169	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At3g01490 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF7747845.1 hypothetical protein DSO57_020938 [Entomophthora muscae]	Mitogen-activated protein kinase kinase kinase 13-A OS=Xenopus laevis OX=8355 GN=map3k13-a PE=2 SV=1

A1170	-	-	GO:0005515(protein binding)	-	-	KOG0291 CE11192 WD40-repeat-containing subunit of the 18S rRNA processing complex	-	Periodic tryptophan protein 2 homolog OS=Caenorhabditis elegans OX=6239 GN=F55F8.3 PE=3 SV=2
A1171	GO:0017183(peptidyl-diphthamide biosynthetic process from peptidyl-histidine)	-	GO:0090560(2-(3-amino-3-carboxypropyl)histidine synthase activity)	K07561 DPH1, dph2; 2-(3-amino-3-carboxypropyl)histidine synthase [EC:2.5.1.108]	-	-	ORX89374.1 hypothetical protein K493DRAFT_233793 [Basidiobolus meristosporus CBS 931.73]	2-(3-amino-3-carboxypropyl)histidine synthase subunit 1 OS=Gallus gallus OX=9031 GN=DPH1 PE=2 SV=1
A1172	-	-	-	-	-	-	-	-
A1173	GO:0006355(regulation of transcription, DNA-templated)	GO:0005730(nucleolus)	GO:0003677(DNA binding),GO:0008134(transcription factor binding)	K02331 POL5, MYBBP1A; DNA polymerase phi [EC:2.7.7.7]	-	KOG1926 At5g64420 Predicted regulator of rRNA gene transcription (MYB-binding protein)	TPX37827.1 hypothetical protein SeMB42_g06860 [Synchytrium endobioticum]	rDNA transcriptional regulator pol5 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=pol5 PE=1 SV=2
A1174	-	-	-	-	-	-	-	-
A1175	-	-	-	-	-	-	-	-
A1176	GO:0008654(phospholipid biosynthetic process)	GO:0016020(membrane)	GO:0016780(phosphotransferase activity, for other substituted phosphate groups)	-	-	KOG2877 At3g25585 sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferases	ORY00406.1 sn-1,2-diacylglycerol cholinephosphotransferase [Basidiobolus meristosporus CBS 931.73]	Uncharacterized CDP-alcohol phosphatidyltransferase class-I family protein 2 OS=Dictyostelium discoideum OX=44689 GN=capt8 PE=3 SV=1
A1177	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	TPX68090.1 isocitrate dehydrogenase (NAD+) [Spizellomyces sp. 'palustris']	Adenylate cyclase type 10 OS=Homo sapiens OX=9606 GN=ADCY10 PE=1 SV=3
A1178	-	-	-	-	-	-	-	-
A1179	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004965(G protein-coupled GABA receptor activity),GO:0004930(G protein-coupled receptor activity)	-	-	-	ORX69814.1 hypothetical protein BCR32DRAFT_272429 [Anaeromyces robustus]	Metabotropic glutamate receptor-like protein F OS=Dictyostelium discoideum OX=44689 GN=grIF PE=2 SV=1
A1180	-	-	-	-	-	-	-	-
A1181	GO:0009143(nucleoside triphosphate catabolic process)	-	GO:0047429(nucleoside-triphosphate diphosphatase activity)	K01519 rdgB, ITPA; XTP/dITP diphosphohydrolase [EC:3.6.1.66]	map00983 Drug metabolism - other enzymes;map00230 Purine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3222 At4g13720 Inosine triphosphate pyrophosphatase	KAG2183537.1 hypothetical protein INT43_006543 [Umbelopsis isabellina]	Inosine triphosphate pyrophosphatase OS=Monosiga brevicollis OX=81824 GN=13033 PE=3 SV=1

A1182	-	-	GO:0003824(catalytic activity)	K05607 AUH; methylglutaryl-CoA hydratase [EC:4.2.1.18]	map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG1680 Hs8923864 Enoyl-CoA hydratase	XP_031023751.1 uncharacterized protein SmJEL517_g04374 [Synchytrium microbalum]	Ethylmalonyl-CoA decarboxylase OS=Xenopus laevis OX=8355 GN=echdc1 PE=2 SV=1
A1183	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	K05657 ABCB10; ATP-binding cassette, subfamily B (MDR/TAP), member 10	map02010 ABC transporters	KOG0058 Hs9961244 Peptide exporter, ABC superfamily	OBZ83293.1 ATP-binding cassette sub-family B member 10, mitochondrial [Choanephora cucurbitarum]	ATP-binding cassette sub-family B member 10, mitochondrial OS=Mus musculus OX=10090 GN=Abcb10 PE=1 SV=1
A1184	GO:0006508(proteolysis)	-	GO:0004222(metalloendopeptidase activity);GO:0008237(metalloproteinase activity)	-	-	KOG3607 Hs4557253 Meltrins, fertilins and related Zn-dependent metalloproteinases of the ADAMs family	XP_036635209.1 uncharacterized protein PC9H_004149 [Pleurotus ostreatus]	Zinc metalloproteinase-disintegrin-like MTP9 OS=Drysdalia coronoides OX=66186 PE=1 SV=1
A1185	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	-	-	-	XP_001876028.1 predicted protein [Laccaria bicolor S238N-H82]	-
A1186	-	-	GO:0005516(protein binding)	K11806 DCAF13, WDSOF1; DDB1- and CUL4-associated factor 13	-	KOG0268 Hs10092627 Sof1-like rRNA processing protein (contains WD40 repeats)	KAG0222797.1 rRNA-processing protein sof1 [Actinomyces rella wolfii]	DDB1- and CUL4-associated factor 13 OS=Xenopus tropicalis OX=8364 GN=dcaf13 PE=2 SV=1
A1187	-	-	-	K09660 MPDU1; mannose-P-dolichol utilization defect 1	-	KOG3211 Hs4759110 Predicted endoplasmic reticulum membrane protein Lec35/MPDU1 involved in monosaccharide-P-dolichol utilization	OZJ04272.1 hypothetical protein BZG36_02478 [Bifiguratus adelaidae]	Mannose-P-dolichol utilization defect 1 protein homolog 2 OS=Arabidopsis thaliana OX=3702 GN=At4g07390 PE=2 SV=1
A1188	-	-	-	-	-	-	-	-
A1189	GO:0016104(triterpenoid biosynthetic process)	GO:0005811(lipid droplet)	GO:0016866(intramolecular transferase activity)	K01852 LSS, ERG7; lanosterol synthase [EC:5.4.99.7]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG0497 At2g07050 Oxidosqualene-lanosterol cyclase and related proteins	XP_006680412.1 uncharacterized protein BATDEDRAFT_35539 [Batrachochytrium dendrobatidis JAM81]	Cycloartenol synthase OS=Arabidopsis thaliana OX=3702 GN=CAS1 PE=1 SV=2
A1190	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding);GO:0016491(oxidoreductase activity)	K00227 SC5DL, ERG3; Delta7-sterol 5-desaturase [EC:1.14.19.20]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG0872 YLR056w Sterol C5 desaturase	PYI29715.1 hypothetical protein BP00DRAFT_427220 [Aspergillus nidulans CBS 114.80]	Alternative squalene epoxidase OS=Phaeodactylum tricornutum (strain CCAP 1055/1) OX=556484 GN=PHATRDRAFT_45494 PE=1 SV=1

A1191	GO:0008299(isoprenoid biosynthetic process), GO:0015936(coenzyme A metabolic process)	-	GO:0004420(hydroxymethylglutaryl-CoA reductase (NADPH) activity),GO:0005515(protein binding),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)	K00021 HMGCR; hydroxymethylglutaryl-CoA reductase (NADPH) [EC:1.1.1.34]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis;map04976 Bile secretion;map04152 AMPK signaling pathway;map01100 Metabolic pathways	KOG2480 At1g76490 3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) reductase	KAG0066969.1 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme, partial [Linnemania elongata]	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 OS=Dictyostelium discoideum OX=44689 GN=hmgA PE=2 SV=1
A1192	GO:0009966(regulation of signal transduction),GO:0043666(regulation of phosphoprotein phosphatase activity),GO:0006457(protein folding)	-	GO:0004864(protein phosphatase inhibitor activity),GO:0005515(protein binding),GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding)	K09553 STIP1; stress-induced-phosphoprotein 1	map05020 Prion disease	KOG0548 Hs5803181 Molecular co-chaperone STI1	KAF5322423.1 hypothetical protein D9619_001064 [Psilocybe cf. subviscida]	Stress-induced-phosphoprotein 1 OS=Cricetulus griseus OX=10029 GN=STIP1 PE=2 SV=1
A1193	-	-	-	-	-	-	-	-
A1194	-	-	-	-	-	-	-	Protein-glutamine gamma-glutamyltransferase E OS=Bos taurus
A1195	-	-	-	-	-	KOG4081 7300373 Dynein light chain	KAG2229887.1 hypothetical protein INT48_001322, partial [Thamnidium elegans]	Dynein light chain Tctex-type OS=Dictyostelium discoideum OX=44689 GN=dlcA PE=3 SV=2
A1196	-	-	GO:0005085(guanine nucleotide exchange factor activity)	K20047 PAN1; actin cytoskeleton-regulatory complex protein PAN1	-	KOG3518 Hs18562992_1 Putative guanine nucleotide exchange factor	SCV75025.1 BQ2448_8054 [Microbryum intermedium]	Pleckstrin homology domain-containing family G member 1 OS=Homo sapiens OX=9606 GN=PLEKHG1 PE=1 SV=2
A1197	-	-	GO:0005509(calcium ion binding)	-	-	KOG0027 At1g24620 Calmodulin and related proteins (EF-Hand superfamily)	-	Probable calcium-binding protein CML18 OS=Oryza sativa subsp. japonica OX=39947 GN=CML18 PE=2 SV=1
A1198	-	-	-	-	-	-	TPX55334.1 hypothetical protein PhCBS80983_g05403 [Powellomyces hirtus]	Cilia- and flagella-associated protein 99 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP99 PE=1 SV=1
A1199	GO:0006413(translational initiation)	-	GO:0003743(translation initiation factor activity),GO:0003723(RNA binding)	K03236 EIF1A; translation initiation factor 1A	-	KOG3403 At2g04520 Translation initiation factor 1A (eIF-1A)	OCB91340.1 nucleic acid-binding protein [Sanguinalia baumii]	Eukaryotic translation initiation factor 1A OS=Onobrychis viciifolia OX=3882 PE=2 SV=2

A1200	-	-	-	-	-	-	RKP03909.1 hypothetical protein CXG81DRAFT _16615 [Caulochytrium protostelioides]	-
A1201	-	-	-	-	-	-	-	-
A1202	-	-	-	-	-	KOG4009 At1g49140 NADH-ubiquinone oxidoreductase, subunit NDUFB10/PDSW	-	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-A OS=Arabidopsis thaliana OX=3702 GN=At1g49140 PE=1 SV=1
A1203	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05665 ABCC1; ATP-binding cassette, subfamily C (CFTR/MRP), member 1 [EC:7.6.2.3]	map04071 Sphingolipid signaling pathway;map01523 Antifolate resistance;map04977 Vitamin digestion and absorption;map02010 ABC transporters;map05206 MicroRNAs in cancer	KOG0054 Hs4557481 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	OBZ82882.1 Metal resistance protein YCF1 [Choanephora cucurbitarum]	Multidrug resistance-associated protein 1 OS=Mus musculus OX=10090 GN=Abcc1 PE=1 SV=1
A1204	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0054 Hs4557481 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	OBZ82882.1 Metal resistance protein YCF1 [Choanephora cucurbitarum]	Multidrug resistance-associated protein 1 OS=Canis lupus familiaris OX=9615 GN=ABCC1 PE=1 SV=1
A1205	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05665 ABCC1; ATP-binding cassette, subfamily C (CFTR/MRP), member 1 [EC:7.6.2.3]	map04071 Sphingolipid signaling pathway;map01523 Antifolate resistance;map04977 Vitamin digestion and absorption;map02010 ABC transporters;map05206 MicroRNAs in cancer	KOG0054 Hs4557481 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	OBZ82882.1 Metal resistance protein YCF1 [Choanephora cucurbitarum]	ATP-binding cassette sub-family C member 2 OS=Homo sapiens OX=9606 GN=ABCC2 PE=1 SV=3
A1206	GO:0097056(selenocysteinyl-tRNA(Sec) biosynthetic process)	-	GO:0016740(transferase activity),GO:0016785(selenotransferase activity),GO:0003824(catalytic activity)	-	-	KOG3843 Hs8393713 Predicted serine hydroxymethyltransferase SLA/LP (autoimmune hepatitis marker in humans)	OZJ02775.1 hypothetical protein BZG36_03480 [Bifiguratus adalaidae]	O-phosphoserine-tRNA(Sec) selenium transferase OS=Xenopus tropicalis OX=8364 GN=sepssec PE=2 SV=1

A1207	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239 At5g54670 Kinesin (KAR3 subfamily)	KXN69631.1 kinesin-domain-containing protein, partial [Conidiobolus coronatus NRRL 28638]	Kinesin-like protein KIN-14N OS=Arabidopsis thaliana OX=3702 GN=KIN14N PE=1 SV=1
A1208	-	-	-	-	-	-	-	-
A1209	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 CE25046 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	RKO99416.1 hypothetical protein CXG81DRAFT_30214 [Caulochytrium protostelioides]	Calcium/calmodulin-dependent protein kinase type 1 OS=Caenorhabditis elegans OX=6239 GN=cmk-1 PE=1 SV=1
A1210	-	-	-	K03098 APOD; apolipoprotein D and lipocalin family protein	-	KOG4824 At5g58070 Apolipoprotein D/Lipocalin	KAG0941766.1 hypothetical protein G6F31_014970 [Rhizopus oryzae]	Temperature-induced lipocalin-1 OS=Arabidopsis thaliana OX=3702 GN=TIL PE=1 SV=1
A1211	-	-	GO:0016407(acyltransferase activity)	-	-	-	KAG1470278.1 hypothetical protein G6F57_011853 [Rhizopus oryzae]	-
A1212	-	-	-	-	-	KOG1928 At4g19900.1 Alpha-1,4-N-acetylglucosaminyltransferase	KAF9956433.1 hypothetical protein BGZ70_009902 [Mortierella alpina]	Uncharacterized protein At4g19900 OS=Arabidopsis thaliana OX=3702 GN=At4g19900 PE=2 SV=1
A1213	-	GO:0034464(BBSome)	GO:0005085(guanylate-nucleotide exchange factor activity)	-	-	KOG3679 Hs13929460 Predicted coiled-coil protein	PIA17812.1 Dbl homology domain-containing protein, partial [Coemansia reversa NRRL 1564]	Protein PTHB1 OS=Homo sapiens OX=9606 GN=BBS9 PE=1 SV=1
A1214	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1215	-	-	-	-	-	-	-	-
A1216	-	-	-	-	-	-	-	-
A1217	GO:0046856(phosphatidylinositol dephosphorylation)	-	GO:0016791(phosphatase activity),GO:0043813(phosphatidylinositol-3,5-bisphosphate 5-phosphatase activity)	K22913 FIG4; phosphatidylinositol 3,5-bisphosphate 5-phosphatase [EC:3.1.3.-]	map05014 Amyotrophic lateral sclerosis;map05022 Pathways of neurodegeneration - multiple diseases;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG1888 At1g22620 Putative phosphoinositide phosphatase	KAG2181956.1 hypothetical protein INT43_006881 [Umbelopsis isabellina]	Phosphatidylinositol-3-phosphatase SAC1 OS=Arabidopsis thaliana OX=3702 GN=SAC1 PE=1 SV=1
A1218	-	-	-	-	-	KOG3961 Hs18564317 Uncharacterized conserved protein	ORZ34611.1 parkin coregulated protein [Catenaria anguillulae PL171]	Parkin coregulated gene protein OS=Bos taurus OX=9913 GN=PACRG PE=1 SV=1

A1219	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1220	-	-	-	-	-	-	-	-
A1221	GO:0007165(signal transduction)	-	-	-	-	-	-	-
A1222	-	-	-	-	-	KOG2130 Hs14769286 Phosphatidylinositol-specific receptor PtdSerR, contains JmjC domain	OAJ42605.1 hypothetical protein BDEG_26046 [Batrachochytrium dendrobatidis JEL423]	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Danio rerio OX=7955 GN=jmjd6 PE=2 SV=2
A1223	GO:0006351(transcription, DNA-templated)	-	GO:0046983(protein dimerization activity),GO:0003899(DNA-directed 5'-3' RNA polymerase activity),GO:0003677(DNA binding)	K03011 RPB3, POLR2C; DNA-directed RNA polymerase II subunit RPB3	map03420 Nucleotide excision repair;map03020 RNA polymerase;map05016 Huntington disease	KOG1522 At2g15430 RNA polymerase II, subunit POLR2C/RPB3	XP_023469750.1 insert subdomain of RNA polymerase alpha subunit [Rhizopus microsporus ATCC 52813]	DNA-directed RNA polymerase II subunit rpb3 OS=Dictyostelium discoideum OX=44689 GN=polr2c PE=3 SV=1
A1224	-	-	GO:0005515(protein binding)	K22073 IBA57; transferase CAF17, mitochondria I [EC:2.1.-.-]	-	KOG2929 7299068 Transcription factor, component of CCR4 transcriptional complex	XP_025378110.1 Aminomethyltransferase folate-binding domain-containing protein [Acaromyces ingoldii]	Putative transferase CAF17, mitochondrial OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=CAF17 PE=3 SV=1
A1225	GO:0035082(axoneme assembly),GO:0060294(cilium movement involved in cell motility)	-	-	-	-	-	RKO94655.1 hypothetical protein BDK51DRAFT_29686 [Blyttomyces helicus]	Cilia- and flagella-associated protein 46 OS=Homo sapiens OX=9606 GN=CFAP46 PE=2 SV=3
A1226	-	-	-	-	-	-	-	-
A1227	GO:0006466(phosphatidylethanolamine biosynthetic process),GO:0009058(biosynthetic process)	-	GO:0004306(ethanolamine-phosphate cytidyltransferase activity),GO:0003824(catalytic activity)	K00967 PCYT2; ethanolamine-phosphate cytidyltransferase [EC:2.7.7.14]	map00440 Phosphonate and phosphinate metabolism;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG2803 At2g38670 Choline phosphate cytidyltransferase/Predicted CDP-ethanolamine synthase	ORY98790.1 hypothetical protein BCR43DRAFT_530230 [Syncephalaster racemosus]	Ethanolamine-phosphate cytidyltransferase OS=Arabidopsis thaliana OX=3702 GN=PECT1 PE=1 SV=1
A1228	-	-	GO:0005515(protein binding)	K14556 DIP2, UTP12, WDR3; U3 small nucleolar RNA-associated protein 12	map03008 Ribosome biogenesis in eukaryotes	-	TPX63875.1 hypothetical protein SpCBS45565_g06304 [Spizellomyces sp. 'palustris']	-

A1229	-	-	GO:0005509(calcium ion binding);GO:0008597(calcium-dependent protein serine/threonine phosphatase regulator activity)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	KOG0034[Hs4506025 Ca2+/calmodulin-dependent protein phosphatase (calcineurin subunit B), EF-Hand superfamily protein	GJH88679.1 hypothetical protein NliqN6_5081 [Naganishia liquefaciens]	Calcineurin subunit B type 2 OS=Homo sapiens OX=9606 GN=PPP3R2 PE=1 SV=3
A1230	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	-	-	-	-	-
A1231	-	-	-	-	-	-	KNE59945.1 hypothetical protein AMAG_05392 [Allomyces macrogynus ATCC 38327]	-
A1232	-	-	-	-	-	-	KAF9425160.1 hypothetical protein BGZ94_007784 [Podila epigama]	-
A1233	-	-	-	-	-	-	-	-
A1234	-	-	-	-	-	-	-	-
A1235	GO:0006850(mitochondrial pyruvate transmembrane transport)	GO:0005743(mitochondrial inner membrane)	-	K22139 MPC2; mitochondrial pyruvate carrier 2	map05415 Diabetic cardiomyopathy	KOG1589[At4g22310 Uncharacterized conserved protein	KAG0230730.1 Mitochondrial pyruvate carrier 2 [Actinomyces rella wolfii]	Mitochondrial pyruvate carrier 4 OS=Arabidopsis thaliana OX=3702 GN=MPC4 PE=3 SV=1
A1236	-	-	-	K00627 DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00620 Pyruvate metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0557[YNL071w Dihydrolipoyl acetyltransferase	KAG5355977.1 Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex [Yarrowia sp. B02]	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=mrp-3 PE=1 SV=2

A1237	-	GO:0016021(integral component of membrane)	GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups),GO:0004659(prenyltransferase activity)	-	-	KOG4581 7298285 Predicted membrane protein	-	UbiA prenyltransferase domain-containing protein 1 OS=Dictyostelium discoideum OX=44689 GN=ubiad1 PE=3 SV=1
A1238	-	-	GO:0016787(hydrolase activity)	K01293 E3.4.17.4; Gly-Xaa carboxypeptidase [EC:3.4.17.4]	-	KOG2275 YJL172w Aminoacylase ACY1 and related metalloexopeptidases	RYO79412.1 hypothetical protein DL763_009289 [Monosporascus cannonballus]	Probable carboxypeptidase S-like 2 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0267984 PE=3 SV=1
A1239	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0003678(DNA helicase activity),GO:0016818(hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides),GO:0003676(nucleic acid binding),GO:0004386(helicase activity),GO:0005524(ATP binding),GO:0003677(DNA binding)	K11273 DDX11, CHL1, CTF1; chromosome transmission fidelity protein 1 [EC:3.6.4.13]	map04110 Cell cycle	KOG1133 Hs13787197 Helicase of the DEAD superfamily	XP_01660399 8.1 DNA repair helicase (rad3) [Spizellomyces punctatus DAOM BR117]	ATP-dependent DNA helicase DDX11 OS=Mus musculus OX=10090 GN=Ddx11 PE=1 SV=2
A1240	-	GO:0016021(integral component of membrane)	GO:0009922(fatty acid elongase activity)	K10245 ELO2; fatty acid elongase 2 [EC:2.3.1.199]	map01110 Biosynthesis of secondary metabolites;map00062 Fatty acid elongation;map01040 Biosynthesis of unsaturated fatty acids;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG3072 7294075 Long chain fatty acid elongase	ORX53925.1 GNS1/SUR4 membrane protein [Hesseltinella vesiculosa]	Very long chain fatty acid elongase 6 OS=Drosophila melanogaster OX=7227 GN=Baldspot PE=1 SV=2
A1241	-	-	-	-	-	KOG1471 At3g24840 Phosphatidylinositol transfer protein SEC14 and related proteins	CCO31683.1 Sec14 cytosolic factor AltName: Full=Phosphatidylinositol/phosphatidylcholine transfer protein [Rhizoctonia solani AG-1 IB]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH9 OS=Arabidopsis thaliana OX=3702 GN=SFH9 PE=2 SV=1
A1242	-	-	-	-	-	-	-	-

A1243	GO:0000413(protein peptidyl-prolyl isomerization)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K01802 E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]	-	KOG0865 YML078w Cyclophilin type peptidyl-prolyl cis-trans isomerase	XP_022676364.1 peptidyl-prolyl cis-trans isomerase C [Kluyveromyces marxianus DMKU3-1042]	Peptidyl-prolyl cis-trans isomerase slr1251 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=slr1251 PE=1 SV=1
A1244	-	-	-	-	-	-	-	-
A1245	-	-	-	-	-	-	-	-
A1246	-	-	-	-	-	-	-	-
A1247	-	-	-	-	-	-	-	-
A1248	-	-	-	-	-	KOG1471 At2g21540 Phosphatidylinositol transfer protein SEC14 and related proteins	KAF9468763.1 CRAL-TRIO domain-containing protein [Lepista nuda]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH3 OS=Arabidopsis thaliana OX=3702 GN=SFH3 PE=2 SV=1
A1249	-	-	-	K08342 ATG4; cysteine protease ATG4 [EC:3.4.22.-]	map04140 Autophagy - animal;map04138 Autophagy - yeast;map04136 Autophagy - other	KOG2674 Hs18378733 Cysteine protease required for autophagy - Apg4p/Aut2p	GAN07444.1 cysteine protease ATG4A isoform X1 [Mucor ambiguus]	Cysteine protease ATG4B OS=Xenopus laevis OX=8355 GN=atg4b PE=2 SV=1
A1250	-	-	-	-	-	-	KAF7749177.1 hypothetical protein DSO57_018839 [Entomophthora muscae]	-
A1251	-	-	GO:0005515(protein binding)	-	-	-	TPX76320.1 hypothetical protein CcCBS67573_g02396 [Chytridiomycota confervae]	-
A1252	-	-	-	-	-	-	-	E3 ubiquitin-protein ligase RNF114 OS=Sus scrofa OX=9823
A1253	GO:0016567(protein ubiquitination)	-	GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity);GO:0004842(ubiquitin-protein transferase activity)	K14571 RIX7, NVL; ribosome biogenesis ATPase	map03008 Ribosome biogenesis in eukaryotes	KOG0733 Hs4505483 Nuclear AAA ATPase (VCP subfamily)	RIB10190.1 AAA-domain-containing protein, partial [Gigaspora rosea]	Nuclear valosin-containing protein-like OS=Homo sapiens OX=9606 GN=NVL PE=1 SV=1
A1254	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	K15628 PXA; ATP-binding cassette, subfamily D (ALD), peroxisomal long-chain fatty acid import protein [EC:7.6.2.4]	map04146 Peroxisome;map02010 ABC transporters	KOG0060 At1g54350 Long-chain acyl-CoA transporter, ABC superfamily (involved in peroxisome organization and biogenesis)	EXF79224.1 ABC transporter transmembrane region 2 [Colletotrichum fioriniae PJ7]	Uncharacterized ABC transporter ATP-binding protein slI0182 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=slI0182 PE=3 SV=1

A1255	-	-	GO:0071949(FAD binding)	K00480 E1.14.13.1; salicylate hydroxylase [EC:1.14.13.1]	map01120 Microbial metabolism in diverse environments;map01220 Degradation of aromatic compounds;map00624 Polycyclic aromatic hydrocarbon degradation;map00626 Naphthalene degradation;map00621 Dioxin degradation;map01100 Metabolic pathways	KOG2614 At5g11330 Kynurenine 3-monooxygenase and related flavoprotein monooxygenases	XP_002484427.1 salicylate hydroxylase, putative [Talaromyces stipitatus ATCC 10500]	3-amino-4-hydroxybenzoate 2-monooxygenase OS=Streptomyces cremusus OX=66881 GN=creL PE=1 SV=1
A1256	-	-	-	-	-	-	OAJ36524.1 hypothetical protein BDEG_20689 [Batrachochytrium dendrobatidis JEL423]	Sperm axonemal maintenance protein CFAP97D1 OS=Mus musculus OX=10090 GN=Cfap97d1 PE=2 SV=1
A1257	GO:0006281(DNA repair)	-	GO:0003887(DNA-directed DNA polymerase activity)	K03511 POLK; DNA polymerase kappa [EC:2.7.7.7]	map05222 Small cell lung cancer;map05223 Non-small cell lung cancer;map05217 Basal cell carcinoma;map05216 Thyroid cancer;map05214 Glioma;map05213 Endometrial cancer;map05212 Pancreatic cancer;map05210 Colorectal cancer;map05218 Melanoma;map05226 Gastric cancer;map05200 Pathways in cancer;map05202 Transcriptional misregulation in cancer;map05225 Hepatocellular carcinoma;map05220 Chronic	KOG2094 At1g49980 Predicted DNA damage inducible protein	RIB02872.1 hypothetical protein C2G38_1990734 [Gigaspora rosea]	DNA polymerase kappa OS=Arabidopsis thaliana OX=3702 GN=POLK PE=1 SV=1
A1258	-	-	-	-	-	-	-	-
A1259	GO:0006072(glycerol-3-phosphate metabolic process), GO:0046168(glycerol-3-phosphate catabolic process), GO:0005975(carbohydrate metabolic process)	GO:0009331(glycerol-3-phosphate dehydrogenase complex)	GO:0004367(glycerol-3-phosphate dehydrogenase [NAD+] activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0051287(NAD binding),GO:0016491(oxidoreductase activity)	-	-	KOG2711 At2g40690 Glycerol-3-phosphate dehydrogenase/dihydroxyacetone 3-phosphate reductase	XP_006683002.1 uncharacterized protein BATDEDRAFT_92784 [Batrachochytrium dendrobatidis JAM81]	Glycerol-3-phosphate dehydrogenase [NAD(+)] 2, chloroplast OS=Arabidopsis thaliana OX=3702 GN=GLY1 PE=1 SV=1

A1260	GO:0000105(histidine biosynthetic process)	-	GO:0003949(1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase activity)	K01814 hisA; phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [EC:5.3.1.16]	map00340 Histidine metabolism;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways	KOG3055 At2g36230 Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase	KAF4602436.1 Enzyme that catalyzes the fourth step in the histidine pathway [Pleurotus pulmonarius]	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=HISN3 PE=1 SV=1
A1261	-	-	GO:0005515(protein binding)	-	-	KOG0676 CE16463 Actin and related proteins	KAF5095009.1 hypothetical protein DV451_004837 [Geotrichum candidum]	Actin OS=Crassostrea gigas OX=29159 PE=2 SV=1
A1262	GO:0006913(nucleocytoplasmic transport)	GO:0005643(nuclear pore)	GO:0017056(structural constituent of nuclear pore)	K14297 NUP98, ADAR2, NUP116; nuclear pore complex protein Nup98-Nup96	map05014 Amyotrophic lateral sclerosis;map03013 Nucleocytoplasmic transport;map05164 Influenza A	KOG0845 Hs21264365 Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116)	KAF9570612.1 Vacuolar fusion protein mon1b [Mortierella alpina]	Nuclear pore complex protein Nup98-Nup96 OS=Drosophila melanogaster OX=7227 GN=Nup98-96 PE=1 SV=3
A1263	-	-	-	-	-	KOG2973 At1g14300 Uncharacterized conserved protein	KXS14969.1 DUF383-domain-containing protein [Gonapodya prolifera JEL478]	Protein HGH1 homolog OS=Danio rerio OX=7955 GN=hgh1 PE=2 SV=1
A1264	-	-	-	-	-	-	KAG1469498.1 hypothetical protein G6F56_003223 [Rhizopus deleamar]	Rhodanese-like domain-containing protein 6 OS=Arabidopsis thaliana OX=3702 GN=STR6 PE=2 SV=1
A1265	-	-	GO:0005267(potassium channel activity)	-	-	-	-	-
A1266	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration;map04024 cAMP signaling pathway;map04020 Calcium signaling pathway;map05414 Dilated cardiomyopathy;map04140 Autophagy - animal;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map01522 Endocrine resistance;map04919 Thyroid hormone signaling pathway;map04918 Thyroid hormone synthesis;map04	KOG0614 CE19898 cGMP-dependent protein kinase	ORY28135.1 kinase-like domain-containing protein [Nematelia encephala]	cGMP-dependent protein kinase egl-4 OS=Caenorhabditis elegans OX=6239 GN=egl-4 PE=1 SV=2
A1267	-	-	-	-	-	-	-	Hepatocyte growth factor receptor OS=Loxodonta africana OX=9785

A1268	-	-	-	-	-	-	XP_038925569.1 uncharacterized protein LCP9604111_8363 [Penicillium roqueforti]	-
A1269	-	-	-	-	-	-	-	-
A1270	GO:0051726(regulation of cell cycle)	-	-	-	-	-	-	-
A1271	-	-	-	-	-	-	-	-
A1272	-	-	GO:0005254(chloride channel activity)	-	-	-	-	-
A1273	GO:0016075(rRNA catabolic process), GO:0090503(RNA phosphodiester bond hydrolysis, exonucleolytic)	-	GO:0000175(3'-5'-exoribonuclease activity),GO:0003723(RNA binding),GO:0004540(ribonuclease activity)	K12585 DIS3, RRP44; exosome complex exonuclease DIS3/RRP44 [EC:3.1.13.-]	map03018 RNA degradation	KOG2102 Hs19115966 Exosomal 3'-5'-exoribonuclease complex, subunit Rrp44/Dis3	ORZ01300.1 hypothetical protein BCR43DRAFT_453736 [Syncephalastrium racemosum]	DIS3-like exonuclease 1 OS=Danio rerio OX=7955 GN=dis3l PE=2 SV=1
A1274	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	-	-	KOG0087 Hs4758984 GTPase Rab11/YPT3, small G protein superfamily	KXS13402.1 Rab11-1c [Gonapodya prolifera JEL478]	Ras-related protein Rab-11A OS=Gallus gallus OX=9031 GN=RAB11A PE=2 SV=1
A1275	-	GO:0016020(membrane)	GO:0051537(2 iron, 2 sulfur cluster binding),GO:0008121(ubiquinol-cytochrome-c reductase activity)	K00411 UQCRCF1, RIP1, petA; ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:7.1.1.8]	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04260 Cardiac muscle contraction;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map02020 Two-component	KOG1671 At5g13430 Ubiquinol cytochrome c reductase, subunit RIP1	KAF9172897.1 hypothetical protein BGX20_004592 [Mortierella sp. AD010]	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Solanum tuberosum OX=4113 GN=FES1 PE=1 SV=1
A1276	GO:0007076(mitotic chromosome condensation)	GO:0000796(condensin complex)	-	K06676 BRN1, CAPH; condensin complex subunit 2	map04111 Cell cycle - yeast	KOG2328 At2g32590 Chromosome condensation complex Condensin, subunit H	TFY75376.1 hypothetical protein EWM64_g8638 [Hericium alpestre]	Condensin complex subunit 2 OS=Arabidopsis thaliana OX=3702 GN=CAPH PE=1 SV=1
A1277	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1278	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A1279	-	-	-	-	-	-	-	-
A1280	-	-	GO:0005515(protein binding),GO:0005085(guanylnucleotide exchange factor activity)	-	-	-	-	-

A1281	GO:0006163(purine nucleotide metabolic process)	-	GO:0004385(guanylate kinase activity)	K00942 gmk, GUK1; guanylate kinase [EC:2.7.4.8]	map00230 Purine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG0707[Hs4504221 Guanylate kinase	PGH28950.1 guanylate kinase, partial [Emmonsia crescens]	Guanylate kinase OS=Mus musculus OX=10090 GN=Guk1 PE=1 SV=2
A1282	-	-	GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	K14789 NOP6; nucleolar protein 6	-	-	OZJ03035.1 hypothetical protein BZG36_03266 [Bifiguratus adalaidae]	Uncharacterized RNA-binding protein C365.04c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC365.04c PE=4 SV=1
A1283	-	-	-	K13291 TUT; terminal uridylyltransferase [EC:2.7.7.52]	-	KOG2277[Hs22044581 S-M checkpoint control protein CID1 and related nucleotidyltransferases	KAG0248260.1 hypothetical protein BG011_000267 [Mortierella polycephala]	UTP:RNA uridylyltransferase 1 OS=Arabidopsis thaliana OX=3702 GN=URT1 PE=1 SV=2
A1284	GO:0042254(ribosome biogenesis)	GO:1990904(ribonucleoprotein complex), GO:0005730(nucleolus)	GO:0003723(RNA binding)	-	-	KOG3387[At5g20160 60S ribosomal protein 15.5kD/SNU13, NHP2/L7A family (includes ribonuclease P subunit p38), involved in splicing	OON10075.1 ribonucleoprotein-associated protein [Batrachochytrium salamandrivorans]	NHP2-like protein 1 homolog OS=Caenorhabditis elegans OX=6239 GN=M28.5 PE=3 SV=1
A1285	-	-	GO:0005515(protein binding)	K10415 DYNC11, DNCL; dynein cytoplasmic 1 intermediate chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG1587[Hs17435098 Cytoplasmic dynein intermediate chain	TPX62281.1 hypothetical protein PhCBS80983_g00515 [Powellomyces hirtus]	Dynein axonemal intermediate chain 3 OS=Macaca fascicularis OX=9541 GN=DNAI3 PE=2 SV=1
A1286	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K06682 TEM1; Gtp-binding protein of the ras superfamily involved in termination of M-phase	map04111 Cell cycle - yeast	-	RIA99144.1 small GTPase [Glomus cerebriiforme]	Septum-promoting GTP-binding protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=spg1 PE=1 SV=1
A1287	GO:0016311(dephosphorylation),GO:0006470(protein dephosphorylation)	-	GO:0005515(protein binding),GO:0008138(protein tyrosine/serine/threonine phosphatase activity),GO:0016791(phosphatase activity)	K14819 DUSP12, YVH1; dual specificity phosphatase 12 [EC:3.1.3.16 3.1.3.48]	-	KOG1716[At3g06110 Dual specificity phosphatase	ORX87467.1 phosphatases II [Anaeromyces robustus]	Dual specificity protein phosphatase 1B OS=Arabidopsis thaliana OX=3702 GN=DSPTP1B PE=1 SV=1

A1288	-	-	GO:0005515(protein binding)	K14012 NSFL1C, UBX1, SHP1; UBX domain-containing protein 1	map04141 Protein processing in endoplasmic reticulum	KOG2086 At4g22150 Protein tyrosine phosphatase SHP1/Cofactor for p97 ATPase-mediated vesicle membrane fusion	KAF9345664.1 hypothetical protein BGX34_004572, partial [Mortierella sp. NVP85]	Plant UBX domain-containing protein 4 OS=Arabidopsis thaliana OX=3702 GN=PUX4 PE=1 SV=1
A1289	GO:0007165(signal transduction)	GO:0000159(protein phosphatase type 2A complex)	GO:0019888(protein phosphatase regulator activity)	K11584 PPP2R5; serine/threonine-protein phosphatase 2A regulatory subunit B'	map04071 Sphingolipid signaling pathway;map04728 Dopaminergic synapse;map04660 T cell receptor signaling pathway;map04261 Adrenergic signaling in cardiomyocytes; map03015 mRNA surveillance pathway;map04152 AMPK signaling pathway;map04151 PI3K-Akt signaling pathway;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04110 Cell cycle;map05165	KOG2085 At3g26020 Serine/threonine protein phosphatase 2A, regulatory subunit	KAF0374545.1 B56-domain-containing protein [Gigaspora margarita]	Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' eta isoform OS=Arabidopsis thaliana OX=3702 GN=B'ETA PE=1 SV=1
A1290	GO:0016311(dephosphorylation);GO:0006470(protein dephosphorylation)	-	GO:0016791(phosphatase activity);GO:0008138(protein tyrosine/serine/threonine phosphatase activity)	K14165 K14165; atypical dual specificity phosphatase [EC:3.1.3.16 3.1.3.48]	-	KOG1716 7298988 Dual specificity phosphatase	XP_025180488.1 protein-tyrosine phosphatase -like protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Dual specificity protein phosphatase 1-A OS=Xenopus laevis OX=8355 GN=dup1-a PE=1 SV=1
A1291	-	-	-	-	-	-	-	-
A1292	-	-	-	-	-	-	-	-
A1293	-	-	-	-	-	-	-	-
A1294	GO:0015031(protein transport)	-	-	-	-	KOG0934 At2g19790 Clathrin adaptor complex, small subunit	XP_025183263.1 clathrin adaptor complex, small subunit [Rhizophagus irregularis DAOM 181602=DAOM 197198]	AP-4 complex subunit sigma OS=Arabidopsis thaliana OX=3702 GN=At2g19790 PE=1 SV=1
A1295	-	-	-	-	-	-	-	-
A1296	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1297	GO:1905515(non-motile cilium assembly)	GO:0034464(BBSome)	GO:0005515(protein binding)	K13342 PEX5, PXR1; peroxin-5	map04146 Peroxisome	KOG1129 Hs21389383 TPR repeat-containing protein	KAG4098491.1 tetratricopeptide repeat protein 8-like protein [Neocallimastix sp. JGI-2020a]	Tetratricopeptide repeat protein 8 OS=Mus musculus OX=10090 GN=Ttc8 PE=1 SV=1
A1298	-	-	-	-	-	-	-	-

A1299	GO:0015914(phospholipid transport)	GO:0016021(integral component of membrane)	GO:0000166(nucleotide binding),GO:0000287(magnesium ion binding),GO:0005524(ATP binding),GO:0140326(ATPase-coupled intramembrane lipid transporter activity),GO:0005215(transporter activity),GO:0016887(ATP hydrolysis activity)	K14802 DRS2, ATP8A; phospholipid-transporting ATPase [EC:7.6.2.1]	-	KOG0206 At3g25610 P-type ATPase	OAJ42700.1 hypothetical protein BDEG_26119 [Batrachochytrium dendrobatidis JEL423]	Phospholipid-transporting ATPase 10 OS=Arabidopsis thaliana OX=3702 GN=ALA10 PE=3 SV=1
A1300	-	-	-	-	-	-	ORZ38713.1 hypothetical protein BCR44DRAFT_1427659 [Catenaria anguillulae PL171]	WW domain-containing protein A OS=Dictyostelium discoideum OX=44689 GN=dwwA PE=1 SV=1
A1301	GO:0006508(proteolysis)	-	GO:0070006(metalloaminopeptidase activity)	K01265 map; methionyl aminopeptidase [EC:3.4.11.18]	-	KOG2738 Hs2044792 Putative methionine aminopeptidase	EPZ34747.1 Methionine aminopeptidase 1 [Rozella allomyces CSF55]	Methionine aminopeptidase 1 OS=Gallus gallus OX=9031 GN=METAP1 PE=2 SV=1
A1302	-	-	-	-	-	KOG2497 7293566 Predicted methyltransferase	EJT97714.1 S-adenosyl-L-methionine-dependent methyltransferase [Dacryopinax primogenitus]	Protein N-lysine methyltransferase METTL21A OS=Danio rerio OX=7955 GN=mettl21a PE=2 SV=1
A1303	GO:0006351(transcription, DNA-templated)	-	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	K03145 TFIIIS; transcription elongation factor S-II	-	KOG1105 At2g38560 Transcription elongation factor TFIIIS/Cofactor of enhancer-binding protein Sp1	PWA02711.1 hypothetical protein BB558_001143 [Smittium angustum]	Transcription elongation factor TFIIIS OS=Arabidopsis thaliana OX=3702 GN=TFIIIS PE=1 SV=1
A1304	-	GO:0016021(integral component of membrane)	-	-	-	KOG4758 At1g33230 Predicted membrane protein	OAJ35774.1 hypothetical protein BDEG_20015 [Batrachochytrium dendrobatidis JEL423]	Transmembrane protein 120 homolog OS=Dictyostelium discoideum OX=44689 GN=tmem120 PE=3 SV=1
A1305	-	-	GO:0016787(hydrolase activity)	-	-	-	ORY97566.1 Alpha/Beta hydrolase protein [Syncephalaster racemosus]	Carboxymethylenebutenolidase homolog OS=Mus musculus OX=10090 GN=Cmb1 PE=1 SV=1
A1306	-	-	-	-	-	-	-	-
A1307	-	-	-	-	-	-	-	-

A1308	-	-	GO:0016787(hydrolase activity)	K24083 ABHD13; abhydrolase domain- containing protein 13 [EC:3.-.-.-]	-	KOG4391 YN L320w Predicted alpha/beta hydrolase BEM46	KAF9138289. 1 hypothetical protein BGX30_00930 9 [Mortierella sp. GBA39]	Uncharacterized protein MT2364 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=MT2364 PE=4 SV=1
A1309	-	-	GO:0005096(GTPase activator activity)	K21766 TBCC; tubulin- specific chaperone C	-	KOG2512 Hs5 902060 Beta- tubulin folding cofactor C	XP_01660858 3.1 hypothetical protein SPPG_04852 [Spizellomyces punctatus DAOM BR117]	Protein XRP2 OS=Danio rerio OX=7955 GN=rp2 PE=1 SV=1
A1310	GO:0032259(methylation)	-	GO:0008168(methyltransferase activity)	-	-	-	XP_02537401. 3.1 methyltransferase [Acaromyces ingoldii]	Putative S-adenosyl-L-methionine-dependent methyltransferase YktD OS=Bacillus subtilis (strain 168) OX=224308 GN=yktD PE=3 SV=1
A1311	GO:0036297(interstrand cross-link repair)	-	GO:0016788(hydrolase activity, acting on ester bonds),GO:0004518(nuclease activity)	K15363 FAN1, MTMR15; fanconi- associated nuclease 1 [EC:3.1.21.- 3.1.4.1]	map03460 Fanconi anemia pathway	KOG2143 At1 g48360 Uncharacterized conserved protein	PJF16464.1 hypothetical protein PSACC_03710 [Paramicrosporidium saccamoebae]	Fanconi-associated nuclease 1 homolog OS=Dictyostelium discoideum OX=44689 GN=mtmr15 PE=3 SV=1
A1312	GO:0055085(transmembrane transport),GO:0098656(anion transmembrane transport)	GO:0005741(mitochondrial outer membrane)	GO:0008308(voltage-gated anion channel activity)	K15040 VDAC2; voltage- dependent anion channel protein 2	map04022 cGMP- PKG signaling pathway;map04020 Calcium signaling pathway;map05415 Diabetic cardiomyopathy; map04216 Ferroptosis;map04217 Necroptosis;map04218 Cellular senescence;map04613 Neutrophil extracellular trap formation;map04621 NOD-like receptor signaling pathway;map04979 Cholesterol metabolism;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple	KOG3126 Hs2 0070212 Porin/voltage- dependent anion- selective channel protein	RPB28311.1 hypothetical protein L211DRAFT_833278 [Terfezia boudieri ATCC MYA- 4762]	Voltage-dependent anion-selective channel protein 3 OS=Sus scrofa OX=9823 GN=VDAC3 PE=2 SV=2
A1313	-	-	GO:0005515(protein binding)	-	-	KOG4308 Hs1 5193292 LRR- containing protein	CCA71349.1 hypothetical protein PIIN_05288 [Serendipita indica DSM 11827]	NACHT, LRR and PYD domains-containing protein 12 OS=Homo sapiens OX=9606 GN=NLRP12 PE=1 SV=2
A1314	-	GO:0016459(myosin complex),GO:0005856(cytoskeleton)	GO:0005515(protein binding),GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At3 g19960 Myosin class V heavy chain	RKP25431.1 P-loop containing nucleoside triphosphate hydrolase protein [Syncephalis pseudoplumigaleata]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1

A1315	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K19800 SCH9; serine/threonine protein kinase SCH9 [EC:2.7.11.1]	map04213 Longevity regulating pathway - multiple species;map04138 Autophagy - yeast	KOG0598[Hs4506739 Ribosomal protein S6 kinase and related proteins	PKK77596.1 kinase-like protein, partial [Rhizophagus irregularis]	Ribosomal protein S6 kinase beta-2 OS=Homo sapiens OX=9606 GN=RPS6KB2 PE=1 SV=2
A1316	-	-	-	-	-	-	-	-
A1317	-	-	-	-	-	-	-	-
A1318	-	-	-	-	-	-	TPX72626.1 hypothetical protein SpCBS45565_g00282 [Spizellomyces sp. 'palustris']	Cilia- and flagella-associated protein 299 OS=Xenopus laevis OX=8355 GN=cfap299 PE=2 SV=1
A1319	-	-	GO:0005509(calcium ion binding)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	KOG0034[At4g33000 Ca2+/calmodulin-dependent protein phosphatase (calcineurin subunit B), EF-Hand superfamily protein	RHZ44981.1 hypothetical protein Glove_701g19 [Diversispora epigaea]	Calcineurin B-like protein 10 OS=Arabidopsis thaliana OX=3702 GN=CBL10 PE=1 SV=1
A1320	-	-	GO:0005515(protein binding);GO:0015035(protein-disulfide reductase activity)	K03671 trxA; thioredoxin 1	map05132 Salmonella infection;map05418 Fluid shear stress and atherosclerosis; map04621 NOD-like receptor signaling pathway;map05012 Parkinson disease	KOG0907[YLR043c Thioredoxin	KAF7740875.1 Cytoplasmic thioredoxin isoenzyme 2 [Entomophthora muscae]	Thioredoxin OS=Echinococcus granulosus OX=6210 GN=TRX PE=3 SV=2
A1321	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG0253[At3g13050 Synaptic vesicle transporter SV2 (major facilitator superfamily)	KAF2235216.1 MFS general substrate transporter [Viridotherium virens]	Synaptic vesicle 2-related protein OS=Mus musculus OX=10090 GN=Svop PE=1 SV=1

A1322	-	-	GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor);GO:0051287(NAD binding)	K00134 GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]	map05415 Diabetic cardiomyopathy; map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00710 Carbon fixation in photosynthetic organisms;map0	KOG0657 YJR009c Glyceraldehyde 3-phosphate dehydrogenase	KAF8426605.1 glyceraldehyde 3-phosphate dehydrogenase [Tirmania nivea]	Glyceraldehyde-3-phosphate dehydrogenase-like protein OS=Pseudomonas aeruginosa (strain UCBPP-PA14) OX=208963 GN=gap2 PE=1 SV=1
A1323	-	-	GO:0003998(acylphosphatase activity)	-	-	KOG3360 Hs4557245 Acylphosphatase	KXS13315.1 acylphosphatase-1-like protein [Gonapodya prolifera JEL478]	Acylphosphatase-1 OS=Sus scrofa OX=9823 GN=ACYP1 PE=1 SV=2
A1324	GO:0006508(proteolysis)	GO:0016020(membrane)	GO:0004190(serine-type endopeptidase activity)	-	-	KOG2718 Hs4506973 Na+-bile acid cotransporter	XP_013312229.1 hypothetical protein PV05_10346 [Exophiala xenobiotica]	Ileal sodium/bile acid cotransporter OS=Homo sapiens OX=9606 GN=SLC10A2 PE=1 SV=2
A1325	-	-	GO:0043169(cation binding)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 At5g24940 Serine/threonine protein phosphatase	ORZ06622.1 phosphatase 2C-like domain-containing protein [Absidia repens]	Probable protein phosphatase 2C 45 OS=Oryza sativa subsp. japonica OX=39947 GN=Os04g0659500 PE=2 SV=2
A1326	-	-	-	-	-	KOG4511 Hs18087843 Uncharacterized conserved protein	TPX59838.1 hypothetical protein PhCBS80983.g02250 [Powellomyces hirtus]	Cilia- and flagella-associated protein 36 OS=Danio rerio OX=7955 GN=cfap36 PE=2 SV=2
A1327	-	-	-	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis -	KOG0867 Hs16167642 Glutathione S-transferase	KAG1258174.1 hypothetical protein G6F65_015664 [Rhizopus oryzae]	Glutathione S-transferase theta-1 OS=Bos taurus OX=9913 GN=GSTT1 PE=2 SV=3

A1328	GO:0008299(isoprenoid biosynthetic process)	-	GO:0005515(protein binding),GO:0003824(catalytic activity)	-	-	KOG0613 Hs20143914 Projectin/twitin and related proteins	-	Anti-sigma-I factor RsgI3 OS=Acetivibrio thermocellus (strain ATCC 27405 / DSM 1237 / JCM 9322 / NBRC 103400 / NCIMB 10682 / NRRL B-4536 / VPI 7372) OX=203119 GN=rsgI3 PE=1 SV=1
A1329	GO:0072488(ammonium transmembrane transport)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 At3g24290 Ammonia permease	KAF9137593.1 hypothetical protein BGX30_010076 [Mortierella sp. GBA39]	Ammonium transporter 1 member 3 OS=Solanum lycopersicum OX=4081 GN=AMT1-3 PE=2 SV=1
A1330	-	-	-	-	-	-	-	-
A1331	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1332	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K22530 ATAD1; ATPase family AAA domain-containing protein 1 [EC:3.6.1.-]	-	KOG0737 At4g27680 AAA+-type ATPase	KAG4091079.1 AAA-domain-containing protein [Neocallimastix sp. JGI-2020a]	Outer mitochondrial transmembrane helix translocase OS=Danio rerio OX=7955 GN=atad1a PE=2 SV=2
A1333	GO:0000226(microtubule cytoskeleton organization),GO:007020(microtubule nucleation)	GO:0000922(spindle pole),GO:0005815(microtubule organizing center)	GO:0043015(gamma-tubulin binding)	K16569 TUBGCP2, GCP2; gamma-tubulin complex component 2	-	KOG2065 Hs7656841 Gamma-tubulin ring complex protein	ORY96653.1 Spc98 family-domain-containing protein [Syncephalaster racemosus]	Gamma-tubulin complex component 4 OS=Mus musculus OX=10090 GN=Tubgcp4 PE=1 SV=2
A1334	GO:0000226(microtubule cytoskeleton organization),GO:007020(microtubule nucleation)	GO:0000922(spindle pole),GO:0005815(microtubule organizing center)	GO:0043015(gamma-tubulin binding)	-	-	KOG2065 Hs7656841 Gamma-tubulin ring complex protein	RUS21296.1 Spc98 family-domain-containing protein [Endogone sp. FLAS-F59071]	Gamma-tubulin complex component 4 OS=Homo sapiens OX=9606 GN=TUBGCP4 PE=1 SV=1
A1335	-	-	-	-	-	-	-	-
A1336	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	-	-	KOG4280 Hs11641245 Kinesin-like protein	XP_016610724.1 hypothetical protein SPPG_01768 [Spizellomyces punctatus DAOM BR117]	Kinesin-like protein KIF9 OS=Homo sapiens OX=9606 GN=KIF9 PE=1 SV=4
A1337	-	-	-	-	-	-	-	-
A1338	-	-	-	K11876 PSMG2, PAC2; proteasome assembly chaperone 2	-	KOG3112 At3g18940 Uncharacterized conserved protein	ORZ35016.1 PAC2 family-domain-containing protein [Catenaria anguillulae PL171]	Proteasome assembly chaperone 2 OS=Xenopus laevis OX=8355 GN=psmg2 PE=2 SV=1
A1339	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K14396 PABPN1, PABP2; polyadenylate-binding protein 2	map03015 mRNA surveillance pathway;map05164 Influenza A	KOG4209 YIR001c Splicing factor RNPS1, SR protein superfamily	TDZ35873.1 Polyadenylate-binding protein 2 [Colletotrichum trifolii]	RNA-binding protein SGN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SGN1 PE=1 SV=1
A1340	-	-	-	-	-	-	-	-
A1341	GO:0071596(ubiquitin-dependent protein catabolic process via the N-end rule pathway)	-	GO:0061630(ubiquitin protein ligase activity),GO:0008270(zinc ion binding)	K10625 UBR1; E3 ubiquitin-protein ligase UBR1 [EC:2.3.2.27]	-	KOG1140 7293307 N-end rule pathway, recognition component UBR1	KAF7357595.1 E3 ubiquitin-protein ligase [Mycena sanguinolenta]	E3 ubiquitin-protein ligase UBR1 OS=Drosophila melanogaster OX=7227 GN=Ubr1 PE=2 SV=2

A1342	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0163 Hs4826846 Myosin class VI heavy chain	XP_007727468.1 hypothetical protein A1O1_08416 [Capronia coronata CBS 617.96]	Unconventional myosin-VI OS=Homo sapiens OX=9606 GN=MYO6 PE=1 SV=4
A1343	GO:0003341(cilium movement),GO:0036158(outer dynein arm assembly)	GO:0005929(cilium)	-	-	-	-	TPX58773.1 hypothetical protein SpCBS45565.g07915 [Spizellomyces sp. 'palustris']	Outer dynein arm-docking complex subunit 3 OS=Mus musculus OX=10090 GN=ODAD3 PE=2 SV=2
A1344	GO:0007059(chromosome segregation)	GO:0031262(Ndc80 complex)	-	K11558 SPC25; kinetochore protein Spc25, fungi type	-	KOG4657 Hs10190716 Uncharacterized conserved protein	GFZ49559.1 Probable kinetochore protein SPC25 [Saitozyma sp. JCM 24511]	Kinetochore protein Spc25 OS=Bos taurus OX=9913 GN=SPC25 PE=2 SV=1
A1345	-	-	-	-	-	-	-	-
A1346	-	-	GO:0016491(oxidoreductase activity)	-	-	-	KAF9078351.1 nitroreductase [Rhodocollybia butyracea]	Chloronitrobenzene nitroreductase OS=Comamonas testosteroni OX=285 GN=cnbA PE=1 SV=1
A1347	GO:0006893(Golgi to plasma membrane transport)	GO:0000145(exocyst)	-	-	-	-	-	-
A1348	-	-	-	-	-	-	-	-
A1349	-	-	GO:0005515(protein binding)	-	-	KOG4310 Hs19923855 Synapse-associated protein	KAF6801170.1 ankyrin repeat protein [Colletotrichum sojae]	Synapse-associated protein 1 OS=Homo sapiens OX=9606 GN=SYAP1 PE=1 SV=1
A1350	-	-	-	K17508 PTC7, PPTC7; protein phosphatase PTC7 [EC:3.1.3.16]	-	KOG1379 At4g16580 Serine/threonine protein phosphatase	KXN72583.1 protein serine/threonine phosphatase 2C [Conidiobolus coronatus NRRL 28638]	Probable protein phosphatase 2C 55 OS=Arabidopsis thaliana OX=3702 GN=At4g16580 PE=2 SV=2
A1351	GO:0043248(proteasome assembly)	-	GO:0060090(molecular adaptor activity)	K11886 ECM29; proteasome component ECM29	-	KOG0915 Hs2045006 Uncharacterized conserved protein	KAG0170361.1 hypothetical protein DFO30_002609 [Apophysomyces sp. BC1015]	Proteasome adapter and scaffold protein ECM29 OS=Homo sapiens OX=9606 GN=ECPAS PE=1 SV=2
A1352	-	-	GO:0005515(protein binding)	K11422 SETD1, SET1; [histone H3]-lysine4 N-trimethyltransferase SETD1 [EC:2.1.1.354]	map00310 Lysine degradation;map01100 Metabolic pathways	KOG1084 Hs7662046 Transcription factor TCF20	PWW72012.1 histone H3-K4 methyltransferase Set1 [Tuber magnatum]	Histone-lysine N-methyltransferase, H3 lysine-4 specific OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=set1 PE=3 SV=1
A1353	GO:0006629(lipid metabolic process)	-	-	-	-	-	RUS31207.1 Alpha/Beta hydrolase protein [Jimgerdmania flammicorona]	-

A1354	GO:0006629(lipid metabolic process)	-	-	-	-	-	ORZ37865.1 class 3-domain-containing protein [Catenaria anguillulae PL171]	-
A1355	GO:0006629(lipid metabolic process)	-	-	-	-	-	XP_038915092.1 lipase [Cantharellus anzutake]	-
A1356	GO:0006629(lipid metabolic process)	-	-	-	-	KOG4569[CE05753 Predicted lipase	TID18915.1 Mitochondrial distribution and morphology protein 10 [Venturia nashicola]	-
A1357	-	-	GO:0005515(protein binding)	-	-	KOG1227[Hs8923676 Putative methyltransferase	RKP18336.1 hypothetical protein ROZALSC1DR AFT_23332 [Rozella allomyces CSF55]	tRNA wybutosine-synthesizing protein 2 homolog OS=Danio rerio OX=7955 GN=trmt12 PE=2 SV=1
A1358	-	-	GO:0003723(RNA binding)	K14844 PUF6; pumilio homology domain family member 6	-	KOG2050[YDR496c Puf family RNA-binding protein	KAG2175748.1 hypothetical protein INT44_000226 [Umbelopsis vinacea]	Pumilio homology domain family member 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUF6 PE=1 SV=1
A1359	GO:0006412(translation)	GO:0030956(glutamyl-tRNA(Gln) amidotransferase complex)	GO:0050567(glutamyl-tRNA synthase (glutamine-hydrolyzing activity),GO:0003824(catalytic activity)	K02433 gatA, QRSL1; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit A [EC:6.3.5.6 6.3.5.7]	map00970 Aminoacyl-tRNA biosynthesis;map01100 Metabolic pathways	KOG1211[7300468 Amidases	KKK18511.1 hypothetical protein AOC00_04395 [Aspergillus ochraceoroseus]	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial OS=Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) OX=447093 GN=HCBG_08377 PE=3 SV=1
A1360	GO:0006457(protein folding)	-	GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding),GO:0005515(protein binding)	K24927 TTC4, CNS1; tetratricopeptide repeat protein 4	-	KOG0548[7295086_1 Molecular co-chaperone ST11	TPX40162.1 hypothetical protein SeLEV6574_g06754 [Synchytrium endobioticum]	Sperm-associated antigen 1 OS=Rattus norvegicus OX=10116 GN=Spag1 PE=1 SV=1
A1361	-	-	-	-	-	-	-	-
A1362	-	-	-	-	-	-	-	-
A1363	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	OZJ05452.1 hypothetical protein BZG36_01642 [Bifiguratus adalaidae]	Sulfoquinovosyl transferase SQD2 OS=Arabidopsis thaliana OX=3702 GN=SQD2 PE=1 SV=1
A1364	GO:0016192(vesicle-mediated transport)	-	-	K20183 VPS39, VAM6; Vam6/Vps39-like protein vacuolar protein sorting-associated protein 39	map04140 Autophagy - animal;map05132 Salmonella infection;map04138 Autophagy - yeast	KOG2063[Hs21359865 Vacuolar assembly/sorting proteins VPS39/VAM6/VPS3	ORX48192.1 hypothetical protein BCR36DRAFT_84127, partial [Piromyces finnis]	Transforming growth factor-beta receptor-associated protein 1 homolog OS=Danio rerio OX=7955 GN=tgfbap1 PE=2 SV=1

A1365	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	-	-	KOG0247 Hs6754472 Kinesin-like protein	ORX77542.1 kinesin-domain-containing protein, partial [Basidiobolus meristosporus CBS 931.73]	Kinesin-like protein KIF23 OS=Mus musculus OX=10090 GN=Kif23 PE=1 SV=1
A1366	-	-	GO:0004386(helicase activity)	K10706 SETX, ALS4; senataxin [EC:5.6.2.-]	map05014 Amyotrophic lateral sclerosis	KOG1801 At2g19120 tRNA-splicing endonuclease positive effector (SEN1)	ORY88412.1 SEN1 N terminal-domain-containing protein [Leucosporidium creatinivorum]	Helicase SEN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEN1 PE=1 SV=2
A1367	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0043 Hs8922436 Uncharacterized conserved protein, contains DM10 domain	ORX56052.1 hypothetical protein BCR36DRAFT_346610 [Piromyces finnis]	EF-hand domain-containing protein 1 OS=Homo sapiens OX=9606 GN=EFHC1 PE=1 SV=1
A1368	-	-	-	-	-	-	KAF9335443.1 hypothetical protein BG006_000081 [Podila minutissima]	-
A1369	-	-	-	-	-	-	-	-
A1370	-	-	-	-	-	-	-	Dynein axonemal assembly factor 9 OS=Mus musculus OX=10090
A1371	-	-	-	-	-	-	-	-
A1372	-	-	-	-	-	-	-	-
A1373	-	-	GO:0010349(L-galactose dehydrogenase activity),GO:0016491(oxidoreductase activity)	K00062 ARA2; D-arabinose 1-dehydrogenase [EC:1.1.1.116]	map00053 Ascorbate and aldarate metabolism;map01100 Metabolic pathways	KOG1576 7299543 Predicted oxidoreductase	KAF9121220.1 hypothetical protein BGX30_002719 [Mortierella sp. GBA39]	L-galactose dehydrogenase OS=Arabidopsis thaliana OX=3702 GN=LGALDH PE=1 SV=1
A1374	-	-	-	-	-	-	-	-
A1375	GO:0051568(histone H3-K4 methylation)	GO:0048188(Set1C/COMPASS complex)	-	K14967 BRE2, CPS60; COMPASS component BRE2	-	KOG2626 At1g51450 Histone H3 (Lys4) methyltransferase complex, subunit CPS60/ASH2/BRE2	KAG2187257.1 hypothetical protein INT44_004942 [Umbelopsis vinacea]	Protein TRAUCO OS=Arabidopsis thaliana OX=3702 GN=TRO PE=1 SV=1
A1376	-	-	GO:0005515(protein binding)	-	-	-	KKK16647.1 TPR domain protein [Aspergillus rambellii]	-
A1377	-	-	-	-	-	-	-	-

A1378	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K08711 PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065 At2g29940 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	KAG0261124.1 hypothetical protein BG011_001337 [Mortierella polycephala]	ABC transporter G family member 31 OS=Arabidopsis thaliana OX=3702 GN=ABCG31 PE=1 SV=1
A1379	-	-	GO:0005515(protein binding),GO:0046872(metal ion binding)	-	-	KOG0230 At3g14270 Phosphatidylinositol-4-phosphate 5-kinase and related FYVE finger-containing proteins	CEI92067.1 hypothetical protein RMCBS344292_06340 [Rhizopus microsporus]	Lateral signaling target protein 2 OS=Caenorhabditis briggsae OX=6238 GN=lst-2 PE=3 SV=1
A1380	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10356 MYO1; myosin I	map05130 Pathogenic Escherichia coli infection,map04814 Motor proteins	KOG0164 CE01061 Myosin class I heavy chain	XP_031027609.1 uncharacterized protein SmJEL517_g00731 [Synchytrium microbalum]	Unconventional myosin-Ia OS=Mus musculus OX=10090 GN=Myo1a PE=2 SV=2
A1381	-	-	-	-	-	-	-	-
A1382	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A1383	-	-	-	-	-	-	KAF5345350.1 hypothetical protein D9758_008466 [Tetrapyrgos nigripes]	L-threonine 3-dehydrogenase OS=Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087) OX=3042615 GN=tdh PE=3 SV=1
A1384	-	-	-	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ12941.1 Transposon TX1 protein [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A1385	-	-	-	-	-	-	PVU87440.1 hypothetical protein BB561_006329, partial [Smittium simulii]	-
A1386	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ28687.1 LINE-1 retrotransposable element ORF2 protein, partial [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A1387	-	-	-	-	-	-	-	-
A1388	-	-	-	-	-	-	-	-
A1389	-	-	-	-	-	-	KAF9208467.1 hypothetical protein BGZ59_010644 [Podila verticillata]	-
A1390	-	-	-	-	-	-	-	-

A1391	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	OJT05228.1 MAP kinase kinase kinase mkh1 [Trametes pubescens]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei brucei OX=5702 GN=CRK2 PE=3 SV=1
A1392	-	-	GO:0035091(phosphatidylinositol binding),GO:0005515(protein binding)	-	-	-	-	Uncharacterized protein MJ0678 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ0678 PE=4 SV=1
A1393	-	-	GO:0005515(protein binding)	K18696 GDE1; glycerophosphodiester phosphodiesterase [EC:3.1.4.46]	map00564 Glycerophospholipid metabolism	KOG3599 Hs4505835 Ca2+-modulated nonselective cation channel polycystin	GES57670.1 hypothetical protein ATETN484_00101088000 [Aspergillus terreus]	Polycystin-2 OS=Bos taurus OX=9913 GN=PKD2 PE=2 SV=1
A1394	-	-	-	-	-	-	ORZ35457.1 hypothetical protein BCR44DRAFT_1499651 [Catenaria anguillulae PL171]	Protein psiP OS=Dictyostelium discoideum OX=44689 GN=psiP PE=3 SV=1
A1395	GO:0006537(glutamate biosynthetic process)	-	GO:0016491(oxidoreductase activity),GO:0016639(oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor),GO:0051536(iron-sulfur cluster binding)	K00264 GLT1; glutamate synthase (NADH) [EC:1.4.1.14]	map00910 Nitrogen metabolism;map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG0399 At5g53460 Glutamate synthase	RCH79684.1 glutamate synthase [NADH], partial [Rhizopus stolonifer]	Glutamate synthase 1 [NADH], chloroplastic OS=Arabidopsis thaliana OX=3702 GN=GLT1 PE=1 SV=2
A1396	GO:0006537(glutamate biosynthetic process), GO:0006807(nitrogen compound metabolic process)	-	GO:0015930(glutamate synthase activity),GO:0016638(oxidoreductase activity, acting on the CH-NH2 group of donors),GO:0016491(oxidoreductase activity)	-	-	KOG0399 At5g53460 Glutamate synthase	RKO91909.1 hypothetical protein BDK51DRAFT_18838 [Blyttiomycetes helicus]	Glutamate synthase 1 [NADH], chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0681900 PE=2 SV=1
A1397	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1398	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	-	-	-

A1399	-	-	-	-	-	KOG4178 At5g53050 Soluble epoxide hydrolase	XP_007360969.1 alpha/beta-hydrolase [Dichomitus squalens LYAD-421 SS1]	Non-heme haloperoxidase OS=Rhodococcus erythropolis OX=1833 GN=thcF PE=3 SV=1
A1400	-	-	-	-	-	-	-	-
A1401	-	-	-	-	-	-	-	-
A1402	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	-	-	KOG2037 CE26776 Guanylate-binding protein	PKY54488.1 GBP-domain-containing protein [Rhizophagus irregularis]	Atlantin-2 OS=Xenopus laevis OX=8355 GN=atl2 PE=2 SV=1
A1403	-	GO:0005737(cytoplasm),GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0003743(translation initiation factor activity),GO:0005515(protein binding)	K15028 EIF3K; translation initiation factor 3 subunit K	-	KOG2106 Hs6912356 Uncharacterized conserved protein, contains HELP and WD40 domains	XP_031023021.1 uncharacterized protein SmJEL517_g05070 [Synchytrium microbalum]	Echinoderm microtubule-associated protein-like 2 OS=Mus musculus OX=10090 GN=Eml2 PE=1 SV=1
A1404	-	-	-	-	-	-	-	-
A1405	GO:0006996(organelle organization)	-	GO:0005515(protein binding)	-	-	-	-	-
A1406	-	-	GO:0005509(calcium ion binding)	-	-	KOG0032 At4g21940 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	QSL66745.1 hypothetical protein MERGE_001131 [Pneumocystis wakefieldiae]	Calcineurin subunit B OS=Naegleria gruberi OX=5762 GN=CNB1 PE=3 SV=1
A1407	-	-	-	-	-	KOG0725 Hs10047132 Reductases with broad range of substrate specificities	OBZ88763.1 3-oxoacyl-[acyl-carrier-protein] reductase FabG [Choanephora cucurbitarum]	3-oxoacyl-[acyl-carrier-protein] reductase FabG OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=fabG PE=3 SV=1
A1408	-	-	GO:0008237(metallopeptidase activity)	-	-	KOG3658 7301878 Tumor necrosis factor-alpha-converting enzyme (TACE/ADAM17) and related metalloproteases	XP_014168470.1 metalloprotease [Grosmannia clavigera kw1407]	Disintegrin and metalloproteinase domain-containing protein B OS=Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) OX=554155 GN=ADM-B PE=3 SV=1
A1409	-	-	-	-	-	-	-	-
A1410	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	-	PPR07393.1 hypothetical protein CVT26_013709 [Gymnopilus dilepis]	Serine/threonine-protein kinase StkP OS=Streptococcus pneumoniae serotype 4 (strain ATCC BAA-334 / TIGR4) OX=170187 GN=stkP PE=1 SV=1
A1411	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding),GO:0005515(protein binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239 At5g65930.2 Kinesin (KAR3 subfamily)	KAF9325430.1 kinesin-like nuclear fusion protein [Podila minutissima]	Kinesin-like protein KIN-14E OS=Arabidopsis thaliana OX=3702 GN=KIN14E PE=1 SV=1

A1412	-	GO:0005643(nuclear pore)	GO:0017056(structural constituent of nuclear pore)	-	-	KOG2168[Hs20561607 Cullins	KAF8943335.1 hypothetical protein BGZ47_005519 [Haplosporangium gracile]	Nuclear pore complex protein Nup93 OS=Danio rerio OX=7955 GN=dye PE=2 SV=1
A1413	-	-	-	K06689 UBE2D, UBC4, UBC5; ubiquitin-conjugating enzyme E2 D [EC:2.3.2.23]	map04141 Protein processing in endoplasmic reticulum;map05131 Shigellosis;map04624 Toll and lmd signaling pathway;map04120 Ubiquitin mediated proteolysis;map03083 Polycomb repressive complex;map04013 MAPK signaling pathway - fly	KOG0417[Hs4507775 Ubiquitin-protein ligase	RKP33521.1 ubiquitin-conjugating enzyme/RWD-like protein [Dimargaris cristalligena]	Ubiquitin-conjugating enzyme E2 D2 OS=Bos taurus OX=9913 GN=UBE2D2 PE=2 SV=1
A1414	-	-	-	K20242 EVI5; ecotropic viral integration site 5 protein	-	KOG1102[At5g15930 Rab6 GTPase activator GAPCenA and related TBC domain proteins	XP_018292416.1 hypothetical protein PHYBLDRAFT_3461, partial [Phycomyces blakesleeana s NRRL 1555(-)]	Ecotropic viral integration site 5 protein homolog OS=Homo sapiens OX=9606 GN=EVI5 PE=1 SV=3
A1415	-	-	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A1416	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity)	-	-	-	-	-
A1417	-	-	GO:0005525(GTP binding);GO:0003924(GTPase activity)	-	-	KOG0098[At4g17170 GTPase Rab2, small G protein superfamily	ORX85488.1 ras-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Ras-related protein Rab-2-A OS=Zea mays OX=4577 GN=RAB2A PE=2 SV=2
A1418	GO:0006432(phenylalanyl-tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0004826(phenylalanine-tRNA ligase activity);GO:0003723(RNA binding);GO:0000287(magnesium ion binding);GO:0005524(ATP binding);GO:0000166(nucleotide binding)	K01890 FARSB, pheT; phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]	map00970 Aminoacyl-tRNA biosynthesis	KOG2472[7301135 Phenylalanyl-tRNA synthetase beta subunit	ORY00806.1 beta subunit of phenylalanyl-tRNA synthetase [Basidiobolus meristosporus CBS 931.73]	Phenylalanine--tRNA ligase beta subunit OS=Drosophila melanogaster OX=7227 GN=beta-PheRS PE=1 SV=1
A1419	-	-	-	-	-	-	-	-
A1420	-	-	-	-	-	-	-	-

A1421	GO:0009098(leucine biosynthetic process)	-	GO:0003862(3-isopropylmalate dehydrogenase activity),GO:000287(magnesium ion binding),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0051287(NAD binding)	K00052 leuB, IMDH; 3-isopropylmalate dehydrogenase [EC:1.1.1.85]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00660 C5-Branched dibasic acid metabolism;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0786 At1g31180 3-isopropylmalate dehydrogenase	CAE6442335.1 unnamed protein product [Rhizoctonia solani]	3-isopropylmalate dehydrogenase OS=Clostridium pasteurianum OX=1501 GN=leuB PE=3 SV=1
A1422	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	-	Probable serine/threonine-protein kinase roco5 OS=Dictyostelium discoideum OX=44689 GN=roco5 PE=3 SV=1
A1423	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1424	-	-	-	-	-	-	-	-
A1425	-	-	-	K01101 E3.1.3.41; 4-nitrophenyl phosphatase [EC:3.1.3.41]	map01120 Microbial metabolism in diverse environments;map00627 Aminobenzoate degradation	KOG2882 YDL236w p-Nitrophenyl phosphatase	RKO94743.1 N-acetylglucosamine-6-phosphate deacetylase, partial [Blyttiomycetes helicus]	Dihydroxyacetone phosphatase OS=Corynebacterium glutamicum (strain R) OX=340322 GN=hdpA PE=1 SV=1
A1426	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0005524(ATP binding),GO:0019205(nucleobase-containing compound kinase activity),GO:0004017(adenylate kinase activity),GO:0016776(phosphotransferase activity, phosphate group as acceptor)	K00939 adk, AK; adenylate kinase [EC:2.7.4.3]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map00730 Thiamine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3078 At5g47840 Adenylate kinase	PVV03164.1 hypothetical protein BB560_002366 [Smittium megazygosporum]	Probable adenylate kinase 2, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os08g0109300 PE=2 SV=1
A1427	-	-	-	-	-	-	KAF9782188.1 hypothetical protein BJ322DRAFT_1100890 [Thelephora terrestris]	UPF0652 protein C22H10.08 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC22H10.08 PE=3 SV=1
A1428	-	-	-	-	-	-	TPX63075.1 hypothetical protein SpCBS45565_g06902 [Spizellomyces sp. 'palustris']	-

A1429	-	-	GO:0008233(peptidase activity),GO:0005515(protein binding)	K22762 DES1, PPPDE2; desumoylating isopeptidase 1 [EC:3.4.-.-]	-	KOG0324 At3g07090 Uncharacterized conserved protein	KAF6812926.1 pul domain-containing protein, partial [Colletotrichum sojae]	Desumoylating isopeptidase 1 OS=Xenopus laevis OX=8355 GN=desi1 PE=2 SV=1
A1430	-	-	GO:0005515(protein binding)	-	-	KOG0401 Hs4503539 Translation initiation factor 4F, ribosome/mRNA-bridging subunit (eIF-4G)	-	Eukaryotic translation initiation factor 4 gamma 2 OS=Mus musculus OX=10090 GN=EIF4G2 PE=1 SV=2
A1431	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1432	-	-	-	-	-	-	-	-
A1433	-	-	GO:0005525(GTP binding)	K16185 RRAGA, B; Ras-related GTP-binding protein A/B	map04140 Autophagy - animal;map05131 Shigellosis;map04150 mTOR signaling pathway	KOG3886 Hs8051629 GTP-binding protein	KAG4096921.1 Gtr1/RagA G protein conserved region-domain-containing protein [Neocallimastix sp. JGI-2020a]	Ras-related GTP-binding protein A OS=Dictyostelium discoideum OX=44689 GN=ragA PE=2 SV=1
A1434	-	-	-	-	-	KOG3286 Hs7706471 Selenoprotein T	-	Thioredoxin reductase-like selenoprotein T OS=Mus musculus OX=10090 GN=SelenoT PE=1 SV=2
A1435	-	-	-	-	-	-	KAG4092705.1 hypothetical protein H8356DRAFT_1429309 [Neocallimastix sp. JGI-2020a]	-
A1436	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1437	-	-	-	-	-	-	-	-
A1438	-	-	-	-	-	-	-	-
A1439	-	-	-	-	-	KOG2223 Hs14733591 Uncharacterized conserved protein, contains TBC domain	-	TBC1 domain family member 14 OS=Bos taurus OX=9913 GN=TBC1D14 PE=2 SV=2
A1440	-	-	GO:0016491(oxidoreductase activity)	-	-	-	KFH67061.1 hypothetical protein MVEG_07584 [Podila verticillata NRRL 6337]	Glycine betaine monooxygenase reductase subunit OS=Pseudomonas aeruginosa (strain UCBPP-PA14) OX=208963 GN=gbcb PE=2 SV=1
A1441	GO:0005992(trehalose biosynthetic process)	-	GO:2001070(starch binding),GO:0030246(carbohydrate binding),GO:0003824(catalytic activity)	K16055 TPS; trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]	map01110 Biosynthesis of secondary metabolites;map00500 Starch and sucrose metabolism;map01100 Metabolic pathways	KOG1050 At1g68020 Trehalose-6-phosphate synthase component TPS1 and related subunits	TPX53521.1 alpha,alpha-trehalose-phosphate synthase (UDP-forming) [Powellomyces hirtus]	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabidopsis thaliana OX=3702 GN=TPS5 PE=1 SV=2
A1442	-	-	-	-	-	-	-	-

A1443	-	GO:0016020(membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	K05681 ABCG2, CD338; ATP-binding cassette, subfamily G (WHITE), member 2	map01523 Antifolate resistance;map04976 Bile secretion;map02010 ABC transporters	KOG0061[Hs8051577 Transporter, ABC superfamily (Breast cancer resistance protein)]	PJF18591.1 ABC-2 type transporter domain-containing protein [Paramicrosporidium saccamoebae]	Protein white OS=Anopheles gambiae OX=7165 GN=w PE=2 SV=1
A1444	-	-	-	-	-	-	-	-
A1445	-	-	-	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG1113[7296360 cAMP-dependent protein kinase types I and II, regulatory subunit	XP_031023584.1 uncharacterized protein SmJEL517_g04538 [Synchytrium microbalum]	cAMP-dependent protein kinase type I regulatory subunit OS=Drosophila melanogaster OX=7227 GN=Pka-R1 PE=1 SV=2
A1446	-	-	GO:0005506(iron ion binding);GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen);GO:0031418(L-ascorbic acid binding)	-	-	-	RUP06760.1 hypothetical protein BC936DRAFT_140269 [Jimgerdemonnia flammicorona]	-
A1447	-	-	GO:0009055(electron transfer activity);GO:0050660(flavin adenine dinucleotide binding)	K03522 fixB, etfA; electron transfer flavoprotein alpha subunit	-	KOG3954[7303574 Electron transfer flavoprotein, alpha subunit	ORX59606.1 electron transfer flavoprotein, alpha subunit [Hesseltinella vesiculosa]	Electron transfer flavoprotein subunit alpha OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=etfA PE=3 SV=1
A1448	-	-	GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0044[7293713 Ca2+ sensor (EF-Hand superfamily)	KXN82946.1 Calmodulin [Leucoagaricus sp. SymC.cos]	Troponin C, isoform 1 OS=Homarus americanus OX=6706 PE=1 SV=1
A1449	-	-	-	-	-	-	-	-
A1450	-	-	-	-	-	-	-	-
A1451	-	-	-	-	-	-	-	-
A1452	-	-	GO:0016491(oxidoreductase activity)	-	-	-	POS80850.1 N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase [Diaporthe helianthi]	Glycine betaine reductase ATRR OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=ATRR PE=1 SV=1

A1453	-	-	GO:0016538(cyclin-dependent protein serine/threonine kinase regulator activity)	K02219 CKS1; cyclin-dependent kinase regulatory subunit CKS1	map05222 Small cell lung cancer;map05200 Pathways in cancer;map04111 Cell cycle - yeast	KOG3484 At2g27970 Cyclin-dependent protein kinase CDC28, regulatory subunit CKS1, and related proteins	KAF7778612.1 hypothetical protein Agabi119p4_2957 [Agaricus bisporus var. burnettii]	Cyclin-dependent kinases regulatory subunit 1 OS=Oryza sativa subsp. indica OX=39946 GN=CKS1 PE=2 SV=1
A1454	-	-	-	-	-	-	-	-
A1455	GO:0007032(endosome organization),GO:2000641(regulation of early endosome to late endosome transport)	-	-	-	-	KOG1789 At2g26890 Endocytosis protein RME-8, contains DnaJ domain	-	DnaJ homolog subfamily C member 13 OS=Homo sapiens OX=9606 GN=DNAJC13 PE=1 SV=5
A1456	-	-	GO:0071949(FAD binding)	-	-	KOG2614 At2g35660 Kynurenine 3-monooxygenase and related flavoprotein monooxygenases	XP_007733952.1 hypothetical protein A1O3_05642 [Capronia epimyces CBS 606.96]	Monooxygenase asqM OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=asqM PE=3 SV=1
A1457	-	-	-	-	-	-	-	-
A1458	-	-	-	K17777 TIM9; mitochondria l import inner membrane translocase subunit TIM9	-	-	KAF7291560.1 zf-Tim10-DDP domain-containing protein [Mycena chlorophos]	Mitochondrial import inner membrane translocase subunit Tim9 OS=Oryza sativa subsp. japonica OX=39947 GN=TIM9 PE=3 SV=2
A1459	-	-	-	-	-	-	KAG1457252.1 hypothetical protein G6F57_014926 [Rhizopus oryzae]	-
A1460	-	-	-	-	-	KOG0048 Hs13641706_1 Transcription factor, Myb superfamily	KXN66846.1 ternary protein-Dna Complex1, partial [Conidiobolus coronatus NRRL 28638]	Transcription factor MYB3R-5 OS=Arabidopsis thaliana OX=3702 GN=MYB3R5 PE=2 SV=1
A1461	-	-	GO:0003824(catalytic activity),GO:0016841(ammonia-lyase activity)	-	-	KOG0222 Hs4504333 Phenylalanine and histidine ammonia-lyase	KNE60686.1 histidine ammonia-lyase [Allomyces macrogynus ATCC 38327]	Histidine ammonia-lyase OS=Bos taurus OX=9913 GN=HAL PE=2 SV=1
A1462	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	-	-	KOG0244 Hs7305205 Kinesin-like protein	KAG2185182.1 hypothetical protein INT44_001972 [Umbelopsis vinacea]	Chromosome-associated kinesin KIF4A OS=Homo sapiens OX=9606 GN=KIF4A PE=1 SV=3
A1463	-	-	GO:0008233(peptidase activity)	-	-	-	-	-

A1464	-	-	-	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0697 730 1459 Protein phosphatase 1B (formerly 2C)	KAG1140359. 1 hypothetical protein G6F38_00916 5 [Rhizopus oryzae]	Protein phosphatase 1B OS=Mus musculus OX=10090 GN=Ppm1b PE=1 SV=1
A1465	-	-	-	-	-	-	-	Vacuolar-sorting receptor 4 OS=Arabidopsis thaliana OX=3702
A1466	-	-	GO:0005509(cal cium ion binding)	-	-	KOG0034 729 6698 Ca2+/calmod ulin- dependent protein phosphatase (calcineurin subunit B), EF-Hand superfamily protein	GJH88679.1 hypothetical protein NliqN6_5081 [Naganishia liquefaciens]	Calcineurin subunit B OS=Naegleria gruberi OX=5762 GN=CNB1 PE=3 SV=1
A1467	GO:00181 93(peptid yl-amino acid modificati on)	-	GO:0008146(sulf otransferase activity)	-	-	-	KAG2177966. 1 hypothetical protein INT43_00321 3 [Umbelopsis isabellina]	Carbohydrate sulfotransferase 15 OS=Mus musculus OX=10090 GN=Chst15 PE=2 SV=1
A1468	-	-	-	-	-	KOG3720 Hs M7705955 Lysosomal & prostatic acid phosphatases	KAG2182975. 1 hypothetical protein INT44_00595 6 [Umbelopsis vinacea]	Lysophosphatidic acid phosphatase type 6 OS=Pongo abelii OX=9601 GN=ACP6 PE=2 SV=1
A1469	-	-	GO:0016491(oxi doreductase activity)	K14157 AASS; alpha- aminoadipic semialdehyde synthase [EC:1.5.1.8 1.5.1.9]	map01110 Biosynthesis of secondary metabolites;map 00310 Lysine degradation;ma p01100 Metabolic pathways	KOG0172 At4 g33150 Lysine- ketoglutarate reductase/sac charopine dehydrogena se	TPX69014.1 hypothetical protein SpCBS45565_ g02736 [Spizellomyces sp. 'palustris']	Alpha-aminoadipic semialdehyde synthase OS=Arabidopsis thaliana OX=3702 GN=LKR/SDH PE=1 SV=1
A1470	-	-	GO:0016620(oxi doreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor);GO:00 16491(oxidore ductase activity);GO:000 4029(aldehyde dehydrogenase (NAD+) activity)	K14085 ALDH7A1; aldehyde dehydrogena se family 7 member A1 [EC:1.2.1.31 1.2.1.8 1.2.1.3]	map00410 beta- Alanine metabolism;map 00340 Histidine metabolism;map 01110 Biosynthesis of secondary metabolites;map 00010 Glycolysis / Gluconeogenesi s;map00330 Arginine and proline metabolism;map 01120 Microbial metabolism in diverse environments;m ap00053 Ascorbate and aldarate metabolism;map 00280 Valine, leucine and isoleucine degradation;ma p00260 Glycine, serine and	KOG2453 At1 g54100 Aldehyde dehydrogena se	KNE58765.1 hypothetical protein AMAG_04318 [Allomyces macrogynus ATCC 38327]	Putative aldehyde dehydrogenase family 7 member A1 homolog OS=Dictyostelium discoideum OX=44689 GN=DDB_G0276821 PE=3 SV=2
A1471	-	-	-	-	-	KOG2458 Hs2 2065884 Endoplasmic reticulum protein EP58, contains filamin rod domain and KDEL motif	KAF8184983. 1 glycosyl transferase family 90- domain- containing protein [Mycena galopus ATCC 62051]	Uncharacterized protein 179R OS=Invertebrate iridescent virus 6 OX=176652 GN=IIV6-179R PE=4 SV=1

A1472	GO:0006508(proteolysis)	-	GO:0046872(metal ion binding),GO:0004222(metalloendopeptidase activity)	K01408 IDE, ide; insulin [EC:3.4.24.56]	map05010 Alzheimer disease;map03266 Virion - Herpesvirus	KOG0959 At1g06900 N-arginine dibasic convertase NRD1 and related Zn2+-dependent endopeptidases, insulinase superfamily	TPX51820.1 hypothetical protein SeLEV6574_g00057 [Synchytrium endobioticum]	Nardilysin-like OS=Arabidopsis thaliana OX=3702 GN=At1g06900 PE=2 SV=1
A1473	-	-	GO:0016791(phosphatase activity)	K15731 CTDSP: carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase [EC:3.1.3.16]	-	KOG1605 Hs5031775 TFIIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	RPA80613.1 NLI interacting factor [Ascobolus immersus RN42]	Probable C-terminal domain small phosphatase OS=Dictyostelium discoideum OX=44689 GN=fcpA PE=3 SV=1
A1474	-	-	GO:0005515(protein binding)	-	-	KOG0266 Hs21450820 WD40 repeat-containing protein	TPX70450.1 hypothetical protein SpCBS45565_g01836 [Spizellomyces sp. 'palustris']	Cilia- and flagella-associated protein 52 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP52 PE=1 SV=1
A1475	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	-	-	-	PMD45483.1 hypothetical protein L207DRAFT_452517 [Hyaloscypha variabilis F]	-
A1476	GO:0032012(regulation of ARF protein signal transduction)	-	GO:0005515(protein binding),GO:0005085(guanylnucleotide exchange factor activity)	K18442 ARFGEF, BIG; brefeldin A-inhibited guanine nucleotide-exchange protein	map04144 Endocytosis	KOG0929 Hs5453571 Guanine nucleotide exchange factor	RIB18551.1 hypothetical protein C2G38_2085322 [Gigaspora rosea]	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Mus musculus OX=10090 GN=Argef1 PE=1 SV=1
A1477	GO:0055085(transmembrane transport)	-	-	K15275 SLC35B1; solute carrier family 35 (UDP-galactose transporter), member B1	-	KOG1581 Hs20555079 UDP-galactose transporter related protein	ORY82122.1 UAA transporter [Protomyces lactucaedebilis]	Adenosine 3'-phospho 5'-phosphosulfate transporter 1 OS=Homo sapiens OX=9606 GN=SLC35B2 PE=1 SV=1
A1478	-	-	-	-	-	-	-	-

A1479	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0019773(proteasome complex, alpha-subunit complex), GO:0005839(proteasome core complex)	-	K02727 PSMA3; 20S proteasome subunit alpha 7 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0184 At2g27020 20S proteasome, regulatory subunit alpha type PSMA3/PRE10	GEM08811.1 20S proteasome subunit alpha 7 [Rhodotorula toruloides]	Proteasome subunit alpha type-3 OS=Dictyostelium discoideum OX=44689 GN=psmA3 PE=2 SV=2
A1480	-	-	-	-	-	-	-	-
A1481	-	-	-	-	-	-	-	-
A1482	-	-	-	-	-	KOG2977 CE05618 Glycosyltransferase	-	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like protein 1 OS=Mus musculus OX=10090 GN=B3gnt11 PE=2 SV=1
A1483	-	-	GO:0005515(protein binding)	-	-	-	KAG0284119.1 hypothetical protein BGZ96_011519 [Linnemannia gamsii]	-
A1484	GO:0006364(rRNA processing)	-	GO:0004222(metalloendopeptidase activity)	-	-	-	KAG1460188.1 hypothetical protein G6F57_014361 [Rhizopus oryzae]	Endoribonuclease YBEY, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=YBEY PE=1 SV=1
A1485	GO:0009058(biosynthetic process)	-	-	K13950 pabAB; para-aminobenzoate synthetase [EC:2.6.1.85]	map01240 Biosynthesis of cofactors;map00790 Folate biosynthesis	KOG1224 At2g28880 Para-aminobenzoate (PABA) synthase ABZ1	ORX91347.1 ADC synthase [Basidiobolus meristosporus CBS 931.73]	Aminodeoxychorismate synthase OS=Streptomyces pristinaespiralis OX=38300 GN=papA PE=3 SV=1
A1486	-	-	-	-	-	-	-	-
A1487	-	-	GO:0005515(protein binding)	-	-	-	-	Regulator of microtubule dynamics protein 1 OS=Mus musculus OX=10090 GN=Rmdn1 PE=1 SV=2
A1488	-	-	-	-	-	-	-	-
A1489	-	-	-	-	-	-	-	-
A1490	GO:0006260(DNA replication)	GO:0005664(nuclear origin of replication recognition complex)	GO:0003677(DNA binding)	-	-	-	-	-
A1491	-	-	GO:0005509(calcium ion binding),GO:0070403(NAD+ binding)	-	-	KOG2684 Hs6912664 Sirtuin 5 and related class III sirtuins (SIR2 family)	XP_035368033.1 NAD-dependent histone deacetylase silent information regulator Sir2 [Lasiodiplodia theobromae]	NAD-dependent deacetylase sir2E OS=Dictyostelium discoideum OX=44689 GN=sir2E PE=2 SV=2
A1492	-	-	-	-	-	-	-	-
A1493	-	-	-	-	-	-	-	-

A1494	-	-	GO:0016409(palmitoyltransferase activity)	-	-	KOG1311 Hs14761406 DHHC-type Zn-finger proteins	CDH53904.1 palmitoyltransferase erf2 [Lichtheimia corymbifera JMRC:FSU:9682]	Palmitoyltransferase ZDHHC14 OS=Mus musculus OX=10090 GN=Zdhhc14 PE=1 SV=1
A1496	-	-	-	-	-	-	-	-
A1497	-	-	-	-	-	-	-	-
A1498	-	-	-	-	-	-	-	-
A1499	-	GO:0030014(CCR4-NOT complex)	GO:0005515(protein binding)	-	-	KOG2471 Hs13123772 TPR repeat-containing protein	-	CCR4-NOT transcription complex subunit 10-A OS=Xenopus laevis OX=8355 GN=cnot10-a PE=2 SV=1
A1500	-	-	GO:0018024(histone-lysine N-methyltransferase activity)	-	-	-	CCG82509.1 protein of unknown function [Taphrina deformans PYCC 5710]	-
A1501	-	-	GO:0016787(hydrolase activity)	-	-	KOG3904 7298591 Predicted hydrolase RP2 (NUDIX/MutT superfamily)	SAM03943.1 hypothetical protein [Absidia glauca]	Acyl-coenzyme A diphosphatase NUDT19 OS=Xenopus laevis OX=8355 GN=nudt19 PE=2 SV=1
A1502	-	-	-	-	-	-	-	-
A1503	GO:0008612(peptidyl-lysine modification to peptidyl-hypusine)	-	-	K00809 DHPS, dys; deoxyhypusine synthase [EC:2.5.1.46]	-	KOG2924 7295142 Deoxyhypusine synthase	ORY04593.1 Deoxyhypusine synthase [Basidiobolus meristosporus CBS 931.73]	Probable deoxyhypusine synthase OS=Drosophila melanogaster OX=7227 GN=CG8005 PE=2 SV=2
A1504	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02902 RP-L28, MRPL28, rpmB; large subunit ribosomal protein L28	map03010 Ribosome	KOG3278 At4g31460 Mitochondrial/chloroplast ribosomal protein L28	KAG0333524.1 39S ribosomal protein L24, mitochondria I [Podila humilis]	Large ribosomal subunit protein bL28 OS=Bartonella quintana (strain Toulouse) OX=283165 GN=rpmB PE=3 SV=1
A1505	-	-	GO:0005515(protein binding)	K03350 APC3, CDC27; anaphase-promoting complex subunit 3	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG1124 Hs14719410 FOG: TPR repeat	KAG4091986.1 sporangia induced Bardet-Biedl syndrome 4 protein [Neocallimastix sp. JGI-2020a]	Bardet-Biedl syndrome 4 protein OS=Homo sapiens OX=9606 GN=BBS4 PE=1 SV=2
A1506	GO:0006412(translation)	-	-	K02838 frr, MRRF, RRF; ribosome recycling factor	-	KOG4759 7294968 Ribosome recycling factor	KAG0162932.1 hypothetical protein DFQ30_00107 [Apophysomyces sp. BC1015]	Ribosome-recycling factor OS=Rhizobium meliloti (strain 1021) OX=266834 GN=frr PE=3 SV=1

A1507	-	-	-	K05740 DIAPH1; diaphanous 1	map05131 Shigellosis;map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04933 AGE-RAGE signaling pathway in diabetic complications	KOG1922 CE23783 Rho GTPase effector BNI1 and related formins	KDR84018.1 hypothetical protein GALMADRAFT_262374 [Galerina marginata CBS 339.88]	Formin-F OS=Dictyostelium discoideum OX=44689 GN=forF PE=1 SV=1
A1508	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	-	-	-	TPX42428.1 hypothetical protein SeLEV6574.g05612 [Synchytrium endobioticum]	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 3 OS=Rattus norvegicus OX=10116 GN=Ogfod3 PE=2 SV=1
A1509	-	-	GO:0004045(aminoacyl-tRNA hydrolase activity)	K01056 PTH1, PTRH1, pth, spoVC; peptidyl-tRNA hydrolase, PTH1 family [EC:3.1.1.29]	-	KOG2255 Hs17449452 Peptidyl-tRNA hydrolase	ORX60654.1 peptidyl-tRNA hydrolase [Hesseltinella vesiculosa]	Peptidyl-tRNA hydrolase OS=Homo sapiens OX=9606 GN=PTRH1 PE=1 SV=1
A1510	GO:0006071(glycerol metabolic process)	-	GO:0004371(glycerone kinase activity)	-	-	KOG2426 At3g17770 Dihydroxyacetone kinase/glycerone kinase	KAF5643319.1 DAK2-dihydroxyacetone kinase [Fusarium sp. NRRL 25303]	Putative 3,4-dihydroxy-2-butanone kinase OS=Solanum lycopersicum OX=4081 GN=DHBK PE=2 SV=1
A1511	-	-	-	-	-	-	-	-
A1512	-	-	-	-	-	-	ORZ36500.1 hypothetical protein BCR44DRAFT_119276 [Catenaria anguillulae PL171]	Coiled-coil domain-containing protein 96 OS=Mus musculus OX=10090 GN=Ccdc96 PE=2 SV=1
A1513	GO:0000070(mitotic sister chromatid segregation),GO:1902412(regulation of mitotic cytokinesis)	-	-	-	-	KOG4456 Hs910376 Inner centromere protein (INCENP), C-terminal domain	RKP22616.1 inner centromere protein [Syncephalis pseudoplumigaleata]	Inner centromere protein OS=Homo sapiens OX=9606 GN=INCENP PE=1 SV=3
A1514	-	-	-	-	-	KOG1326 Hs4758856 Membrane-associated protein FER-1 and related ferlins, contain multiple C2 domains	KAF0449901.1 C2 domain containing protein [Gigaspora margarita]	Otoferlin OS=Danio rerio OX=7955 GN=otof PE=3 SV=1

A1515	-	-	-	-	-	KOG1303 At1g25530 Amino acid transporters	XP_016235708.1 hypothetical protein PV08_05538 [Exophiala spinifera]	Amino acid transporter AVT1B OS=Arabidopsis thaliana OX=3702 GN=AVT1B PE=3 SV=2
A1516	-	-	-	-	-	-	-	-
A1517	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0046872(metal ion binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0033 Hs14141724 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KNE62784.1 CAMK/CAMK1 protein kinase [Allomyces macrogynus ATCC 38327]	Probable myosin light chain kinase DDB_G0271550 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0271550 PE=3 SV=1
A1518	-	-	GO:0010181(FMN binding),GO:0016491(oxidoreductase activity),GO:0020037(heme binding)	-	-	-	CAE6459180.1 unnamed protein product [Rhizoctonia solani]	Fumarate reductase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=osm1 PE=3 SV=1
A1519	-	-	GO:0005515(protein binding)	-	-	-	TKA77672.1 hypothetical protein B0A49_02194 [Cryomyces minteri]	Adenylate cyclase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=cyr1 PE=1 SV=1
A1520	-	-	-	-	-	-	-	-
A1521	-	-	-	-	-	-	-	-
A1522	-	-	-	-	-	-	KAG2177195.1 hypothetical protein INT43_007852 [Umbelopsis isabellina]	-
A1523	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At4g14780 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAG0258387.1 hypothetical protein DFQ27_004656 [Actinomortierella ambigua]	Putative serine/threonine-protein kinase/receptor R831 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_R831 PE=3 SV=2
A1524	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity)	-	-	KOG3040 Hs14149777 Predicted sugar phosphatase (HAD superfamily)	KZT62386.1 hypothetical protein CALCODRAFT_446211, partial [Calocera cornea HHB12733]	Haloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Rattus norvegicus OX=10116 GN=Hdh2 PE=2 SV=1

A1525	GO:0000105(histidine biosynthetic process)	-	GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0046872(metal ion binding),GO:0051287(NAD binding),GO:0016491(oxidoreductase activity),GO:0004399(histidinol dehydrogenase activity)	-	-	KOG2697 At5g63890 Histidinol dehydrogenase	THZ49932.1 histidinol dehydrogenase [Aureobasidium pullulans]	Histidinol dehydrogenase OS=Thermus thermophilus (strain ATCC BAA-163 / DSM 7039 / HB27) OX=262724 GN=hisD PE=3 SV=1
A1526	-	-	-	-	-	-	-	-
A1527	GO:0007165(signal transduction)	-	-	-	-	KOG2372 Hs22054257 Oxidation resistance protein	OUM57377.1 hypothetical protein PIROE2DRAFT_28581, partial [Piromyces sp. E2]	TLD domain-containing protein 2 OS=Mus musculus OX=10090 GN=Tldc2 PE=3 SV=1
A1528	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K11498 CENPE, KIF10; centromeric protein E	map04814 Motor proteins	KOG0242 7297839_1 Kinesin-like protein	RUS29389.1 hypothetical protein BC938DRAFT_480720 [Jimgerdeman nia flammicorona]	Kinesin-like protein KIN-7D, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=KIN7D PE=1 SV=2
A1529	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0005524(ATP binding),GO:0019205(nucleobase-containing compound kinase activity),GO:0004017(adenylate kinase activity),GO:0016776(phosphotransferase activity, phosphate group as acceptor)	K00939 adk, AK; adenylate kinase [EC:2.7.4.3]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map00730 Thiamine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3078 At5g63400 Adenylate kinase	EPZ35724.1 Adenylate kinase [Rozella allomycis CSF55]	Adenylate kinase 4 OS=Arabidopsis thaliana OX=3702 GN=ADK1 PE=1 SV=2
A1530	-	-	GO:0005515(protein binding),GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K11661 SRCAP, SWR1; helicase SRCAP/SWR1 [EC:5.6.2.-]	map03082 ATP-dependent chromatin remodeling	KOG0391 At3g12810 SNF2 family DNA-dependent ATPase	CAD6613054.1 BJ4_G0049040.mRNA.1.CDS.1 [Saccharomyces cerevisiae]	Protein PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1 OS=Arabidopsis thaliana OX=3702 GN=PIE1 PE=1 SV=1

A1531	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K06641 CHEK2; serine/threonine-protein kinase CHEK2 [EC:2.7.11.1]	map04218 Cellular senescence;map04115 p53 signaling pathway;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG0032[Hs4826684_1 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORX91130.1 Pkinase-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Probable myosin light chain kinase DDB_G0271550 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0271550 PE=3 SV=1
A1532	GO:0006629(lipid metabolic process),GO:0006488(dolichol-linked oligosaccharide biosynthetic process)	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0003865(3-oxo-5-alpha-steroid 4-dehydrogenase activity)	K12345 SRD5A3; 3-oxo-5-alpha-steroid 4-dehydrogenase 3 / polyprenol reductase [EC:1.3.1.22 1.3.1.94]	map00510 N-Glycan biosynthesis;map00140 Steroid hormone biosynthesis;map01100 Metabolic pathways	KOG1640[At2g16530 Predicted steroid reductase	KAF9955577.1 Steroid 5 alpha-reductase 3 [Mortierella alpina]	Polyprenol reductase 2 OS=Arabidopsis thaliana OX=3702 GN=PPRD2 PE=1 SV=2
A1533	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity)	K18083 MTMR6_7_8; myotubularin-related protein 6/7/8 [EC:3.1.3.64 3.1.3.95]	map04070 Phosphatidylinositol signaling system;map04138 Autophagy - yeast;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG4471[Hs705564 Phosphatidylinositol 3-phosphate 3-phosphatase myotubularin MTM1	XP_018231485.1 hypothetical protein T551_00278 [Pneumocystis jirovecii RU7]	Myotubularin-related protein 2 OS=Gallus gallus OX=9031 GN=MTMR2 PE=2 SV=1
A1534	GO:0006508(proteolysis)	-	GO:0004185(serine-type carboxypeptidase activity)	-	-	KOG1282[At3g10410 Serine carboxypeptidases (lysosomal cathepsin A)	TPX58515.1 hypothetical protein PhCBS80983_g03085 [Powellomyces hirtus]	Serine carboxypeptidase S10 family member 1 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0291912 PE=3 SV=1
A1535	-	-	GO:0000166(nucleotide binding),GO:0003676(nucleic acid binding),GO:0003887(DNA-directed DNA polymerase activity),GO:0003677(DNA binding)	K02327 POLD1; DNA polymerase delta subunit 1 [EC:2.7.7.7]	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03440 Homologous recombination;map03430 Mismatch repair	KOG0969[Hs4505933 DNA polymerase delta, catalytic subunit	KAG0235930.1 DNA-directed DNA polymerase delta [Actinomortierella wolffii]	DNA polymerase delta catalytic subunit OS=Oryza sativa subsp. japonica OX=39947 GN=POLD1 PE=2 SV=1
A1536	-	-	-	-	-	-	-	-
A1537	-	-	-	-	-	-	-	-
A1538	-	-	-	-	-	-	-	-
A1539	GO:0043666(regulation of phosphoprotein phosphatase activity)	-	GO:0019211(phosphatase activator activity)	K17605 PPP2R4, PTPA; serine/threonine-protein phosphatase 2A activator	map05415 Diabetic cardiomyopathy;map04931 Insulin resistance	KOG2867[At4g08960 Phosphotyrosyl phosphatase activator	KIJ16527.1 hypothetical protein PAXINDRAFT_180335 [Paxillus involutus ATCC 200175]	Serine/threonine-protein phosphatase 2A activator 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rrd2 PE=3 SV=1

A1540	-	-	GO:0018580(nitronate monooxygenase activity)	K23948 E1.6.5.9; NADH:quinone reductase (non-electrogenic) [EC:1.6.5.9]	-	-	TPX72943.1 nitronate monooxygenase [Spizellomyces sp. 'palustris']	NADH:quinone reductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA1024 PE=1 SV=1
A1541	-	-	-	-	-	-	-	-
A1542	GO:0006468(protein phosphorylation),GO:0007165(signal transduction)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	-	-
A1543	GO:0006914(autophagy)	GO:0005737(cytoplasm)	-	K08339 ATG5; autophagy-related protein 5	map04140 Autophagy - animal;map05131 Shigellosis;map04216 Ferroptosis;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map04138 Autophagy - yeast;map04137 Mitophagy - animal;map04136 Autophagy - other;map04621 NOD-like receptor signaling pathway;map04622 RIG-I-like receptor signaling pathway	KOG2976[Hs4757798 Protein involved in autophagy and nutrient starvation	TPX33535.1 hypothetical protein SeMB42_g07464 [Synchytrium endobioticum]	Autophagy protein 5 OS=Mus musculus OX=10090 GN=Atg5 PE=1 SV=1
A1544	GO:0006637(acyl-CoA metabolic process)	-	GO:0047617(acyl-CoA hydrolase activity)	-	-	KOG3016[Hs4885565 Acyl-CoA thioesterase	KAG1255965.1 hypothetical protein G6F65_016521 [Rhizopus oryzae]	Acyl-CoA thioesterase 2 OS=Escherichia coli O157:H7 OX=83334 GN=tesB PE=3 SV=2
A1545	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration;map04024 cAMP signaling pathway;map04020 Calcium signaling pathway;map05414 Dilated cardiomyopathy;map04140 Autophagy - animal;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map01522 Endocrine resistance;map04919 Thyroid hormone signaling pathway;map04918 Thyroid hormone synthesis;map04	KOG0614[Hs10835242 cGMP-dependent protein kinase	XP_007911114.1 putative camp-dependent protein kinase catalytic subunit protein [Phaeoacremonium minimum UCRPA7]	cGMP-dependent protein kinase 1 OS=Homo sapiens OX=9606 GN=PRKG1 PE=1 SV=3

A1546	GO:000929(thiamine diphosphate biosynthetic process), GO:0006772(thiamine metabolic process)	-	GO:0003677(DNA binding),GO:0004788(thiamine diphosphokinase activity),GO:0005524(ATP binding),GO:0030975(thiamine binding)	K00949 thiN, TPK1, THI80; thiamine pyrophosphokinase [EC:2.7.6.2]	map00730 Thiamine metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG3153[Hs21362110 Thiamine pyrophosphokinase	RHZ79632.1 hypothetical protein Glove_143g46 [Diversispora epigaea]	Thiamin pyrophosphokinase 1 OS=Homo sapiens OX=9606 GN=TPK1 PE=1 SV=1
A1547	-	-	-	-	-	-	-	-
A1548	-	-	-	-	-	-	-	-
A1549	GO:0046856(phosphatidylinositol dephosphorylation)	-	GO:0016791(phosphatase activity)	K20279 SYNJ; synaptotjanin [EC:3.1.3.36]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0565[Hs4755142_1 Inositol polyphosphate 5-phosphatase and related proteins	KAF9109704.1 hypothetical protein BGX27_007295 [Mortierella sp. AM989]	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Sus scrofa OX=9823 GN=INPL1 PE=1 SV=2
A1550	-	-	-	-	-	KOG1426[At5g63860 FOG:RCC1 domain	RIB03142.1 regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II, partial [Gigaspora rosea]	Ultraviolet-B receptor UVR8 OS=Arabidopsis thaliana OX=3702 GN=UVR8 PE=1 SV=1
A1551	-	-	-	-	-	-	-	-
A1552	GO:0006508(proteolysis)	-	GO:0004198(calcium-dependent cysteine-type endopeptidase activity)	-	-	KOG0045[At1g55350 Cytosolic Ca2+-dependent cysteine protease (calpain), large subunit (EF-Hand protein superfamily)	KAF9359528.1 hypothetical protein BGX34_008316 [Mortierella sp. NVP85]	Calpain-type cysteine protease DEK1 OS=Zea mays OX=4577 GN=DEK1 PE=1 SV=2
A1553	-	-	-	K24970 TCF25, RQC1; transcription factor 25	-	KOG2422[Hs14149657 Uncharacterized conserved protein	XP_018281331.1 DUF654-domain-containing protein [Cutaneotrichosporon oleaginosum]	Ribosome quality control complex subunit TCF25 OS=Homo sapiens OX=9606 GN=TCF25 PE=1 SV=1
A1554	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K14837 NOP12; nucleolar protein 12	-	-	KAG0053196.1 Nucleolar protein 12 [Gryganskiella cystojenkini]	Nucleolar protein 12 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / BCRC 21394 / JCM 1990 / NBRC 0083 / IGC 2968) OX=284592 GN=NOP12 PE=3 SV=2
A1555	GO:0006457(protein folding)	GO:0005737(cytoplasm)	GO:0051082(unfolded protein binding)	-	-	-	-	33 kDa chaperonin OS=Levilactobacillus brevis (strain ATCC 367 / BCRC 12310 / CIP 105137 / JCM 1170 / LMG 11437 / NCIMB 947 / NCTC 947) OX=387344 GN=hslo PE=3 SV=1
A1556	GO:0006325(chromatin organization),GO:0006355(regulation of transcription, DNA-templated)	GO:0005634(nucleus)	-	K11339 MORF4L1, MRG15, EAF3; mortality factor 4-like protein 1	map03082 ATP-dependent chromatin remodeling	-	ODV91922.1 hypothetical protein CANCADRAFT_18276, partial [Tortispora caseinolytica NRRL Y-17796]	Chromatin modification-related protein eaf3 OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=eaf3 PE=3 SV=1

A1557	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	-	-	KOG0387 At2g18760 Transcription-coupled repair protein CSB/RAD26 (contains SNF2 family DNA-dependent ATPase domain)	CEG84102.1 Putative YALI0C16643 p [Rhizopus microsporus]	DNA excision repair protein CSB OS=Oryza sativa subsp. japonica OX=39947 GN=CSB PE=2 SV=1
A1558	-	-	GO:0004582(dolichyl-phosphate beta-D-mannosyltransferase activity)	K00721 DPM1: dolichol-phosphate mannosyltransferase [EC:2.4.1.83]	map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG2978 YP R183w Dolichol-phosphate mannosyltransferase	XP_007363392.1 uncharacterized protein DICSQDRAFT_101599 [Dichomitus squalens LYAD-421 SS1]	Dolichol-phosphate mannosyltransferase OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=DPM1 PE=3 SV=2
A1559	GO:0006096(glycolytic process)	GO:000015(phosphopyruvate hydratase complex)	GO:0000287(magnesium ion binding),GO:0004634(phosphopyruvate hydratase activity)	K01689 ENO, eno; enolase [EC:4.2.1.11]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00680 Methane metabolism;map03018 RNA degradation;map01100 Metabolic pathways;map04066 HIF-1 signaling pathway	KOG2670 Hs4503571 Enolase	PVU98140.1 hypothetical protein BB559_001774 [Furculomyces boomerangs]	Enolase OS=Oryza sativa subsp. japonica OX=39947 GN=ENO1 PE=1 SV=2
A1560	-	-	-	-	-	-	-	-
A1561	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A1562	-	-	-	-	-	KOG2668 7303053 Flotillins	KAF9121765.1 hypothetical protein BGX30_002395, partial [Mortierella sp. GBA39]	Flotillin-2 OS=Drosophila melanogaster OX=7227 GN=Flot2 PE=2 SV=3
A1563	-	-	-	-	-	-	-	-
A1564	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02913 RP-L33, MRPL33, rpmG; large subunit ribosomal protein L33	map03010 Ribosome	KOG3505 At3g06320 Mitochondrial/chloroplast ribosomal protein L33-like	KAG0923746.1 hypothetical protein G6F31_019385 [Rhizopus oryzae]	Large ribosomal subunit protein bL33 OS=Deinococcus geothermalis (strain DSM 11300 / AG-3a) OX=319795 GN=rpmG PE=3 SV=1

A1565	GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	KOG1485 At1g79520 Mitochondrial Fe2+ transporter MMT1 and related transporters (cation diffusion facilitator superfamily)	RKP09675.1 cation efflux family-domain-containing protein [Thamnocephalis sphaerospora]	Metal tolerance protein 9 OS=Arabidopsis thaliana OX=3702 GN=MTP9 PE=3 SV=2
A1566	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1567	-	-	GO:0003682(chromatin binding)	-	-	-	RKP07077.1 hypothetical protein THASP1DRAFT_24705 [Thamnocephalis sphaerospora]	-
A1568	GO:0016311(dephosphorylation),GO:006470(protein dephosphorylation),GO:0007096(regulation of exit from mitosis)	-	GO:0016791(phosphatase activity),GO:0008138(protein tyrosine/serine/threonine phosphatase activity),GO:0004721(phosphoprotein phosphatase activity)	K06639 CDC14; cell division cycle 14 [EC:3.1.3.16 3.1.3.48]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG1720 Hs15451933 Protein tyrosine phosphatase CDC14	TPX65103.1 hypothetical protein SpCBS45565_g05373 [Spizellomyces sp. 'palustris']	Dual specificity protein phosphatase CDC14A OS=Mus musculus OX=10090 GN=Cdc14a PE=1 SV=2
A1569	-	-	GO:0005524(ATP binding),GO:0046872(metal ion binding)	K01968 E6.4.1.4A; 3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4]	map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG0238 Hs4557833 3-Methylcrotonyl-CoA carboxylase, biotin-containing subunit/Propionyl-CoA carboxylase, alpha chain/Acetyl-CoA carboxylase, biotin carboxylase subunit	ORX89120.1 hypothetical protein K493DRAFT_267496 [Basidiobolus meristosporus CBS 931.73]	Propionyl-CoA carboxylase alpha chain OS=Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) OX=246200 GN=pccA PE=1 SV=1
A1570	GO:0008033(tRNA processing)	-	GO:0017150(tRNA dihydrouridine synthase activity),GO:0050660(flavin adenine dinucleotide binding)	K05542 DUS1; tRNA-dihydrouridine synthase 1 [EC:1.3.1.88]	-	KOG2335 At5g67220 tRNA-dihydrouridine synthase	OAC98556.1 hypothetical protein MUCCIDRAFT_119003, partial [Mucor lusitanicus CBS 277.49]	tRNA-dihydrouridine(16/17) synthase [NAD(P)(+)]-like OS=Rattus norvegicus OX=10116 GN=Dus1 PE=2 SV=1
A1571	GO:0007010(cytoskeleton organization)	-	GO:0003779(action binding)	-	-	-	ORX84484.1 hypothetical protein BCR32DRAFT_230388 [Anaeromyces robustus]	-
A1572	-	-	-	-	-	-	-	-
A1573	-	-	GO:0005515(protein binding)	-	-	KOG3953 7303345 SOCS box protein SSB-1, contains SPRY domain	PKC16632.1 BTB-domain-containing protein [Rhizophagus irregularis]	F-box/SPRY domain-containing protein 1 OS=Drosophila yakuba OX=7245 GN=Fsn PE=3 SV=1

A1574	-	-	-	K11493 RCC1; regulator of chromosome condensation	-	KOG1426 At5 g63860 FOG: RCC1 domain	KAF9945743. 1 hypothetical protein BGZ72_00105 8 [Mortierella alpina]	Ultraviolet-B receptor UVR8 OS=Arabidopsis thaliana OX=3702 GN=UVR8 PE=1 SV=1
A1575	-	-	-	-	-	-	-	-
A1576	-	-	-	-	-	-	-	-
A1577	-	-	-	K00942 gmk, GUK1; guanylate kinase [EC:2.7.4.8]	map00230 Purine metabolism;map 01232 Nucleotide metabolism;map 01100 Metabolic pathways	KOG0707 Hs4 504221 Guanylate kinase	TGZ84310.1 guanylate kinase [Ascodesmis nigricans]	Guanylate kinase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=GK1 PE=2 SV=2
A1578	-	-	-	-	-	-	-	-
A1579	-	-	-	-	-	KOG2401 YPL 199c Predicted MutS-related protein involved in mismatch repair	XP_02006626 5.1 DUF1771- domain- containing protein [Suhomyces tanzawaensis NRRL Y- 17324]	Smr domain-containing protein YPL199C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPL199C PE=1 SV=1
A1580	-	-	-	-	-	KOG3961 Hs1 8564317 Uncharacteriz ed conserved protein	XP_03102570 8.1 uncharacteriz ed protein SmJEL517_g0 2437 [Synchytrium microbalum]	Parkin coregulated gene protein OS=Bos taurus OX=9913 GN=PACRG PE=1 SV=1
A1581	-	GO:00056 34(nucleu s)	-	-	-	KOG1949 Hs M8923293 Uncharacteriz ed conserved protein	KXS20665.1 hypothetical protein M427DRAFT_ 142851 [Gonapodya prolifera JEL478]	Condensin-2 complex subunit G2 OS=Homo sapiens OX=9606 GN=NCAPG2 PE=1 SV=1
A1582	-	-	GO:0005506(iron ion binding),GO:001 6705(oxidoredu ctase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:003 1418(L-ascorbic acid binding)	-	-	-	-	-
A1583	-	-	GO:0046983(pro tein dimerization activity)	-	-	-	-	-
A1584	-	-	GO:0008270(zin c ion binding)	-	-	-	KAE8237392. 1 hypothetical protein A4X13_0g880 7 [Tilletia indica]	-
A1585	-	-	-	-	-	-	-	-
A1586	-	-	-	-	-	-	-	-
A1587	-	-	-	-	-	-	-	-

A1588	-	-	-	-	-	-	TPX77863.1 hypothetical protein CcCBS67573_ g00888 [Chytridiomyc s confervae]	E3 ubiquitin-protein ligase WAV3 OS=Arabidopsis thaliana OX=3702 GN=WAV3 PE=1 SV=1
A1589	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02882 RP-L18Ae, RPL18A; large subunit ribosomal protein L18Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0829 At2g34480 60S ribosomal protein L18A	XP_013019438.1 60S ribosomal protein L20 [Schizosaccharomyces octosporus yFS286]	Large ribosomal subunit protein eL20y OS=Arabidopsis thaliana OX=3702 GN=RPL18AB PE=1 SV=2
A1590	-	-	GO:0005515(protein binding)	K17970 MDV1, FIS2; mitochondrial division protein 1	-	KOG4155 YKR036c FOG: WD40 repeat	KXJ85813.1 WD40-repeat-containing domain protein [Microdochium bolleyi]	CCR4-associated factor 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAF4 PE=1 SV=3
A1591	-	-	-	K00784 rnz; ribonuclease Z [EC:3.1.26.11]	-	-	PWI69118.1 hypothetical protein PCL_01503 [Purpureocillium lilacinum]	tRNase Z TRZ2, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=TRZ2 PE=2 SV=1
A1592	GO:0006633(fatty acid biosynthetic process)	-	GO:0016746(acyltransferase activity),GO:0004315(3-oxoacyl-[acyl-carrier-protein] synthase activity),GO:0016740(transferase activity)	K01043 SWNK; reducing polyketide synthase SwnK [EC:2.3.1.-]	-	KOG1202 CE09880 Animal-type fatty acid synthase and related proteins	KID83603.1 polyketide synthase [Metarhizium guizhouense ARSEF 977]	Polyunsaturated fatty acid synthase subunit A OS=Thraustochytrium sp. (strain ATCC 26185 / S-3) OX=672127 GN=ORF-A PE=1 SV=1
A1593	-	-	GO:0016746(acyltransferase activity),GO:0016740(transferase activity)	-	-	KOG1202 CE04187.1 Animal-type fatty acid synthase and related proteins	KAF9395587.1 hypothetical protein CPC16_007748 [Podila verticillata]	Polyunsaturated fatty acid synthase subunit B OS=Thraustochytrium sp. (strain ATCC 26185 / S-3) OX=672127 GN=ORF-B PE=1 SV=1
A1594	-	-	GO:0016740(transferase activity)	K10669 TRPT1, TPT1; 2'-phosphotransferase [EC:2.7.1.160]	-	KOG2278 At2g45330 RNA:NAD 2'-phosphotransferase TPT1	RIA85631.1 KptA family-domain-containing protein [Glomus cerebriforme]	tRNA 2'-phosphotransferase 1 OS=Danio rerio OX=7955 GN=trpt1 PE=2 SV=2
A1595	-	-	-	K05687 PARK7; protein DJ-1 [EC:3.5.1.124]	map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease	KOG2764 CE07740 Putative transcriptional regulator DJ-1	ORY46879.1 DJ-1-like protein [Rhizoclostium globosum]	Glutathione-independent glyoxalase DJR-1.1 OS=Caenorhabditis elegans OX=6239 GN=djr-1.1 PE=1 SV=1
A1596	-	-	-	-	-	-	-	-

A1597	-	-	-	K01738 cysK; cysteine synthase [EC:2.5.1.47]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00920 Sulfur metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	-	TPX42630.1 hypothetical protein SeLEV6574.g05499 [Synchytrium endobioticum]	Cysteine synthase 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=cys12 PE=3 SV=1
A1598	-	-	-	K19199 SETD3; protein-histidine N-methyltransferase [EC:2.1.1.85]	-	KOG1337 Hs14149938 N-methyltransferase	TPX76020.1 hypothetical protein CcCBS67573.g02708 [Chytrium confervae]	Actin-histidine N-methyltransferase OS=Rhinolophus ferrumequinum OX=59479 GN=SETD3 PE=3 SV=1
A1599	-	-	-	K22696 EEF2KMT; protein-lysine N-methyltransferase EEF2KMT [EC:2.1.1.-]	-	KOG2497 Hs20562158 Predicted methyltransferase	RFN49149.1 protein fam86a [Fusarium flagelliforme]	Putative protein N-methyltransferase FAM86B1 OS=Homo sapiens OX=9606 GN=FAM86B1 PE=2 SV=2
A1600	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0659 7300773 Cdk activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH/TFIIK, kinase subunit CDK7	KAF2461127.1 kinase-like domain-containing protein [Lineolata rhizophorae]	Probable inactive protein kinase At3g63330 OS=Arabidopsis thaliana OX=3702 GN=At3g63330 PE=2 SV=1
A1601	-	-	-	-	-	-	KAF2105573.1 S-adenosyl-L-methionine-dependent methyltransferase [Lophiotrema nucula]	-
A1602	-	-	-	K01934 MTHFS; 5-formyltetrahydrofolate cyclo-ligase [EC:6.3.3.2]	map00670 One carbon pool by folate;map01100 Metabolic pathways	KOG3093 Hs5453746 5-formyltetrahydrofolate cyclo-ligase	KAF1803403.1 5-formyltetrahydrofolate cyclo-ligase [Mucor lusitanicus]	5-formyltetrahydrofolate cyclo-ligase OS=Oryctolagus cuniculus OX=9986 GN=MTHFS PE=1 SV=1
A1603	-	GO:0000922(spindle pole),GO:0005813(cytosol)	-	-	-	-	-	-

A1604	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At3g06620 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	XP_025362569.1 Pkinase-domain-containing protein, partial [Jaminaea rosea]	Putative serine/threonine-protein kinase/receptor R831 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_R831 PE=3 SV=2
A1605	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05681 ABCG2, CD338; ATP-binding cassette, subfamily G (WHITE), member 2	map01523 Antifolate resistance;map04976 Bile secretion;map02010 ABC transporters	KOG0061 Hs4757850 Transporter, ABC superfamily (Breast cancer resistance protein)	ORZ41275.1 P-loop containing nucleoside triphosphate hydrolase protein [Catenaria anguillulae PL171]	Broad substrate specificity ATP-binding cassette transporter ABCG2 OS=Bos taurus OX=9913 GN=ABCG2 PE=3 SV=2
A1606	-	-	-	-	-	-	-	-
A1607	-	-	GO:0047617(acyl-CoA hydrolase activity)	-	-	-	TVY75571.1 Uncharacterized protein LSUE1_G004615, partial [Lachnellula suecica]	-
A1608	GO:0006450(regulation of translational fidelity),GO:0051083('de novo' cotranslational protein folding)	-	GO:0030544(Hsp70 protein binding),GO:0043022(ribosome binding)	K09522 DNAJC2; DnaJ homolog subfamily C member 2	-	KOG0724 Hs20543026 Zuotin and related molecular chaperones (DnaJ superfamily), contains DNA-binding domains	TPX65842.1 hypothetical protein SpCBS45565_g04887 [Spizellomyces sp. 'palustris']	DnaJ homolog subfamily C member 2 OS=Mus musculus OX=10090 GN=Dnajc2 PE=1 SV=2
A1609	-	-	-	-	-	KOG1700 Hs4503049 Regulatory protein MLP and related LIM proteins	TPX62594.1 hypothetical protein PhCBS80983_g00407 [Powellomyces hirtus]	Cysteine-rich protein 2 OS=Homo sapiens OX=9606 GN=CRIP2 PE=1 SV=1
A1610	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02884 RP-L19, MRPL19, rplS; large subunit ribosomal protein L19	map03010 Ribosome	KOG1698 At4g11630 Mitochondrial/chloroplast ribosomal protein L19	OLL22971.1 54S ribosomal subunit img1, mitochondrial [Neoelecta irregularis DAH-3]	Large ribosomal subunit protein bL19 OS=Thermus thermophilus (strain ATCC BAA-163 / DSM 7039 / HB27) OX=262724 GN=rplS PE=1 SV=1
A1611	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10401 KIF18A; kinesin family member 18A	map04814 Motor proteins	KOG0242 At3g49650 Kinesin-like protein	RKP21684.1 kinesin-domain-containing protein, partial [Rozella allomycis CSF55]	Kinesin-like protein KIF19 OS=Xenopus laevis OX=8355 GN=kif19 PE=2 SV=1
A1612	-	-	-	-	-	-	-	-
A1613	-	-	GO:0008146(sulfotransferase activity)	-	-	KOG3704 Hs18585335 Heparan sulfate D-glucosaminyl 3-O-sulfotransferase	-	Heparan sulfate glucosamine 3-O-sulfotransferase 3A1 OS=Mus musculus OX=10090 GN=Hs3st3a1 PE=2 SV=1
A1614	-	-	GO:0008146(sulfotransferase activity)	-	-	-	-	Carbohydrate sulfotransferase 15 OS=Homo sapiens OX=9606 GN=CHST15 PE=1 SV=1
A1615	-	-	GO:0005515(protein binding)	-	-	-	-	-

A1616	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02966 RP-S19e, RPS19; small subunit ribosomal protein S19e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3411 At5g15520 40S ribosomal protein S19	TPX60859.1 hypothetical protein CcCBS67573_g08972 [Chytridiomycota confervae]	Small ribosomal subunit protein eS19y OS=Arabidopsis thaliana OX=3702 GN=RPS19B PE=2 SV=1
A1617	-	-	-	-	-	-	-	-
A1618	-	-	-	-	-	KOG0048 Hs4505293_1 Transcription factor, Myb superfamily	EHY66387.1 MYB domain-containing protein [Nematocida sp. 1 ERTm2]	Myb-related protein B OS=Xenopus laevis OX=8355 GN=mybl2 PE=2 SV=2
A1619	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1620	-	-	-	-	-	KOG1032 At1g03370_2 Uncharacterized conserved protein, contains GRAM domain	KAF7747578.1 hypothetical protein DSO57_015300 [Entomophthora muscae]	C2 and GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana OX=3702 GN=At1g03370 PE=2 SV=4
A1621	-	-	-	K00477 PHYH; phytanoyl-CoA hydroxylase [EC:1.14.11.18]	map04146 Peroxisome	KOG3290 CE24085 Peroxisomal phytanoyl-CoA hydroxylase	KAF9421336.1 hypothetical protein BGZ94_008854 [Podila epigama]	Phytanoyl-CoA dioxygenase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PHYHD1 PE=1 SV=2
A1622	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	-	-	KOG1868 HsM19923759 Ubiquitin C-terminal hydrolase	OAD00670.1 hypothetical protein MUCCIDRAFT_14515, partial [Mucor lusitanicus CBS 277.49]	Ubiquitin carboxyl-terminal hydrolase 2 OS=Rattus norvegicus OX=10116 GN=Usp2 PE=1 SV=1
A1623	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10398 KIF11, EG5; kinesin family member 11	map04814 Motor proteins	KOG0243 At2g36200 Kinesin-like protein	ORX87825.1 kinesin-domain-containing protein [Anaeromyces robustus]	Kinesin-like protein KIN-5C OS=Nicotiana tabacum OX=4097 GN=KIN5C PE=1 SV=1
A1624	-	-	-	-	-	-	-	-
A1625	GO:0070588(calcium ion transmembrane transport),GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0005886(plasma membrane),GO:0005891(voltage-gated calcium channel complex),GO:0016020(membrane)	GO:0005261(cation channel activity),GO:0005245(voltage-gated calcium channel activity),GO:0005216(ion channel activity)	K21864 CCH1; voltage-dependent calcium channel	-	KOG2301 Hs19923117 Voltage-gated Ca2+ channels, alpha1 subunits	RKP08010.1 ion transport protein-domain-containing protein [Thamnocephalus sphaerosporus]	Voltage-dependent L-type calcium channel subunit alpha-1S OS=Aquarana catesbeiana OX=8400 PE=2 SV=1
A1626	GO:0000398(mRNA splicing, via spliceosome)	GO:0005681(spliceosomal complex)	-	K06063 SNW1, SKIIP, SKIP; SNW domain-containing protein 1	map03040 Spliceosome;map05203 Viral carcinogenesis; map04330 Notch signaling pathway;map05169 Epstein-Barr virus infection	KOG2441 At1g77180 mRNA splicing factor/probable chromatin binding snw family nuclear protein	KAG2185902.1 hypothetical protein INT43_002340 [Umbelopsis isabellina]	SNW/SKI-interacting protein A OS=Oryza sativa subsp. japonica OX=39947 GN=SKIPA PE=1 SV=1

A1627	-	-	-	K26544 SEC14, SEC14L; phosphatidyli nositol/phosp hatidylcholin e transfer protein	-	KOG1471 CE 07556 Phosphatidyl nositol transfer protein SEC14 and related proteins	KAA8908082. 1 hypothetical protein TRICL_004833 [Trichomonas ciferrii]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH14 OS=Arabidopsis thaliana OX=3702 GN=SFH14 PE=2 SV=1
A1628	-	-	-	-	-	-	-	-
A1629	-	-	-	-	-	KOG0718 Hs8 922629 Molecular chaperone (DnaJ superfamily)	XP_00732764 1.1 hypothetical protein AGAB11DRAFT_126182 [Agaricus bisporus var. burnettii JB137-S8]	Chaperone protein DnaJ OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) OX=322710 GN=dnaJ PE=3 SV=1
A1630	GO:00090 73(aromat ic amino acid family biosynthe tic process)	-	GO:0003849(3- deoxy-7- phosphoheptul onate synthase activity)	K01626 E2.5.1.54, aroF, aroG, aroH; 3- deoxy-7- phosphohept ulonate synthase [EC:2.5.1.54]	map01110 Biosynthesis of secondary metabolites;map 01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;ma p02024 Quorum sensing;map011 00 Metabolic pathways	-	KAG0242227. 1 hypothetical protein BGW41_0046 59 [Actinomortie rella wolfii]	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=aro-8 PE=1 SV=2
A1631	-	-	GO:0003677(DN A binding),GO:000 3678(DNA helicase activity),GO:000 5524(ATP binding),GO:001 6787(hydrolase activity)	K10300 FBH1, FBXO18; F- box DNA helicase 1 [EC:5.6.2.4]	-	KOG2108 Hs M14249492 3'-5' DNA helicase	KAG0769089. 1 hypothetical protein G6F24_00136 7 [Rhizopus oryzae]	F-box DNA helicase 1 OS=Homo sapiens OX=9606 GN=FBH1 PE=1 SV=2
A1632	-	-	-	-	-	KOG0101 Hs1 8576822 Molecular chaperones HSP70/HSC7 0, HSP70 superfamily	RGB26169.1 hypothetical protein C1646_77078 6 [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Heat shock 70 kDa protein 12A OS=Mus musculus OX=10090 GN=Hspa12a PE=1 SV=1
A1633	-	-	-	K17408 DAP3, MRPS29; small subunit ribosomal protein S29	-	KOG3928 At1 g16870 Mitochondria l ribosome small subunit component, mediator of apoptosis DAP3	KAF8230539. 1 hypothetical protein L208DRAFT_1 423806 [Tricholoma matsutake 945]	Small ribosomal subunit protein mS29 OS=Homo sapiens OX=9606 GN=DAP3 PE=1 SV=1
A1634	-	GO:00160 21(integra l compone nt of membran e)	GO:0004190(asp artic-type endopeptidase activity)	K09595 HM13; minor histocompati bility antigen H13 [EC:3.4.23.-]	-	KOG2442 Hs2 0514780 Uncharacteriz ed conserved protein, contains PA domain	KAF9146950. 1 Signal peptide peptidase- like 2A [Mortierella sp. GBA39]	Signal peptide peptidase-like 3 OS=Arabidopsis thaliana OX=3702 GN=SPPL3 PE=2 SV=1

A1635	GO:0017121(plasma membrane phospholipid scrambling)	-	GO:0017128(phospholipid scramblase activity)	-	-	KOG0621 Hs10863877 Phospholipid scramblase	-	Phospholipid scramblase 1 OS=Homo sapiens OX=9606 GN=PLSCR1 PE=1 SV=1
A1636	GO:0046314(phosphocreatine biosynthetic process)	-	GO:0016301(kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups),GO:0004111(creatine kinase activity),GO:0003824(catalytic activity)	-	-	KOG3581 7294999 Creatine kinases	KAF9118610.1 hypothetical protein BGX30_004456 [Mortierella sp. GBA39]	Arginine kinase OS=Anthopleura japonica OX=67755 PE=1 SV=1
A1637	-	-	-	K15283 SLC35E1; solute carrier family 35, member E1	-	KOG1441 At1g61800 Glucose-6-phosphate/p-phosphate and phosphoenolpyruvate/phosphate antiporter	KAF3000889.1 suppressor of loss of ypt1 [Curvularia kusanoi]	Glucose-6-phosphate/phosphate translocator 2, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=GPT2 PE=2 SV=2
A1638	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0286 Hs11321585 G-protein beta subunit	KAF7115753.1 hypothetical protein CNMCM5793_003256 [Aspergillus hiratsukae]	Guanine nucleotide-binding protein subunit beta OS=Cryphonectria parasitica OX=5116 GN=GB-1 PE=3 SV=1
A1639	GO:0006412(translation)	GO:0015934(large ribosomal subunit),GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02876 RP-L15, MRPL15, rplO; large subunit ribosomal protein L15	map03010 Ribosome	-	KAF9411817.1 YmL10 [Podila epigama]	Large ribosomal subunit protein uL15 OS=Methylobacterium nodulans (strain LMG 21967 / CNCM I-2342 / ORS 2060) OX=460265 GN=rplO PE=3 SV=1
A1640	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs6005990 Sulfatase	TQV91287.1 sulfatase [Cordyceps javanica]	Arylsulfatase A OS=Homo sapiens OX=9606 GN=ARSA PE=1 SV=3
A1641	-	-	-	-	-	KOG1179 Hs4503653 Very long-chain acyl-CoA synthetase/fatty acid transporter	KAF9950570.1 hypothetical protein BGZ72_007792 [Mortierella alpina]	Long-chain fatty acid transport protein 4 OS=Homo sapiens OX=9606 GN=SLC27A4 PE=1 SV=1
A1642	-	-	-	-	-	-	KAF2752184.1 glycoside hydrolase family 114 protein [Sporormia fimetaria CBS 119925]	-
A1643	-	-	-	-	-	-	KAG4089158.1 hypothetical protein H8356DRAFT_957104 [Neocallimastix sp. JGI-2020a]	-
A1644	-	-	-	-	-	-	-	UPF0489 protein C5orf22 homolog OS=Danio rerio OX=7955

A1645	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	PKY39010.1 hypothetical protein RhiirA4_439755 [Rhizophagus irregularis]	-
A1646	-	-	-	-	-	-	-	-
A1647	GO:0034551(mitochondrial respiratory chain complex III assembly)	-	-	-	-	-	XP_025343560.1 hypothetical protein CXQ85_005194 [[Candida] haemulonii]	-
A1648	GO:0006468(protein phosphorylation),GO:0000289(nuclear-transcribed mRNA poly(A) tail shortening),GO:0006397(mRNA processing)	GO:0031251(PAN complex)	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0003723(RNA binding)	K12572 PAN3; PAB-dependent poly(A)-specific ribonuclease subunit 3	map03018 RNA degradation	KOG3741[7292306 Poly(A) ribonuclease subunit	ORX41514.1 hypothetical protein BCR36DRAFT_587953 [Piromyces finnis]	PAN2-PAN3 deadenylation complex subunit pan3 OS=Dictyostelium discoideum OX=44689 GN=pan3 PE=3 SV=1
A1649	GO:0008299(isoprenoid biosynthetic process)	-	-	-	-	-	-	Short chain isoprenyl diphosphate synthase OS=Methanothermobacter thermautotrophicus (strain ATCC 29096 / DSM 1053 / JCM 10044 / NBRC 100330 / Delta H) OX=187420 GN=idsA PE=3 SV=1
A1650	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG1362[CE04499 Choline transporter-like protein	ORZ33107.1 plasma-membrane choline transporter-domain-containing protein [Catenaria anguillulae PL171]	Choline transporter-like protein 2 OS=Dictyostelium discoideum OX=44689 GN=slc44a2 PE=3 SV=1
A1651	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0157[CE02952 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	XP_018298657.1 CYP5210 protein [Phycomyces blakesleeana NRRL 1555(-)]	Cytochrome P450 714B1 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP714B1 PE=1 SV=2
A1652	-	-	GO:0005515(protein binding)	-	-	-	XP_009266643.1 26S proteasome non-ATPase regulatory subunit 10 [Wallemia ichthyophaga EXF-994]	-

A1653	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin---tyrosine ligase [EC:6.3.2.25]	-	-	OTB11179.1 hypothetical protein K445DRAFT_322365 [Daldinia sp. EC12]	-
A1654	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	GEM08218.1 MFS multidrug transporter [Rhodotorula toruloides]	-
A1655	-	-	-	-	-	-	-	-
A1656	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1657	-	-	GO:0005515(protein binding)	K18726 FAF2, UBXD8; FAS-associated factor 2	-	KOG1363 At4g10790 Predicted regulator of the ubiquitin pathway (contains UAS and UBX domains)	OON04364.1 hypothetical protein BSLG_05522 [Batrachochytrium salamandrivorans]	FAS-associated factor 2 OS=Rattus norvegicus OX=10116 GN=Faf2 PE=2 SV=1
A1658	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At4g35780 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	ORZ30046.1 kinase-like domain-containing protein [Catenaria anguillulae PL171]	Probable serine/threonine-protein kinase drkA OS=Dictyostelium discoideum OX=44689 GN=drkA PE=3 SV=1
A1659	-	-	-	-	-	-	-	-
A1660	GO:0006564(L-serine biosynthetic process)	-	GO:0004648(O-phospho-L-serine:2-oxoglutarate aminotransferase activity),GO:0003824(catalytic activity)	-	-	-	ELR04293.1 hypothetical protein GMDG_09019, partial [Pseudogymnoascus destructans 20631-21]	Phosphoserine aminotransferase OS=Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A) OX=188937 GN=serC PE=3 SV=1
A1661	-	-	-	K15692 RNF13, RZF; E3 ubiquitin-protein ligase RNF13 [EC:2.3.2.27]	-	KOG4628 Hs6005864 Predicted E3 ubiquitin ligase	TRM62468.1 hypothetical protein BD626DRAFT_497484 [Auriculariopsis ampla]	E3 ubiquitin-protein ligase RNF13 OS=Bos taurus OX=9913 GN=RNF13 PE=2 SV=1
A1662	-	-	GO:0005515(protein binding)	-	-	KOG1587 Hs16418347 Cytoplasmic dynein intermediate chain	OON07203.1 hypothetical protein BSLG_03283 [Batrachochytrium salamandrivorans]	Cytoplasmic dynein 2 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC2I2 PE=1 SV=2
A1663	-	-	-	-	-	-	-	-
A1664	GO:0006629(lipid metabolic process)	-	-	-	-	KOG0513 At2g26560 Ca2+-independent phospholipase A2	RGB32971.1 acyl transferase/acyl hydrolase/lyso-phospholipase [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Protein teg OS=Priestia megaterium (strain ATCC 14581 / DSM 32 / CCUG 1817 / JCM 2506 / NBRC 15308 / NCIMB 9376 / NCTC 10342 / NRRL B-14308 / VKM B-512 / Ford 19) OX=1348623 GN=teg PE=3 SV=1

A1665	GO:0031929(TOR signaling)	GO:0031932(TORC2 complex)	-	K08267 RICTOR; rapamycin-insensitive companion of mTOR	map04150 mTOR signaling pathway	KOG3694 Hs2047806 Protein required for meiosis	OZJ02093.1 hypothetical protein BZG36_04577 [Bifiguratus adalaidae]	Protein pianissimo A OS=Dictyostelium discoideum OX=44689 GN=piaA PE=1 SV=1
A1666	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	TPX76941.1 hypothetical protein CcBS67573_g01807 [Chytrium confervae]	-
A1667	-	-	-	-	-	-	KZM27989.1 hypothetical protein ST47_g860 [Ascochyta rabiei]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A1668	-	-	-	-	-	-	-	-
A1669	-	-	-	-	-	-	-	-
A1670	-	-	-	-	-	-	-	-
A1671	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ28687.1 LINE-1 retrotransposable element ORF2 protein, partial [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A1672	-	-	-	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ12941.1 Transposon TX1 protein [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A1673	-	-	-	K17675 SUPV3L1, SUV3; ATP-dependent RNA helicase SUPV3L1/SUV3 [EC:3.6.4.13]	-	KOG0953 At4g14790 Mitochondrial RNA helicase SUV3, DEAD-box superfamily	KNE72769.1 hypothetical protein AMAG_17098 [Allomyces macrogynus ATCC 38327]	DExH-box ATP-dependent RNA helicase DExH16, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=SUV3 PE=1 SV=1
A1674	-	-	-	-	-	-	-	-
A1675	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02866 RP-L10e, RPL10; large subunit ribosomal protein L10e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	-	XP_002175295.1 60S ribosomal protein L10 [Schizosaccharomyces japonicus yFS275]	Large ribosomal subunit protein uL16A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rpl1001 PE=1 SV=2
A1676	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	-	-	-	KAF9138565.1 hypothetical protein BGX30_009003 [Mortierella sp. GBA39]	-
A1677	-	-	GO:0005525(GTP binding);GO:0003924(GTPase activity)	K12852 EFTUD2; 116 kDa U5 small nuclear ribonucleoprotein component	map03040 Spliceosome	KOG0468 Hs4759280 U5 snRNP-specific protein	KAG2225669.1 hypothetical protein INT45_012141 [Mucor circinatus]	116 kDa U5 small nuclear ribonucleoprotein component OS=Gallus gallus OX=9031 GN=EFTUD2 PE=2 SV=1

A1678	GO:0006520 (cellular amino acid metabolic process)	-	GO:0016639 (oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor), GO:0016491 (oxidoreductase activity)	K00262 E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	map00910 Nitrogen metabolism; map01120 Microbial metabolism in diverse environments; map00250 Alanine, aspartate and glutamate metabolism; map00220 Arginine biosynthesis; map01100 Metabolic pathways	KOG2250 [YOR375c] Glutamate/leucine/phenylalanine/valine dehydrogenases	KAG1262871.1 hypothetical protein G6F65_014604 [Rhizopus oryzae]	Glutamate dehydrogenase OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / JCM 5827 / CCUG 10774 / NCTC 10582 / VPI-5482 / E50) OX=226186 GN=gdhA PE=3 SV=2
A1679	GO:0032543 (mitochondrial translation)	-	GO:0003735 (structural constituent of ribosome)	K17424 MRPL43; large subunit ribosomal protein L43	-	KOG3445 [At3g59650] Mitochondrial/chloroplast ribosomal protein 36a	GAM90691.1 hypothetical protein ANO11243.087360 [fungal sp. No.11243]	Large ribosomal subunit protein mL43 OS=Mus musculus OX=10090 GN=Mrpl43 PE=1 SV=1
A1680	-	-	-	-	-	-	-	-
A1681	-	GO:0016459 (myosin complex)	GO:0005515 (protein binding), GO:0003774 (motor activity), GO:0005524 (ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection; map04814 Motor proteins	KOG0160 [At4g28710] Myosin class V heavy chain	ORX76076.1 hypothetical protein BCR32DRAFT_209564, partial [Anaeromyces robustus]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1
A1682	GO:0006511 (ubiquitin-dependent protein catabolic process)	-	-	K03872 ELOC, TCEB1; elongin-C	map05170 Human immunodeficiency virus 1 infection; map05211 Renal cell carcinoma; map04120 Ubiquitin mediated proteolysis; map05200 Pathways in cancer; map04066 HIF-1 signaling pathway	KOG3473 [Hs5032161] RNA polymerase II transcription elongation factor Elongin/SIII, subunit elongin C	OAJ43561.1 hypothetical protein BDEG_26911 [Batrachochytrium dendrobatidis JEL423]	Elongin-C OS=Bos taurus OX=9913 GN=ELOC PE=1 SV=1
A1683	GO:0006479 (protein methylation)	-	GO:0008276 (protein methyltransferase activity)	K22696 EEF2KMT; protein-lysine N-methyltransferase EEF2KMT [EC:2.1.1.-]	-	KOG2793 [At1g73320] Putative N2,N2-dimethylguanosine tRNA methyltransferase	GAO51010.1 hypothetical protein G7K_5122-t1 [Saitoella complicata NRRL Y-17804]	Protein N-lysine methyltransferase METTL21A OS=Danio rerio OX=7955 GN=mettl21a PE=2 SV=1
A1684	-	GO:0016020 (membrane)	GO:0005524 (ATP binding), GO:0140359 (ABC-type transporter activity)	K05681 ABCG2, CD338; ATP-binding cassette, subfamily G (WHITE), member 2	map01523 Antifolate resistance; map04976 Bile secretion; map02010 ABC transporters	KOG0061 [Hs4757850] Transporter, ABC superfamily (Breast cancer resistance protein)	RUS17489.1 hypothetical protein BC937DRAFT_89917 [Endogone sp. FLAS-F59071]	Broad substrate specificity ATP-binding cassette transporter ABCG2 OS=Homo sapiens OX=9606 GN=ABCG2 PE=1 SV=3
A1685	-	-	-	-	-	-	-	-
A1686	-	-	-	-	-	-	-	-

A1687	GO:0006457(protein folding)	-	GO:0005524(ATP binding)	K04078 groES, HSPE1; chaperonin GroES	-	KOG1641 Hs4504523 Mitochondrial chaperonin	KUL86617.1 hypothetical protein ZTR_03040 [Talaromyces verruculosus]	10 kDa heat shock protein, mitochondrial OS=Oryzias latipes OX=8090 GN=hspe1 PE=3 SV=1
A1688	-	-	-	-	-	-	-	-
A1689	GO:0007165(signal transduction)	-	-	-	-	KOG4270 Hs13775230 GTPase-activator protein	-	Rho GTPase-activating protein 24 OS=Homo sapiens OX=9606 GN=ARHGAP24 PE=1 SV=2
A1690	-	-	-	-	-	-	-	-
A1691	-	-	-	-	-	-	-	-
A1692	GO:0006260(DNA replication)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0005515(protein binding),GO:0003677(DNA binding)	K10755 RFC2_4; replication factor C subunit 2/4	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03430 Mismatch repair	KOG0991 Hs4506487 Replication factor C, subunit RFC2	TPX63579.1 hypothetical protein CcCBS67573_g08639 [Chytridiomycetes confervae]	Replication factor C subunit 2 OS=Bos taurus OX=9913 GN=RFC2 PE=2 SV=1
A1693	-	-	-	-	-	-	XP_016605183.1 hypothetical protein SPPG_07534 [Spizellomyces punctatus DAOM BR117]	KIF-binding protein OS=Bos taurus OX=9913 GN=KIFBP PE=2 SV=1
A1694	-	-	-	-	-	-	-	-
A1695	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1696	-	-	-	-	-	-	-	-
A1697	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	-	-	KOG0736 YNL329c Peroxisome assembly factor 2 containing the AAA+ type ATPase domain	SAL97339.1 hypothetical protein [Absidia glauca]	Peroxisomal ATPase PEX6 OS=Pichia angusta OX=870730 GN=PEX6 PE=1 SV=1
A1698	-	-	-	-	-	-	-	-
A1699	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07904 RAB11A; Ras-related protein Rab-11A	map04144 Endocytosis;map04972 Pancreatic secretion;map04962 Vasopressin-regulated water reabsorption;map04961 Endocrine and other factor-regulated calcium reabsorption;map05164 Influenza A	KOG0087 Hs5902038 GTPase Rab11/YPT3, small G protein superfamily	KNE58784.1 small GTP-binding protein domain [Allomyces macrogynus ATCC 38327]	Rab-like protein 2A OS=Pongo abelii OX=9601 GN=RABL2A PE=2 SV=1
A1700	-	-	-	-	-	-	-	-

A1701	GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K13303 SGK2;serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0690[Hs4502023 Serine/threonine protein kinase	RKP17416.1 Pkinase-domain-containing protein [Rozella allomycis CSF55]	RAC-beta serine/threonine-protein kinase A OS=Xenopus laevis OX=8355 GN=akt2-a PE=2 SV=1
A1702	-	-	-	-	-	-	-	-
A1703	-	-	-	-	-	-	-	-
A1704	-	-	-	-	-	-	-	-
A1705	-	-	GO:0005515(protein binding)	K14554 UTP21, WDR36; U3 small nucleolar RNA-associated protein 21	map03008 Ribosome biogenesis in eukaryotes	-	OAJ37219.1 hypothetical protein BDEG_21268 [Batrachochytrium dendrobatidis JEL423]	WD repeat-containing protein 87 OS=Homo sapiens OX=9606 GN=WDR87 PE=1 SV=4
A1706	GO:0006011(UDP-glucose metabolic process), GO:0009058(biosynthetic process)	-	GO:0003983(UTP:glucose-1-phosphate uridylyltransferase activity),GO:0005524(ATP binding),GO:0016779(nucleotidyl transferase activity)	-	-	-	KAF9124464.1 hypothetical protein BGX30_000926 [Mortierella sp. GBA39]	UTP--glucose-1-phosphate uridylyltransferase OS=Rhizobium meliloti (strain 1021) OX=266834 GN=exoN PE=3 SV=2
A1707	-	-	-	-	-	-	-	-
A1708	GO:0016559(peroxisome fission)	GO:0005779(integral component of peroxisomal membrane)	-	-	-	-	EPZ36382.1 Peroxisomal biogenesis factor 11 domain-containing protein [Rozella allomycis CSF55]	-
A1709	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05657 ABCB10; ATP-binding cassette, subfamily B (MDR/TAP), member 10	map02010 ABC transporters	KOG0058[7292782 Peptide exporter, ABC superfamily	TPX68436.1 hypothetical protein CcCBS67573_g07190 [Chytridiomycetes confervae]	ABC transporter B family member 4 OS=Dictyostelium discoideum OX=44689 GN=abcB4 PE=3 SV=1
A1710	GO:0006468(protein phosphorylation)	-	GO:0004707(MAP kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K04464 MAPK7; mitogen-activated protein kinase 7 [EC:2.7.11.24]	map04722 Neurotrophin signaling pathway;map04912 GnRH signaling pathway;map05418 Fluid shear stress and atherosclerosis; map04657 IL-17 signaling pathway;map04139 Mitophagy - yeast;map04138 Autophagy - yeast;map04540 Gap junction;map05206 MicroRNAs in cancer;map04010 MAPK signaling pathway;map04011 MAPK signaling pathway - yeast;map04921 Oxytocin signaling	KOG0660[At2g43790 Mitogen-activated protein kinase	OCL09066.1 cell wall integrity MAP kinase [Glonium stellatum]	Mitogen-activated protein kinase homolog MMK1 OS=Medicago sativa OX=3879 GN=MMK1 PE=1 SV=1

A1711	-	-	-	K24083 ABHD13; abhydrolase domain- containing protein 13 [EC:3.-.-.-]	-	KOG1552 At3 g23540 Predicted alpha/beta hydrolase	KAF9144194. 1 hypothetical protein BGX30_01351 1 [Mortierella sp. GBA39]	Uncharacterized protein YqkD OS=Bacillus subtilis (strain 168) OX=224308 GN=yqkD PE=4 SV=1
A1712	-	-	-	K18164 NDUFAF7; NADH dehydrogena se [ubiquinone] 1 alpha subcomplex assembly factor 7	map04714 Thermogenesis	KOG2901 At3 g28700 Uncharacteriz ed conserved protein	ORZ35504.1 S-adenosyl- L- methionine- dependent methyltransfe rase [Catenaria anguillulae PL171]	Protein arginine methyltransferase NDUFAF7 homolog, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=midA PE=1 SV=1
A1713	GO:00064 57(protein folding)	GO:00057 83(endopl asmic reticulum)	GO:0005509(cal cium ion binding),GO:005 1082(unfolded protein binding),GO:000 5515(protein binding)	K08054 CANX; calnexin	map04145 Phagosome;map 04141 Protein processing in endoplasmic reticulum;map04 918 Thyroid hormone synthesis;map04 612 Antigen processing and presentation;ma p05166 Human T-cell leukemia virus 1 infection	KOG0674 At1 g56340 Calreticulin	ORX91885.1 Calreticulin [Basidiobolus meristosporu s CBS 931.73]	Calreticulin OS=Chlamydomonas reinhardtii OX=3055 PE=2 SV=1
A1714	-	-	-	K07390 grxD, GLRX5; monothiol glutaredoxin	-	KOG0911 YPL 059w Glutaredoxin -related protein	QID88373.1 monothiol glutaredoxin grx5 [Saccharomy ces pastorianus]	Monothiol glutaredoxin-5, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GRX5 PE=1 SV=1
A1715	-	GO:00165 92(mediat or complex)	-	-	-	-	-	-
A1716	GO:00065 08(proteo lysis)	-	GO:0004252(seri ne-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map 04972 Pancreatic secretion;map04 080 Neuroactive ligand-receptor interaction;map0 5164 Influenza A	KOG3627 Hs4 758508 Trypsin	XP_01455559 2.1 hypothetical protein COCVIDRAFT _27497 [Bipolaris victoriae FI3]	Transmembrane protease serine 12 OS=Homo sapiens OX=9606 GN=TMPRSS12 PE=1 SV=2
A1717	GO:00068 11(ion transport), GO:00550 85(transm embrane transport)	GO:00160 20(membr ane),GO: 0016021(i ntegral compone nt of membran e)	GO:0022857(tra nsmembrane transporter activity),GO:001 5377(cation:chlo ride symporter activity)	K14429 SLC12A9, CCC6; solute carrier family 12 (potassium/c hloride transporters), member 9	-	KOG2083 Hs4 506975 Na+/K+ symporter	RKP21424.1 hypothetical protein ROZALSC1DR AFT_27160 [Rozella allomycis CSF55]	Solute carrier family 12 member 2 OS=Homo sapiens OX=9606 GN=SLC12A2 PE=1 SV=1
A1718	-	-	-	-	-	-	-	-

A1719	GO:0006468(protein phosphorylation),GO:0007165(signal transduction)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0667[Hs1386209 Dual-specificity tyrosine-phosphorylation regulated kinase	-	Homeodomain-interacting protein kinase 3 OS=Homo sapiens OX=9606 GN=HIPK3 PE=1 SV=1
A1720	-	-	GO:0005515(protein binding)	K04555 UBE2G2, UBC7; ubiquitin-conjugating enzyme E2 G2 [EC:2.3.2.23]	map04141 Protein processing in endoplasmic reticulum;map04120 Ubiquitin mediated proteolysis;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease	KOG0426[Hs14780721 Ubiquitin-protein ligase	KAG0233236.1 Ubiquitin-conjugating enzyme E2 G2 [Actinomortierella wolffii]	Ubiquitin-conjugating enzyme E2 G2 OS=Bos taurus OX=9913 GN=UBE2G2 PE=2 SV=1
A1721	GO:0006352(DNA-templated transcription, initiation),GO:0070897(transcription preinitiation complex assembly),GO:0006383(transcription by RNA polymerase III)	GO:0000126(transcription factor TFIIIB complex)	GO:0017025(TBP-class protein binding),GO:0000995(RNA polymerase III general transcription initiation factor activity)	K15196 BRF1, GTF3B; transcription factor IIIB 90 kDa subunit	-	KOG1598[Hs22035556 Transcription initiation factor TFIIIB, Brf1 subunit	PJF19050.1 Subunit Brf1 of transcription factor TFIIIB complex [Paramicrosporidium saccamoebae]	Transcription factor IIIB 90 kDa subunit OS=Mus musculus OX=10090 GN=Brf1 PE=1 SV=1
A1722	GO:0006561(proline biosynthetic process)	-	GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor),GO:0016491(oxidoreductase activity),GO:0004350(glutamate-5-semialdehyde dehydrogenase activity)	K00147 proA; glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41]	map01110 Biosynthesis of secondary metabolites;map00332 Carbapenem biosynthesis;map00330 Arginine and proline metabolism;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways	-	XP_025174663.1 glutamate-5-semialdehyde dehydrogenase [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Gamma-glutamyl phosphate reductase OS=Pelotomaculum thermopropionicum (strain DSM 13744 / JCM 10971 / Si) OX=370438 GN=proA PE=3 SV=1
A1723	-	-	-	-	-	-	-	-

A1724	GO:0006635(fatty acid beta-oxidation),GO:0006631(fatty acid metabolic process)	GO:0005777(peroxisome)	GO:0003997(acyl-CoA oxidase activity),GO:0071949(FAD binding),GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding)	K00232 E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00410 beta-Alanine metabolism;map03320 PPAR signaling pathway;map04024 cAMP signaling pathway;map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00640 Propanoate metabolism;map01040 Biosynthesis of unsaturated fatty acids;map04936 Alcoholic liver disease;map00592 alpha-Linolenic acid metabolism;map	KOG0136 Hs4757712 Acyl-CoA oxidase	XP_016607254.1 hypothetical protein SPPG_05470 [Spizellomyces punctatus DAOM BR117]	Peroxisomal acyl-coenzyme A oxidase 1 OS=Cavia porcellus OX=10141 GN=ACOX1 PE=2 SV=1
A1725	-	-	-	-	-	-	RCI06979.1 hypothetical protein CU098_013918 [Rhizopus stolonifer]	Vacuolar membrane protein YPL162C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPL162C PE=1 SV=1
A1726	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K09569 FKBP2; FK506-binding protein 2 [EC:5.2.1.8]	-	KOG0549 Hs17149842 FKBP-type peptidyl-prolyl cis-trans isomerase	KAE8210813.1 hypothetical protein CF327_g5367 [Tilletia walkeri]	Macrophage infectivity potentiator OS=Trypanosoma cruzi OX=5693 GN=MIP PE=1 SV=1
A1727	-	-	-	-	-	-	-	-
A1728	GO:0006668(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004713(protein tyrosine kinase activity)	K21157 SAK1; SNF1-activating kinase 1 [EC:2.7.11.1]	map04138 Autophagy - yeast	KOG0197 7292519 Tyrosine kinases	RKP21201.1 kinase-like protein [Rozella allomyces CSF55]	Tyrosine-protein kinase Src64B OS=Drosophila melanogaster OX=7227 GN=Src64B PE=1 SV=3
A1729	-	-	GO:0003779(actin binding)	-	-	-	KAG0659039.1 hypothetical protein C6P46_005335 [Rhodotorula mucilaginosa]	Coactosin OS=Dictyostelium discoideum OX=44689 GN=coaA PE=1 SV=1
A1730	GO:0006668(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K11226 STE7; mitogen-activated protein kinase kinase [EC:2.7.12.2]	map04011 MAPK signaling pathway - yeast	KOG0581 At4g26070 Mitogen-activated protein kinase kinase (MAP2K)	TPX68515.1 hypothetical protein SpCBS45565_g03055 [Spizellomyces sp. 'palustris']	Mitogen-activated protein kinase kinase 1 OS=Arabidopsis thaliana OX=3702 GN=MKK1 PE=1 SV=2
A1731	-	-	-	-	-	KOG1498 Hs4506221 26S proteasome regulatory complex, subunit RPN5/PSMD12	ORY01231.1 PCI-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	26S proteasome non-ATPase regulatory subunit 12 OS=Pongo abelii OX=9601 GN=PSMD12 PE=2 SV=3
A1732	-	-	GO:0008289(lipid binding)	-	-	-	-	-
A1733	-	-	-	-	-	-	-	-
A1734	-	-	GO:0005515(protein binding)	-	-	-	-	Tetrapeptide repeat protein 16 OS=Macaca fascicularis OX=9541 GN=TTC16 PE=2 SV=1

A1735	GO:007248(ammonium transmembrane transport)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 CE27655 Ammonia permease	KAF9137593.1 hypothetical protein BGX30_010076 [Mortierella sp. GBA39]	Putative ammonium transporter sll0108 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=sll0108 PE=3 SV=1
A1736	GO:0007030(Golgi organization)	-	-	-	-	KOG4677 Hs4826748 Golgi integral membrane protein	-	Golgin-84 OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0744400 PE=2 SV=1
A1737	GO:0003352(regulation of cilium movement)	-	-	-	-	-	TPX53932.1 hypothetical protein PhCBS80983_g06108 [Powellomyces hirtus]	Cilia- and flagella-associated protein 298-B OS=Xenopus laevis OX=8355 GN=cfap298-b PE=3 SV=1
A1738	-	-	-	-	-	-	-	-
A1739	-	-	GO:0047793(cycloecalenol cycloisomerase activity)	-	-	-	XP_033455321.1 uncharacterized protein K489DRAFT_385067 [Dissoconium aciculare CBS 342.82]	Cycloecalenol cycloisomerase OS=Arabidopsis thaliana OX=3702 GN=CPI1 PE=2 SV=1
A1740	-	-	GO:0016872(intramolecular lyase activity)	-	-	-	-	-
A1741	-	-	-	-	-	-	-	-
A1742	-	-	-	-	-	-	-	-
A1743	GO:0000398(mRNA splicing, via spliceosome)	-	GO:0005515(protein binding)	-	-	KOG0504 7304080 FOG: Ankyrin repeat	KAG2176591.1 hypothetical protein INT44_007255 [Umbelopsis vinacea]	Nuclear distribution protein PAC1 OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) OX=663331 GN=PAC1 PE=3 SV=1
A1744	-	-	-	K15109 SLC25A20_29, CACT, CACL, CRC1; solute carrier family 25 (mitochondrial carnitine/acyl carnitine transporter), member 20/29	map04714 Thermogenesis	KOG0758 Hs4557403 Mitochondrial carnitine-acylcarnitine carrier protein	EPZ34510.1 Mitochondrial substrate/solute carrier domain-containing protein [Rozella allomyces CSF55]	Mitochondrial carnitine/acylcarnitine carrier protein OS=Rattus norvegicus OX=10116 GN=Slc25a20 PE=1 SV=1
A1745	GO:0007034(vacuolar transport)	-	-	K12194 CHMP4A_B, SNF7, VPS32A_B; charged multivesicular body protein 4A/B	map04144 Endocytosis;map03250 Viral life cycle - HIV-1;map04217 Necroptosis	KOG1656 At4g29160 Protein involved in glucose derepression and pre-vacuolar endosome protein sorting	XP_006680691.1 uncharacterized protein BATDEDRAFT_26522 [Batrachochytrium dendrobatidis JAM81]	Vacuolar protein sorting-associated protein 32 homolog 2 OS=Arabidopsis thaliana OX=3702 GN=VPS32.2 PE=1 SV=1
A1746	-	-	GO:0005509(calcium ion binding);GO:0017110(nucleoside-diphosphatase activity)	-	-	KOG4494 Hs20270339 Cell surface ATP diphosphohydrolase Apyrase	-	Soluble calcium-activated nucleotidase 1 OS=Mus musculus OX=10090 GN=Cant1 PE=2 SV=1
A1747	-	-	-	-	-	-	-	-

A1748	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0005515(protein binding)	K12196 VPS4; vacuolar protein-sorting-associated protein 4	map04144 Endocytosis;map03250 Viral life cycle - HIV-1;map04217 Necroptosis	KOG0738 At2g34560 AAA+-type ATPase	XP_031027255.1 uncharacterized protein SmJEL517_g01070 [Synchytrium microbalum]	Katanin p60 ATPase-containing subunit A-like 2 OS=Xenopus tropicalis OX=8364 GN=katnal2 PE=2 SV=1
A1749	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0619 7300644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A1750	-	-	GO:0015035(protein-disulfide reductase activity)	-	-	-	KAG1317554.1 hypothetical protein G6F63_015623 [Rhizopus oryzae]	Uncharacterized protein YuxK OS=Bacillus subtilis (strain 168) OX=224308 GN=yuxK PE=3 SV=1
A1751	-	-	-	-	-	-	-	Protein dispatched homolog 1 OS=Danio rerio OX=7955 GN=disp1
A1752	-	GO:0016021(integral component of membrane)	-	-	-	KOG3664 7296658 Predicted patched transmembrane receptor	-	Protein dispatched homolog 1 OS=Danio rerio OX=7955 GN=disp1 PE=2 SV=1
A1753	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	TPX57928.1 hypothetical protein PhCBS80983_g03512 [Powellomyces hirtus]	Riboflavin transporter RfnT OS=Brucella anthropi (strain ATCC 49188 / DSM 6882 / CCUG 24695 / JCM 21032 / LMG 3331 / NBRC 15819 / NCTC 12168 / Alc 37) OX=439375 GN=rfnT PE=1 SV=1
A1754	GO:0006508(proteolysis)	-	GO:0004222(metalloendopeptidase activity),GO:0008237(metalloproteinase activity)	K01415 ECE; endothelin-converting enzyme [EC:3.4.24.71]	-	KOG3624 Hs4503443 M13 family peptidase	ORY45062.1 zincin [Rhizoclostium globosum]	Neutral endopeptidase OS=Lactococcus lactis subsp. lactis (strain IL1403) OX=272623 GN=pepO PE=1 SV=3
A1755	GO:0016255(attachment of GPI anchor to protein)	GO:0042765(GPI-anchor transamidase complex)	-	K05291 PIGS; GPI-anchor transamidase subunit S	map00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis;map01100 Metabolic pathways	-	KAG2187653.1 hypothetical protein INT44_005343 [Umbelopsis vinacea]	GPI transamidase component PIG-S OS=Bos taurus OX=9913 GN=PIGS PE=2 SV=3
A1756	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs4502557 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KAG4090790.1 Pkinase-domain-containing protein [Neocallimastix sp. JGI-2020a]	Calcium/calmodulin-dependent protein kinase type IV OS=Homo sapiens OX=9606 GN=CAMK4 PE=1 SV=1
A1757	-	-	-	K00681 ggt; gamma-glutamyltranspeptidase / glutathione hydrolase [EC:2.3.2.2 3.4.19.13]	map00460 Cyanoamino acid metabolism;map00480 Glutathione metabolism;map00430 Taurine and hypotaurine metabolism;map01100 Metabolic pathways	KOG2410 At4g29210 Gamma-glutamyltransferase	KXN74495.1 gamma-glutamyltranspeptidase [Conidiobolus coronatus NRRL 28638]	Glutathione hydrolase-like YwrD proenzyme OS=Bacillus subtilis (strain 168) OX=224308 GN=ywrD PE=1 SV=1

A1758	-	-	-	-	-	-	-	-
A1759	GO:0006072(glycerol-3-phosphate metabolic process), GO:0005975(carbohydrate metabolic process)	-	GO:0004370(glycerol kinase activity), GO:0016773(phosphotransferase activity, alcohol group as acceptor), GO:0016301(kinase activity)	-	-	KOG2517 At1g80460 Ribulose kinase and related carbohydrate kinases	KZM27614.1 hypothetical protein ST47_g1322 [Ascochyta rabiei]	Glycerol kinase OS=Brucella anthropi (strain ATCC 49188 / DSM 6882 / CCUG 24695 / JCM 21032 / LMG 3331 / NBRC 15819 / NCTC 12168 / Alc 37) OX=439375 GN=glpK PE=3 SV=1
A1760	-	-	GO:0016301(kinase activity)	K04718 SPHK; sphingosine kinase [EC:2.7.1.91]	map04020 Calcium signaling pathway; map04071 Sphingolipid signaling pathway; map04072 Phospholipase D signaling pathway; map00600 Sphingolipid metabolism; map04666 Fc gamma R-mediated phagocytosis; map04371 Apelin signaling pathway; map04370 VEGF signaling pathway; map05152 Tuberculosis; map01100 Metabolic pathways	KOG1116 HsM11464967 Sphingosine kinase, involved in sphingolipid metabolism	XP_033404065.1 sphingoid long chain base kinase 4 [Arthroderma uncinatum]	Sphingosine kinase 1 OS=Arabidopsis thaliana OX=3702 GN=SPHK1 PE=1 SV=1
A1761	-	-	-	-	-	-	-	-
A1762	GO:0006644(phospholipid metabolic process)	-	-	K18693 DPP1, DPPL, PLPP4_5; diacylglycerol diphosphate phosphatase / phosphatidate phosphatase [EC:3.6.1.75 3.1.3.4]	map01110 Biosynthesis of secondary metabolites; map00564 Glycerophospholipid metabolism; map00561 Glycerolipid metabolism	KOG3030 At3g18220 Lipid phosphate phosphatase and related enzymes of the PAP2 family	XP_456680.2 DEHA2A08052p [Debaryomyces hansenii CBS767]	Probable lipid phosphate phosphatase 4 OS=Arabidopsis thaliana OX=3702 GN=LPP4 PE=2 SV=1
A1763	-	-	GO:0004672(protein kinase activity)	K00898 PDK2_3_4; pyruvate dehydrogenase kinase 2/3/4 [EC:2.7.11.2]	map05415 Diabetic cardiomyopathy	KOG0787 At3g06483 Dehydrogenase kinase	XP_035320625.1 uncharacterized protein GMORB2_7566 [Geosmithia morbida]	[Pyruvate dehydrogenase (acetyl-transferring)] kinase, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=PDK PE=1 SV=1
A1764	-	-	GO:0016409(palmitoyltransferase activity)	-	-	KOG1311 Hs21361910 DHHC-type Zn-finger proteins	RLV94261.1 Palmitoyltransferase ERF2 [Spathaspora sp. JA1]	Putative ZDHHC-type palmitoyltransferase 7 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0276017 PE=2 SV=1
A1765	GO:0006298(mismatch repair)	-	GO:0005524(ATP binding), GO:0030983(mismatched DNA binding)	K08736 MSH3; DNA mismatch repair protein MSH3	map01524 Platinum drug resistance; map05210 Colorectal cancer; map05200 Pathways in cancer; map03430 Mismatch repair	KOG0218 Hs4505249 Mismatch repair MSH3	KUM55520.1 hypothetical protein ACN42_g11743 [Penicillium freii]	DNA mismatch repair protein msh3 OS=Aspergillus fumigatus (strain CBS 144.89 / FGSC A1163 / CEA10) OX=451804 GN=msh3 PE=3 SV=1

A1766	GO:0015986(ATP synthesis coupled proton transport)	GO:0000276(mitochondrial proton-transporting ATP synthase complex, coupling factor F(o))	GO:0015078(proton transmembrane transporter activity)	-	-	KOG3366 At3g52300 Mitochondrial F1F0-ATP synthase, subunit d/ATP7	-	ATP synthase subunit d, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At3g52300 PE=1 SV=3
A1767	-	-	GO:0009777(RNA polymerase II transcription regulatory region sequence-specific DNA binding),GO:0032422(purine-rich negative regulatory element binding)	-	-	KOG3074 At2g32080 Transcriptional regulator of the PUR family, single-stranded-DNA-binding	-	Transcription factor Pur-alpha 1 OS=Arabidopsis thaliana OX=3702 GN=PURA1 PE=1 SV=2
A1768	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity),GO:0004674(protein serine/threonine kinase activity)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0598 CE14798 Ribosomal protein S6 kinase and related proteins	RKP23074.1 kinase-like domain-containing protein [Syncephalis pseudoplumigaleata]	Serine/threonine-protein kinase sgk-1 OS=Caenorhabditis elegans OX=6239 GN=sgk-1 PE=1 SV=1
A1769	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07943 ARL2; ADP-ribosylation factor-like protein 2	-	KOG0074 CE15872 GTP-binding ADP-ribosylation factor-like protein ARL3	KWU47289.1 GTP-binding protein [Rhodotorula sp. JG-1b]	ADP-ribosylation factor-like protein 13B OS=Chlamydomonas reinhardtii OX=3055 GN=ARL13 PE=1 SV=1
A1770	-	GO:0016020(membrane),GO:0016021(integral component of membrane)	-	K15289 SLC35F5; solute carrier family 35, member F5	-	KOG2765 At3g07080 Predicted membrane protein	CDS10060.1 hypothetical protein LRAMOSA02737 [Lichtheimia ramosa]	Uncharacterized transporter C405.03c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC405.03c PE=3 SV=1
A1771	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG4022 Z7294987 Dihydropteridine reductase DHPR/QDPR	KAG0168305.1 hypothetical protein DFQ30_004952 [Apophysomyces sp. BC1015]	Dihydropteridine reductase OS=Rattus norvegicus OX=10116 GN=Qdpr PE=1 SV=1
A1772	-	-	-	-	-	-	-	-
A1773	-	-	-	-	-	KOG0048 At4g18770 Transcription factor, Myb superfamily	ORY70773.1 C-Myb R2r3, partial [Leucosporidium creatinivorum]	Transcription factor MYB98 OS=Arabidopsis thaliana OX=3702 GN=MYB98 PE=2 SV=1
A1774	-	-	-	-	-	-	-	GREB1-like protein OS=Mus musculus OX=10090 GN=Greb1 PE=2
A1775	-	-	-	-	-	-	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A1776	-	-	-	-	-	-	-	-
A1777	-	-	-	-	-	KOG0048 At1g73410 Transcription factor, Myb superfamily	KLO20426.1 hypothetical protein SCHPADRAFT_5966 [Schizopora paradoxa]	Transcription factor MYB118 OS=Arabidopsis thaliana OX=3702 GN=MYB118 PE=2 SV=1

A1778	GO:0000338(protein deneddylation)	GO:0008180(COP9 signalosome)	GO:0005515(protein binding),GO:0008233(peptidase activity),GO:0008237(metalloproteinase activity)	K12179 COPS6, CSN6; COP9 signalosome complex subunit 6	-	KOG3050[Hs5803096 COP9 signalosome, subunit CSN6	ORY51857.1 hypothetical protein BCR33DRAFT_675637 [Rhizoclostium globosum]	COP9 signalosome complex subunit 6 OS=Dictyostelium discoideum OX=44689 GN=csn6 PE=1 SV=1
A1779	GO:0006289(nucleotide-excision repair),GO:0045737(positive regulation of cyclin-dependent protein serine/threonine kinase activity)	GO:0005675(transcription factor TFIIF holo complex)	GO:0061575(cyclin-dependent protein serine/threonine kinase activator activity)	K10842 MNAT1; CDK-activating kinase assembly factor MAT1	map03420 Nucleotide excision repair;map03022 Basal transcription factors	-	XP_020070625.1 subunit of TFIIF [Cyberlindnera jadinii NRRL Y-1542]	RNA polymerase II transcription factor B subunit 3 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / BCRC 21394 / JCM 1990 / NBRC 0083 / IGC 2968) OX=284592 GN=TFB3 PE=3 SV=2
A1780	-	-	GO:0003824(catalytic activity)	K02805 wecE; rffA; dTDP-4-aminoo-4,6-dideoxygalactose transaminase [EC:2.6.1.59]	map01250 Biosynthesis of nucleotide sugars;map00541 O-Antigen nucleotide sugar biosynthesis;map01100 Metabolic pathways	-	TAQ84944.1 hypothetical protein B7494_g6732 [Chlorociboria aeruginascens]	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase OS=Pseudomonas syringae pv. syringae (strain B728a) OX=205918 GN=arnB PE=3 SV=1
A1781	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1782	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A1783	-	-	-	-	-	-	KIM52504.1 hypothetical protein SCLCIDRAFT_1223705 [Scleroderma citrinum Foug A]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A1784	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A1785	-	GO:0005929(cilium)	-	-	-	-	-	Cilia- and flagella-associated protein 157 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP157 PE=1 SV=1
A1786	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471[Hs4506867 Phosphatidylinositol transfer protein SEC14 and related proteins	CUS12340.1 unnamed protein product [Tuber aestivum]	Protein real-time OS=Aedes aegypti OX=7159 GN=retm PE=3 SV=1
A1787	-	-	-	-	-	-	-	-
A1788	-	-	-	-	-	-	-	-
A1789	-	-	-	K10798 PARP2_3_4; poly [ADP-ribose] polymerase 2/3/4 [EC:2.4.2.30]	map04210 Apoptosis;map04212 Longevity regulating pathway - worm;map03410 Base excision repair	-	RIA89135.1 arsenite methyltransferase [Glomus cerebriiforme]	Arsenite methyltransferase OS=Pseudomonas alcaligenes (strain ATCC 14909 / DSM 50342 / JCM 20561 / NBRC 14159 / NCIMB 9945 / NCTC 10367 / 1577) OX=1215092 GN=arsM PE=1 SV=1

A1790	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 Hs18561812 Uncharacterized conserved protein	SPQ26039.1 a016cd25-6611-415c-a03e-0e2c81ace22c [Thermophilus avoides terrestris]	Probable magnesium transporter NIPA7 OS=Arabidopsis thaliana OX=3702 GN=At4g38730 PE=2 SV=1
A1791	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2156 Hs7661970 Tubulin-tyrosine ligase-related protein	XP_016608407.1 hypothetical protein SPPG_04692 [Spizellomyces punctatus DAOM BR117]	Tubulin monoglutamylase TTL4 OS=Homo sapiens OX=9606 GN=TTL4 PE=1 SV=2
A1792	-	-	GO:0004674(protein serine/threonine kinase activity),GO:0005515(protein binding),GO:0044877(protein-containing complex binding),GO:0016301(kinase activity)	K07203 MTOR, FRAP, TOR; serine/threonine-protein kinase mTOR [EC:2.7.11.1]	map04361 Axon regeneration;map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map04140 Autophagy - animal;map05131 Shigellosis;map04211 Longevity regulating pathway;map04212 Longevity regulating pathway - worm;map04213 Longevity regulating pathway - multiple species;map04218 Cellular senescence;map04072 Phospholipase D signaling	-	TPX48075.1 hypothetical protein SeLEV6574_g02255 [Synchytrium endobioticum]	Serine/threonine-protein kinase tor OS=Dictyostelium discoideum OX=44689 GN=tor PE=1 SV=1
A1793	-	-	-	-	-	-	PRQ69998.1 Armadillo-type fold [Rhodotorula toruloides]	-
A1794	-	-	-	-	-	-	KAG1716737.1 hypothetical protein ID866_431 [Astraeus odoratus]	Methylthioribose kinase OS=Arabidopsis thaliana OX=3702 GN=MTK PE=1 SV=1
A1795	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0005515(protein binding),GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	KOG1971 Hs4557837 Lysyl hydroxylase	RUP06760.1 hypothetical protein BC936DRAFT_140269 [Jimgerdemia flammicorona]	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Rattus norvegicus OX=10116 GN=Plod3 PE=1 SV=1

A1796	GO:0006784(heme A biosynthetic process)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0016653(oxidoreductase activity, acting on NAD(P)H, heme protein as acceptor)	K02259 COX15, ctaA; heme a synthase [EC:1.17.99.9]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map04714 Thermogenesis;map00190 Oxidative phosphorylation;map02020 Two-component system;map01100 Metabolic pathways	KOG2725[At5g56090 Cytochrome oxidase assembly factor COX15	KAG0042725.1 Cytochrome c oxidase assembly protein cox15 [Gryganskiella cystojenkini]	Cytochrome c oxidase assembly protein COX15 OS=Arabidopsis thaliana OX=3702 GN=COX15 PE=2 SV=1
A1797	-	GO:0030014(CCR4-NOT complex)	GO:0004535(poly(A)-specific ribonuclease activity),GO:0003676(nucleic acid binding)	K12581 CNOT7.8, CAF1, POP2; CCR4-NOT transcription complex subunit 7/8	map03018 RNA degradation	KOG0304[Hs21361073 mRNA deadenylase subunit	TPX39321.1 hypothetical protein SeLEV6574.g07301 [Synchytrium endobioticum]	CCR4-NOT transcription complex subunit 7 OS=Bos taurus OX=9913 GN=CNOT7 PE=2 SV=1
A1798	-	-	GO:0016746(acyltransferase activity)	-	-	-	-	-
A1799	-	-	-	-	-	-	-	-
A1800	-	-	-	-	-	-	-	-
A1801	-	-	-	-	-	-	-	-
A1802	-	-	-	K01426 E3.5.1.4, amiE; amidase [EC:3.5.1.4]	map00330 Arginine and proline metabolism;map01120 Microbial metabolism in diverse environments;map00643 Styrene degradation;map00627 Aminobenzoate degradation;map00360 Phenylalanine metabolism;map00380 Tryptophan metabolism;map01100 Metabolic pathways	KOG1212[7303473 Amidases	ORX70476.1 amidase signature enzyme [Linderina pennisporea]	Fatty-acid amide hydrolase 2-B OS=Danio rerio OX=7955 GN=faah2b PE=2 SV=1
A1803	-	-	GO:0016491(oxidoreductase activity)	K00326 CYB5R; cytochrome-b5 reductase [EC:1.6.2.2]	map00520 Amino sugar and nucleotide sugar metabolism	KOG0534[YIL043c NADH-cytochrome b-5 reductase	PLW47181.1 hypothetical protein PCASD_02388 [Puccinia coronata f. sp. avenae]	NADH-cytochrome b5 reductase 1 OS=Dictyostelium discoideum OX=44689 GN=cyb5r1 PE=3 SV=1

A1804	GO:0045454(cell redox homeostasis)	-	GO:0004148(dihydrolipoyl dehydrogenase activity),GO:0050660(flavin adenine dinucleotide binding),GO:0016491(oxidoreductase activity),GO:0016668(oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor)	K00382 DLD, lpd, pdhD; dihydrolipoyl dehydrogenase [EC:1.8.1.4]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00020 Citrate cycle (TCA cycle);map00280 Valine, leucine and isoleucine degradation;map00260 Glycine, serine and	KOG1335[At1g48030 Dihydrolipoyl dehydrogenase	TPX55737.1 dihydrolipoyl dehydrogenase [Powellomyces hirtus]	Dihydrolipoyl dehydrogenase 1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=LPD1 PE=1 SV=2
A1805	GO:0006729(tetrahydrobiopterin biosynthetic process)	-	GO:0008124(4-alpha-hydroxytetrahydrobiopterin dehydratase activity)	-	-	-	-	Putative pterin-4-alpha-carbinolamine dehydratase 2 OS=Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) OX=251221 GN=gs1645 PE=3 SV=1
A1806	-	-	-	-	-	KOG1981[Hs8924256 SOK1 kinase belonging to the STE20/SPS1/GC kinase family	KXS12057.1 Tcp11-domain-containing protein [Gonapodya prolifera JEL478]	T-complex protein 11-like X-linked protein 2 OS=Homo sapiens OX=9606 GN=TCP11X2 PE=3 SV=2
A1807	-	-	-	-	-	-	-	-
A1808	-	-	-	-	-	-	-	-
A1809	-	-	-	-	-	-	XP_037211063.1 trypsin inhibitor like cysteine rich domain protein [Fusarium tjaetaba]	von Willebrand factor OS=Mus musculus OX=10090 GN=Vwf PE=1 SV=2
A1810	-	-	-	-	-	-	-	-
A1811	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity)	-	-	-	KAG0196171.1 hypothetical protein BGX28_010466 [Mortierella sp. GBA30]	-
A1812	-	-	-	-	-	-	-	-
A1813	-	-	GO:0005524(ATP binding),GO:0046872(metal ion binding)	-	-	-	TLD31313.1 hypothetical protein PspLS_01707 [Pyricularia sp. CBS 133598]	Carnosine synthase 1 OS=Gallus gallus OX=9031 GN=CARNS1 PE=1 SV=1
A1814	-	-	-	-	-	KOG1176[At1g65060 Acyl-CoA synthetase	XP_031027085.1 uncharacterized protein SmJEL517_g01067 [Synchytrium microbalum]	Steroid-24-oyl-CoA synthetase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=casG PE=1 SV=1

A1815	-	-	-	-	-	KOG1177 CE20812 Long chain fatty acid acyl-CoA ligase	XP_031023411.1 uncharacterized protein SmJEL517_g04694 [Synchytrium microbalum]	Steroid-24-oyl-CoA synthetase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=casG PE=1 SV=1
A1816	-	-	-	-	-	KOG1176 At4g05160 Acyl-CoA synthetase	XP_031027085.1 uncharacterized protein SmJEL517_g01067 [Synchytrium microbalum]	Steroid-24-oyl-CoA synthetase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=casG PE=1 SV=1
A1817	GO:000956(nuclear-transcribed mRNA catabolic process)	-	GO:0008409(5'-3' exonuclease activity),GO:0003676(nucleic acid binding),GO:0004527(exonuclease activity)	K12618 XRN1, SEP1, KEM1; 5'-3' exoribonuclease 1 [EC:3.1.13.-]	map03018 RNA degradation;map03008 Ribosome biogenesis in eukaryotes	-	KAG2221227.1 hypothetical protein INT45_013938, partial [Mucor circinatus]	5'-3' exoribonuclease 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=exo2 PE=1 SV=1
A1818	-	-	-	-	-	KOG1177 CE20812 Long chain fatty acid acyl-CoA ligase	XP_031027085.1 uncharacterized protein SmJEL517_g01067 [Synchytrium microbalum]	Steroid-24-oyl-CoA synthetase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=casG PE=1 SV=1
A1819	-	-	-	-	-	KOG1176 At1g65060 Acyl-CoA synthetase	XP_031027085.1 uncharacterized protein SmJEL517_g01067 [Synchytrium microbalum]	Steroid-24-oyl-CoA synthetase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=casG PE=1 SV=1
A1820	GO:0008654(phospholipid biosynthetic process)	GO:0016020(membrane)	GO:0016780(phosphotransferase activity, for other substituted phosphate groups)	-	-	KOG3240 Hs5453906 Phosphatidylinositol synthase	RKO99836.1 hypothetical protein CXG81DRAFT_3890, partial [Caulochytrium protostelioides]	CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Mus musculus OX=10090 GN=Cdipt PE=1 SV=1
A1821	-	-	-	-	-	-	-	-
A1822	-	-	-	-	-	-	-	-
A1823	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1824	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1543 At2g27420 Cysteine proteinase Cathepsin L	KFH62689.1 hypothetical protein MVEG_12081 [Podilla verticillata NRRL 6337]	Cysteine proteinase 3 OS=Dictyostelium discoideum OX=44689 GN=cprC PE=3 SV=2
A1825	-	-	-	-	-	-	-	-
A1826	GO:0045892(negative regulation of transcription, DNA-templated)	-	GO:0003714(transcription corepressor activity)	K26244 PHF12, RCO1; transcriptional regulatory protein PHF12/RCO1	-	-	XP_007729944.1 hypothetical protein A1O3_01610 [Capronia epimyces CBS 606.96]	Chromodomain-helicase-DNA-binding protein 5 OS=Mus musculus OX=10090 GN=Chd5 PE=1 SV=1

A1827	GO:0001522(pseudouridine synthesis), GO:0009451(RNA modification)	-	GO:0003723(RNA binding), GO:0009982(pseudouridine synthase activity)	-	-	KOG2364 Hs21389307 Predicted pseudouridylate synthase	ORX92575.1 pseudouridylate synthase-like protein 10 [Basidiobolus meristosporus CBS 931.73]	tRNA pseudouridine synthase Pus10 OS=Homo sapiens OX=9606 GN=PUS10 PE=1 SV=1
A1828	-	-	-	K17973 NAA25, MDM20; N-terminal acetyltransferase B complex non-catalytic subunit	-	KOG2053 7300581 Mitochondrial inheritance and actin cytoskeleton organization protein	RIA93418.1 N-acetyltransferase B complex non-catalytic subunit-domain-containing protein [Glomus cerebriforme]	Phagocyte signaling-impaired protein OS=Anopheles gambiae OX=7165 GN=psidin PE=3 SV=5
A1829	-	-	GO:0005515(protein binding)	K13137 STRAP, UNRIP; serine-threonine kinase receptor-associated protein	-	KOG0278 At3g15610 Serine/threonine kinase receptor-associated protein	KAG0210577.1 hypothetical protein BGX28_009213 [Mortierella sp. GBA30]	Serine-threonine kinase receptor-associated protein OS=Dictyostelium discoideum OX=44689 GN=strap PE=3 SV=1
A1830	-	-	-	K11153 RDH12; retinol dehydrogenase 12 [EC:1.1.1.300]	map01240 Biosynthesis of cofactors; map00830 Retinol metabolism; map01100 Metabolic pathways	KOG1208 Hs7706523 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	RHZ71731.1 hypothetical protein Glove_255g7 [Diversispora epigaea]	WW domain-containing oxidoreductase OS=Danio rerio OX=7955 GN=wwox PE=2 SV=1
A1831	-	-	-	-	-	-	-	-
A1832	-	-	-	-	-	-	-	-
A1833	-	-	-	-	-	KOG2502 Hs19923167 Tub family proteins	EXX51827.1 hypothetical protein RirG_258260 [Rhizophagus irregularis DAOM 197198w]	Tubby protein homolog OS=Homo sapiens OX=9606 GN=TUB PE=1 SV=1
A1834	-	-	-	-	-	-	-	-
A1835	GO:0006821(chloride transport), GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005247(voltage-gated chloride channel activity)	K05012 CLCN3_4_5; chloride channel 3/4/5	map04613 Neutrophil extracellular trap formation	KOG0476 Hs5597006 Cl-channel CLC-2 and related proteins (CLC superfamily)	EZF33371.1 hypothetical protein H101_03058 [Trichophyton interdigitale H6]	Chloride channel protein 2 OS=Oryctolagus cuniculus OX=9986 GN=CLCN2 PE=2 SV=1
A1836	-	-	GO:0002161(aminoacyl-tRNA editing activity), GO:0000049(tRNA binding)	K15437 AIMP1, ARC1; aminoacyl-tRNA synthase complex-interacting multifunctional protein 1	-	KOG2241 CE06007_2 tRNA-binding protein	KAG4085405.1 YbaK/ProRS associated domain-containing protein [Neocallimastix sp. JGI-2020a]	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus OX=10090 GN=Aimp1 PE=1 SV=2
A1837	-	-	-	-	-	KOG1555 7297828_1 26S proteasome regulatory complex, subunit RPN11	-	MPN domain-containing protein OS=Mus musculus OX=10090 GN=Mpnd PE=1 SV=2

A1838	-	-	-	-	-	-	XP_016612431.1 hypothetical protein SPPG_00123 [Spizellomyces punctatus DAOM BR117]	-
A1839	-	-	-	-	-	-	-	-
A1840	-	-	-	-	-	-	-	-
A1841	-	-	-	-	-	-	-	-
A1842	-	-	GO:0005515(protein binding)	-	-	KOG1787 Hs2042385 Kinase A-anchor protein Neurobeachin and related BEACH and WD40 repeat proteins	EXX77184.1 Bph1p [Rhizophagus irregularis DAOM 197198w]	Neurobeachin-like protein 2 OS=Mus musculus OX=10090 GN=Nbeal2 PE=1 SV=2
A1843	GO:0008033(tRNA processing)	-	GO:0017150(tRNA dihydrouridine synthase activity),GO:0050660(flavin adenine dinucleotide binding)	K05544 DUS3; tRNA-dihydrouridine synthase 3 [EC:1.3.1.89]	-	KOG2333 At4g38890 Uncharacterized conserved protein	KAF9973903.1 tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like protein [Actinomyces rella ambigua]	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like OS=Oryza sativa subsp. japonica OX=39947 GN=Os04g0117600 PE=2 SV=2
A1844	-	-	GO:0005509(calcium ion binding)	-	-	KOG1012 At5g11100 Ca2+-dependent lipid-binding protein CLB1/vesicle protein vp115/Granophilin A, contains C2 domain	KNE58026.1 hypothetical protein AMAG_04852 [Allomyces macrogynus ATCC 38327]	Synaptotagmin-4 OS=Arabidopsis thaliana OX=3702 GN=SYT4 PE=2 SV=1
A1845	-	-	-	-	-	-	-	CBY1-interacting BAR domain-containing protein 1-A OS=Xenopus
A1846	-	-	-	-	-	-	-	-
A1847	GO:0007156(homophilic cell adhesion via plasma membrane adhesion molecules)	GO:0016020(membrane)	GO:0005509(calcium ion binding)	-	-	KOG3594 Hs17438356 FOG: Cadherin repeats	-	Protocadherin Fat 4 OS=Mus musculus OX=10090 GN=Fat4 PE=1 SV=2
A1848	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K16196 EIF2AK4; eukaryotic translation initiation factor 2-alpha kinase 4 [EC:2.7.11.1]	map04140 Autophagy - animal;map04138 Autophagy - yeast;map05160 Hepatitis C;map05162 Measles;map05168 Herpes simplex virus 1 infection	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAG0248455.1 hypothetical protein BG011_010259 [Mortierella polycephala]	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK1 OS=Oryza sativa subsp. indica OX=39946 GN=LECRK1 PE=1 SV=2
A1849	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	-	-

A1850	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K06641 CHEK2; serine/threonine-protein kinase CHEK2 [EC:2.7.11.1]	map04218 Cellular senescence;map04115 p53 signaling pathway;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG0587[Hs20544910.1 Traf2- and Nck-interacting kinase and related germinal center kinase (GCK) family protein kinases	KOS19551.1 putative serine/threonine-protein kinase [Escovopsis weberi]	Myosin-IIIa OS=Homo sapiens OX=9606 GN=MYO3A PE=1 SV=2
A1851	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A1852	-	-	-	-	-	-	KAF8273130.1 NADP+-dependent D-mannitol dehydrogenase [Lactarius quietus]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A1853	-	-	GO:0003824(catalytic activity)	-	-	KOG1075[CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A1854	GO:0006265(DNA topological change)	-	GO:0003677(DNA binding),GO:0003918(DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity),GO:0005524(ATP binding)	-	-	-	-	DNA topoisomerase 6 subunit B OS=Arabidopsis thaliana OX=3702 GN=TOP6B PE=1 SV=1
A1855	-	-	-	-	-	-	-	-
A1856	-	-	-	K10576 UBE2H, UBC8; ubiquitin-conjugating enzyme E2 H [EC:2.3.2.23]	map04120 Ubiquitin mediated proteolysis	KOG0416[At5g41340 Ubiquitin-protein ligase	RIA81522.1 ubiquitin-conjugating enzyme/RWD-like protein [Glomus cerebriiforme]	Ubiquitin-conjugating enzyme E2-23 kDa OS=Triticum aestivum OX=4565 GN=UBC4 PE=1 SV=1
A1857	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A1858	-	-	-	-	-	-	-	-
A1859	GO:0006364(rRNA processing)	-	GO:0019843(rRNA binding),GO:0042134(rRNA primary transcript binding)	K14846 RPF1; ribosome production factor 1	-	KOG2780[CE28332 Ribosome biogenesis protein RPF1, contains IMP4 domain	KNE59137.1 hypothetical protein AMAG_03473 [Allomyces macrogynus ATCC 38327]	Brix domain-containing protein F44G4.1 OS=Caenorhabditis elegans OX=6239 GN=F44G4.1 PE=4 SV=4
A1860	-	-	-	-	-	-	-	-

A1861	-	-	GO:0005524(ATP binding),GO:0046872(metal ion binding)	-	-	KOG0237 7297208_2 Glycinamide ribonucleotide synthetase (GARS)/Aminimidazole ribonucleotide synthetase (AIRS)	OCL12795.1 glutathione synthetase ATP-binding domain-like protein [Glonium stellatum]	Carnosine synthase 1 OS=Gallus gallus OX=9031 GN=CARNS1 PE=1 SV=1
A1862	-	-	GO:0035091(phosphatidylinositol binding)	-	-	-	-	-
A1863	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding),GO:0008270(zinc ion binding)	-	-	-	-	-
A1864	-	-	-	K18183 COX19; cytochrome c oxidase assembly protein subunit 19	map04714 Thermogenesis	KOG3477 At1g69750 Putative cytochrome c oxidase, subunit COX19	XP_025363734.1 hypothetical protein BDZ90DRAFT_206332, partial [Jaminaea rosea]	Cytochrome c oxidase assembly protein COX19 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=COX19 PE=3 SV=2
A1865	GO:0006729(tetrahydropterin biosynthetic process)	-	GO:0008124(4-alpha-hydroxytetrahydropterin dehydratase activity)	K01724 PCBD, phhB; 4a-hydroxytetrahydropterin dehydratase [EC:4.2.1.96]	map01100 Metabolic pathways;map00790 Folate biosynthesis	KOG4073 Hs14149825 Pterin carbinolamine dehydratase PCBD/dimerization cofactor of HNF1	ORY42202.1 transcriptional coactivator/pterin dehydratase [Rhizoclostium globosum]	Putative pterin-4- α -carbinolamine dehydratase OS=Brucella anthropi (strain ATCC 49188 / DSM 6882 / CCUG 24695 / JCM 21032 / LMG 3331 / NBRC 15819 / NCTC 12168 / Alc 37) OX=439375 GN=Oant_0094 PE=3 SV=1
A1866	-	-	-	-	-	-	-	-
A1867	-	-	-	-	-	KOG4254 Hs8923275 Phytoene desaturase	KAG4433279.1 hypothetical protein IFR05_011249 [Cadophora sp. M221]	All-trans-retinol 13,14-reductase OS=Danio rerio OX=7955 GN=retsat PE=1 SV=1
A1868	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY27051.1 TPR-like protein [Rhizoclostium globosum]	-
A1869	-	-	-	-	-	-	-	-
A1870	-	-	-	K07019 K07019; uncharacterized protein	-	KOG1838 At5g49950 Alpha/beta hydrolase	KAF7752801.1 hypothetical protein DSO57_021681 [Entomophthora muscae]	Phospholipase ABHD3 OS=Homo sapiens OX=9606 GN=ABHD3 PE=2 SV=2
A1871	-	-	-	-	-	KOG1575 At1g04690 Voltage-gated shaker-like K ⁺ channel, subunit beta/KCNAB	KAG0251692.1 hypothetical protein BG011_007444 [Mortierella polycephala]	Probable voltage-gated potassium channel subunit beta OS=Oryza sativa subsp. japonica OX=39947 GN=KOB1 PE=1 SV=2
A1872	-	-	-	-	-	-	-	-

A1873	-	-	-	K22696 EEF2KMT; protein- lysine N- methyltransfe rase EEF2KMT [EC:2.1.1.-]	-	KOG2497 CE 00292 Predicted methyltransfe rase	KAG0771584. 1 hypothetical protein G6F22_01635 5 [Rhizopus oryzae]	Putative uncharacterized protein DDB_G0277003 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0277003 PE=4 SV=2
A1874	GO:00091 66(nucleo tide catabolic process)	-	GO:0016787(hy drolase activity)	K01081 E3.1.3.5; 5'- nucleotidase [EC:3.1.3.5]	map00230 Purine metabolism;map 01110 Biosynthesis of secondary metabolites;map 00240 Pyrimidine metabolism;map 01232 Nucleotide metabolism;map 00760 Nicotinate and nicotinamide metabolism;map 01100 Metabolic pathways	KOG4419 730 3718 5' nucleotidase	ORY02418.1 Metallo- dependent phosphatase [Basidiobolus meristosporu s CBS 931.73]	Trifunctional nucleotide phosphoesterase protein YfkN OS=Bacillus subtilis (strain 168) OX=224308 GN=yfkN PE=1 SV=1
A1875	GO:00514 09(respon se to nitrosative stress)	-	GO:0016491(oxi doreductase activity),GO:000 8941(nitric oxide dioxygenase activity),GO:001 9825(oxygen binding),GO:002 0037(heme binding),GO:007 1949(FAD binding)	K05916 hmp, YHB1; nitric oxide dioxygenase [EC:1.14.12.1 7]	-	KOG3378 YG R234w Globins and related hemoprotein s	XP_01622232 7.1 hypothetical protein PV10_05377 [Exophiala mesophila]	Flavohemoprotein OS=Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) OX=243365 GN=hmp PE=3 SV=1
A1876	-	-	-	-	-	-	-	-
A1877	GO:00094 11(respon se to UV)	-	-	-	-	-	-	-
A1878	-	-	-	K14997 SLC38A11; solute carrier family 38 (sodium- coupled neutral amino acid transporter), member 11	-	KOG1304 At3 g11900 Amino acid transporters	OAL70691.1 amino acid transporter [Trichophyto n violaceum]	Amino acid transporter ANT1 OS=Arabidopsis thaliana OX=3702 GN=ANT1 PE=1 SV=1
A1879	-	-	GO:0008146(sulf otransferase activity)	-	-	KOG3703 Hs1 2007650 Heparan sulfate N- deacetylase/ N- sulfotransfera se	KAG1473248. 1 hypothetical protein G6F56_00105 9 [Rhizopus delemar]	Membrane-associated sulfotransferase kil1 OS=Dictyostelium discoideum OX=44689 GN=kil1 PE=3 SV=1
A1880	-	GO:00057 37(cytopl asm),GO: 0005852(eukaryotic translatio n initiation factor 3 complex)	GO:0003743(tran slation initiation factor activity)	K03250 EIF3E, INT6; translation initiation factor 3 subunit E	map05160 Hepatitis C	KOG2758 Hs4 503521 Translation initiation factor 3, subunit e (eIF-3e)	KAG0270153. 1 eukaryotic translation initiation factor 3 subunit E [Actinomortie rella ambigua]	Eukaryotic translation initiation factor 3 subunit E OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1 / QM 1276 / 107) OX=344612 GN=int6 PE=3 SV=1

A1881	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity);GO:0005524(ATP binding);GO:0008017(microtubule binding)	-	-	KOG4280[Hs6857804 Kinesin-like protein	RMY46902.1 hypothetical protein D0865_08995 [Hortaea werneckii]	Kinesin-like protein FLA10 OS=Chlamydomonas reinhardtii OX=3055 GN=FLA10 PE=1 SV=1
A1882	-	-	GO:0005515(protein binding)	-	-	-	-	-
A1883	GO:0006749(glutathione metabolic process)	-	GO:0050313(sulfur dioxygenase activity)	K01069 gloB, gloC, HAGH; hydroxyacylglutathione hydrolase [EC:3.1.2.6]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG0814[CE15664 Glyoxylase	ORY23475.1 putative ETHE1 protein [Rhizoclostium globosum]	Persulfide dioxygenase ETHE1, mitochondrial OS=Mus musculus OX=10090 GN=Ethe1 PE=1 SV=2
A1884	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02891 RP-L22e, RPL22; large subunit ribosomal protein L22e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3434[Hs4506613 60S ribosomal protein L22	KJ45645.1 hypothetical protein M422DRAFT_227339 [Sphaerobolus stellatus SS14]	Large ribosomal subunit protein eL22 OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=2
A1885	-	-	GO:0010181(FMN binding);GO:0016491(oxidoreductase activity)	K00354 E1.6.99.1; NADPH2 dehydrogenase [EC:1.6.99.1]	-	KOG0134[At1g76680 NADH:flavin oxidoreductase/12-oxophytodienate reductase	RKP26572.1 NADH:flavin oxidoreductase [Syncephalis pseudoplumigaleata]	N-ethylmaleimide reductase OS=Escherichia coli (strain K12) OX=83333 GN=nemA PE=1 SV=1
A1886	-	-	GO:0010181(FMN binding);GO:0016491(oxidoreductase activity)	-	-	KOG0134[At1g76680 NADH:flavin oxidoreductase/12-oxophytodienate reductase	ORZ02802.1 hypothetical protein BCR43DRAFT_449831 [Syncephalastrium racemosum]	N-ethylmaleimide reductase OS=Escherichia coli (strain K12) OX=83333 GN=nemA PE=1 SV=1
A1887	GO:0018193(peptidyl-amino acid modification)	-	GO:0005515(protein binding);GO:0004842(ubiquitin-protein transferase activity)	K10592 HUWE1, MULE, ARF-BP1, TOM1; E3 ubiquitin-protein ligase HUWE1 [EC:2.3.2.26]	map04120 Ubiquitin mediated proteolysis	KOG1426[Hs4557026 FOG:RCC1 domain	TKA55752.1 hypothetical protein B0A53_02888 [Rhodotorula sp. CCFE 5036]	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens OX=9606 GN=HERC1 PE=1 SV=2
A1888	-	-	GO:0016783(sulfurtransferase activity)	-	-	KOG1529[At1g79230 Mercaptopyruvate sulfurtransferase/thiosulfate sulfurtransferase	KAF9577050.1 hypothetical protein BGW38_00796 [Lunasporengiospora selenospora]	3-mercaptopyruvate sulfurtransferase OS=Escherichia coli O157:H7 OX=83334 GN=sseA PE=3 SV=2
A1889	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0725[Hs10337605 Reductases with broad range of substrate specificities	RKP28010.1 dehydrogenase [Syncephalis pseudoplumigaleata]	Dehydrogenase/reductase SDR family member 4 OS=Homo sapiens OX=9606 GN=DHRS4 PE=1 SV=3
A1890	GO:0044237(cellular metabolic process)	-	GO:000166(nucleotide binding)	-	-	-	-	-
A1891	-	-	-	-	-	-	-	-

A1892	-	-	-	-	-	-	KAF4465721.1 glycoside hydrolase family 43 [Fusarium albosuccineum]	-
A1893	GO:0006418(tRNA aminoacylation for protein translation),GO:0006421(asparaginyl-tRNA aminoacylation)	GO:0016021(integral component of membrane)	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0016757(glycosyltransferase activity),GO:0004816(asparagine-tRNA ligase activity)	K01893 NARS, asnS; asparaginyl-tRNA synthetase [EC:6.1.1.22]	map00970 Aminoacyl-tRNA biosynthesis	KOG0554 At4g17300 Asparaginyl-tRNA synthetase (mitochondrial)	KAF7722092.1 hypothetical protein EC973_003707 [Apophysomyces ossiformis]	Asparagine--tRNA ligase OS=Desulfovibrio vulgaris (strain ATCC 29579 / DSM 644 / NCIMB 8303 / VKM B-1760 / Hildenborough) OX=882 GN=asnS PE=3 SV=1
A1894	-	-	-	-	-	-	-	-
A1895	GO:0006260(DNA replication)	GO:0000808(origin recognition complex),GO:0005634(nucleus)	-	K02607 ORC5; origin recognition complex subunit 5	map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG2543 Hs4505525 Origin recognition complex, subunit 5	KAG0323423.1 Origin recognition complex subunit 5 [Podila horticola]	Origin recognition complex subunit 5 OS=Mus musculus OX=10090 GN=Orc5 PE=2 SV=1
A1896	-	-	-	-	-	-	-	-
A1897	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG0192 At3g63260 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KXS14371.1 kinase-like protein [Gonapodya prolifera JEL478]	RGS domain-containing serine/threonine-protein kinase A OS=Dictyostelium discoideum OX=44689 GN=rckA PE=1 SV=1
A1898	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	-	-	KOG0614 Hs10835242 cGMP-dependent protein kinase	KAG4100598.1 camp-dependent protein kinase catalytic subunit PRKX-like protein [Neocallimastix sp. JGI-2020a]	cGMP-dependent protein kinase 1 OS=Mus musculus OX=10090 GN=Prkg1 PE=1 SV=1
A1899	-	-	-	-	-	-	-	-
A1900	-	-	GO:0005509(calmodium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027 At2g41100 Calmodulin and related proteins (EF-Hand superfamily)	KAG2235520.1 hypothetical protein INT48_003083 [Thamnidium elegans]	Calmodulin-like protein 12 OS=Arabidopsis thaliana OX=3702 GN=CML12 PE=1 SV=3

A1901	GO:0035494(SNARE complex disassembly)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K06027 NSF, SEC18; vesicle-fusing ATPase [EC:3.6.4.6]	map04138 Autophagy - yeast;map04727 GABAergic synapse;map04721 Synaptic vesicle cycle;map04962 Vasopressin-regulated water reabsorption	KOG0741 Hs11079228 AAA+ -type ATPase	XP_007862247.1 vesicular-fusion protein SEC18 [Gloeophyllum trabeum ATCC 11539]	Vesicle-fusing ATPase OS=Pongo abelii OX=9601 GN=NSF PE=2 SV=1
A1902	-	-	-	-	-	-	-	-
A1903	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs4502553 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	RGB35544.1 kinase-like domain-containing protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Calcium/calmodulin-dependent protein kinase type 1 OS=Mus musculus OX=10090 GN=Camk1 PE=1 SV=1
A1904	-	-	GO:0005515(protein binding)	-	-	KOG0166 At3g06720 Karyopherin (importin) alpha	-	Importin subunit alpha-1a OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0253300 PE=1 SV=2
A1905	GO:0042819(vitamin B6 biosynthetic process), GO:0042823(pyridoxal phosphate biosynthetic process)	-	GO:0004359(glutaminase activity)	K08681 pdxT, pdx2; pyridoxal 5'-phosphate synthase pdxT subunit [EC:4.3.3.6]	map01240 Biosynthesis of cofactors;map00750 Vitamin B6 metabolism;map01100 Metabolic pathways	KOG3210 At5g60540 Imidazoleglycerol-phosphate synthase subunit H-like	XP_016608748.1 pyridoxal 5'-phosphate synthase, glutaminase subunit Pdx2 [Spizellomyces punctatus DAOM BR117]	Probable pyridoxal 5'-phosphate synthase subunit PDX2 OS=Arabidopsis thaliana OX=3702 GN=PDX2 PE=1 SV=1
A1907	-	-	-	-	-	-	-	-
A1908	GO:0006744(ubiquinone biosynthetic process)	-	GO:0005515(protein binding),GO:0008168(methyltransferase activity),GO:0008425(2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity)	K00591 COQ3; polyprenyldihydroxybenzoate methyltransferase / 3-demethylubiquinol 3-O-methyltransferase [EC:2.1.1.114 2.1.1.64]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00130 Ubiquinone and other terpenoid-quinone biosynthesis;map01100 Metabolic pathways	KOG1270 At2g30920 Methyltransferases	XP_016611829.1 3-demethylubiquinone-9 3-O-methyltransferase [Spizellomyces punctatus DAOM BR117]	Ubiquinone biosynthesis O-methyltransferase OS=Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966) OX=402881 GN=ubiG PE=3 SV=1
A1909	-	-	-	-	-	-	-	-

A1910	GO:0009098(leucine biosynthetic process), GO:0019752(carboxylic acid metabolic process)	-	GO:0003852(2-isopropylmalate synthase activity),GO:0046912(acyltransferase, acyl groups converted into alkyl on transfer),GO:0003824(catalytic activity)	K01655 LYS21, LYS20, homocitrate synthase [EC:2.3.3.14]	map00300 Lysine biosynthesis;map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00620 Pyruvate metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG2367 At1g74040 Alpha-isopropylmalate synthase/homocitrate synthase	RHZ80289.1 hypothetical protein Glove_137g53 [Diversispora epigaea]	2-isopropylmalate synthase 2, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=IPMS2 PE=1 SV=1
A1911	-	-	-	-	-	KOG2502 Hs6715610 Tub family proteins	RKP07880.1 tubby C-terminal-like domain-containing protein [Thamnocephalis sphaerospora]	Protein king tubby 2 OS=Culex quinquefasciatus OX=7176 GN=king-tubby2 PE=3 SV=2
A1912	-	-	-	K22075 BOLA3; BoA-like protein 3	-	-	XP_013955361.1 hypothetical protein TRIV DRAFT_153169 [Trichoderma virens Gv29-8]	Uncharacterized bolA-like protein C4B3.11c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC4B3.11c PE=3 SV=1
A1913	GO:0016567(protein ubiquitination)	-	GO:0005515(protein binding),GO:0004842(ubiquitin-protein transferase activity),GO:0046872(metal ion binding)	-	-	KOG0895 Hs10442822_2 Ubiquitin-conjugating enzyme	OCH94539.1 ubiquitin conjugating enzyme family protein [Obba rivulosa]	Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens OX=9606 GN=BIRC6 PE=1 SV=3
A1914	GO:0006402(mRNA catabolic process)	GO:0030014(CCR4-NOT complex)	-	K12606 RCD1, CNOT9, CAF40; CCR4-NOT transcription complex subunit 9	map03018 RNA degradation	KOG3036 At3g20800 Protein involved in cell differentiation/sexual development	XP_031026987.1 uncharacterized protein SmJEL517_g01085 [Synchytrium microbalum]	CCR4-NOT transcription complex subunit 9 OS=Danio rerio OX=7955 GN=cnot9 PE=2 SV=1
A1915	-	-	-	-	-	KOG3374 Hs4503037 Cellular repressor of transcription	-	Protein CREG1 OS=Mus musculus OX=10090 GN=Creg1 PE=1 SV=1
A1916	-	-	-	-	-	-	-	-
A1917	-	-	-	-	-	-	-	-
A1918	GO:0007064(mitotic sister chromatid cohesion)	GO:0031390(Ctf18 RFC-like complex)	-	K11270 CTF8; chromosome transmission fidelity protein 8	-	KOG4487 CE06492 Uncharacterized conserved protein	KAF8486228.1 Ctf8-domain-containing protein [Russula ochroleuca]	Chromosome transmission fidelity protein 8 homolog OS=Homo sapiens OX=9606 GN=CHTF8 PE=1 SV=1

A1919	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding),GO:0003995(acyl-CoA dehydrogenase activity)	K00253 IVD, ivd; isovaleryl-CoA dehydrogenase [EC:1.3.8.4]	map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG0141 Hs4504799 Isovaleryl-CoA dehydrogenase	KAG0345915.1 hypothetical protein BG005_001041 [Podila minutissima]	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ivd PE=1 SV=2
A1920	-	-	-	K01768 E4.6.1.1; adenylate cyclase [EC:4.6.1.1]	map00230 Purine metabolism;map04213 Longevity regulating pathway - multiple species;map02025 Biofilm formation - Pseudomonas aeruginosa;map04113 Meiosis - yeast;map01100 Metabolic pathways	KOG0698 At3g02750 Serine/threonine protein phosphatase	XP_016611041.1 hypothetical protein SPPG_08981 [Spizellomyces punctatus DAOM BR117]	Probable protein phosphatase 2C 73 OS=Oryza sativa subsp. japonica OX=39947 GN=Os11g0109000 PE=2 SV=1
A1921	GO:0000413(protein peptidyl-prolyl isomerization),GO:0006457(protein folding)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K09567 PPIH, CYPH; peptidyl-prolyl isomerase H (cyclophilin H) [EC:5.2.1.8]	map03040 Spliceosome	KOG0879 Hs5454154 U-snRNP-associated cyclophilin type peptidyl-prolyl cis-trans isomerase	ORX88462.1 hypothetical protein K493DRAFT_290577 [Basidiobolus meristosporus CBS 931.73]	Peptidyl-prolyl cis-trans isomerase H OS=Bos taurus OX=9913 GN=PPIH PE=2 SV=1
A1922	-	-	-	-	-	-	-	-
A1923	-	-	-	-	-	-	-	-
A1924	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG1287 At3g19553 Amino acid transporters	KXN69737.1 amino acid transporter [Conidiobolus coronatus NRRL 28638]	Probable polyamine transporter At3g19553 OS=Arabidopsis thaliana OX=3702 GN=At3g19553 PE=3 SV=1
A1925	GO:0043066(negative regulation of apoptotic process)	-	-	-	-	-	-	-
A1926	GO:0006479(protein methylation)	-	GO:0008276(protein methyltransferase activity),GO:0008168(methyltransferase activity)	-	-	KOG2904 Hs7705409 Predicted methyltransferase	ESK96567.1 protein-(glutamine-n5) release factor-specific [Moniliophthora roreri MCA 2997]	Release factor glutamine methyltransferase OS=Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIMB 8255 / S1) OX=269796 GN=prmC PE=3 SV=1
A1927	-	-	-	-	-	KOG4167 Hs14149979 Predicted DNA-binding protein, contains SANT and ELM2 domains	KAG0344618.1 putative PHD type zinc finger protein with BAH domain-containing protein [Podila humilis]	Zinc finger protein 541 OS=Mus musculus OX=10090 GN=Znf541 PE=1 SV=1

A1928	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02923 RP-L38e, RPL38; large subunit ribosomal protein L38e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3499 728 9476 60S ribosomal protein L38	TPX54781.1 hypothetical protein PhCBS80983.g05751 [Powellomyces hirtus]	Large ribosomal subunit protein eL38 OS=Argas monolakensis OX=34602 GN=Rpl38 PE=3 SV=1
A1929	GO:0006364(rRNA processing),GO:0000027(ribosomal large subunit assembly),GO:0000470(maturation of LSU-rRNA)	-	GO:0019843(rRNA binding)	K14847 RPF2; ribosome production factor 2	-	KOG3031 Hs20551627 Protein required for biogenesis of the ribosomal 60S subunit	RHZ82180.1 hypothetical protein Glove_113g47 [Diversispora epigaea]	Ribosome production factor 2 homolog OS=Bos taurus OX=9913 GN=RPF2 PE=2 SV=1
A1930	-	-	GO:0016301(kinase activity)	K00852 rbsK, RBKS; ribokinase [EC:2.7.1.15]	map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG2855 CE03147 Ribokinase	QPG94843.1 hypothetical protein CcBS67573.g04719 [Epichloe festucae F11]	Ribokinase OS=Leishmania major OX=5664 GN=LMJF_27_0420 PE=1 SV=1
A1931	-	-	-	K07019 K07019; uncharacterized protein	-	KOG1838 At5g49950 Alpha/beta hydrolase	TPX74009.1 hypothetical protein CcBS67573.g04719 [Chytriumyces confervae]	Embryogenesis-associated protein EMB8 OS=Picea glauca OX=3330 GN=EMB8 PE=2 SV=1
A1932	GO:0016567(protein ubiquitination),GO:0006511(ubiquitin-dependent protein catabolic process),GO:0030433(ubiquitin-dependent ERAD pathway)	GO:0000151(ubiquitin ligase complex)	GO:0004842(ubiquitin-protein transferase activity),GO:0034450(ubiquitin-ubiquitin ligase activity)	K10597 UBE4B, UFD2; ubiquitin conjugation factor E4 B [EC:2.3.2.27]	map04141 Protein processing in endoplasmic reticulum;map04120 Ubiquitin mediated proteolysis	KOG2042 At5g15400 Ubiquitin fusion degradation protein-2	KAG2202131.1 hypothetical protein INT47_008103 [Mucor saturninus]	Probable ubiquitin conjugation factor E4 OS=Arabidopsis thaliana OX=3702 GN=PUB1 PE=2 SV=1
A1933	-	-	GO:0005509(calcium ion binding),GO:0008597(calcium-dependent protein serine/threonine phosphatase regulator activity)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	KOG0034 CE23771 Ca2+/calmodulin-dependent protein phosphatase (calcineurin subunit B), EF-Hand superfamily protein	RKP40314.1 calcineurin subunit B [Dimargaris cristalligena]	Calcineurin subunit B OS=Naegleria gruberi OX=5762 GN=CNB1 PE=3 SV=1
A1934	-	-	-	-	-	-	KAF5345350.1 hypothetical protein D9758_008466 [Tetrapyrgos nigripes]	L-threonine 3-dehydrogenase OS=Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087) OX=3042615 GN=tdh PE=3 SV=1

A1935	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A1936	-	-	-	-	-	-	-	-
A1937	GO:0060271(cilium assembly),GO:0070507(regulation of microtubule cytoskeleton organization)	GO:0005813(centrosome)	GO:0043015(gamma-tubulin binding)	-	-	-	KNE67282.1 hypothetical protein AMAG_12346 [Allomyces macrogynus ATCC 38327]	-
A1938	-	-	-	-	-	KOG1212 Hs4557575 Amidases	KAG1770925.1 amidase signature domain-containing protein [Suillus occidentalis]	Fatty-acid amide hydrolase 1 OS=Rattus norvegicus OX=10116 GN=Faah PE=1 SV=1
A1939	-	-	GO:0010181(FMN binding),GO:0016491(oxidoreductase activity)	-	-	KOG1159 Hs7657393 NADP-dependent flavoprotein reductase	RIB26496.1 hypothetical protein C2G38_2138268 [Gigaspora rosea]	NADPH-dependent diflavin oxidoreductase 1 OS=Danio rerio OX=7955 GN=ndor1 PE=2 SV=1
A1940	-	-	GO:0003756(protein disulfide isomerase activity)	K09580 PDIA1, P4HB; protein disulfide-isomerase A1 [EC:5.3.4.1]	map04141 Protein processing in endoplasmic reticulum	KOG0190 CE03972 Protein disulfide isomerase (prolyl 4-hydroxylase beta subunit)	OJT03774.1 Protein disulfide-isomerase [Trametes pubescens]	Protein disulfide-isomerase 2 OS=Caenorhabditis elegans OX=6239 GN=pdi-2 PE=1 SV=1
A1941	-	-	-	-	-	-	-	-
A1942	-	-	-	K10703 HACD, PHS1, PAS2; very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase [EC:4.2.1.134]	map01110 Biosynthesis of secondary metabolites;map00062 Fatty acid elongation;map01040 Biosynthesis of unsaturated fatty acids;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG3187 CE13650 Protein tyrosine phosphatase-like protein PTPLA (contains Pro instead of catalytic Arg)	KXS14873.1 hypothetical protein M427DRAFT_135548 [Gonapodya prolifera JEL478]	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase hpo-8 OS=Caenorhabditis elegans OX=6239 GN=hpo-8 PE=3 SV=2
A1943	-	-	-	-	-	-	-	-
A1944	GO:0055085(transmembrane transport)	GO:0016020(membrane)	-	-	-	-	-	-
A1945	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	-	-	-	KOG1307 Hs9966787 K+-dependent Ca2+/Na+ exchanger NCKX1 and related proteins	-	Sodium/potassium/calcium exchanger 2 OS=Homo sapiens OX=9606 GN=SLC24A2 PE=1 SV=1

A1946	-	-	-	-	-	-	KAF9764195.1 hypothetical protein IL306_002869 [Fusarium sp. DS 682]	-
A1947	-	-	-	-	-	-	-	-
A1948	-	-	-	-	-	-	TPX55172.1 hypothetical protein PhC8S80983_g05545 [Powellomyces hirtus]	-
A1949	GO:0043631(RNA polyadenylation),GO:0031123(RNA 3'-end processing)	GO:0005634(nucleus)	GO:0003723(RNA binding),GO:0004652(polynucleotide adenylyltransferase activity),GO:0016779(nucleotidyl transferase activity)	K14376 PAP; poly(A) polymerase [EC:2.7.7.19]	map03015 mRNA surveillance pathway	KOG2245 At2g25850 Poly(A) polymerase and related nucleotidyltransferases	KXN74824.1 Poly(A) polymerase [Conidiobolus coronatus NRRL 28638]	Poly(A) polymerase OS=Dictyostelium discoideum OX=44689 GN=papA PE=3 SV=1
A1950	-	-	-	K23451 LCB3; dihydrosphingosine 1-phosphate phosphatase [EC:3.1.3.-]	map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG2822 At3g58490 Sphingoid base-phosphate phosphatase	XP_016604135.1 hypothetical protein SPPG_08481 [Spizellomyces punctatus DAOM BR117]	Lipid phosphate phosphatase delta OS=Arabidopsis thaliana OX=3702 GN=LPPD PE=2 SV=1
A1951	-	-	GO:0005524(ATP binding)	K05658 ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:7.6.2.2]	map04976 Bile secretion;map02010 ABC transporters;map05226 Gastric cancer;map05206 MicroRNAs in cancer	KOG0055 At4g18050 Multidrug/pheromone exporter, ABC superfamily	KAF7755262.1 hypothetical protein DSO57_011322 [Entomophthora muscae]	Probable multidrug resistance ABC transporter ATP-binding/permease protein Yhel OS=Bacillus subtilis (strain 168) OX=224308 GN=yhel PE=1 SV=1
A1952	GO:0006367(transcription initiation from RNA polymerase II promoter)	-	GO:0005515(protein binding)	K06062 PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]	map03250 Viral life cycle - HIV-1;map04919 Thyroid hormone signaling pathway;map05203 Viral carcinogenesis;map04330 Notch signaling pathway;map05166 Human T-cell leukemia virus 1 infection	KOG1472 YGR252w Histone acetyltransferase SAGA/ADA, catalytic subunit PCAF/GCN5 and related proteins	KAG2223511.1 hypothetical protein INT45_000831, partial [Mucor circinatus]	Histone acetyltransferase GCN5 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / BCRC 21394 / JCM 1990 / NBRC 0083 / IGC 2968) OX=284592 GN=GCN5 PE=3 SV=2
A1953	-	-	-	-	-	-	-	-
A1954	GO:0030490(maturation of SSU-rRNA)	-	GO:0003724(RNA helicase activity),GO:0005524(ATP binding),GO:0003676(nucleic acid binding)	K14779 DDX52, ROK1; ATP-dependent RNA helicase DDX52/ROK1 [EC:3.6.4.13]	-	KOG0344 Hs15316941 ATP-dependent RNA helicase	KAG1459933.1 hypothetical protein G6F56_006056 [Rhizopus delemar]	ATP-dependent RNA helicase ROK1 OS=Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) OX=322104 GN=ROK1 PE=3 SV=1

A1955	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	K14264 BNA3; kynurenine aminotransferase [EC:2.6.1.7]	map00380 Tryptophan metabolism;map01100 Metabolic pathways	KOG0256 At4g26200 1-aminocyclopropane-1-carboxylate synthase, and related proteins	KGQ03899.1 Cystathionine beta-lyase PatB [Beauveria bassiana D1-5]	Cystathionine beta-lyase PatB OS=Bacillus subtilis (strain 168) OX=224308 GN=patB PE=1 SV=1
A1956	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity),GO:0015112(nitrate transmembrane transporter activity)	K02575 NRT2, narK, nrtP, nasA; MFS transporter, NNP family, nitrate/nitrite transporter	map00910 Nitrogen metabolism	-	EXX76102.1 hypothetical protein RirG_036130 [Rhizophagus irregularis DAOM 197198w]	High affinity nitrate transporter 2.5 OS=Arabidopsis thaliana OX=3702 GN=NRT2.5 PE=1 SV=1
A1957	GO:0042128(nitrate assimilation)	-	GO:0016491(oxidoreductase activity),GO:0051537(2 iron, 2 sulfur cluster binding),GO:0008942(nitrite reductase [NAD(P)H] activity),GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding),GO:0020037(heme binding),GO:0051536(iron-sulfur cluster binding)	K17877 NIT-6; nitrite reductase (NAD(P)H) [EC:1.7.1.4]	map00910 Nitrogen metabolism;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG1336 Hs21389617 Monodehydroascorbate/ferredoxin reductase	KAF0539739.1 nitrite reductase NADPH small subunit [Gigaspora margarita]	Nitrite reductase [NAD(P)H] OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=niiA PE=3 SV=2
A1958	-	-	GO:0016491(oxidoreductase activity),GO:0030151(molybdenum ion binding),GO:0020037(heme binding)	K10534 NR; nitrate reductase (NAD(P)H) [EC:1.7.1.1 1.7.1.2 1.7.1.3]	map00910 Nitrogen metabolism;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG0535 At1g77760.1 Sulfite oxidase, molybdopterin-binding component	XP_025189456.1 nitrate reductase [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Nitrate reductase [NADH] 1 OS=Oryza sativa subsp. japonica OX=39947 GN=NIA1 PE=2 SV=3
A1959	-	-	-	-	-	-	-	-
A1960	GO:0006457(protein folding),GO:0009408(response to heat)	-	GO:0051082(unfolded protein binding),GO:0031072(heat shock protein binding),GO:0005524(ATP binding)	K03686 dnaJ; molecular chaperone DnaJ	-	KOG0715 At2g22360 Molecular chaperone (DnaJ superfamily)	XP_025380046.1 hypothetical protein FA10DRAFT_263594 [Acaromyces ingoldii]	Chaperone protein DnaJ OS=Psychrobacter cryohalolentis (strain ATCC BAA-1226 / DSM 17306 / VKM B-2378 / K5) OX=335284 GN=dnaJ PE=3 SV=1
A1961	-	-	-	K14209 SLC36A, PAT; solute carrier family 36 (proton-coupled amino acid transporter)	map04138 Autophagy - yeast;map04974 Protein digestion and absorption	KOG1304 At5g65990 Amino acid transporters	KAG0173226.1 neutral amino acid transporter [Apophysomyces sp. BC1015]	Amino acid transporter AVT3A OS=Arabidopsis thaliana OX=3702 GN=AVT3A PE=1 SV=1

A1962	-	-	-	-	-	KOG2342 Hs20561163 Uncharacterized conserved protein	XP_025599894.1 DUF833-domain-containing protein [Tilletiopsis washingtonensis]	Transport and Golgi organization 2 homolog OS=Mus musculus OX=10090 GN=Tango2 PE=1 SV=2
A1963	-	-	GO:0003824(catalytic activity),GO:0031177(phosphopantetheine binding)	K12743 PCBAB; N-(5-amino-5-carboxypentamoyl)-L-cysteinyl-D-valine synthase [EC:6.3.2.26]	map01110 Biosynthesis of secondary metabolites;map00311 Penicillin and cephalosporin biosynthesis;map01100 Metabolic pathways	-	KAF9955515.1 hypothetical protein BGZ72_003654 [Mortierella alpina]	Linear gramicidin synthase subunit D OS=Brevibacillus parabrevis OX=54914 GN=IgrD PE=1 SV=1
A1964	GO:0009073(aromatic amino acid family biosynthetic process), GO:0046417(chorismate metabolic process)	-	GO:0004106(chorismate mutase activity)	K01850 E5.4.99.5; chorismate mutase [EC:5.4.99.5]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map01100 Metabolic pathways	-	XP_022471896.1 chorismate mutase [Colletotrichum orchidophilum]	Chorismate mutase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=aro7 PE=3 SV=1
A1965	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005515(protein binding),GO:0046872(metal ion binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At4g28710 Myosin class V heavy chain	KXS20837.1 myosin [Gonapodya prolifera JEL478]	Myosin-9 OS=Arabidopsis thaliana OX=3702 GN=XI-C PE=2 SV=1
A1966	GO:0006261(DNA-dependent DNA replication)	-	-	K10735 GINS4, SLD5; GINS complex subunit 4	-	KOG3176 At5g49010 Predicted alpha-helical protein, potentially involved in replication/repair	RKP39485.1 hypothetical protein BJ085DRAFT_15087 [Dimargaris cristalligena]	DNA replication complex GINS protein SLD5 OS=Arabidopsis thaliana OX=3702 GN=SLD5 PE=1 SV=1
A1967	-	-	GO:0005515(protein binding)	K20242 EVI5; ecotropic viral integration site 5 protein	-	KOG1102 At5g15930 Rab6 GTPase activator GAPCenA and related TBC domain proteins	OAD06601.1 hypothetical protein MUCCIDRAFT_13924, partial [Mucor lusitanicus CBS 277.49]	Rab GTPase-activating protein eat-17 OS=Caenorhabditis elegans OX=6239 GN=eat-17 PE=1 SV=1
A1968	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0030317(flagellated sperm motility)	GO:0016020(membrane),GO:0036128(CatSper complex)	GO:0005216(ion channel activity),GO:0005227(calcium activated cation channel activity)	-	-	KOG2302 Hs16596698 T-type voltage-gated Ca2+ channel, pore-forming alpha1 subunit	ORX51366.1 hypothetical protein BCR36DRAFT_582910, partial [Piromyces finnis]	Cation channel sperm-associated protein 1 OS=Mus musculus OX=10090 GN=Catsper1 PE=1 SV=1
A1969	-	-	-	-	-	-	-	-

A1970	GO:1902975(mitotic DNA replication initiation),GO:0006260(DNA replication)	-	GO:0000166(nucleotide binding),GO:0003677(DNA binding),GO:0003887(DNA-directed DNA polymerase activity),GO:0003676(nucleic acid binding)	K02320 POLA1; DNA polymerase alpha subunit A [EC:2.7.7.7]	map03030 DNA replication	KOG0970[Hs8393995 DNA polymerase alpha, catalytic subunit	ORZ24563.1 DNA polymerase family B-domain-containing protein [Absidia repens]	DNA polymerase alpha catalytic subunit OS=Homo sapiens OX=9606 GN=POLA1 PE=1 SV=2
A1971	GO:0034599(cellular response to oxidative stress),GO:0006979(response to oxidative stress)	-	GO:0004601(peroxidase activity),GO:0020037(heme binding)	K00428 E1.1.1.1.5; cytochrome c peroxidase [EC:1.11.1.5]	-	-	KNE67634.1 hypothetical protein AMAG_12087 [Allomyces macrogynus ATCC 38327]	Putative heme-binding peroxidase OS=Pyricularia oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) OX=242507 GN=MGG_10368 PE=3 SV=1
A1972	-	-	-	-	-	-	EGU11874.1 MesA protein [Rhodotorula toruloides ATCC 204091]	-
A1973	GO:0006164(purine nucleotide biosynthetic process)	-	GO:0003938(IMP dehydrogenase activity),GO:0003824(catalytic activity),GO:0016491(oxidoreductase activity)	K00088 IMPDH, guaB; IMP dehydrogenase [EC:1.1.1.205]	map00983 Drug metabolism - other enzymes;map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG2550[7291188 IMP dehydrogenase/GMP reductase	RHZ64138.1 hypothetical protein Glove_326g73 [Diversispora epigaea]	Inosine-5'-monophosphate dehydrogenase OS=Dictyostelium discoideum OX=44689 GN=impdh PE=1 SV=1
A1974	-	-	-	-	-	KOG4829[7292231 Uncharacterized conserved protein	ORY56236.1 hypothetical protein LY90DRAFT_669421 [Neocallimastix californiae]	-
A1975	-	-	-	K15109 SLC25A20_29, CACT, CACL, CRC1; solute carrier family 25 (mitochondrial carnitine/acyl carnitine transporter), member 20/29	map04714 Thermogenesis	KOG0758[At5g46800 Mitochondrial carnitine-acylcarnitine carrier protein	KAF7729471.1 Mitochondrial carrier protein ymc2 [Apophysomyces ossiformis]	Mitochondrial substrate carrier family protein G OS=Dictyostelium discoideum OX=44689 GN=mcfG PE=2 SV=1

A1976	-	-	GO:0003824(catalytic activity)	K00830 AGXT; alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase [EC:2.6.1.44 2.6.1.45 2.6.1.51]	map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00680 Methane metabolism;map00250 Alanine, aspartate and glutamate metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism;map00630	KOG2862[Hs4 557289 Alanine-glyoxylate aminotransferase AGT1	TFK74906.1 PLP-dependent transferase [Pluteus cervinus]	Serine-pyruvate aminotransferase OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=TM_1400 PE=1 SV=1
A1977	-	-	-	-	-	-	-	-
A1978	GO:0006412(translation)	GO:0005840(ribosome)	GO:0005515(protein binding),GO:0003735(structural constituent of ribosome)	K02927 RP-L40e, RPL40, UBA52; ubiquitin-large subunit ribosomal protein L40e	map04140 Autophagy - animal;map05131 Shigellosis;map05171 Coronavirus disease - COVID-19;map04137 Mitophagy - animal;map04120 Ubiquitin mediated proteolysis;map03010 Ribosome;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease;map05167 Kaposi sarcoma-associated herpesvirus infection	-	EPB88316.1 ubiquitin-60S ribosomal protein L40 [Mucor circinelloides 1006PhL]	Ubiquitin-ribosomal protein eL40 fusion protein OS=Eimeria bovis OX=5803 PE=2 SV=2
A1979	-	-	-	-	-	-	-	-
A1980	-	GO:0016020(membrane)	-	K17081 PHB2; prohibitin 2	-	KOG3090[Hs6 005854 Prohibitin-like protein	RIB22284.1 prohibitin-2 [Gigaspora rosea]	Prohibitin-2 OS=Dictyostelium discoideum OX=44689 GN=phbB PE=3 SV=1
A1981	-	GO:0016020(membrane)	-	K23544 SERINC1; serine incorporator 1	-	KOG2592[Hs6 4110 Tumor differentially expressed (TDE) protein	KXS20326.1 TMS membrane protein/tumor differentially expressed protein [Gonapodya prolifera JEL478]	Serine incorporator 3 OS=Pongo abelii OX=9601 GN=SERINC3 PE=2 SV=1
A1982	GO:0030488(tRNA methylation)	GO:0031515(tRNA (m1A) methyltransferase complex)	GO:0016429(tRNA (adenine-N1)-methyltransferase activity)	K07442 TRM61, GCD14; tRNA (adenine57-N1/adenine58-N1)-methyltransferase catalytic subunit [EC:2.1.1.219 2.1.1.220]	-	KOG2915[Hs6 1439 tRNA(1-methyladenosine) methyltransferase, subunit GCD14	RKP13534.1 tRNA methyltransferase complex GCD14 subunit-domain-containing protein [Piptocephalis cylindrospora]	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A OS=Bos taurus OX=9913 GN=TRMT61A PE=2 SV=1
A1983	-	-	-	-	-	-	-	-

A1984	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07897 RAB7A; Ras-related protein Rab-7A	map04144 Endocytosis;map04145 Phagosome;map04140 Autophagy - animal;map05132 Salmonella infection;map04138 Autophagy - yeast;map04137 Mitophagy - animal;map05146 Amoebiasis;map05152 Tuberculosis	-	KAG4087419.1 P-loop containing nucleoside triphosphate hydrolase protein [Neocallimastix sp. JGI-2020a]	Intraflagellar transport protein 22 homolog OS=Danio rerio OX=7955 GN=ift22 PE=2 SV=1
A1985	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A1986	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A1987	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	-	-
A1988	-	-	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A1989	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A1990	-	-	GO:0003723(RNA binding)	-	-	KOG2945[At4g16830 Predicted RNA-binding protein	-	RGG repeats nuclear RNA binding protein A (Fragment) OS=Nicotiana tabacum OX=4097 GN=RggA PE=2 SV=1
A1991	-	-	-	-	-	-	-	-
A1992	-	-	GO:0003677(DNA binding)	-	-	KOG2186[Hs8923398 Cell growth-regulating nucleolar protein	KAF9923602.1 hypothetical protein FBU30_006378 [Linnemannia zychnae]	Cell growth-regulating nucleolar protein OS=Mus musculus OX=10090 GN=Lyar PE=1 SV=2
A1993	-	-	-	-	-	-	OZJ03940.1 hypothetical protein BZG36_02936 [Bifiguratus adalaidae]	Heme-binding-like protein At3g10130, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=At3g10130 PE=1 SV=1

A1994	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02993 RP-S7e, RPS7; small subunit ribosomal protein S7e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3320 Hs4506741.40S ribosomal protein S7	TPX55385.1 hypothetical protein PhCBS80983.g05347 [Powellomyces hirtus]	Small ribosomal subunit protein eS7 OS=Danio rerio OX=7955 GN=rps7 PE=1 SV=1
A1995	-	-	GO:0016614(oxidoreductase activity, acting on CH-OH group of donors),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG1238 Hs18556423 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	XP_01661142.4.1 hypothetical protein SPPG_00874 [Spizellomyces punctatus DAOM BR117]	Alcohol dehydrogenase [acceptor] OS=Pseudomonas putida OX=303 GN=alkJ PE=3 SV=1
A1996	-	-	GO:0050660(flavin adenine dinucleotide binding),GO:0016614(oxidoreductase activity, acting on CH-OH group of donors)	-	-	KOG1238 Hs18556423 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	XP_01661142.4.1 hypothetical protein SPPG_00874 [Spizellomyces punctatus DAOM BR117]	Alcohol dehydrogenase [acceptor] OS=Pseudomonas putida OX=303 GN=alkJ PE=3 SV=1
A1997	-	-	GO:0016614(oxidoreductase activity, acting on CH-OH group of donors),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG1238 7293011 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	XP_01661142.4.1 hypothetical protein SPPG_00874 [Spizellomyces punctatus DAOM BR117]	Alcohol dehydrogenase [acceptor] OS=Pseudomonas putida OX=303 GN=alkJ PE=3 SV=1
A1998	-	-	GO:0016614(oxidoreductase activity, acting on CH-OH group of donors),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG1238 7301449 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	XP_01661142.4.1 hypothetical protein SPPG_00874 [Spizellomyces punctatus DAOM BR117]	Alcohol dehydrogenase [acceptor] OS=Pseudomonas putida OX=303 GN=alkJ PE=3 SV=1
A1999	-	-	GO:0016614(oxidoreductase activity, acting on CH-OH group of donors),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG1238 7293011 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	XP_01661142.4.1 hypothetical protein SPPG_00874 [Spizellomyces punctatus DAOM BR117]	Alcohol dehydrogenase [acceptor] OS=Pseudomonas putida OX=303 GN=alkJ PE=3 SV=1
A2000	-	-	-	-	-	-	KXS19169.1 molybdopterin binding oxidoreductase [Gonapodya prolifera JEL478]	Uncharacterized oxidoreductase YuiH OS=Bacillus subtilis (strain 168) OX=224308 GN=yuiH PE=3 SV=1
A2001	-	-	-	-	-	-	-	-
A2002	-	-	GO:0005509(calcium ion binding)	-	-	-	-	Putative calcium-binding protein CML23 OS=Oryza sativa subsp. japonica OX=39947 GN=CML23 PE=3 SV=1
A2003	-	-	-	-	-	-	-	-

A2004	-	-	GO:0050660(flavin adenine dinucleotide binding),GO:0016614(oxidoreductase activity, acting on CH-OH group of donors)	-	-	KOG1238 Z93009 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	XP_016611424.1 hypothetical protein SPPG_00874 [Spizellomyces punctatus DAOM BR117]	Alcohol dehydrogenase [acceptor] OS=Pseudomonas putida OX=303 GN=alkJ PE=3 SV=1
A2005	-	-	-	-	-	-	-	-
A2006	-	-	-	-	-	-	-	-
A2007	-	-	-	-	-	KOG3706 Hs13375885 Uncharacterized conserved protein	-	Ribosomal oxygenase 1 OS=Mus musculus OX=10090 GN=Riox1 PE=1 SV=2
A2008	GO:0006351(transcription, DNA-templated),GO:0016558(protein import into peroxisome matrix)	-	GO:0005515(protein binding),GO:0005053(peroxisome matrix targeting signal-2 binding)	-	-	KOG0277 Hs4505731 Peroxisomal targeting signal type 2 receptor	XP_006682476.1 uncharacterized protein BATDEDRAFT_92122 [Batrachochytrium dendrobatidis JAM81]	Peroxisomal targeting signal 2 receptor OS=Dictyostelium discoideum OX=44689 GN=pex7 PE=3 SV=1
A2009	-	-	-	-	-	-	-	-
A2010	GO:0006629(lipid metabolic process)	-	-	-	-	-	KNE57373.1 hypothetical protein AMAG_03094 [Allomyces macrogynus ATCC 38327]	-
A2011	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2012	-	GO:0016021(integral component of membrane)	GO:0004252(serine-type endopeptidase activity)	-	-	-	-	-
A2013	-	GO:0019867(outer membrane)	-	K07277 SAM50, TOB55, bamA; outer membrane protein insertion porin family	-	KOG2602 At3g11070 Predicted cell surface protein homologous to bacterial outer membrane proteins	KAG2186123.1 hypothetical protein INT43_002561 [Umbelopsis isabellina]	SAM50-like protein SPAC17C9.06 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC17C9.06 PE=3 SV=1
A2014	-	-	-	-	-	KOG1843 At1g29800 Uncharacterized conserved protein	-	-

A2015	GO:0046854(phosphatidylinositol phosphate biosynthetic process), GO:0048015(phosphatidylinositol-mediated signaling)	-	GO:0016301(kinase activity), GO:0005515(protein binding)	K00914 PIK3C3, VPS34; phosphatidylinositol 3-kinase [EC:2.7.1.137]	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map04140 Autophagy - animal;map05132 Salmonella infection;map05131 Shigellosis;map04070 Phosphatidylinositol signaling system;map04138 Autophagy - yeast;map04136 Autophagy - other;map05022 Pathways of neurodegeneration - multiple diseases;map04371 Apelin signaling pathway;map00562 Inositol phosphate	KOG0904[Hs5453894 Phosphatidylinositol 3-kinase catalytic subunit (p110)	RKP20799.1 kinase-like protein, partial [Rozella allomyces CSF55]	Phosphatidylinositol 3-kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pikB PE=2 SV=2
A2016	-	-	-	-	-	-	-	-
A2017	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0140359(ABC-type transporter activity), GO:0005524(ATP binding)	-	-	KOG0059[Hs4501849 Lipid exporter ABCA1 and related proteins, ABC superfamily	ORX93119.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	ABC transporter A family member 2 OS=Dictyostelium discoideum OX=44689 GN=abcA2 PE=3 SV=1
A2018	GO:0006777(Mo-molybdopterin cofactor biosynthetic process)	-	-	-	-	KOG2876[J294773 Molybdenum cofactor biosynthesis pathway protein	RKP15081.1 hypothetical protein BJ684DRAFT_22371 [Piptocephalis cylindrospora]	Cyclic pyranopterin monophosphate synthase OS=Xanthomonas campestris pv. campestris (strain B100) OX=509169 GN=moaC PE=3 SV=1
A2019	-	-	-	-	-	-	-	Calcium-regulated actin-bundling protein OS=Dictyostelium
A2020	-	-	-	-	-	-	-	-
A2021	-	-	GO:0003676(nucleic acid binding), GO:0005524(ATP binding), GO:0003724(RNA helicase activity)	K12858 DDX23, PRP28; ATP-dependent RNA helicase DDX23/PRP28 [EC:3.6.4.13]	map03040 Spliceosome	KOG0333[At2g33730 U5 snRNP-like RNA helicase subunit	KAG4099835.1 P-loop containing nucleoside triphosphate hydrolase protein [Neocallimastix sp. JGI-2020a]	ATP-dependent RNA helicase ddx23 OS=Dictyostelium discoideum OX=44689 GN=helB2 PE=2 SV=1
A2022	-	-	-	-	-	-	KNE61759.1 fibro-slime domain-containing protein [Allomyces macrogynus ATCC 38327]	Protein psiR OS=Dictyostelium discoideum OX=44689 GN=psiR PE=3 SV=1
A2023	GO:0006811(ion transport), GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane), GO:0016020(membrane)	GO:0015377(cation:chloride symporter activity)	K14429 SLC12A9, CCC6; solute carrier family 12 (potassium/c chloride transporters), member 9	-	KOG1288[Hs910386 Amino acid transporters	TGZ79296.1 hypothetical protein EX30DRAFT_309012 [Ascodesmis nigricans]	Solute carrier family 12 member 9 OS=Danio rerio OX=7955 GN=slc12a9 PE=3 SV=1

A2024	GO:0006744(ubiquitination biosynthetic process), GO:0045333(cellular respiration)	-	GO:0048039(ubiquinone binding),GO:0005509(calcium ion binding)	K18588 COQ10; coenzyme Q-binding protein COQ10	-	KOG3177 7302281 Oligoketide cyclase/lipid transport protein	XP_025356635.1 uncharacterized protein FA14DRAFT_161089 [Meiramiltonrushii]	Coenzyme Q-binding protein COQ10, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Coq10 PE=2 SV=1
A2025	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG4280 7294670 Kinesin-like protein	XP_007671712.1 uncharacterized protein BAUCODRAFT_28874 [Baudoinia panamericana UAMH 10762]	Centromere-associated protein E OS=Mus musculus OX=10090 GN=Cenpe PE=1 SV=1
A2026	-	GO:0016021(integral component of membrane)	GO:0016787(hydrolase activity)	-	-	KOG3664 Hs17448847 Predicted patched transmembrane receptor	XP_016294601.1 hypothetical protein PSEUBRA_SC AF10g05546 [Kalmatozymbasilensis GHG001]	Palmitoleoyl-protein carboxylesterase notum1a OS=Danio rerio OX=7955 GN=notum1a PE=2 SV=1
A2027	-	-	-	-	-	-	-	-
A2028	-	-	GO:0008757(S-adenosylmethionine-dependent methyltransferase activity)	K19787 CARNMT1; carnosine N-methyltransferase [EC:2.1.1.22]	map00340 Histidine metabolism;map01100 Metabolic pathways	KOG2798 CE16654 Putative trehalase	KAG1141237.1 hypothetical protein G6F38_008564 [Rhizopus oryzae]	Carnosine N-methyltransferase OS=Gallus gallus OX=9031 GN=CARNMT1 PE=1 SV=2
A2029	-	-	GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding),GO:0004499(N,N-dimethylaniline monooxygenase activity)	-	-	KOG1399 CE06138 Flavin-containing monooxygenase	PUU76745.1 flavin monooxygenase-like protein [Tuber borchii]	Flavin-containing monooxygenase 5 OS=Oryctolagus cuniculus OX=9986 GN=FMO5 PE=1 SV=2
A2030	-	-	GO:0008017(microtubule binding),GO:0005515(protein binding)	K10436 MAPRE; microtubule-associated protein, RP/EB family	-	KOG3000 At5g62500 Microtubule-binding protein involved in cell cycle control	ORX77246.1 hypothetical protein BCR32DRAFT_328993 [Anaeromyces robustus]	Microtubule-associated protein RP/EB family member 1B OS=Arabidopsis thaliana OX=3702 GN=EB1B PE=1 SV=1

A2031	-	GO:0016021(integral component of membrane)	-	K01649 leuA, IMS; 2-isopropylmalate synthase [EC:2.3.3.13]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00620 Pyruvate metabolism;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	-	KAG2181753.1 hypothetical protein INT44_008568 [Umbelopsis vinacea]	Uncharacterized TLC domain-containing protein C17A2.02c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC17A2.02c PE=4 SV=1
A2032	GO:0006556(S-adenosylmethionine biosynthetic process)	-	GO:0004478(methionine adenosyltransferase activity),GO:0005524(ATP binding)	K00789 metK, MAT; S-adenosylmethionine synthetase [EC:2.5.1.6]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map01230 Biosynthesis of amino acids;map00999 Biosynthesis of various plant secondary metabolites;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG1506 At4g01850 S-adenosylmethionine synthetase	RGP74354.1 s-adenosylmethionine synthase [Fusarium longipes]	S-adenosylmethionine synthase 3 OS=Populus trichocarpa OX=3694 GN=METK3 PE=2 SV=1
A2033	GO:0006366(transcription by RNA polymerase II)	-	GO:0046982(protein heterodimerization activity)	K03127 TAF13; transcription initiation factor TFIID subunit 13	map03022 Basal transcription factors	KOG3901 Hs032155 Transcription initiation factor IID subunit	KLO13525.1 transcription initiation factor IID, 18 kDa subunit, partial [Schizopora paradoxa]	Transcription initiation factor TFIID subunit 13 OS=Dictyostelium discoideum OX=44689 GN=taf13 PE=3 SV=1
A2034	-	-	GO:0005509(calcium ion binding)	K14684 SLC25A23S; solute carrier family 25 (mitochondrial phosphate transporter), member 23/24/25/41	-	KOG0036 At5g07320 Predicted mitochondrial carrier protein	KMU81776.1 hypothetical protein C1SG_02794 [Coccidioides immitis RMSCC 3703]	Calcium-dependent mitochondrial ATP-magnesium/phosphate carrier protein 3 OS=Arabidopsis thaliana OX=3702 GN=APC3 PE=1 SV=1
A2035	-	-	GO:0003824(catalytic activity)	-	-	-	XP_013256715.1 4-oxalocrotonate decarboxylase [Exophiala aquamarina CBS 119918]	2-keto-4-pentenoate hydratase 1 OS=Pseudomonas putida OX=303 GN=mhpD1 PE=3 SV=1

A2036	-	-	-	-	-	KOG4044 7291830 Mitochondrial associated endoribonuclease MAR1 (isochorismatase superfamily)	XP_021881249.1 Isochorismatase-like protein [Lobosporangium transversale]	Secreted isochorismatase effector Isc1 OS=Phytophthora sojae (strain P6497) OX=1094619 GN=Isc1 PE=1 SV=1
A2037	-	-	GO:0008270(zinc ion binding)	-	-	KOG2177 Hs5453569 Predicted E3 ubiquitin ligase	-	E3 ubiquitin-protein ligase TRIM45 OS=Mus musculus OX=10090 GN=Trim45 PE=2 SV=2
A2038	GO:0009231(riboflavin biosynthetic process)	GO:0009349(riboflavin synthase complex)	GO:000906(6,7-dimethyl-8-ribityllumazine synthase activity)	K00794 ribH, RIB4; 6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00740 Riboflavin metabolism;map01100 Metabolic pathways	-	ORY08108.1 6,7-dimethyl-8-ribityllumazine synthase [Basidiobolus meristosporus CBS 931.73]	6,7-dimethyl-8-ribityllumazine synthase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rib4 PE=1 SV=1
A2039	-	-	-	-	-	-	-	-
A2040	-	-	GO:0005515(protein binding)	-	-	-	PSS32132.1 hypothetical protein PHL_CEN_2v2088 [Phlebia centrifuga]	SET domain-containing protein 5 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=set5 PE=1 SV=1
A2041	-	-	GO:0003723(RNA binding)	-	-	KOG2375 YGR178c Protein interacting with poly(A)-binding protein	XP_025369386.1 hypothetical protein IE81DRAFT_347637 [Ceraceosorus guamensis]	Ataxin-2 homolog OS=Dictyostelium discoideum OX=44689 GN=atxn2 PE=3 SV=1
A2042	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0051082(unfolded protein binding),GO:0016887(ATP hydrolysis activity)	K09497 CCT5; T-complex protein 1 subunit epsilon	-	KOG0357 At1g24510 Chaperonin complex component, TCP-1 epsilon subunit (CCT5)	XP_025186940.1 chaperonin Cpn60/TCP-1 family [Rhizophagus irregularis DAOM 181602=DAOM 197198]	T-complex protein 1 subunit epsilon OS=Arabidopsis thaliana OX=3702 GN=CCT5 PE=1 SV=1
A2043	GO:0005975(carbohydrate metabolic process)	-	GO:0016853(isomerase activity),GO:0003824(catalytic activity),GO:0030246(carbohydrate binding)	K01792 E5.1.3.15; glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG1594 At4g23730 Uncharacterized enzymes related to aldose 1-epimerase	XP_002849713.1 UPF0010 protein [Microsporium canis CBS 113480]	Putative glucose-6-phosphate 1-epimerase OS=Cenchrus ciliaris OX=35872 PE=2 SV=1

A2044	GO:0006470(protein dephosphorylation)	-	GO:0046872(metal ion binding),GO:0004722(protein serine/threonine phosphatase activity),GO:0043169(cation binding)	-	-	KOG0698 At1g09160 Serine/threonine protein phosphatase	-	Probable protein phosphatase 2C 5 OS=Arabidopsis thaliana OX=3702 GN=At1g09160 PE=2 SV=1
A2045	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10352 MYH9s; myosin heavy chain 9/10/11/14	map05130 Pathogenic Escherichia coli infection;map04810 Regulation of actin cytoskeleton;map04814 Motor proteins;map04530 Tight junction;map04270 Vascular smooth muscle contraction	KOG0160 At4g28710 Myosin class V heavy chain	CCE86957.1 Piso0_005481 [Milleromyia farinosa CBS 7064]	Myosin-2 heavy chain OS=Dictyostelium discoideum OX=44689 GN=mhcA PE=1 SV=3
A2046	-	-	GO:0005515(protein binding)	-	-	-	-	F-box only protein 15 OS=Homo sapiens OX=9606 GN=FBXO15 PE=1 SV=2
A2047	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1198 Hs14776255 Zinc-binding oxidoreductase	XP_025188114.1 chaperonin 10-like protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Synaptic vesicle membrane protein VAT-1 homolog-like OS=Mus musculus OX=10090 GN=Vat1l PE=1 SV=2
A2048	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2049	-	GO:0016021(integral component of membrane)	-	K12385 NPC1; Niemann-Pick C1 protein	map04142 Lysosome;map04979 Cholesterol metabolism	KOG3664 Hs17448847 Predicted patched transmembrane receptor	CAF9922216.1 hypothetical protein IMSHALPRED_005622 [Imshaugia aleurites]	Protein dispatched homolog 1 OS=Danio rerio OX=7955 GN=disp1 PE=2 SV=1
A2050	-	-	-	-	-	KOG3664 Hs17448847 Predicted patched transmembrane receptor	-	Protein dispatched homolog 3 OS=Mus musculus OX=10090 GN=Disp3 PE=2 SV=1
A2051	-	-	GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding),GO:0004499(N,N-dimethylaniline monooxygenase activity)	-	-	KOG1399 CE06138 Flavin-containing monooxygenase	XP_006674885.1 uncharacterized protein BATDEDRAFT_1833, partial [Batrachochytrium dendrobatidis JAM81]	Dimethylaniline monooxygenase [N-oxide-forming] 2 OS=Pongo abelii OX=9601 GN=FMO2 PE=2 SV=3
A2052	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-

A2053	-	-	GO:0003676(nucleic acid binding),GO:0004386(helicase activity),GO:0005524(ATP binding)	K18995 DHX29; ATP-dependent RNA helicase DHX29 [EC:3.6.4.13]	-	KOG0920 At2g30800 ATP-dependent RNA helicase A	KAF1805523.1 P-loop containing nucleoside triphosphate hydrolase protein [Mucor lusitanicus]	3'-5' RNA helicase YTHDC2 OS=Pongo abelii OX=9601 GN=YTHDC2 PE=2 SV=2
A2054	-	-	-	-	-	KOG0714 Hs9558755 Molecular chaperone (DnaJ superfamily)	KIY44118.1 DnaJ-domain-containing protein [Fistulina hepatica ATCC 64428]	DnaJ homolog subfamily B member 9 OS=Cricetulus griseus OX=10029 GN=DNAJB9 PE=1 SV=1
A2055	-	-	-	-	-	KOG1208 Hs10190746 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	KAG0021602.1 hypothetical protein BGZ81_008845 [Podila clonocystis]	Retinol dehydrogenase 14 OS=Homo sapiens OX=9606 GN=RDH14 PE=1 SV=1
A2056	-	-	-	-	-	KOG1208 Hs10190746 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	KFH63134.1 hypothetical protein MVEG_11171 [Podila verticillata NRRL 6337]	Retinol dehydrogenase 14 OS=Mus musculus OX=10090 GN=Rdh14 PE=1 SV=1
A2057	GO:0031124(mRNA 3'-end processing)	-	GO:0003676(nucleic acid binding),GO:0005515(protein binding)	K15542 PFS2; polyadenylation factor subunit 2	map03015 mRNA surveillance pathway	KOG0284 Hs19923529 Polyadenylation factor I complex, subunit PFS2	QIX00520.1 hypothetical protein AMS68_006037 [Peltaster fructicola]	pre-mRNA 3' end processing protein WDR33 OS=Mus musculus OX=10090 GN=Wdr33 PE=1 SV=1
A2058	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG0253 Hs22060805 Synaptic vesicle transporter SV2 (major facilitator superfamily)	XP_025376273.1 MFS general substrate transporter [Acaromyces ingoldii]	Synaptic vesicle 2-related protein OS=Rattus norvegicus OX=10116 GN=Svop PE=1 SV=1
A2059	GO:0006281(DNA repair)	-	-	K03510 POLI; DNA polymerase iota [EC:2.7.7.7]	map03460 Fanconi anemia pathway	KOG2095 Hs6005848 DNA polymerase iota/DNA damage inducible protein	XP_025381270.1 DNA/RNA polymerase [Acaromyces ingoldii]	DNA polymerase iota OS=Homo sapiens OX=9606 GN=POLI PE=1 SV=3
A2060	-	-	GO:0043023(ribosomal large subunit binding)	K07562 NMD3; 60S ribosomal export protein NMD3	map03013 Nucleocytoplasmic transport;map03008 Ribosome biogenesis in eukaryotes	KOG2613 Hs19923796 NMD protein affecting ribosome stability and mRNA decay	RHZ80547.1 hypothetical protein Glove_134g186 [Diversispora epigaea]	60S ribosomal export protein NMD3 OS=Dictyostelium discoideum OX=44689 GN=nmd3 PE=3 SV=1
A2061	-	GO:0016021(integral component of membrane)	-	K12385 NPC1; Niemann-Pick C1 protein	map04142 Lysosome;map04979 Cholesterol metabolism	KOG1933 Hs4557803 Cholesterol transport protein (Niemann-Pick C disease protein)	KAG2175248.1 hypothetical protein INT44_007736 [Umbelopsis vinacea]	NPC intracellular cholesterol transporter 1 OS=Homo sapiens OX=9606 GN=NPC1 PE=1 SV=2

A2062	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0004713(protein tyrosine kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At2g24360 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9644875.1 kinase-like protein [Thelephora ganbajun]	Putative serine/threonine-protein kinase/receptor R831 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_R831 PE=3 SV=2
A2063	-	-	-	K19219 JMD7; peptidyl-lysine (3S)-dioxygenase / protease [EC:1.14.11.6 3 3.4.-.-]	-	KOG2132 Hs21314714.1 Uncharacterized conserved protein, contains JmjC domain	KIM46181.1 hypothetical protein M413DRAFT_23953 [Hebeloma cylindrosporum h7]	HSPB1-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Hspbap1 PE=1 SV=1
A2064	-	-	-	-	-	-	-	-
A2065	-	-	-	-	-	-	-	-
A2066	-	-	-	-	-	-	-	-
A2067	GO:0006213(pyrimidine nucleoside metabolic process), GO:0006206(pyrimidine nucleobase metabolic process)	-	GO:0016763(pentose transferase activity),GO:0004645(1,4-alpha-D-glucan phosphorylase activity),GO:0016757(glycosyltransferase activity),GO:0016154(pyrimidine-nucleoside phosphorylase activity)	-	-	-	KAF9123525.1 hypothetical protein BGX30_001420 [Mortierella sp. GBA39]	Pyrimidine-nucleoside phosphorylase OS=Geobacillus stearothermophilus OX=1422 GN=pdp PE=1 SV=1
A2068	-	-	-	-	-	-	RUS19902.1 hypothetical protein BC937DRAFT_86735 [Endogone sp. FLAS-F59071]	-
A2069	-	GO:0005737(cytoplasm)	GO:0005515(protein binding)	-	-	-	-	-
A2070	-	-	-	-	-	-	-	-
A2071	-	-	GO:0004843(thiol-dependent deubiquitinase), GO:1990380(Lys48-specific deubiquitinase activity)	K01309 MINDY1_2; ubiquitin carboxyl-terminal hydrolase MINDY-1/2 [EC:3.4.19.12]	-	KOG2427 Hs14785441 Uncharacterized conserved protein	KAG1143035.1 hypothetical protein G6F38_007331 [Rhizopus oryzae]	Ubiquitin carboxyl-terminal hydrolase MINDY-1 OS=Danio rerio OX=7955 GN=mindy1 PE=3 SV=1

A2072	GO:0015986(ATP synthesis coupled proton transport)	GO:0045261(proton-transporting ATP synthase complex, catalytic core F(1))	GO:0046933(proton-transporting ATP synthase activity, rotational mechanism)	K02134 ATPeF1D, ATP5D, ATP16; F-type H+-transporting ATPase subunit delta	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map04714 Thermogenesis;map00190 Oxidative phosphorylation;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease;map01100 Metabolic pathways	KOG1758 7291126 Mitochondrial F1F0-ATP synthase, subunit delta/ATP16	OBZ83218.1 ATP synthase subunit delta, mitochondria [Choanephora cucurbitarum]	ATP synthase subunit delta, mitochondrial OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=ATP16 PE=1 SV=2
A2073	GO:0006777(Mo-molybdopterin cofactor biosynthetic process)	GO:0005829(cytosol),GO:0019008(molybdopterin synthase complex)	GO:0030366(molybdopterin synthase activity)	K03635 MOCS2B, moaE; molybdopterin synthase catalytic subunit [EC:2.8.1.12]	map01240 Biosynthesis of cofactors;map04122 Sulfur relay system;map01100 Metabolic pathways;map00790 Folate biosynthesis	KOG3307 Hs4758732 Molybdopterin converting factor subunit 2	KAF9429017.1 Molybdopterin synthase catalytic subunit [Entomortierella beljakovae]	Molybdopterin synthase catalytic subunit OS=Taeniopygia guttata OX=59729 GN=MOCS2 PE=2 SV=1
A2074	-	-	-	-	-	-	-	-
A2075	GO:0006177(GMP biosynthetic process), GO:0006164(purine nucleotide biosynthetic process)	-	GO:0003922(GMP synthase (glutamine-hydrolyzing) activity),GO:0005524(ATP binding),GO:0003921(GMP synthase activity)	K01951 guaA, GMPs; GMP synthase (glutamine-hydrolyzing) [EC:6.3.5.2]	map00983 Drug metabolism - other enzymes;map00230 Purine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG1622 YMR217w GMP synthase	KAG0234322.1 GMP synthase (glutamine-hydrolyzing) [Actinomortierella wolffii]	GMP synthase [glutamine-hydrolyzing] OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=GUA1 PE=3 SV=1
A2076	-	-	-	-	-	-	-	-
A2077	-	-	-	-	-	-	-	-
A2078	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	KAF9026798.1 hypothetical protein BGZ52_005686, partial [Haplosporangium bisporale]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A2079	-	-	-	-	-	-	-	-
A2080	-	-	GO:0003677(DNA binding)	K03627 MBF1; putative transcription factor	-	KOG3398 At2g42680 Transcription factor MBF1	KAF5104848.1 hypothetical protein DV451_000241 [Geotrichum candidum]	Multiprotein-bridging factor 1a OS=Arabidopsis thaliana OX=3702 GN=MBF1A PE=2 SV=1
A2081	-	-	-	K01101 E3.1.3.41; 4-nitrophenyl phosphatase [EC:3.1.3.41]	map01120 Microbial metabolism in diverse environments;map00627 Aminobenzoate degradation	KOG2882 At5g36790 p-nitrophenyl phosphatase	KAF9114657.1 hypothetical protein BGX27_010234 [Mortierella sp. AM989]	Glycerol-3-phosphate phosphatase OS=Gallus gallus OX=9031 GN=PGP PE=2 SV=1

A2082	GO:0000350(generation of catalytic spliceosome for second transesterification step)	-	-	K12870 ISY1; pre-mRNA-splicing factor ISY1	map03040 Spliceosome	KOG3068 At3g18790 mRNA splicing factor	KAF0492483.1 pre-mRNA-splicing factor ISY1-like [Gigaspora margarita]	Protein isy-1 OS=Caenorhabditis elegans OX=6239 GN=isy-1 PE=1 SV=1
A2083	-	-	-	K11493 RCC1; regulator of chromosome condensation	-	-	KAG2233476.1 hypothetical protein INT48_003182, partial [Thamnidium elegans]	Protein pim1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=pim1 PE=1 SV=2
A2084	-	-	-	-	-	-	-	-
A2085	-	-	-	-	-	-	-	-
A2086	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	K00472 P4HA; prolyl 4-hydroxylase [EC:1.14.11.2]	map00330 Arginine and proline metabolism;map01100 Metabolic pathways	KOG1591 At1g20270 Prolyl 4-hydroxylase alpha subunit	OAL05793.1 hypothetical protein IQ06DRAFT_343048 [Stagonospora sp. SRC1sM3a]	Probable prolyl 4-hydroxylase 3 OS=Arabidopsis thaliana OX=3702 GN=P4H3 PE=2 SV=1
A2087	-	-	-	K19219 JMJD7; peptidyl-lysine (3S)-dioxygenase / protease [EC:1.14.11.63 3.4.-.-]	-	KOG2508 7294469 Predicted phospholipase	PIL37318.1 transcription factor [Ganoderma sinense ZZ0214-1]	Bifunctional peptidase and (3S)-lysyl hydroxylase JMJD7 OS=Homo sapiens OX=9606 GN=JMJD7 PE=1 SV=1
A2088	GO:0006396(RNA processing),GO:0045292(mRNA cis splicing, via spliceosome)	-	GO:0003723(RNA binding)	K12825 SF3A1, SAP114; splicing factor 3A subunit 1	map03040 Spliceosome	KOG0007 At1g14650 Splicing factor 3a, subunit 1	EPB88936.1 hypothetical protein HMPREF1544_04196 [Mucor circinelloides 1006PhL]	Probable splicing factor 3A subunit 1 OS=Arabidopsis thaliana OX=3702 GN=At1g14650 PE=1 SV=2
A2089	GO:0006414(translational elongation)	-	GO:0003746(translation elongation factor activity)	K03233 EEF1G; elongation factor 1-gamma	map05134 Legionellosis	KOG1627 YPL048w_2 Translation elongation factor EF-1 gamma	XP_006680023.1 uncharacterized protein BATDEDRAFT_37118 [Batrachochytrium dendrobatidis JAM81]	Elongation factor 1-gamma-A OS=Xenopus laevis OX=8355 GN=eef1g-a PE=1 SV=1
A2090	GO:0000413(protein peptidyl-prolyl isomerization),GO:006457(protein folding)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity),GO:0005515(protein binding)	K05864 PPID; CYPD; peptidyl-prolyl isomerase D [EC:5.2.1.8]	map05131 Shigellosis;map04217 Necroptosis;map04218 Cellular senescence;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease	KOG0865 CE22213 Cyclophilin type peptidyl-prolyl cis-trans isomerase	VUG18836.1 cyp41 [Brettanomyces bruxellensis]	Peptidyl-prolyl cis-trans isomerase OS=Hemicentrotus pulcherrimus OX=7650 PE=2 SV=1

A2091	GO:0006749(glutathione metabolic process)	-	GO:0050313(sulfur dioxygenase activity)	K01069 gloB; gloC, HAGH; hydroxyacylglutathione hydrolase [EC:3.1.2.6]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG0814 At1g53580 Glyoxylase	ORY23475.1 putative ETHE1 protein [Rhizoclostium globosum]	Persulfide dioxygenase ETHE1 homolog, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=GLY3 PE=1 SV=3
A2092	-	-	GO:0003723(RNA binding);GO:0003676(nucleic acid binding)	-	-	KOG4207 7297948 Predicted splicing factor, SR protein superfamily	-	Serine/arginine-rich splicing factor 8 OS=Homo sapiens OX=9606 GN=SRSF8 PE=1 SV=1
A2093	-	-	GO:0005515(protein binding)	-	-	-	RLL93055.1 hypothetical protein CFD26_100455 [Aspergillus turcosus]	-
A2094	-	-	-	-	-	-	ORY64240.1 phosphotransferase enzyme family protein [Pseudomonas ariella vexata]	-
A2095	-	-	-	-	-	-	-	-
A2096	-	-	-	-	-	KOG3290 CE20432 Peroxisomal phytanoyl-CoA hydroxylase	KXS16117.1 hypothetical protein M427DRAFT_56012 [Gonapodya prolifera JEL478]	Phytanoyl-CoA dioxygenase, peroxisomal OS=Rattus norvegicus OX=10116 GN=Phyh PE=1 SV=2
A2097	-	-	-	K00477 PHYH; phytanoyl-CoA hydroxylase [EC:1.14.11.18]	map04146 Peroxisome	KOG3290 Hs545384 Peroxisomal phytanoyl-CoA hydroxylase	KXS14453.1 PhyH-domain-containing protein, partial [Gonapodya prolifera JEL478]	Phytanoyl-CoA dioxygenase, peroxisomal OS=Rattus norvegicus OX=10116 GN=Phyh PE=1 SV=2
A2098	-	-	-	-	-	-	-	-
A2099	-	-	-	K24083 ABHD13; abhydrolase domain-containing protein 13 [EC:3.-.-.-]	-	KOG1552 At1g32190_1 Predicted alpha/beta hydrolase	RUS12691.1 Alpha/Beta hydrolase protein [Endogone sp. FLAS-F59071]	Alpha/beta hydrolase domain-containing protein 17C OS=Danio rerio OX=7955 GN=abhd17c PE=2 SV=1
A2100	GO:0006003(fructose 2,6-bisphosphate metabolic process), GO:0006000(fructose metabolic process)	-	GO:0003824(catalytic activity);GO:0005524(ATP binding);GO:0003873(6-phosphofructose-2-kinase activity)	K19029 PFKFB2; 6-phosphofructose-2-kinase / fructose-2,6-bisphosphatase 2 [EC:2.7.1.1053.1.3.46]	map04919 Thyroid hormone signaling pathway;map00051 Fructose and mannose metabolism;map04152 AMPK signaling pathway;map01100 Metabolic pathways	KOG0234 At1g07110 Fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase	XP_001588298.1 hypothetical protein SS1G_10745 [Sclerotinia sclerotiorum 1980 UF-70]	6-phosphofructose-2-kinase/fructose-2,6-bisphosphatase OS=Arabidopsis thaliana OX=3702 GN=FKFBP PE=1 SV=1
A2101	GO:0000398(mRNA splicing, via spliceosome)	-	GO:0005515(protein binding)	K12862 PLRG1, PRL1, PRP46; pleiotropic regulator 1	map03040 Spliceosome	KOG0285 Hs4505895 Pleiotropic regulator 1	RKP14141.1 WD40-repeat-containing domain protein [Piptopezalis cylindrospora]	Pleiotropic regulator 1 OS=Homo sapiens OX=9606 GN=PLRG1 PE=1 SV=1

A2102	-	-	-	-	-	KOG1618 YK R070w Predicted phosphatase	KAF9203732.1 hypothetical protein BGZ49_006113 [Haplosporangium sp. Z 27]	Mitochondrial hydrolase YKR070W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YKR070W PE=1 SV=1
A2103	GO:0051016(barbed-end actin filament capping)	GO:0008290(F-actin capping protein complex)	-	K10364 CAPZA; F-actin-capping protein subunit alpha	map04144 Endocytosis;map04814 Motor proteins	KOG0836 Hs5453599 F-actin capping protein, alpha subunit	XP_01660592.2.1 hypothetical protein SPPG_09418 [Spizellomyces punctatus DAOM BR117]	F-actin-capping protein subunit alpha-2 OS=Gallus gallus OX=9031 GN=CAPZA2 PE=1 SV=1
A2104	GO:0070682(proteasome regulatory particle assembly)	-	GO:0005515(protein binding)	K06693 PSMD9, RPN4; 26S proteasome regulatory subunit N4	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG3129 At5g957950 26S proteasome regulatory complex, subunit PSMD9	KAF9920135.1 hypothetical protein FBU30_010063 [Linnemanniacybae]	26S proteasome non-ATPase regulatory subunit 9 OS=Mus musculus OX=10090 GN=Psmd9 PE=1 SV=1
A2105	-	-	-	-	-	-	-	-
A2106	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015297(antporter activity),GO:0042910(xenobiotic transmembrane transporter activity)	K03327 TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family	-	KOG1347 Hs8922709 Uncharacterized membrane protein, predicted efflux pump	KAF0546341.1 MATE efflux family protein [Gigaspora margarita]	Multidrug and toxin extrusion protein 1 OS=Pongo abelii OX=9601 GN=SLC47A1 PE=2 SV=1
A2107	GO:0006542(glutamine biosynthetic process), GO:0006807(nitrogen compound metabolic process)	-	GO:0004356(glutamate-ammonia ligase activity),GO:0003824(catalytic activity)	K01915 glnA, GLUL; glutamine synthetase [EC:6.3.1.2]	map00910 Nitrogen metabolism;map04217 Necroptosis;map01120 Microbial metabolism in diverse environments;map04724 Glutamatergic synapse;map04727 GABAergic synapse;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map02020 Two-component system;map00220 Arginine biosynthesis;map01100 Metabolic pathways;map00630 Glyoxylate	KOG0683 At5g35630 Glutamine synthetase	RIB08118.1 glutamine synthetase [Gigaspora rosea]	Glutamine synthetase cytosolic isozyme OS=Daucus carota OX=4039 GN=GLN1 PE=2 SV=1

A2108	GO:0006542(glutamine biosynthetic process), GO:0006807(nitrogen compound metabolic process)	-	GO:0004356(glutamate-ammonia ligase activity), GO:0003824(catalytic activity)	K01915 glnA, GLUL; glutamine synthetase [EC:6.3.1.2]	map00910 Nitrogen metabolism;map04217 Necroptosis;map01120 Microbial metabolism in diverse environments;map04724 Glutamatergic synapse;map04727 GABAergic synapse;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map02020 Two-component system;map00220 Arginine biosynthesis;map01100 Metabolic pathways;map00630 Glyoxylate	KOG0683 At5g37600 Glutamine synthetase	RUS20061.1 glutamine synthetase 1 [Endogone sp. FLAS-F59071]	Glutamine synthetase OS=Lactuca sativa OX=4236 PE=2 SV=2
A2109	-	-	-	-	-	-	-	-
A2110	-	-	-	-	-	-	-	-
A2111	-	-	-	-	-	-	-	-
A2112	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding), GO:0004672(protein kinase activity), GO:0005524(ATP binding)	K21157 SAK1; SNF1-activating kinase 1 [EC:2.7.11.1]	map04138 Autophagy - yeast	KOG0032 Hs21389439 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	CAF9920635.1 hypothetical protein HETSPECPRD_004321 [Heterodermis speciosa]	Ribosomal protein S6 kinase alpha-5 OS=Pongo abelii OX=9601 GN=RPS6KA5 PE=2 SV=1
A2113	GO:0072488(ammonium transmembrane transport)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 At3g24300 Ammonia permease	KAF9121223.1 hypothetical protein BGX30_00272 [Mortierella sp. GBA39]	Ammonium transporter 1 member 3 OS=Solanum lycopersicum OX=4081 GN=AMT1-3 PE=2 SV=1
A2114	GO:0072488(ammonium transmembrane transport), GO:0042981(regulation of apoptotic process)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 At3g24300 Ammonia permease	KAF9137593.1 hypothetical protein BGX30_010076 [Mortierella sp. GBA39]	Ammonium transporter 1 member 3 OS=Solanum lycopersicum OX=4081 GN=AMT1-3 PE=2 SV=1
A2115	-	GO:0005783(endoplasmic reticulum), GO:0016021(integral component of membrane), GO:0072546(EMC complex)	-	K23567 EMC6, TMEM93; ER membrane protein complex subunit 6	-	KOG4455 Hs13775220 Uncharacterized conserved protein	XP_007302545.1 hypothetical protein STEHIDRAFT_155151 [Stereum hirsutum FP-91666 SS1]	ER membrane protein complex subunit 6 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC1020.11c PE=3 SV=2
A2116	-	-	GO:0016791(phosphatase activity)	K18043 OCA1; tyrosine-protein phosphatase OCA1 [EC:3.1.3.48]	-	KOG1572 At1g05000 Predicted protein tyrosine phosphatase	KNE63235.1 hypothetical protein AMAG_08384 [Allomyces macrogynus ATCC 38327]	Probable tyrosine-protein phosphatase DG1060 OS=Dictyostelium discoideum OX=44689 GN=DG1060 PE=3 SV=1
A2117	-	GO:0016021(integral component of membrane)	GO:0008146(sulfotransferase activity)	-	-	KOG3922 Hs5032219 Sulfotransferases	-	Uronyl 2-sulfotransferase OS=Mus musculus OX=10090 GN=Ust PE=2 SV=3

A2118	-	-	GO:0016746(acyltransferase activity),GO:0008374(O-acyltransferase activity)	K13506 GPAT3.4, AGPAT9, AGPAT6; glycerol-3-phosphate O-acyltransferase 3/4 [EC:2.3.1.15]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	KOG2898 At5g60620 Predicted phosphate acyltransferase, contains PlsC domain	RKO89322.1 hypothetical protein BDK51DRAFT_12602, partial [Blyttomyces helicus]	Glycerol-3-phosphate acyltransferase 9 OS=Arabidopsis thaliana OX=3702 GN=GPAT9 PE=1 SV=1
A2119	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	-	-
A2120	GO:1902600(proton transmembrane transport)	GO:0016020(membrane)	GO:0004427(inorganic diphosphatase activity),GO:0009678(pyrophosphate hydrolysis-driven proton transmembrane transporter activity)	-	-	-	KAG1209907.1 hypothetical protein G6F35_010653 [Rhizopus oryzae]	Pyrophosphate-energized membrane proton pump 3 OS=Arabidopsis thaliana OX=3702 GN=AVPL2 PE=3 SV=1
A2121	GO:0006891(intra-Golgi vesicle-mediated transport)	GO:0017119(Golgi transport complex)	-	-	-	KOG2033 At5g16300 Low density lipoprotein B-like protein	-	Conserved oligomeric Golgi complex subunit 1 OS=Arabidopsis thaliana OX=3702 GN=COG1 PE=1 SV=1
A2122	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K24887 GTPBP1; GTP-binding protein 1	-	KOG0463 Hs4758490 GTP-binding protein GP-1	ORY37466.1 P-loop containing nucleoside triphosphate hydrolase protein [Rhizoclostium globosum]	GTP-binding protein 1 (Fragment) OS=Pongo abelii OX=9601 GN=GTPBP1 PE=2 SV=2
A2123	GO:0000160(phosphorelay signal transduction system),GO:0006355(regulation of transcription, DNA-templated),GO:0009584(detection of visible light),GO:0016310(phosphorylation),GO:0007165(signal transduction)	-	GO:0005515(protein binding),GO:0016772(transferase activity, transferring phosphorus-containing groups),GO:0000155(phosphorelay sensor kinase activity)	-	-	KOG0519 At1g27320 Sensory transduction histidine kinase	TFY65059.1 hypothetical protein EVJ58_g2200, partial [Fomitopsis rosea]	Cyanobacterial phytochrome A OS=Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) OX=103690 GN=aphA PE=3 SV=1

A2124	GO:0006508(proteolysis)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0004176(ATP-dependent peptidase activity),GO:0004222(metalloendopeptidase activity),GO:0008270(zinc ion binding)	K08956 AFG3; AFG3 family protein [EC:3.4.24.-]	map05017 Spinocerebellar ataxia	-	ORX95647.1 ATP-dependent metalloproteinase Hfl [Basidiobolus meristosporus CBS 931.73]	Mitochondrial respiratory chain complexes assembly protein rca1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=yta12 PE=3 SV=1
A2125	-	-	GO:0019787(ubiquitin-like protein transferase activity)	K08343 ATG3; ubiquitin-like-conjugating enzyme ATG3	map04140 Autophagy - animal;map04138 Autophagy - yeast;map04136 Autophagy - other;map05167 Kaposi sarcoma-associated herpesvirus infection	KOG2981 7293868 Protein involved in autophagocytosis during starvation	ORX83196.1 hypothetical protein K493DRAFT_269782 [Basidiobolus meristosporus CBS 931.73]	Ubiquitin-like-conjugating enzyme ATG3 OS=Mus musculus OX=10090 GN=Atg3 PE=1 SV=1
A2126	-	GO:0005743(mitochondrial inner membrane),GO:0005747(mitochondrial respiratory chain complex I)	-	-	-	-	XP_031854611.1 uncharacterized protein SAPINGB_P004005 [Saprochaete ingens]	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2 OS=Arabidopsis thaliana OX=3702 GN=At1g76200 PE=1 SV=1
A2127	GO:0006364(rRNA processing)	-	GO:0019843(rRNA binding)	K14820 BRX1, BRX1; ribosome biogenesis protein BRX1	-	KOG2971 Hs20545215 RNA-binding protein required for biogenesis of the ribosomal 60S subunit	KAG0264122.1 Ribosome biogenesis protein brx1 [Actinomyces rella ambigua]	Ribosome biogenesis protein BRX1 homolog OS=Xenopus laevis OX=8355 GN=brx1 PE=2 SV=1
A2128	-	-	-	-	-	-	KAG0354549.1 hypothetical protein BG005_006406 [Podila minutissima]	-
A2129	-	-	GO:0003824(catalytic activity),GO:0005515(protein binding)	K12603 CNOT6, CCR4; CCR4-NOT transcription complex subunit 6 [EC:3.1.13.4]	map03018 RNA degradation	KOG0620 At3g58580 Glucose-repressible alcohol dehydrogenase transcriptional effector CCR4 and related proteins	ORY49370.1 hypothetical protein BCR33DRAFT_757418 [Rhizoclostium globosum]	Carbon catabolite repressor protein 4 homolog 2 OS=Arabidopsis thaliana OX=3702 GN=CCR4-2 PE=2 SV=2
A2130	-	-	-	-	-	-	-	-
A2131	-	-	-	-	-	-	-	-
A2132	-	-	-	-	-	-	KXS21091.1 NAD(P)-binding protein [Gonapodya prolifera JEL478]	-

A2133	-	-	-	-	-	KOG0048 At5g02320 Transcription factor, Myb superfamily	KXN66846.1 ternary protein-Dna Complex1, partial [Conidiobolus coronatus NRRL 28638]	Transcription factor MYB3R-5 OS=Arabidopsis thaliana OX=3702 GN=MYB3R5 PE=2 SV=1
A2134	GO:0006750(glutathione biosynthetic process)	-	GO:0004363(glutathione synthase activity),GO:0005524(ATP binding),GO:0016874(ligase activity)	-	-	KOG0021 At5g27380 Glutathione synthetase	TPX72981.1 glutathione synthase [Spizellomyces sp. 'palustris']	Glutathione synthetase, chloroplastic OS=Solanum lycopersicum OX=4081 GN=GSH2 PE=2 SV=1
A2135	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K07359 CAMKK2; calcium/calmodulin-dependent protein kinase kinase 2 [EC:2.7.11.17]	map04140 Autophagy - animal;map04211 Longevity regulating pathway;map05034 Alcoholism;map04936 Alcoholic liver disease;map04152 AMPK signaling pathway;map04920 Adipocytokine signaling pathway;map04921 Oxytocin signaling pathway	KOG0585 Hs17933758 Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	KAG0365213.1 hypothetical protein BGZ54_006754 [Gamsiella multidivariata]	Calcium/calmodulin-dependent protein kinase kinase 2 OS=Homo sapiens OX=9606 GN=CAMKK2 PE=1 SV=2
A2136	GO:0051603(proteolysis involved in cellular protein catabolic process), GO:0006508(proteolysis)	GO:0005839(proteasome complex), GO:0009376(HslUV protease complex)	GO:0004298(threonine-type endopeptidase activity)	-	-	-	KAG0298491.1 hypothetical protein BGZ96_011420, partial [Linnemannia gamsii]	ATP-dependent protease subunit HslV OS=Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966) OX=402881 GN=hslV PE=3 SV=1
A2137	-	-	-	-	-	-	-	-
A2138	-	-	-	K14823 EBP2, EBNA1BP2; rRNA-processing protein EBP2	-	KOG3080 YKL172w Nucleolar protein-like/EBNA1-binding protein	KAG2176537.1 hypothetical protein INT44_007200 [Umbelopsis vinacea]	rRNA-processing protein EBP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EBP2 PE=1 SV=1
A2139	-	-	GO:0046872(metal ion binding)	-	-	-	XP_020063750.1 heavy metal translocatin [Suhomyces tanzawaensis NRRL Y-17324]	Copper-transporting P-type ATPase OS=Sinorhizobium medicae (strain WSM419) OX=366394 GN=actP PE=1 SV=1
A2140	-	-	-	-	-	-	TPX75085.1 hypothetical protein CcCBS67573_g03643 [Chytridiomycetes confervae]	Cilia- and flagella-associated protein 61 OS=Mus musculus OX=10090 GN=Cfap61 PE=1 SV=2

A2141	GO:0030163(protein catabolic process)	GO:0005737(cytoplasm)	GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity);GO:0036402(proteasome-activating activity)	K03064 PSMC6, RPT4; 26S proteasome regulatory subunit T4	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG0651 At5g43010 26S proteasome regulatory complex, ATPase RPT4	XP_01660926.1.1 26S protease regulatory subunit 10B [Spizellomyces punctatus DAOM BR117]	26S proteasome regulatory subunit 10B homolog A OS=Arabidopsis thaliana OX=3702 GN=RPT4A PE=1 SV=1
A2142	GO:0006221(pyrimidine nucleotide biosynthetic process), GO:0006241(CTP biosynthetic process)	-	GO:0003883(CTP synthase activity)	K01937 pyrG, CTPS; CTP synthase [EC:6.3.4.2]	map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG2387 At3g12670 CTP synthase (UTP-ammonia lyase)	RUP43153.1 hypothetical protein BC936DRAFT_137543 [Jimgerdeman nia flammicorona]	CTP synthase 1-A OS=Xenopus laevis OX=8355 GN=ctps1-a PE=2 SV=1
A2143	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map04972 Pancreatic secretion;map04080 Neuroactive ligand-receptor interaction;map05164 Influenza A	KOG3627 7295687 Trypsin	KFH43498.1 Trypsin-like protein [Acremonium chrysogenum ATCC 11550]	Vitamin K-dependent protein C OS=Rattus norvegicus OX=10116 GN=Proc PE=2 SV=1
A2144	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG2325 At4g22990_2 Predicted transporter/transmembrane protein	KAF8623864.1 hypothetical protein AX17_007266 [Amanita inopinata Kibby_2008]	SPX domain-containing membrane protein OsI_17046 OS=Oryza sativa subsp. indica OX=39946 GN=OsI_17046 PE=3 SV=1
A2145	-	-	-	-	-	-	KAG1458467.1 hypothetical protein G6F57_014680 [Rhizopus oryzae]	-
A2146	-	-	GO:0005515(protein binding)	-	-	-	ORZ40864.1 hypothetical protein BCR44DRAFT_1423932, partial [Catenaria anguillulae PL171]	-
A2147	-	-	-	-	-	-	-	-
A2148	-	-	-	-	-	-	-	-

A2149	-	-	GO:0005085(guanyl-nucleotide exchange factor activity)	K20047 PAN1; actin cytoskeleton-regulatory complex protein PAN1	-	KOG4424 7295262 Predicted Rho/Rac guanine nucleotide exchange factor/faciog enital dysplasia protein 3	ORX70034.1 Dbl homology domain-containing protein [Linderina pennisporea]	FYVE, RhoGEF and PH domain-containing protein 6 OS=Homo sapiens OX=9606 GN=FGD6 PE=1 SV=2
A2150	GO:0034453(microtubule anchoring)	GO:0005815(microtubule organizing center)	GO:0005515(protein binding)	-	-	-	TPX71440.1 hypothetical protein SpCBS45565_g00997 [Spizellomyces sp. 'palustris']	Centrosomal protein 43 OS=Macaca fascicularis OX=9541 GN=CEP43 PE=2 SV=1
A2151	-	-	-	-	-	-	-	-
A2152	-	-	-	-	-	-	-	-
A2153	-	-	GO:0005515(protein binding)	-	-	KOG3595 7300687 Dyneins, heavy chain	-	Dynein beta chain, ciliary OS=Triploneustes gratilla OX=7673 PE=1 SV=1
A2154	GO:0006281(DNA repair)	-	GO:0003824(catalytic activity);GO:0003677(DNA binding)	K10801 MBD4; methyl-CpG-binding domain protein 4 [EC:3.2.2.-]	map03410 Base excision repair	-	RIB15589.1 DNA glycosylase [Gigaspora rosea]	Methyl-CpG-binding domain protein 4-like protein OS=Arabidopsis thaliana OX=3702 GN=MBD4L PE=1 SV=1
A2155	-	-	GO:0008270(zinc ion binding)	-	-	-	TPX64073.1 hypothetical protein SpCBS45565_g06174 [Spizellomyces sp. 'palustris']	Uncharacterized protein C18H10.09 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC18H10.09 PE=4 SV=2
A2156	-	-	-	-	-	-	-	-
A2157	GO:0055085(transmembrane transport);GO:0140021(mitochondrial ADP transmembrane transport);GO:1990544(mitochondrial ATP transmembrane transport)	GO:0005743(mitochondrial inner membrane)	GO:0005471(ATP:ADP antiporter activity)	K05863 SLC25A4S, ANT; solute carrier family 25 (mitochondrial adenine nucleotide translocator), member 4/5/6/31	map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05415 Diabetic cardiomyopathy;map04217 Necroptosis;map04218 Cellular senescence;map04613 Neutrophil extracellular trap formation;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05010 Alzheimer disease;map05012 Parkinson	KOG0749 Hs20554413 Mitochondrial ADP/ATP carrier proteins	TPX68954.1 hypothetical protein CcCBS67573_g07010 [Chytridiomycetes confervae]	ADP,ATP carrier protein OS=Parachlorella kessleri OX=3074 PE=3 SV=1

A2158	GO:0055085(transmembrane transport), GO:0140021(mitochondrial ADP transmembrane transport), GO:1990544(mitochondrial ATP transmembrane transport)	GO:0005743(mitochondrial inner membrane)	GO:0005471(ATP:ADP antiporter activity)	K05863 SLC25A4S, ANT; solute carrier family 25 (mitochondrial adenine nucleotide translocator), member 4/5/6/31	map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05415 Diabetic cardiomyopathy; map04217 Necroptosis;map04218 Cellular senescence;map04613 Neutrophil extracellular trap formation;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05010 Alzheimer disease;map05012 Parkinson	KOG0749 7292557 Mitochondrial ADP/ATP carrier proteins	TPX68954.1 hypothetical protein CcCBS67573_g07010 [Chytridiomycota confervae]	ADP,ATP carrier protein OS=Parachlorella kessleri OX=3074 PE=3 SV=1
A2159	-	-	-	-	-	-	-	-
A2160	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K08793 STK32, YANK; serine/threonine kinase 32 [EC:2.7.11.1]	-	KOG0986 7302050 G protein-coupled receptor kinase	RKP17416.1 Pkinase-domain-containing protein [Rozella allomyces CSF55]	G protein-coupled receptor kinase 2 OS=Drosophila melanogaster OX=7227 GN=Gprk2 PE=1 SV=3
A2161	GO:0006281(DNA repair)	-	-	-	-	KOG4712 HsM14861832 Uncharacterized conserved protein	KAG2226033.1 hypothetical protein INT45_002499 [Mucor circinatus]	Fanconi anemia group D2 protein OS=Homo sapiens OX=9606 GN=FANCD2 PE=1 SV=2
A2162	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	K08176 PHO84; MFS transporter, PHS family, inorganic phosphate transporter	-	KOG0252 At1g76430 Inorganic phosphate transporter	KAF9140505.1 Inorganic phosphate transporter pho84 [Mortierella sp. GBA39]	Probable inorganic phosphate transporter 1-9 OS=Arabidopsis thaliana OX=3702 GN=PHT1-9 PE=2 SV=1
A2163	-	-	-	-	-	-	-	-
A2164	GO:0055085(transmembrane transport)	-	-	K13577 SLC25A10, DIC; solute carrier family 25 (mitochondrial dicarboxylate transporter), member 10	map04964 Proximal tubule bicarbonate reclamation	KOG0759 At4g24570 Mitochondrial oxoglutarate/malate carrier proteins	XP_022457802.1 uncharacterized protein KUCA_T00001761001 [Kuraishia capsulata CBS 1993]	Mitochondrial uncoupling protein 4 OS=Arabidopsis thaliana OX=3702 GN=PUMP4 PE=2 SV=1
A2165	-	-	-	-	-	KOG2641 Hs8922707 Predicted seven transmembrane receptor - rhodopsin family	RIA99579.1 organic solute transporter Ostalpa-domain-containing protein [Glomus cerebriiforme]	Transmembrane protein 184C OS=Xenopus tropicalis OX=8364 GN=tmem184c PE=2 SV=1
A2166	-	-	-	-	-	-	-	-
A2167	-	-	-	-	-	-	TPX73331.1 hypothetical protein CcCBS67573_g05394 [Chytridiomycota confervae]	-
A2168	-	-	-	-	-	-	-	-

A2169	-	-	GO:0005515(protein binding)	-	-	KOG0504[7296935 FOG: Ankyrin repeat	KAF2105358.1 ankyrin repeat-containing domain protein, partial [Lophiotrema nucula]	-
A2170	-	-	-	-	-	-	XP_01660550.0.1 hypothetical protein SPPG_07378 [Spizellomyces punctatus DAOM BR117]	SANT and BTB domain regulator of class switch recombination OS=Xenopus laevis OX=8355 GN=sanbr PE=2 SV=1
A2171	-	-	-	-	-	-	-	-
A2172	GO:0006412(translation),GO:0000463(maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA))	GO:0005840(ribosome),GO:0022625(cytosolic large ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02918 RP-L35e, RPL35; large subunit ribosomal protein L35e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3436[Hs6005860 60S ribosomal protein L35	KAF7739645.1 60S ribosomal protein L35 [Entomophthora muscae]	Large ribosomal subunit protein uL29 OS=Mus musculus OX=10090 GN=Rpl35 PE=1 SV=1
A2173	-	GO:0015935(small ribosomal subunit)	GO:0005515(protein binding),GO:0043022(ribosome binding)	K14753 RACK1; guanine nucleotide-binding protein subunit beta-2-like 1 protein	map05162 Measles	KOG0279[Hs5174447 G protein beta subunit-like protein	KAG2178958.1 hypothetical protein INT43_001805 [Umberlopsis isabellina]	Small ribosomal subunit protein RACK1 OS=Macaca fascicularis OX=9541 GN=GNB2L1 PE=2 SV=3
A2174	-	-	-	-	-	-	-	-
A2175	-	-	-	-	-	-	-	-
A2176	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2177	GO:0043039(tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation),GO:0006412(translation)	GO:0005737(cytoplasm)	GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0000166(nucleotide binding)	K01885 EARS; gltX; glutamyl-tRNA synthetase [EC:6.1.1.17]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map00970 Aminoacyl-tRNA biosynthesis;map01100 Metabolic pathways	-	KAF7322471.1 Glutamate-tRNA ligase [Mycena chlorophos]	Probable glutamate--tRNA ligase, cytoplasmic OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=gus1 PE=1 SV=1
A2178	-	-	-	-	-	-	-	-
A2179	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0000981(DNA-binding transcription factor activity, RNA polymerase II-specific),GO:0008270(zinc ion binding)	-	-	-	-	-
A2180	-	-	-	-	-	-	-	-
A2181	-	-	-	-	-	-	-	-
A2182	-	-	-	-	-	-	-	-

A2183	GO:0098869 (cellular oxidant detoxification)	-	GO:0016209 (antioxidant activity), GO:0016491 (oxidoreductase activity), GO:0051920 (peroxidase activity)	-	-	KOG0854 Hs4758638 Alkyl hydroperoxide reductase, thiol specific antioxidant and related enzymes	KAF7730301.1 hypothetical protein EC973_002545 [Apophysomyces ossiformis]	1-Cys peroxiredoxin OS=Dictyostelium discoideum OX=44689 GN=DDB_G0282517 PE=3 SV=1
A2184	-	-	GO:0005515 (protein binding)	-	-	KOG3689 7298454 Cyclic nucleotide phosphodiesterase	RKP17717.1 hypothetical protein ROZALSC1DR AFT_30510, partial [Rozella allomycis CSF55]	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11 OS=Drosophila melanogaster OX=7227 GN=Pde11 PE=1 SV=4
A2185	-	-	-	-	-	-	-	-
A2186	-	-	GO:0046982 (protein heterodimerization activity)	K08066 NFYC, HAP5; nuclear transcription factor Y, gamma	map04612 Antigen processing and presentation; map05152 Tuberculosis	KOG1657 YOR358w CCAAT-binding factor, subunit C (HAP5)	ORZ13112.1 histone-fold-containing protein [Absidia repens]	Transcriptional activator HAP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HAP5 PE=1 SV=1
A2187	-	-	GO:0016491 (oxidoreductase activity)	-	-	KOG2733 7299619 Uncharacterized membrane protein	ORX99326.1 saccharopine dehydrogenase [Basidiobolus meristosporus CBS 931.73]	Putative trans-acting enoyl reductase Rv2449c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2449c PE=1 SV=3
A2188	-	-	GO:0003824 (catalytic activity)	K12603 CNOT6, CCR4; CCR4-NOT transcription complex subunit 6 [EC:3.1.13.4]	map03018 RNA degradation	KOG2338 Hs14784709 Transcriptional effector CCR4-related protein	XP_016608952.1 hypothetical protein SPPG_04013 [Spizellomyces punctatus DAOM BR117]	Protein angel homolog 2 OS=Danio rerio OX=7955 GN=angel2 PE=2 SV=1
A2189	-	-	-	-	-	KOG1205 Hs7706318 Predicted dehydrogenase	KAF5724881.1 ketoreductase [Fusarium mundagurra]	Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens OX=9606 GN=DHRS7 PE=1 SV=1
A2190	-	-	-	-	-	-	-	-
A2191	-	-	-	-	-	-	-	-
A2192	-	-	-	-	-	-	OON04310.1 hypothetical protein BSLG_05565 [Batrachochytrium salamandrivorans]	Cilia- and flagella-associated protein 74 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP74 PE=1 SV=1
A2193	-	-	-	-	-	-	-	-
A2194	-	-	-	-	-	KOG2381 At5g24240.2 Phosphatidylinositol 4-kinase	-	Phosphatidylinositol 4-kinase gamma 4 OS=Oryza sativa subsp. japonica OX=39947 GN=PI4KG4 PE=1 SV=1
A2195	-	-	-	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG1113 7303815 cAMP-dependent protein kinase types I and II, regulatory subunit	OON08583.1 hypothetical protein BSLG_02183 [Batrachochytrium salamandrivorans]	cAMP-dependent protein kinase type II regulatory subunit OS=Strongylocentrotus purpuratus OX=7668 PE=2 SV=1

A2196	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors);GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG0141 Hs4501857 Isovaleryl-CoA dehydrogenase	CDS12487.1 hypothetical protein LRAMOSA04681 [Lichtheimia ramosa]	Acyl-CoA dehydrogenase apdG OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=apdG PE=2 SV=1
A2197	-	-	GO:0008270(zinc ion binding)	-	-	-	-	Protein translocase subunit SecA OS=Maridesulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIMB 8403 / VKM B-1763) OX=526222 GN=secA PE=3 SV=1
A2198	-	-	GO:0005515(protein binding)	K10752 RBBP4, HAT2; CAF1, MIS16; histone-binding protein RBBP4	map04218 Cellular senescence;map03082 ATP-dependent chromatin remodeling;map03083 Polycomb repressive complex	KOG0264 Hs20551282 Nucleosome remodeling factor, subunit CAF1/NURF55/MSI1	XP_018988854.1 histone acetyltransferase type B subunit 2 [Cryptococcus amyloletus CBS 6039]	Histone-binding protein RBBP7 OS=Pongo abelii OX=9601 GN=RBBP7 PE=3 SV=1
A2199	-	-	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	-	-	KOG0061 At2g37010 Transporter, ABC superfamily (Breast cancer resistance protein)	TKW55380.1 ABC transporter G family member 24 [Colletotrichum tanacetii]	Putative white-brown complex homolog protein 30 OS=Arabidopsis thaliana OX=3702 GN=WBC30 PE=1 SV=3
A2200	GO:0006364(rRNA processing)	-	GO:0003723(RNA binding);GO:0008168(methyltransferase activity)	-	-	KOG1596 Hs12056465 Fibrillarin and related nucleolar RNA-binding proteins	RKP08637.1 Fibrillarin-domain-containing protein [Thamnocephalus sphaerospora]	rRNA 2'-O-methyltransferase fibrillarin OS=Xenopus laevis OX=8355 GN=fbl PE=2 SV=1
A2201	-	-	-	-	-	KOG4538 Hs13129104.2 Predicted coiled-coil protein	-	-
A2202	GO:0036211(protein modification process)	-	GO:0004719(protein-L-isoaspartate (D-aspartate) O-methyltransferase activity)	K00573 E2.1.1.77, pcm; protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77]	-	KOG1661 Hs4885539 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	XP_024337967.1 hypothetical protein POSPLADRAFT_1058102 [Postia placenta MAD-698-R-SB12]	Protein-L-isoaspartate O-methyltransferase OS=Triticum aestivum OX=4565 GN=PCM PE=1 SV=1
A2203	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A2204	-	-	-	-	-	-	XP_503106.1 YALI0D21318p [Yarrowia lipolytica CLIB122]	Phosphoglycolate phosphatase OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=gph PE=3 SV=1
A2205	-	-	-	-	-	-	PIA15707.1 CRAL/TRIO domain-containing protein [Coemansia reversa NRRL 1564]	CRAL-TRIO domain-containing protein C589.09, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC589.09 PE=4 SV=1
A2206	GO:0045892(negative regulation of transcription, DNA-templated)	GO:0005634(nucleus)	GO:0005515(protein binding)	-	-	-	RKP05516.1 TH1 protein-domain-containing protein [Thamnocephalus sphaerospora]	Negative elongation factor D OS=Drosophila melanogaster OX=7227 GN=TH1 PE=1 SV=2

A2207	-	-	GO:0051287(NAD binding)	-	-	-	KAF9120706.1 hypothetical protein BGX30_003000 [Mortierella sp. GBA39]	Glyoxylate reductase OS=Thermofilum pendens (strain DSM 2475 / Hrk 5) OX=368408 GN=gyaR PE=3 SV=1
A2208	-	-	GO:0051287(NAD binding)	-	-	KOG0069 7298717 Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	XP_019049856.1 hypothetical protein I302_00275 [Kwoniella bestiolae CBS 10118]	Glyoxylate reductase OS=Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1) OX=186497 GN=gyaR PE=1 SV=1
A2209	-	-	-	-	-	-	-	Wings apart-like protein 1 OS=Arabidopsis thaliana OX=3702
A2210	GO:0006289(nucleotide-excision repair),GO:0006367(transcription initiation from RNA polymerase II promoter)	-	GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0016787(hydrolase activity),GO:0003678(DNA helicase activity)	K10843 ERCC3, XPB; DNA excision repair protein ERCC-3 [EC:5.6.2.4]	map03420 Nucleotide excision repair;map03022 Basal transcription factors	-	KAF9976124.1 DNA repair helicase RAD25 [Actinomortierella ambigua]	General transcription and DNA repair factor IIH helicase subunit XPB OS=Dictyostelium discoideum OX=44689 GN=repB PE=2 SV=1
A2211	-	-	GO:0016491(oxidoreductase activity)	K17743 XYL1, XYRA; D-xylose reductase [EC:1.1.1.307 1.1.1.430 1.1.1.431]	map00040 Pentose and glucuronate interconversions;map01100 Metabolic pathways	KOG1577 YHR104w Aldo/keto reductase family proteins	KAF8948477.1 NAD(P)H-dependent D-xylose reductase (XR) [Haplosporangium gracile]	Probable NAD(P)H-dependent D-xylose reductase xyl1 OS=Emmericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=xyl1 PE=3 SV=1
A2212	GO:0036158(outer dynein arm assembly),GO:0036159(inner dynein arm assembly)	GO:0005930(axoneme)	GO:0070840(dynein complex binding),GO:0005515(protein binding)	-	-	-	KXS09247.1 outer arm dynein light chain 1 [Gonapodya prolifera JEL478]	Dynein axonemal assembly factor 1 OS=Bos taurus OX=9913 GN=DNAAF1 PE=2 SV=2
A2213	GO:0090266(regulation of mitotic cell cycle spindle assembly checkpoint)	GO:0005680(anaphase-promoting complex)	GO:0003824(catalytic activity)	-	-	KOG4178 At4g02340 Soluble epoxide hydrolase	KAF4240593.1 hypothetical protein CNMCM6457_007171 [Aspergillus fumigatus affinis]	3-oxoadipate enol-lactonase 1 OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=pcaD PE=4 SV=2
A2214	-	-	GO:0005515(protein binding)	-	-	-	KAG1122277.1 hypothetical protein G6F42_011632 [Rhizopus oryzae]	Mitochondrial division protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=mdv1 PE=3 SV=1
A2215	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A2216	-	-	-	-	-	-	-	-
A2217	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02919 RP-L36, MRPL36, rpmJ; large subunit ribosomal protein L36	map03010 Ribosome	KOG4122 At5g20180 Mitochondrial/chloroplast ribosomal protein L36	XP_025361815.1 hypothetical protein BDZ90DRAFT_260867 [Jaminaea rosea]	Large ribosomal subunit protein bL36 OS=Buchnera aphidicola subsp. Baizongia pistaciae (strain Bp) OX=224915 GN=rpmJ PE=3 SV=1

A2218	-	-	GO:0051287(NA D binding)	-	-	KOG0068 At1g17740 D-3-phosphoglycerate dehydrogenase, D-isomer-specific 2-hydroxy acid dehydrogenase superfamily	XP_019049856.1 hypothetical protein [302_00275 [Kwoniella bestiolae CBS 101118]	Glyoxylate reductase OS=Thermofilum pendens (strain DSM 2475 / Hrk 5) OX=368408 GN=gyaR PE=3 SV=1
A2219	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	-	ORX51081.1 kinesin-domain-containing protein, partial [Piromyces finnis]	Kinesin-related protein 3 OS=Dictyostelium discoideum OX=44689 GN=kif3 PE=1 SV=1
A2220	-	-	GO:0005515(protein binding)	K18730 GIGYF; PERQ amino acid-rich with GYF domain-containing protein	-	KOG1862 Hs12007656 GYF domain containing proteins	-	GRB10-interacting GYF protein 2 OS=Mus musculus OX=10090 GN=Gigyf2 PE=1 SV=2
A2221	-	-	GO:0016787(hydrolase activity)	K03426 E3.6.1.22, NUDT12, nudC; NAD+ diphosphatase [EC:3.6.1.22]	map04146 Peroxisome;map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	KOG3084 Hs13899267_2 NADH pyrophosphatase I of the Nudix family of hydrolases	ORX81315.1 hypothetical protein K493DRAFT_320706 [Basidiobolus meristosporus CBS 931.73]	NAD-capped RNA hydrolase NUDT12 OS=Homo sapiens OX=9606 GN=NUDT12 PE=1 SV=1
A2222	GO:0006094(gluconeogenesis)	-	GO:0003941(L-serine ammonia-lyase activity),GO:0051539(4 iron, 4 sulfur cluster binding)	-	-	-	KAF0432778.1 L-serine ammonia-lyase [Gigaspora margarita]	L-serine dehydratase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=sdaA PE=3 SV=1
A2223	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0157 At1g67110 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	XP_031025487.1 uncharacterized protein SmJEL517_g02588 [Synchytrium microbalum]	Cytokinin hydroxylase OS=Arabidopsis thaliana OX=3702 GN=CYP735A2 PE=1 SV=1

A2224	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAG2188994.1 hypothetical protein INT44_004136 [Umbelopsis vinacea]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei OX=5702 GN=CRK2 PE=3 SV=1
A2225	-	-	-	-	-	-	-	-
A2226	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A2227	-	-	-	-	-	-	PVU87440.1 hypothetical protein BB561_006329, partial [Smittium simulii]	-
A2228	-	-	-	-	-	-	KIM52504.1 hypothetical protein SCLCIDRAFT_1223705 [Scleroderma citrinum Foug A]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A2229	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A2230	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	-	-
A2231	-	-	-	-	-	-	-	-
A2232	-	-	-	-	-	-	ORY75863.1 hypothetical protein LY90DRAFT_314474, partial [Neocallimastix californiae]	-
A2233	-	-	-	-	-	KOG3399 Hs9558721 Predicted Yippee-type zinc-binding protein	KDQ21711.1 hypothetical protein BOTBODRAFT_26141 [Botryobasidium botryosum FD-172 SS1]	Protein yippee-like 1 OS=Mus musculus OX=10090 GN=Ypel1 PE=2 SV=1
A2234	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	KAG4088656.1 hypothetical protein H8356DRAFT_1724123 [Neocallimastix sp. JGI-2020a]	Adenylate cyclase type 10 OS=Oryctolagus cuniculus OX=9986 GN=ADCY10 PE=2 SV=1

A2235	GO:0006644(phospholipid metabolic process)	-	-	K18693 DPP1, DPPL, PLPP4_5; diacylglycerol diphosphate phosphatase / phosphatidate phosphatase [EC:3.6.1.75 3.1.3.4]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism	KOG3030 At3g02600 Lipid phosphate phosphatase and related enzymes of the PAP2 family	KAG2179354.1 hypothetical protein INT44_006200 [Umbelopsis vinacea]	Putative lipid phosphate phosphatase 3, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=LPP3 PE=2 SV=1
A2236	GO:0035556(intracellular signal transduction);GO:0045454(cell redox homeostasis)	-	GO:0016491(oxidoreductase activity);GO:0050660(flavin adenine dinucleotide binding);GO:0016668(oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor)	K00382 DLDLpd, pdhD; dihydrolipoyl dehydrogenase [EC:1.8.1.4]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00020 Citrate cycle (TCA cycle);map00280 Valine, leucine and isoleucine degradation;map00260 Glycine, serine and	KOG1335 At3g17240 Dihydrolipoamide dehydrogenase	RKP39590.1 hypothetical protein BJ085DRAFT_38114 [Dimargaris cristalligena]	Mercuric reductase OS=Lysinibacillus sphaericus OX=1421 GN=merA PE=1 SV=2
A2237	-	-	-	-	-	-	-	-
A2238	-	-	-	-	-	-	-	-
A2239	-	-	-	K14405 FIP1L1, FIP1; pre-mRNA 3'-end-processing factor FIP1	map03015 mRNA surveillance pathway	KOG1049 CE09873 Polyadenylation factor I complex, subunit FIP1	XP_008075042.1 hypothetical protein VCUG_02028 [Vavraia culicis subsp. floridensis]	Pre-mRNA 3'-end-processing factor FIP1 OS=Rattus norvegicus OX=10116 GN=Fip111 PE=1 SV=1
A2240	GO:0036211(protein modification process);GO:0018095(protein polyglutamylation)	-	GO:0003676(nucleic acid binding);GO:0004523(RNA-DNA hybrid ribonuclease activity)	K06047 TTL; tubulin-tyrosine ligase [EC:6.3.2.25]	-	KOG2157 Hs11068135 Predicted tubulin-tyrosine ligase	ORX65268.1 putative tubulin polyglutamylase TTL1 [Anaeromyces robustus]	Probable alpha-tubulin polyglutamylase Ttl1 OS=Tetrahymena thermophila (strain SB210) OX=312017 GN=Ttl1 PE=3 SV=2
A2241	GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity);GO:0005524(ATP binding)	-	-	-	XP_962102.1 hypothetical protein NCU07969 [Neurospora crassa OR74A]	Eukaryotic elongation factor 2 kinase OS=Mus musculus OX=10090 GN=Eef2k PE=1 SV=1
A2242	-	-	GO:0003824(catalytic activity)	-	-	KOG1680 At4g16210 Enoyl-CoA hydratase	XP_031025469.1 uncharacterized protein SmJEL517_g02574 [Synchytrium microbalum]	Probable enoyl-CoA hydratase echA12 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=echA12 PE=3 SV=1

A2243	-	GO:0016020(membrane)	-	K14998 SURF1, SHY1; surf1 locus 1 family protein	-	KOG1563 7295311 Mitochondrial protein Surf1 1/SURF1/SHY1, required for expression of cytochrome oxidase	KAG2182410.1 hypothetical protein INT43_007340 [Umbelopsis isabellina]	Surfeit locus protein 1 OS=Arabidopsis thaliana OX=3702 GN=SURF1 PE=2 SV=1
A2244	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	XP_025349929.1 UDP-Glycosyltransferase/glycogen phosphorylase [Pseudomonas stroma glucosiphilum]	N-acetyl-alpha-D-glucosaminyl L-malate synthase OS=Bacillus subtilis (strain 168) OX=224308 GN=bshA PE=1 SV=2
A2245	-	-	-	-	-	-	-	-
A2246	GO:0019752(carboxylic acid metabolic process)	-	GO:0004451(isocitrate lyase activity),GO:0003824(catalytic activity)	K01637 E4.1.3.1, aceA; isocitrate lyase [EC:4.1.3.1]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways;map00630 Glyoxylate and dicarboxylate metabolism	KOG1260 At3g21720 Isocitrate lyase	TNY19743.1 isocitrate lyase [Rhodotorula diobovata]	Isocitrate lyase OS=Arabidopsis thaliana OX=3702 GN=ICL PE=1 SV=2
A2247	GO:0071704(organic substance metabolic process), GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	-	-	-	RKP18466.1 glycoside hydrolase [Rozella allomyces CSF55]	Glucosylceramidase OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) OX=246409 GN=ERC1 PE=1 SV=1
A2248	-	-	-	-	-	-	ORX68112.1 hypothetical protein DL89DRAFT_294055 [Linderina pennisporea]	-
A2249	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity)	K02201 E2.7.7.3B; pantetheine-phosphate adenylyltransferase [EC:2.7.7.3]	map00770 Pantothenate and CoA biosynthesis;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG3351 YGR277c Predicted nucleotidyltransferase	ORZ00508.1 hypothetical protein BCR43DRAFT_408388, partial [Syncephalastrium racemosum]	Phosphopantetheine adenylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAB4 PE=1 SV=1

A2250	GO:0007165(signal transduction)	-	GO:0008081(phosphoric diester hydrolase activity);GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity)	K18436 PDE7; high affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7 [EC:3.1.4.53]	map00230 Purine metabolism;map05032 Morphine addiction;map01100 Metabolic pathways	KOG3689[Hs4505663 Cyclic nucleotide phosphodiesterase	XP_006676931.1 uncharacterized protein BATDEDRAFT_86647 [Batrachochytrium dendrobatidis JAM81]	3',5'-cyclic-AMP phosphodiesterase 4C OS=Homo sapiens OX=9606 GN=PDE4C PE=1 SV=2
A2251	-	-	GO:0016491(oxidoreductase activity)	K00521 E1.16.1.7; ferric-chelate reductase [EC:1.16.1.7]	-	KOG0039[At1g01580 Ferric reductase, NADH/NADPH oxidase and related proteins	RKO91938.1 FAD-binding domain-containing protein [Blyttomyces helicus]	Ferric reduction oxidase 2 OS=Arabidopsis thaliana OX=3702 GN=FRO2 PE=1 SV=2
A2252	-	-	-	-	-	KOG0039[At5g50160 Ferric reductase, NADH/NADPH oxidase and related proteins	RKO91938.1 FAD-binding domain-containing protein [Blyttomyces helicus]	Ferric reduction oxidase 8, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=FRO8 PE=1 SV=1
A2253	-	GO:0005634(nucleus)	GO:0003677(DNA binding)	K09272 SSRP1, POB3; FACT complex subunit SSRP1/POB3	-	KOG0526[Hs4507241 Nucleosome-binding factor SPN, POB3 subunit	KXL49201.1 hypothetical protein FE78DRAFT_275644 [Acidomyces sp. 'richmondensis']	FACT complex subunit SSRP1 OS=Dictyostelium discoideum OX=44689 GN=ssrp1 PE=3 SV=1
A2254	-	-	-	K01897 ACSL fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04146 Peroxisome;map04216 Ferroptosis;map04714 Thermogenesis;map00061 Fatty acid biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation;map04920 Adipocytokine signaling pathway	KOG1256[Hs7706449 Long-chain acyl-CoA synthetases (AMP-forming)	XP_016606276.1 hypothetical protein SPPG_06636 [Spizellomyces punctatus DAOM BR117]	Fatty acyl-CoA synthetase A OS=Dictyostelium discoideum OX=44689 GN=fcsA PE=1 SV=1
A2255	-	-	GO:0004518(nuclease activity)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518[YO R033c 5'-3' exonuclease	PNY27590.1 Exodeoxyribonuclease 1 [Tolypodladium capitatum]	Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EXO1 PE=1 SV=2
A2256	GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	K01811 xylS, yicI; alpha-D-xyloside xylohydrolase [EC:3.2.1.177]	-	KOG1066[HsM7661898 Glucosidase II catalytic (alpha) subunit and related enzymes, glycosyl hydrolase family 31	KAF5565280.1 alpha-d-xyloside xylohydrolase [Fusarium phyllophilum]	Sulfoquinovosidase OS=Escherichia coli (strain K12) OX=83333 GN=yihQ PE=1 SV=3

A2257	GO:0036211(protein modification process)	-	GO:0004719(protein-L-isoaspartate (D-aspartate) O-methyltransferase activity)	K00573 E2.1.1.77, pcm; protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77]	-	KOG1661 Hs4885539 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	KAF0478503.1 Protein-L-isoaspartate O-methyltransferase [Gigaspora margarita]	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Gallus gallus OX=9031 GN=PCMT1 PE=2 SV=3
A2258	-	-	-	-	-	-	-	-
A2259	-	-	-	-	-	-	-	-
A2260	-	-	-	-	-	-	-	-
A2261	-	-	GO:0005515(protein binding)	K20241 WDR44, RAB11BP; WD repeat-containing protein 44	-	KOG0283 At1g48870 WD40 repeat-containing protein	RKP14680.1 WD40-repeat-containing domain protein, partial [Piptocephalis cylindrospora]	WD repeat-containing protein 44 OS=Bos taurus OX=9913 GN=WDR44 PE=1 SV=1
A2262	-	-	-	-	-	-	-	-
A2263	-	-	-	-	-	-	-	-
A2264	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A2265	-	-	-	-	-	-	-	-
A2266	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K18669 DYRK2_3_4; dual specificity tyrosine-phosphorylation-regulated kinase 2/3/4 [EC:2.7.12.1]	map04111 Cell cycle - yeast	KOG0667 At2g40120 Dual-specificity tyrosine-phosphorylation regulated kinase	ODV92608.1 hypothetical protein CANCADRAFT_20444, partial [Tortispora caseinolytica NRRL Y-17796]	Serine/threonine-protein kinase ppk5 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ppk5 PE=1 SV=1
A2267	-	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups),GO:0016746(acyltransferase activity)	K07513 ACAA1; acetyl-CoA acyltransferase 1 [EC:2.3.1.16]	map03320 PPAR signaling pathway;map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map01040 Biosynthesis of unsaturated fatty acids;map00592 alpha-Linolenic acid metabolism;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG1391 Hs5174429 Acetyl-CoA acyltransferase	KXS15223.1 acetyl-CoA acetyltransferase [Gonapodya prolifera JEL478]	Steroid 3-ketoacyl-CoA thiolase FadA6 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=fadA6 PE=1 SV=2

A2268	GO:0030071(regulation of mitotic metaphase/anaphase transition),GO:003145(anaphase-promoting complex-dependent catabolic process)	GO:0005680(anaphase-promoting complex)	GO:0005515(protein binding)	K03351 APC4, ANAPC4; anaphase-promoting complex subunit 4	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG4640 Hs2044133 Anaphase-promoting complex (APC), subunit 4	ORX98889.1 hypothetical protein K493DRAFT_299660 [Basidiobolus meristosporus CBS 931.73]	Anaphase-promoting complex subunit 4 OS=Arabidopsis thaliana OX=3702 GN=APC4 PE=2 SV=2
A2269	-	-	-	K20526 TAGLN; transgelin	-	KOG2046 7303337 Calponin	ORY22996.1 hypothetical protein BCR33DRAFT_760114 [Rhizoclostium globosum]	Muscle-specific protein 20 OS=Drosophila melanogaster OX=7227 GN=Mp20 PE=2 SV=2
A2270	-	-	-	-	-	-	KDE02271.1 non-histone chromosomal protein 6 [Microbotryum lychnidis-dioicae p1A1 Lamole]	Non-histone chromosomal protein 6 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=NHP6 PE=3 SV=2
A2271	GO:0006666(3-ketosphinganine metabolic process), GO:0030148(sphingolipid biosynthetic process)	-	GO:0047560(3-dehydrosphinganine reductase activity)	K04708 KDSR; 3-dehydrosphinganine reductase [EC:1.1.1.102]	map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG1210 Hs4503817 Predicted 3-ketosphinganine reductase	GAW07131.1 3-ketodihydrosphingosine reductase tsc10 [Lentinula edodes]	3-ketodihydrosphingosine reductase OS=Dictyostelium discoideum OX=44689 GN=ksrA-1 PE=3 SV=1
A2272	GO:0000160(phosphorelay signal transduction system)	-	GO:0005515(protein binding)	-	-	KOG1601 At5g24470 GATA-4/5/6 transcription factors	KAG1435916.1 hypothetical protein G6F57_020903 [Rhizopus oryzae]	Chemotaxis protein CheY OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=cheY PE=3 SV=1
A2273	-	-	-	-	-	KOG4199 Hs15529984 Uncharacterized conserved protein	-	Armadillo repeat-containing protein 6 OS=Mus musculus OX=10090 GN=Armc6 PE=1 SV=1
A2274	-	-	-	-	-	KOG2177 Hs15011941 Predicted E3 ubiquitin ligase	KAF1994003.1 RING-14 protein-like protein [Amniculicola lignicola CBS 123094]	E3 ubiquitin-protein ligase TRIM4 OS=Homo sapiens OX=9606 GN=TRIM4 PE=1 SV=2

A2275	GO:0006725(cellular aromatic compound metabolic process)	-	GO:0008198(ferrous iron binding),GO:0016491(oxidoreductase activity),GO:0008270(zinc ion binding),GO:0016701(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen)	-	-	-	KXS15563.1 Extradiol aromatic ring-opening dioxygenase [Gonapodya prolifera JEL478]	4,5-DOPA dioxygenase extradiol OS=Beta vulgaris OX=161934 GN=DODA PE=1 SV=1	
A2276	-	-	-	-	-	-	-	-	
A2277	GO:0007154(cell communication)	-	GO:0016021(integral component of membrane)	-	K03332 fruA; fructan beta-fructosidase [EC:3.2.1.80]	map00051 Fructose and mannose metabolism	-	KUL83293.1 hypothetical protein ZTR_09138 [Talaromyces verruculosus]	Putative glycosyl hydrolase ecdE OS=Aspergillus rugulosus OX=41736 GN=ecdE PE=3 SV=1
A2278	-	-	GO:0005515(protein binding)	-	-	-	-	PJF18463.1 hypothetical protein PSACC_01723 [Paramicrosporidium saccamoebae]	Keratocan OS=Danio rerio OX=7955 GN=kera PE=1 SV=1
A2279	-	-	GO:0005515(protein binding)	-	K09527 DNAJC7; DnaJ homolog subfamily C member 7	-	KOG0550 Hs4507713 Molecular chaperone (DnaJ superfamily)	KAF2728643.1 TPR-like protein [Polyplosphaeria fusca]	DnaJ homolog subfamily C member 7 OS=Pongo abelii OX=9601 GN=DNAJC7 PE=2 SV=1
A2280	-	-	GO:0005515(protein binding)	-	-	-	KOG4199 Hs15529984 Uncharacterized conserved protein	-	Armadillo repeat-containing protein 6 OS=Homo sapiens OX=9606 GN=ARMC6 PE=1 SV=2
A2281	-	-	-	-	-	-	-	-	-
A2282	-	-	-	-	-	-	-	RUS15932.1 Alpha/Beta hydrolase protein, partial [Endogone sp. FLAS-F59071]	-
A2283	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity),GO:0000166(nucleotide binding),GO:0005215(transporter activity),GO:0016887(ATP hydrolysis activity),GO:0015444(P-type magnesium transporter activity)	-	K01531 mgtA, mgtB; P-type Mg2+ transporter [EC:7.2.2.14]	-	KOG1016 Hs20538502 Predicted DNA helicase, DEAD-box superfamily	RYO75852.1 hypothetical protein DL763_010986 [Monosporascus cannonballus]	Magnesium-transporting ATPase, P-type 1 OS=Escherichia coli O157:H7 OX=83334 GN=mgtA PE=3 SV=1

A2284	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	-	Hydroxyproline O-arabinosyltransferase RDN2 OS=Medicago truncatula OX=3880 GN=RDN2 PE=3 SV=1
A2285	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A2286	GO:0070475(rRNA base methylation)	-	GO:0070042(rRNA (uridine-N3-)-methyltransferase activity)	K19307 BMT5; 25S rRNA (uracil2634-N3)-methyltransferase [EC:2.1.1.313]	-	-	KAF7732751.1 hypothetical protein EC973_000023 [Apophysomyces ossiformis]	25S rRNA (uridine-N(3))-methyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=bmt5 PE=3 SV=1
A2287	-	-	GO:0008270(zinc ion binding),GO:0003682(chromatin binding)	-	-	-	TCD61797.1 hypothetical protein EIP91_007883 [Steccherinum ochraceum]	Lysine-specific demethylase 5B-B OS=Danio rerio OX=7955 GN=kdm5bb PE=2 SV=2
A2288	-	-	-	-	-	-	-	-
A2289	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	-	K13754 SLC24A6, NCKX6; solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	-	KOG1307[Hs10190740 K+-dependent Ca2+/Na+ exchanger NCKX1 and related proteins	RPA82908.1 hypothetical protein BJ508DRAFT_305206 [Ascobolus immersus RN42]	Sodium/potassium/calcium exchanger 4 OS=Homo sapiens OX=9606 GN=SLC24A4 PE=1 SV=2
A2290	GO:0007165(signal transduction)	GO:0000159(protein phosphatase type 2A complex)	GO:0019888(protein phosphatase regulator activity)	-	-	-	-	-
A2291	GO:000909(regulation of flower development)	-	GO:0005515(protein binding)	-	-	-	-	-
A2292	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2293	-	-	-	-	-	-	-	Folate receptor alpha OS=Mus musculus OX=10090 GN=Folr1 PE=1
A2294	-	-	-	-	-	-	-	-
A2295	-	-	GO:0016491(oxidoreductase activity),GO:0046872(metal ion binding)	K13954 yiaY; alcohol dehydrogenase [EC:1.1.1.1]	map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01220 Degradation of aromatic compounds;map00625 Chloroalkane and chloroalkene degradation;map00626 Naphthalene degradation;map00620 Pyruvate metabolism;map00350 Tyrosine metabolism;map01100 Metabolic pathways;map00	KOG3857[YGL256w Alcohol dehydrogenase, class IV	KXS18892.1 iron-containing alcohol dehydrogenase [Gonapodya prolifera JEL478]	Probable alcohol dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=yiaY PE=3 SV=4

A2296	-	-	GO:0003824(catalytic activity)	K08726 EPHX2; soluble epoxide hydrolase / lipid-phosphate phosphatase [EC:3.3.2.10 3.1.3.76]	map04146 Peroxisome;map01120 Microbial metabolism in diverse environments;map00590 Arachidonic acid metabolism;map05207 Chemical carcinogenesis - receptor activation;map05208 Chemical carcinogenesis - reactive oxygen species;map00625 Chloroalkane and chloroalkene degradation;map01100 Metabolic pathways	KOG4178[Hs14743830_2 Soluble epoxide hydrolase	XP_033605933.1 alpha/beta-hydrolase [Pseudovirgaria hyperparasitica]	Bifunctional epoxide hydrolase 2 OS=Rattus norvegicus OX=10116 GN=Ephx2 PE=1 SV=1
A2297	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0159 7300481 Cytochrome P450 CYP11/CYP12/CYP24/CYP27 subfamilies	KAG1736243.1 cytochrome P450 [Suillus lakei]	Probable cytochrome P450 12c1, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Cyp12c1 PE=2 SV=2
A2298	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0004497(monoxygenase activity),GO:0020037(heme binding)	-	-	KOG0159 7300481 Cytochrome P450 CYP11/CYP12/CYP24/CYP27 subfamilies	KNE64035.1 hypothetical protein AMAG_19100 [Allomyces macrogynus ATCC 38327]	Cytochrome P450 CYP12A2 OS=Musca domestica OX=7370 GN=CYP12A2 PE=2 SV=1
A2299	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0159 7300481 Cytochrome P450 CYP11/CYP12/CYP24/CYP27 subfamilies	TRM68995.1 cytochrome P450 [Auriculariopsis amplia]	Probable cytochrome P450 12d1 proximal, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Cyp12d1-p PE=2 SV=3

A2301	-	GO:0005956(protein kinase CK2 complex)	GO:0019887(protein kinase regulator activity)	K03115 CSNK2B; casein kinase II subunit beta	map04310 Vhl signaling pathway;map04139 Mitophagy - yeast;map04137 Mitophagy - animal;map04712 Circadian rhythm - plant;map03083 Polycomb repressive complex;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05235 PD-L1 expression and PD-1 checkpoint pathway in cancer;map04520 Adherens junction;map03008 Ribosome biogenesis in	KOG3092[CE18168 Casein kinase II, beta subunit	XP_006675102.1 uncharacterized protein BATDEDRAFT_15229 [Batrachochytrium dendrobatidis JAM81]	Casein kinase II subunit beta OS=Dictyostelium discoideum OX=44689 GN=csnk2b PE=3 SV=1
A2302	GO:0007017(microtubule-based process)	GO:0005874(microtubule)	GO:0005525(GTP binding);GO:0005200(structural constituent of cytoskeleton)	K07374 TUBA; tubulin alpha	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins;map04210 Apoptosis;map04540 Gap junction;map04530 Tight junction;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map050	KOG1376[Hs17986283 Alpha tubulin	RKO92378.1 tubulin, alpha, ubiquitous, partial [Blyttiomycetes helicus]	Tubulin alpha-1A chain OS=Cricetulus griseus OX=10029 GN=TUBA1A PE=2 SV=1
A2303	GO:0000398(mRNA splicing, via spliceosome)	GO:0089701(U2AF complex)	GO:0046872(metal ion binding);GO:0003676(nucleic acid binding);GO:0003723(RNA binding)	K12836 U2AF1; splicing factor U2AF 35 kDa subunit	map03040 Spliceosome;map05131 Shigellosis	KOG2202[7296221 U2 snRNP splicing factor, small subunit, and related proteins	OLY85380.1 Splicing factor U2AF 23 kDa subunit [Smittium mucronatum]	Splicing factor U2af small subunit A OS=Oryza sativa subsp. japonica OX=39947 GN=U2AF35A PE=2 SV=1
A2304	-	-	-	-	-	-	-	-
A2305	GO:0090481(pyrimidine nucleotide-sugar transmembrane transport)	GO:0000139(Golgi membrane);GO:0016021(integral component of membrane)	GO:0015165(pyrimidine nucleotide-sugar transmembrane transporter activity)	K15272 SLC35A1_2_3; solute carrier family 35 (UDP-sugar transporter), member A1/2/3	-	KOG2234[Hs5453621 Predicted UDP-galactose transporter	ORY48303.1 UDP-N-acetylglucosamine transporter [Rhizoclostium globosum]	CMP-sialic acid transporter OS=Mus musculus OX=10090 GN=Slc35a1 PE=1 SV=2
A2306	-	-	-	-	-	-	-	-
A2307	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity);GO:0003677(DNA binding)	-	-	KOG1601[At4g31920 GATA-4/5/6 transcription factors	-	Two-component response regulator ORR24 OS=Oryza sativa subsp. indica OX=39946 GN=RR24 PE=3 SV=1

A2308	-	-	GO:0003676(nucleic acid binding)	K23719 SAC3; nuclear mRNA export protein SAC3	-	-	XP_01629451.4.1 hypothetical protein PSEUBRA_SC AF10g05495 [Kalmatozym a brasiliensis GHG001]	SAC3 family protein 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC70.06 PE=3 SV=1
A2309	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016459(myosin complex),GO:0016020(membrane)	GO:0005515(protein binding),GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005509(calcium ion binding),GO:0005216(ion channel activity)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection,map04814 Motor proteins	KOG0160 At4g33200 Myosin class V heavy chain	RKP01558.1 hypothetical protein CXG81DRAFT_571, partial [Caulochytrium protostelioides]	Myosin-15 OS=Arabidopsis thaliana OX=3702 GN=XI-I PE=1 SV=1
A2310	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG3888 Hs4502369 Gamma-butyrobetaine, 2-oxoglutarate dioxygenase	TPX45556.1 hypothetical protein SeMB42_g03973 [Synchytrium endobioticum]	Gamma-butyrobetaine dioxygenase OS=Mus musculus OX=10090 GN=Bbox1 PE=1 SV=1
A2311	GO:0006614(SRP-dependent cotranslational protein targeting to membrane)	GO:0005786(signal recognition particle, endoplasmic reticulum targeting)	GO:0005047(signal recognition particle binding),GO:0008312(7S RNA binding),GO:000942(endoplasmic reticulum signal peptide binding),GO:0003723(RNA binding)	K03107 SRP68; signal recognition particle subunit SRP68	map03060 Protein export	KOG2460 Hs22062290 Signal recognition particle, subunit Srp68	RHZ50001.1 hypothetical protein Glove_508g19 [Diversispora epigaea]	Signal recognition particle subunit SRP68 OS=Mus musculus OX=10090 GN=Srp68 PE=1 SV=2
A2312	-	-	-	-	-	-	-	-
A2313	-	-	-	-	-	-	-	-
A2314	-	-	-	-	-	-	-	-
A2315	-	-	-	-	-	-	-	-
A2316	-	-	-	-	-	-	-	-
A2317	GO:0017121(plasma membrane phospholipid scrambling)	-	GO:0017128(phospholipid scramblase activity)	-	-	-	-	Phospholipid scramblase 3 OS=Rattus norvegicus OX=10116 GN=Plscr3 PE=1 SV=1
A2318	-	-	GO:0005515(protein binding)	-	-	-	-	-

A2319	-	-	-	K01539 ATP1A; sodium/potas- sium-transporting ATPase subunit alpha [EC:7.2.2.13]	map04024 cAMP signaling pathway;map04 022 cGMP-PKG signaling pathway;map04 919 Thyroid hormone signaling pathway;map04 918 Thyroid hormone synthesis;map04 911 Insulin secretion;map04 261 Adrenergic signaling in cardiomyocytes; map04260 Cardiac muscle contraction;map 04978 Mineral absorption;map 04974 Protein digestion and absorption;map 04976 Bile secretion;map04 971 Gastric acid secretion;map04	KOG0203 Hs M4502269 Na+/K+ ATPase, alpha subunit	XP_00802625 4.1 uncharacteriz ed protein SETTUDRAFT _151418 [Exserohilum turcica Et28A]	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Gallus gallus OX=9031 GN=ATP1A2 PE=2 SV=1
A2320	GO:0006122(mitochondrial electron transport, ubiquinol to cytochrome c)	GO:0005750(mitochondrial respiratory chain complex III)	-	K00417 QCR7, UQCRB; ubiquinol-cytochrome c reductase subunit 7	map05014 Amyotrophic lateral sclerosis;map054 15 Diabetic cardiomyopathy; map04260 Cardiac muscle contraction;map 04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map050 22 Pathways of neurodegeneration - multiple diseases;map052 08 Chemical carcinogenesis - reactive oxygen species;map049 32 Non-alcoholic fatty liver disease;map050 10 Alzheimer disease;map050	KOG3440 At5 g25450 Ubiquinol cytochrome c reductase, subunit QCR7	XP_02535628 2.1 14 kDa subunit of cytochrome bd ubiquinol oxidase [Meira miltonrushii]	Cytochrome b-c1 complex subunit 7-2, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=QCR7-2 PE=1 SV=1
A2321	-	-	-	-	-	-	XP_01902097 2.1 uncharacteriz ed protein SAICODRAFT _28020 [Saitoella complicata NRRL Y- 17804]	-
A2322	-	-	-	-	-	-	-	-
A2323	GO:0016579(protein deubiquitination),GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase)	K11853 USP34; ubiquitin carboxyl-terminal hydrolase 34 [EC:3.4.19.12]	-	KOG1866 Hs2 2043041 Ubiquitin carboxyl-terminal hydrolase	RUS20937.1 hypothetical protein BC937DRAFT _93997 [Endogone sp. FLAS- F59071]	Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens OX=9606 GN=USP34 PE=1 SV=2
A2324	-	-	GO:0046982(protein heterodimerization activity)	-	-	-	-	-

A2325	-	GO:0005737(cytoplasm),GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0003743(translation initiation factor activity),GO:0005515(protein binding),GO:0008233(peptidase activity),GO:0008237(metalloproteinase activity)	K03247 EIF3H; translation initiation factor 3 subunit H	map05162 Measles	KOG1560 At1g10840 Translation initiation factor 3, subunit h (eIF-3h)	RHZ45050.1 hypothetical protein Glove_692g8 [Diversispora epigaea]	Eukaryotic translation initiation factor 3 subunit H OS=Arabidopsis thaliana OX=3702 GN=TIF3H1 PE=1 SV=2
A2326	GO:0006355(regulation of transcription, DNA-templated)	GO:0005634(nucleus),GO:0030015(CCR4-NOT core complex)	-	K12580 CNOT3, NOT3; CCR4-NOT transcription complex subunit 3	map03018 RNA degradation	KOG2150 Hs7657387 CCR4-NOT transcriptional regulation complex, NOT5 subunit	PKY45097.1 hypothetical protein RhiirA4_434713 [Rhizophagus irregularis]	CCR4-NOT transcription complex subunit 3 OS=Mus musculus OX=10090 GN=Cnot3 PE=1 SV=1
A2327	-	-	-	K06630 YWHAZ; 14-3-3 protein epsilon	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04722 Neurotrophin signaling pathway;map04621 NOD-like receptor signaling pathway;map05203 Viral carcinogenesis; map04151 PI3K-Akt signaling pathway;map04011 MAPK signaling pathway - yeast;map04114 Oocyte meiosis;map04110 Cell cycle;map05160 Hepatitis C	KOG0841 Hs4507953 Multifunctional chaperone (14-3-3 family)	KOS21192.1 14-3-3 protein -like protein [Escovopsis weberi]	14-3-3 protein zeta/delta OS=Bos taurus OX=9913 GN=YWHAZ PE=1 SV=1
A2328	GO:0006629(lipid metabolic process)	-	-	-	-	KOG2088 Hs21040277 Predicted lipase/calmodulin-binding heat-shock protein	XP_016610904.1 hypothetical protein SPPG_01945 [Spizellomyces punctatus DAOM BR117]	Diacylglycerol lipase-beta OS=Homo sapiens OX=9606 GN=DAGLB PE=1 SV=2
A2329	GO:012009(intermembrane lipid transfer)	GO:0005737(cytoplasm)	GO:0120013(lipid transfer activity)	-	-	KOG4189 7291276.2 Uncharacterized conserved protein	KAF9452770.1 glycolipid transfer protein [Macrolepiota fuliginosa MF-IS2]	Ceramide-1-phosphate transfer protein OS=Danio rerio OX=7955 GN=cptp PE=2 SV=1
A2330	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	K14264 BNA3; kynurenine aminotransferase [EC:2.6.1.7]	map00380 Tryptophan metabolism;map01100 Metabolic pathways	KOG0257 At1g77670 Kynurenine aminotransferase, glutamine transaminase K	XP_027610663.1 Uncharacterized aminotransferase [Sparassis crispa]	Probable N-succinyl-diaminopimelate aminotransferase DapC OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=dapC PE=1 SV=1
A2331	-	GO:0016021(integral component of membrane)	-	K13348 MPV17; protein Mpv17	map04146 Peroxisome	KOG1944 At5g19750 Peroxisomal membrane protein MPV17 and related proteins	KAF8003305.1 hypothetical protein HF325_002550 [Metschnikowia persimmonensis]	PXMP2/4 family protein 4 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0290631 PE=3 SV=1

A2332	-	-	GO:0000030(mannosyltransferase activity),GO:0016757(glycosyltransferase activity)	K03842 ALG1; beta-1,4-mannosyltransferase [EC:2.4.1.142]	map00513 Various types of N-glycan biosynthesis;map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG2941 730314 Beta-1,4-mannosyltransferase	ORX92561.1 UDP-Glycosyltransferase/glycogen phosphorylase [Basidiobolus meristosporus CBS 931.73]	Chitobiosyldiphosphodolichol beta-mannosyltransferase OS=Mus musculus OX=10090 GN=Alg1 PE=1 SV=3
A2333	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0606 At1g45160 Microtubule-associated serine/threonine kinase and related proteins	KAG1580476.1 hypothetical protein G6F48_010427 [Rhizopus deleamar]	Probable serine/threonine protein kinase IRE4 OS=Arabidopsis thaliana OX=3702 GN=IRE4 PE=2 SV=1
A2334	-	-	GO:0005458(GDP-P-mannose transmembrane transporter activity)	K15356 GONST1_2, VRG4; GDP-mannose transporter	-	-	KAG2202790.1 hypothetical protein INT47_004814 [Mucor saturninus]	GDP-mannose transporter GONST1 OS=Arabidopsis thaliana OX=3702 GN=GONST1 PE=1 SV=2
A2335	-	-	-	-	-	KOG1030 Hs21362014 Predicted Ca2+-dependent phospholipid-binding protein	EPS35070.1 hypothetical protein H072_11610 [Dactylellina haptotyla CBS 200.50]	Multiple C2 and transmembrane domain-containing protein 1 OS=Mus musculus OX=10090 GN=Mctp1 PE=1 SV=1
A2336	-	-	-	-	-	-	-	-
A2337	GO:0071596(ubiquitin-dependent protein catabolic process via the N-end rule pathway)	-	GO:0008270(zinc ion binding),GO:0061630(ubiquitin protein ligase activity)	K10625 UBR1; E3 ubiquitin-protein ligase UBR1 [EC:2.3.2.27]	-	KOG1140 7293307 N-end rule pathway, recognition component UBR1	KAF8957057.1 hypothetical protein BDZ97DRAFT_1954955 [Flammula alnicola]	E3 ubiquitin-protein ligase UBR1 OS=Homo sapiens OX=9606 GN=UBR1 PE=1 SV=1
A2338	GO:0006289(nucleotide-excision repair),GO:0043161(proteasome-mediated ubiquitin-dependent protein catabolic process)	-	GO:0005515(protein binding),GO:0003684(damaged DNA binding)	K10839 RAD23, HR23; UV excision repair protein RAD23	map04141 Protein processing in endoplasmic reticulum;map03420 Nucleotide excision repair	-	ORX90166.1 UV excision repair protein Rad23 [Basidiobolus meristosporus CBS 931.73]	UV excision repair protein rhp23 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rhp23 PE=1 SV=1
A2339	GO:0006807(nitrogen compound metabolic process)	-	GO:0036361(racemase activity, acting on amino acids and derivatives),GO:0016855(racemase and epimerase activity, acting on amino acids and derivatives)	-	-	-	-	Aspartate racemase OS=Pyrococcus horikoshii (strain ATCC 700860 / DSM 12428 / JCM 9974 / NBRC 100139 / OT-3) OX=70601 GN=PH0670 PE=1 SV=1
A2340	-	-	-	-	-	KOG1502 At1g09480 Flavonol reductase/cinnamoyl-CoA reductase	KZT02568.1 NAD-P-binding protein [Laetiporus sulphureus 93-53]	Phenylacetaldehyde reductase OS=Rosa hybrid cultivar OX=128735 GN=PAR PE=1 SV=1
A2341	-	-	-	-	-	-	-	-

A2342	GO:0030041(actin filament polymerization),GO:0034314(Arp2/3 complex-mediated actin nucleation),GO:0030833(regulation of actin filament polymerization)	GO:0005885(Arp2/3 protein complex),GO:0015629(actin cytoskeleton)	-	K05755 ARPC4; actin related protein 2/3 complex, subunit 4	map04144 Endocytosis;map05135 Yersinia infection;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04810 Regulation of actin cytoskeleton;map04138 Autophagy - yeast;map05100 Bacterial invasion of epithelial cells;map04666 Fc gamma R-mediated phagocytosis;map04530 Tight junction	KOG1876 7297077 Actin-related protein Arp2/3 complex, subunit ARPC4	SPO43277.1 probable ARP2/3 complex 20 kDa subunit [Moesziomyces antarcticus]	Actin-related protein 2/3 complex subunit 4 OS=Bos taurus OX=9913 GN=ARPC4 PE=1 SV=3
A2343	-	-	-	-	-	KOG0370 YOR303w Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phosphate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)	CDH52300.1 carbamoyl-phosphate synthase [Lichtheimia corymbifera JMR:FSU:9682]	Carbamoyl phosphate synthase arginine-specific small chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CPA1 PE=1 SV=1
A2344	-	-	-	K01956 carA, CPA1; carbamoyl-phosphate synthase small subunit [EC:6.3.5.5]	map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG0370 CE03105 Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phosphate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)	KAF7752952.1 Gly-Xaa carboxypeptidase, partial [Entomophthora muscae]	Multifunctional protein CAD OS=Mesocricetus auratus OX=10036 GN=CAD PE=1 SV=4
A2345	GO:0006807(nitrogen compound metabolic process)	-	GO:0005524(ATP binding),GO:0046872(metal ion binding)	K11541 URA2; carbamoyl-phosphate synthase / aspartate carbamoyltransferase [EC:6.3.5.5.2.1.3.2]	map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG0370 YJL130c Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phosphate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)	XP_018287077.1 hypothetical protein PHYBLDRAFT_74982 [Phycomyces blakesleeanus NRRL 1555(-)]	Multifunctional protein pyrABCN OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=pyrABCN PE=3 SV=2

A2346	-	-	-	K11541 URA2: carbamoyl- phosphate synthase / aspartate carbamoyltra nsferase [EC:6.3.5.5 2.1.3.2]	map00240 Pyrimidine metabolism;map 01240 Biosynthesis of cofactors;map00 250 Alanine, aspartate and glutamate metabolism;map 01100 Metabolic pathways	KOG0370 YJL 130c Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl- phosphate synthetase, aspartate transcarbamy lase, and glutamine amidotransfe rase)	POY71469.1 putative Carbamoyl- phosphate synthase (glutamine- hydrolyzing) [Rhodotorula taiwanensis]	Multifunctional protein URA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA2 PE=1 SV=5
A2347	GO:0007165(signal transduction);GO:0007186(G protein-coupled receptor signaling pathway)	-	GO:0003924(GTPase activity);GO:0019001(guanylnucleotide binding);GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide- binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04730 Long-term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082 Hs20542545 G-protein alpha subunit (small G protein superfamily)	OSD04117.1 heterotrimeric G protein alpha subunit B [Trametes coccinea BRFM310]	Guanine nucleotide-binding protein G(t) subunit alpha-3 OS=Bos taurus OX=9913 GN=GNAT3 PE=1 SV=1
A2348	-	-	-	-	-	KOG0750 YDL198c Mitochondrial solute carrier protein	CDS10033.1 hypothetical protein LRAMOSA02710 [Lichtheimia ramosa]	Mitochondrial GTP/GDP carrier protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GGC1 PE=1 SV=1
A2349	-	-	-	-	-	-	-	-
A2350	GO:0043248(proteasome assembly)	-	-	-	-	-	KAG2182222.1 hypothetical protein INT43_007149 [Umbelopsis isabellina]	-
A2351	-	GO:0071203(WASH complex)	GO:0005515(protein binding)	-	-	-	-	-
A2352	-	-	GO:0016787(hydrolase activity);GO:0010945(CoA pyrophosphatase activity)	-	-	-	KAF9430523.1 hypothetical protein BGZ94_006318 [Podila epigama]	-
A2353	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity);GO:0043169(cation binding)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 At4g31860 Serine/threonine protein phosphatase	XP_016294271.1 Protein phosphatase Mg+2 or Mn+2 dependent - PPM [Kalmanozyma brasiliensis GHG001]	Probable protein phosphatase 2C 60 OS=Arabidopsis thaliana OX=3702 GN=At4g31860 PE=2 SV=1
A2354	-	-	-	-	-	-	-	-

A2355	GO:0006914(autophagy),GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08269 ULK2, ATG1; serine/threonine-protein kinase ULK2 [EC:2.7.11.1]	map05014 Amyotrophic lateral sclerosis;map04140 Autophagy - animal;map04212 Longevity regulating pathway - worm;map04139 Mitophagy - yeast;map04138 Autophagy - yeast;map04136 Autophagy - other;map05022 Pathways of neurodegeneration - multiple diseases;map04150 mTOR signaling pathway;map05010 Alzheimer disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0595 At2g37840 Serine/threonine-protein kinase involved in autophagy	CEP19209.1 hypothetical protein [Parasitella parasitica]	Serine/threonine-protein kinase ATG1 OS=Komagataella pastoris OX=4922 GN=ATG1 PE=3 SV=1
A2356	-	-	-	K02947 RP-S10e, RPS10; small subunit ribosomal protein S10e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3344 YOR293w 40s ribosomal protein s10	KAF8805333.1 hypothetical protein BYT27DRAFT_7169466 [Cortinarius glaucopus]	Small ribosomal subunit protein eS10 OS=Lumbricus rubellus OX=35632 GN=RPS10 PE=2 SV=1
A2357	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02894 RP-L23e, RPL23; large subunit ribosomal protein L23e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	-	OUM58395.1 hypothetical protein PIROE2DRAFT_52402 [Piromyces sp. E2]	Large ribosomal subunit protein uL14A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rpl2301 PE=1 SV=1
A2358	-	-	-	-	-	-	-	-
A2359	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity),GO:0043169(cation binding)	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698 At5g24940 Serine/threonine protein phosphatase	XP_024663803.1 Protein phosphatase 2C 1 [Wickerhamia sorbophila]	Probable protein phosphatase 2C 69 OS=Arabidopsis thaliana OX=3702 GN=At5g10740 PE=2 SV=1
A2360	GO:0009235(cobalamin metabolic process)	-	-	-	-	KOG3945 CE04947_2 Uncharacterized conserved protein	KAG0207804.1 hypothetical protein BGX28_001050 [Mortierella sp. GBA30]	Mitochondrial fission process protein 1 OS=Caenorhabditis elegans OX=6239 GN=mtp-18 PE=3 SV=2
A2361	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2362	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08793 STK32, YANK; serine/threonine kinase 32 [EC:2.7.11.1]	-	KOG0598 Hs8923754 Ribosomal protein S6 kinase and related proteins	EPZ33161.1 Protein kinase, catalytic domain-containing protein [Rozella allomycis CSF55]	Serine/threonine-protein kinase 32B OS=Homo sapiens OX=9606 GN=STK32B PE=2 SV=1
A2363	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding),GO:0016491(oxidoreductase activity)	-	-	-	TPX54413.1 hypothetical protein PhCBS80983_g05938 [Powellomyces hirtus]	-

A2364	GO:003420(ion transmembrane transport);GO:0006811(ion transport)	GO:0016021(integral component of membrane)	GO:0004888(transmembrane signaling receptor activity);GO:0005216(ion channel activity);GO:0005230(extracellular ligand-gated ion channel activity)	-	-	-	-	-
A2365	-	-	-	-	-	-	-	-
A2366	-	-	GO:0016491(oxidoreductase activity);GO:0010181(FMN binding)	K11517 HAO; (S)-2-hydroxy-acid oxidase [EC:1.1.3.15]	map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways;map00630 Glyoxylate and dicarboxylate metabolism	KOG0538 At3g14150 Glycolate oxidase	KAG4087762.1 Hydroxyacid oxidase 2 [Neocallimastix sp. JGI-2020a]	Peroxisomal (S)-2-hydroxyacid oxidase GLO3 OS=Arabidopsis thaliana OX=3702 GN=GLO3 PE=1 SV=1
A2367	-	-	-	K18172 CMC2; COX assembly mitochondrial protein 2	-	-	ORY88989.1 cytochrome c oxidase biogenesis protein Cmc1-like protein [Leucosporidium creatinivorum]	COX assembly mitochondrial protein 2 homolog OS=Danio rerio OX=7955 GN=cmc2 PE=3 SV=1
A2368	-	-	GO:0005524(ATP binding);GO:0140658(ATPase-dependent chromatin remodeler activity)	-	-	KOG0384 Hs2047300 Chromodomain-helicase DNA-binding protein	TPX54401.1 hypothetical protein PhCBS80983.g05948 [Powellomyces hirtus]	Chromodomain-helicase-DNA-binding protein 7 OS=Mus musculus OX=10090 GN=Chd7 PE=1 SV=1
A2369	-	-	-	-	-	-	-	-
A2370	GO:0006648(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K08842 TESK2; testis-specific kinase 2 [EC:2.7.12.1]	-	KOG0192 At2g17700 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KXS19920.1 kinase-like protein [Gonapodya prolifera JEL478]	Probable serine/threonine-protein kinase drkA OS=Dictyostelium discoideum OX=44689 GN=drkA PE=3 SV=1
A2371	GO:0006629(lipid metabolic process)	-	-	K13806 DAGL; sn1-specific diacylglycerol lipase [EC:3.1.1.116]	map04723 Retrograde endocannabinoid signaling;map04745 Phototransduction - fly;map04925 Aldosterone synthesis and secretion	KOG2088 Hs21040277 Predicted lipase/calmodulin-binding heat-shock protein	TPX65219.1 hypothetical protein SpCBS45565.g05341 [Spizellomyces sp. 'palustris']	Diacylglycerol lipase-alpha OS=Mus musculus OX=10090 GN=Dagla PE=1 SV=2

A2372	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K06276 PDPK1; 3-phosphoinositide dependent protein kinase-1 [EC:2.7.11.1]	map04360 Axon guidance;map03320 PPAR signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map05223 Non-small cell lung cancer;map04722 Neurotrophin signaling pathway;map04510 Focal adhesion;map04210 Apoptosis;map04071 Sphingolipid signaling pathway;map01524 Platinum drug resistance;map04919 Thyroid hormone signaling	KOG0603[Hs19923570 Ribosomal protein S6 kinase	OBZ91519.1 Serine/threonine-protein kinase 32A, partial [Choanephora cucurbitarum]	Ribosomal protein S6 kinase 2 alpha OS=Gallus gallus OX=9031 GN=RPS6KA PE=2 SV=1
A2373	GO:000079(regulation of cyclin-dependent protein serine/threonine kinase activity)	-	GO:0019901(protein kinase binding)	-	-	KOG1674[At3g60550 Cyclin	XP_026607833.1 hypothetical protein DSM5745_02654 [Aspergillus mulundensis]	Cyclin-U2-2 OS=Arabidopsis thaliana OX=3702 GN=CYCU2-2 PE=1 SV=1
A2374	-	-	-	-	-	-	-	-
A2375	GO:000079(regulation of cyclin-dependent protein serine/threonine kinase activity)	-	GO:0019901(protein kinase binding)	-	-	KOG1674[At3g60550 Cyclin	XP_026607833.1 hypothetical protein DSM5745_02654 [Aspergillus mulundensis]	Cyclin-U2-2 OS=Arabidopsis thaliana OX=3702 GN=CYCU2-2 PE=1 SV=1
A2376	-	-	-	-	-	-	-	-
A2377	-	-	GO:0003697(single-stranded DNA binding),GO:0003676(nucleic acid binding)	-	-	-	-	-
A2378	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239[At5g54670 Kinesin (KAR3 subfamily)	TPX76853.1 hypothetical protein CcCBS67573_g01876 [Chytridiomycota confervae]	Kinesin-like protein KIN-14H OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14H PE=2 SV=1
A2379	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1543[Hs14786522 Cysteine proteinase Cathepsin L	ORX50197.1 peptidase C1A [Hesseltinella vesiculosa]	Cathepsin Z OS=Mus musculus OX=10090 GN=Ctsz PE=1 SV=1
A2380	-	-	-	K18158 NCA2; nuclear control of ATPase protein 2	-	-	KAG0299223.1 Nuclear control of ATPase protein 2, partial [Dissophora globulifera]	Nuclear control of ATPase protein 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=nca2 PE=3 SV=1
A2381	-	-	-	K02295 CRY; cryptochrome	map04710 Circadian rhythm	KOG0133[At3g15620 Deoxyribodipyrimidine photolase/cryptochrome	KAF7756459.1 (6-4)DNA photolase [Entomophthora muscae]	(6-4)DNA photolase OS=Oryza sativa subsp. japonica OX=39947 GN=UVR3 PE=3 SV=1

A2382	GO:0006886 (intracellular protein transport), GO:0016192 (vesicle-mediated transport), GO:0015031 (protein transport)	GO:0030117 (membrane coat)	-	K12394 AP1S1_2; AP-1 complex subunit sigma 1/2	map04142 Lysosome; map05170 Human immunodeficiency virus 1 infection	KOG0934 At4g35410 Clathrin adaptor complex, small subunit	OAQ35374.1 Adaptor protein complex sigma subunit [Linnemannia elongata AG-77]	AP-1 complex subunit sigma-2 OS=Dictyostelium discoideum OX=44689 GN=ap1s2 PE=3 SV=1
A2383	GO:0042073 (intracellular transport), GO:0060271 (cilium assembly)	GO:0030992 (intracellular transport particle B)	GO:0048487 (beta-tubulin binding)	-	-	-	XP_01660872.1 hypothetical protein SPPG_03805 [Spizellomyces punctatus DAOM BR117]	Intraflagellar transport protein 74 OS=Chlamydomonas reinhardtii OX=3055 GN=IFT74 PE=1 SV=1
A2384	GO:0006468 (protein phosphorylation)	-	GO:0004672 (protein kinase activity), GO:0005524 (ATP binding)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration; map04024 cAMP signaling pathway; map04020 Calcium signaling pathway; map05414 Dilated cardiomyopathy; map04140 Autophagy - animal; map04211 Longevity regulating pathway; map04213 Longevity regulating pathway - multiple species; map01522 Endocrine resistance; map04919 Thyroid hormone signaling pathway; map04918 Thyroid hormone synthesis; map04	-	RKP19300.1 Kinase-domain-containing protein [Rozella allomycis CSF55]	Serine/threonine-protein kinase sck1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=sck1 PE=1 SV=2
A2385	GO:0001510 (RNA methylation)	-	GO:0008168 (methyltransferase activity)	K15264 NSUN5, WBSCR20, RCM1; 25S rRNA (cytosine2278-C5)-methyltransferase [EC:2.1.1.311]	-	KOG2360 At5g26180 Proliferation-associated nucleolar protein (NOL1)	TPX58127.1 hypothetical protein PhCBS80983_g03355 [Powellomyces hirtus]	28S rRNA (cytosine-C(5))-methyltransferase OS=Mus musculus OX=10090 GN=Nsun5 PE=1 SV=2
A2386	-	-	-	-	-	-	-	-
A2387	-	-	-	-	-	KOG1726 CE02055 HVA22/DP1 gene product-related proteins	KAF0488450.1 receptor expression enhancing protein 3 [Gigaspora margarita]	Receptor expression-enhancing protein 4 OS=Rattus norvegicus OX=10116 GN=Reep4 PE=1 SV=1
A2388	GO:0042254 (ribosome biogenesis)	GO:0005634 (nucleus)	GO:0005525 (GTP binding)	K14569 BMS1; ribosome biogenesis protein BMS1	map03008 Ribosome biogenesis in eukaryotes	KOG1951 Hs7661980 GTP-binding protein AARP2 involved in 40S ribosome biogenesis	ORY01638.1 DUF663-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens OX=9606 GN=BMS1 PE=1 SV=1
A2389	GO:0006364 (rRNA processing)	GO:0030688 (ribosome, small subunit precursor)	-	K14849 RRP1; ribosomal RNA-processing protein 1	-	KOG3911 Hs4503247 Nucleolar protein NOP52/RRP1	XP_03359100.4.1 nucleolar protein, Nop52-domain-containing protein [Neohortaea acidophila]	Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens OX=9606 GN=RRP1 PE=1 SV=1

A2390	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	-	-	-
A2391	-	-	-	-	-	-	-	-
A2392	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 CE25046 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	XP_018284599.1 hypothetical protein PHYBLDRAFT_152360 [Phycomyces blakesleeana NRRL 1555(-)]	Calcium/calmodulin-dependent protein kinase type 1 OS=Macrobrachium nipponense OX=159736 GN=CaMKI PE=2 SV=1
A2393	-	-	GO:0005509(calcium ion binding)	-	-	KOG0027 Hs4507617 Calmodulin and related proteins (EF-Hand superfamily)	-	-
A2394	-	-	-	-	-	-	-	-
A2395	-	-	-	-	-	KOG3699 Hs710117 Cytoskeletal protein Adducin	KAG1463373.1 hypothetical protein G6F57_013770 [Rhizopus oryzae]	Putative aldolase class 2 protein PA3430 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA3430 PE=3 SV=1
A2396	GO:0006457(protein folding)	-	GO:0005515(protein binding),GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding)	K09553 STIP1; stress-induced-phosphoprotein 1	map05020 Prion disease	KOG0548 Hs5803181 Molecular chaperone STI1	KAG4107925.1 heat shock protein STI-like protein [Neocallimastix sp. JGI-2020a]	Protein STIP1 homolog OS=Dictyostelium discoideum OX=44689 GN=sti1 PE=3 SV=1
A2397	-	-	GO:0005515(protein binding)	K11684 BDF1; bromodomain-containing factor 1	-	KOG1474 At1g73150 Transcription initiation factor TFIID, subunit BDF1 and related bromodomain proteins	KAG2225900.1 hypothetical protein INT45_006596, partial [Mucor circinatus]	Bromodomain-containing protein 4A OS=Xenopus laevis OX=8355 GN=brd4-a PE=2 SV=1
A2398	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02991 RP-S6e, RPS6; small subunit ribosomal protein S6e	map01521 EGFR tyrosine kinase inhibitor resistance;map04910 Insulin signaling pathway;map05171 Coronavirus disease - COVID-19;map04714 Thermogenesis; map03010 Ribosome;map05205 Proteoglycans in cancer;map04371 Apelin signaling pathway;map04151 PI3K-Akt signaling pathway;map04150 mTOR signaling pathway;map04066 HIF-1 signaling pathway	KOG1646 Hs17158044 40S ribosomal protein S6	OUM65570.1 hypothetical protein PIROE2DRAFT_51017 [Piromyces sp. E2]	Small ribosomal subunit protein eS6 OS=Aplysia californica OX=6500 GN=RPS6 PE=2 SV=1

A2399	-	-	-	-	-	KOG0048 Hs13641706_1 Transcription factor, Myb superfamily	KAF9981062.1 Transcription factor myb3r-5 [Mortierella antarctica]	Transcription factor MYB3R-5 OS=Arabidopsis thaliana OX=3702 GN=MYB3R5 PE=2 SV=1
A2400	GO:0043551(regulation of phosphatidylinositol 3-kinase activity);GO:0045022(early endosome to late endosome transport)	-	GO:0005515(protein binding)	-	-	KOG1333 Hs7661754 Uncharacterized conserved protein	GBC31664.1 wd repeat-containing protein 91 [Rhizophagus irregularis DAOM 181602=DAOM 197198]	WD repeat-containing protein 91 OS=Homo sapiens OX=9606 GN=WDR91 PE=1 SV=2
A2401	GO:0051726(regulation of cell cycle);GO:0006357(regulation of transcription by RNA polymerase II)	GO:0005634(nucleus)	-	-	-	KOG1010 Hs20547701 Rb (Retinoblastoma tumor suppressor)-related protein	EPZ33476.1 Retinoblastoma-associated protein, A-box domain-containing protein [Rozella allomyces CSF55]	Retinoblastoma-associated protein OS=Gallus gallus OX=9031 GN=RB1 PE=1 SV=1
A2402	-	-	GO:0003714(transcription corepressor activity)	K19765 HSBP1; heat shock factor-binding protein 1	map04212 Longevity regulating pathway - worm	-	ORZ35763.1 heat shock factor binding protein 1-domain-containing protein [Catenaria anguillulae PL171]	Heat shock factor-binding protein OS=Arabidopsis thaliana OX=3702 GN=HSBP PE=1 SV=1
A2403	GO:1902600(proton transmembrane transport)	GO:0016020(membrane)	GO:0004427(inorganic diphosphatase activity);GO:0009678(pyrophosphate hydrolysis-driven proton transmembrane transporter activity)	-	-	-	KAG1209907.1 hypothetical protein G6F35_010653 [Rhizopus oryzae]	Pyrophosphate-energized vacuolar membrane proton pump OS=Vigna radiata var. radiata OX=3916 PE=1 SV=4
A2404	-	-	-	K18803 HPM1; protein-histidine N-methyltransferase [EC:2.1.1.85]	-	KOG2920 7295858 Predicted methyltransferase	RKP07647.1 hypothetical protein THASP1DRAFT_16736, partial [Thamnocephalis sphaerospora]	Histidine protein methyltransferase 1 homolog OS=Dictyostelium discoideum OX=44689 GN=DDB_G0270580 PE=3 SV=1
A2405	-	-	-	-	-	-	-	-
A2406	GO:0046952(ketone body catabolic process)	-	GO:0008410(CoA-transferase activity)	K01027 OXC1; 3-oxoacid CoA-transferase [EC:2.8.3.5]	map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map01100 Metabolic pathways	KOG3822 Hs4557817 Succinyl-CoA:alpha-ketoacid-CoA transferase	KXN71530.1 3-oxoacid CoA transferase 1 [Conidiobolus coronatus NRRL 28638]	Probable succinyl-CoA:3-ketoacid coenzyme A transferase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=oxct1 PE=3 SV=1

A2407	GO:0006788(heme oxidation)	-	GO:0004392(heme oxygenase (decyclizing) activity)	K21480 HO, pbsA1, hmuO; heme oxygenase (biliverdin-producing, ferredoxin) [EC:1.14.15.20]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01100 Metabolic pathways	KOG4480[Hs4504437 Heme oxygenase	ORY02253.1 hypothetical protein K493DRAFT_386863 [Basidiobolus meristosporus CBS 931.73]	Heme oxygenase 1 OS=Homo sapiens OX=9606 GN=HMOX1 PE=1 SV=1
A2408	GO:0007165(signal transduction)	-	-	-	-	-	-	Rho GTPase-activating protein gacY OS=Dictyostelium discoideum OX=44689 GN=gacY PE=3 SV=1
A2409	-	-	-	-	-	-	-	-
A2410	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0004497(monooxygenase activity),GO:0020037(heme binding)	K05917 CYP51; sterol 14alpha-demethylase [EC:1.14.14.154 1.14.15.36]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG0684[At1g11680 Cytochrome P450	TPX40754.1 hypothetical protein SeMB42_g05887 [Synchytrium endobioticum]	Sterol 14-demethylase OS=Arabidopsis thaliana OX=3702 GN=CYP51G1 PE=1 SV=1
A2411	-	-	GO:0008146(sulfotransferase activity)	-	-	KOG3703[Hs4758766 Heparan sulfate N-deacetylase/N-sulfotransferase	-	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 3 OS=Homo sapiens OX=9606 GN=NDST3 PE=1 SV=1
A2412	GO:0019441(tryptophan catabolic process to kynurenine)	-	GO:0020037(heme binding),GO:0046872(metal ion binding)	K00463 IDO, INDO; indoleamine 2,3-dioxygenase [EC:1.13.11.52]	map01240 Biosynthesis of cofactors;map05143 African trypanosomiasis;map00380 Tryptophan metabolism;map01100 Metabolic pathways	-	KAG1291855.1 hypothetical protein G6F66_007482 [Rhizopus oryzae]	Indoleamine 2,3-dioxygenase 1 OS=Rattus norvegicus OX=10116 GN=Ido1 PE=2 SV=1
A2413	-	GO:0016021(integral component of membrane)	-	-	-	KOG2569[At3g09570 G protein-coupled seven transmembrane receptor	RCI01907.1 hypothetical protein CU098_000946, partial [Rhizopus stolonifer]	Protein CANDIDATE G-PROTEIN COUPLED RECEPTOR 7 OS=Arabidopsis thaliana OX=3702 GN=CAND7 PE=2 SV=1
A2414	-	-	-	-	-	-	KAF9119979.1 hypothetical protein BGX30_003476, partial [Mortierella sp. GBA39]	Capsule biosynthesis protein CapA OS=Bacillus anthracis OX=1392 GN=capA PE=2 SV=2

A2415	GO:0007205(protein kinase C-activating G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0004143(diacylglycerol kinase activity),GO:0016301(kinase activity)	-	-	KOG1169 At5g63770 Diacylglycerol kinase	TPX66194.1 diacylglycerol kinase (ATP) [Spizellomyces sp. 'palustris']	Diacylglycerol kinase 2 OS=Arabidopsis thaliana OX=3702 GN=DGK2 PE=1 SV=1
A2416	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2417	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0157 Hs4503235 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	XP_031026519.1 uncharacterized protein SmJEL517_g01523 [Synchytrium microbalum]	Cytochrome P450 4V2 OS=Homo sapiens OX=9606 GN=CYP4V2 PE=1 SV=2
A2418	-	-	-	-	-	KOG3589 Hs4506511 G protein signaling regulators	-	Regulator of G-protein signaling 13 OS=Homo sapiens OX=9606 GN=RGS13 PE=1 SV=1
A2419	GO:0000160(phosphorelay signal transduction system)	-	-	-	-	-	-	-
A2420	-	-	-	-	-	-	-	-
A2421	-	-	-	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG1113 CE28749 cAMP-dependent protein kinase types I and II, regulatory subunit	XP_028477874.1 hypothetical protein EHS24_005947 [Apiotrichum porosum]	cGMP-dependent 3',5'-cGMP phosphodiesterase A OS=Dictyostelium discoideum OX=44689 GN=pdeD PE=1 SV=1
A2422	-	-	-	-	-	-	-	-
A2423	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	-	-	KOG1971 CE03397 Lysyl hydroxylase	RCH81117.1 hypothetical protein CU098_006192 [Rhizopus stolonifer]	Multifunctional procollagen lysine hydroxylase and glycosyltransferase OS=Caenorhabditis elegans OX=6239 GN=let-268 PE=1 SV=1
A2424	-	-	-	-	-	-	-	-
A2425	-	-	-	-	-	KOG4386 At5g65950 Uncharacterized conserved protein	-	-

A2426	-	-	-	-	-	-	XP_016605326.1 hypothetical protein SPPG_07215 [Spizellomyces punctatus DAOM BR117]	-
A2427	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A2428	GO:0006465(signal peptide processing),GO:0006508(protolysis),GO:0006627(protein processing involved in protein targeting to mitochondrion)	GO:0016020(membrane),GO:0042720(mitochondrial inner membrane peptidase complex)	GO:0004252(serine-type endopeptidase activity),GO:0008236(serine-type peptidase activity)	K09648 IMP2; mitochondrial inner membrane protease subunit 2 [EC:3.4.21.-]	map03060 Protein export	KOG1568 At3g08980 Mitochondrial inner membrane protease, subunit IMP2	KAG1268741.1 hypothetical protein G6F68_000870 [Rhizopus microsporus]	Mitochondrial inner membrane protease subunit 2 OS=Danio rerio OX=7955 GN=immp2l PE=2 SV=1
A2429	-	-	-	-	-	KOG3377 Hs14249520 Uncharacterized conserved protein	-	Protein FAM136A OS=Homo sapiens OX=9606 GN=FAM136A PE=1 SV=1
A2430	-	-	-	-	-	-	-	-
A2431	-	-	-	-	-	-	-	-
A2432	GO:0006298(mismatch repair)	-	GO:0005524(ATP binding),GO:0030983(mismatched DNA binding)	K08741 MSH5; DNA mismatch repair protein MSH5	-	KOG0221 Hs4505253 Mismatch repair ATPase MSH5 (MutS family)	XP_007732180.1 hypothetical protein AIO3_03855 [Capronia epimyces CBS 606.96]	MutS protein homolog 5 OS=Mus musculus OX=10090 GN=Msh5 PE=1 SV=1
A2433	-	-	-	-	-	-	-	-
A2434	GO:0006629(lipid metabolic process)	-	-	-	-	KOG4569 At5g18630 Predicted lipase	KAF9120150.1 hypothetical protein BGX30_003339 [Mortierella sp. GBA39]	-
A2435	-	-	-	-	-	-	-	-
A2436	GO:0016226(iron-sulfur cluster assembly)	-	GO:0005506(iron ion binding),GO:0051536(iron-sulfur cluster binding)	-	-	KOG2358 At1g51390 NifU-like domain-containing proteins	EGA61437.1 Nfu1p [Saccharomyces cerevisiae FostersO]	NifU-like protein 5, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=NIFU5 PE=2 SV=1
A2437	GO:0017196(N-terminal peptidyl-methionine acetylation)	GO:0031417(NatC complex)	-	K20823 NAA35, MAK10; N-alpha-acetyltransferase 35, NatC auxiliary subunit	-	KOG2343 Hs11345464 Glucose-repressible protein and related proteins	ORX56320.1 Mak10-domain-containing protein [Hesseltinella vesiculosa]	N-alpha-acetyltransferase 35, NatC auxiliary subunit OS=Danio rerio OX=7955 GN=naa35 PE=2 SV=1
A2438	-	-	-	-	-	-	-	-
A2439	-	-	-	K15198 BDP1, TFC5; transcription factor TFIIIB component B''	-	-	KAF3226896.1 Transcription factor TFIIIB component B, partial [Orbilia oligospora]	Transcription factor TFIIIB component B'' OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=bdp1 PE=3 SV=2

A2440	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0005509(calcium ion binding)	K18798 AFG1, LACE1; peroxisome-assembly ATPase [EC:3.6.4.7]	-	KOG2383 Hs21918872 Predicted ATPase	KEP55334.1 AFG1 family ATPase [Rhizoctonia solani 123E]	AFG1-like ATPase OS=Rattus norvegicus OX=10116 GN=Afg1l PE=2 SV=1
A2441	-	-	-	-	-	-	-	-
A2442	-	-	GO:0008194(UDP-glycosyltransferase activity)	K05841 E2.4.1.173; sterol 3beta-glucosyltransferase [EC:2.4.1.173]	-	KOG1192 YLR189c UDP-glucuronosyl and UDP-glucosyl transferase	KAF5314999.1 hypothetical protein D9619_007125 [Psilocybe cf. subviscida]	Sterol 3-beta-glucosyltransferase OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294 / BCRC 21397 / CBS 2163 / NBRC 10782 / NRRL Y-8283 / UCD 57-17) OX=436907 GN=ATG26 PE=3 SV=1
A2443	-	-	-	-	-	-	-	Protein ENHANCED DISEASE RESISTANCE 2-like OS=Arabidopsis
A2444	GO:0001510(RNA methylation),GO:0006396(RNA processing)	-	GO:0008168(methyltransferase activity),GO:0003723(RNA binding),GO:0008757(S-adenosylmethionine-dependent methyltransferase activity)	K14835 NOP2; 25S rRNA (cytosine2870-C5)-methyltransferase [EC:2.1.1.310]	-	-	RKP09852.1 NOL1/NOP2/sun family-domain-containing protein [Thamnocephalis sphaerospora]	Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Mus musculus OX=10090 GN=Nop2 PE=1 SV=1
A2445	GO:0006298(mismatch repair)	GO:0032300(mismatch repair complex)	GO:0005524(ATP binding),GO:0030983(mismatched DNA binding),GO:0003677(DNA binding)	-	-	KOG0219 Hs4557761 Mismatch repair ATPase MSH2 (MutS family)	KAG2175155.1 hypothetical protein INT44_007643 [Umbelopsis vinacea]	DNA mismatch repair protein Msh2 OS=Mus musculus OX=10090 GN=Msh2 PE=1 SV=1
A2446	GO:0006400(tRNA modification)	-	GO:0016763(pentose transferase activity)	K15407 QTRT2, QTRTD1; queuine tRNA-ribosyltransferase accessory subunit	-	KOG3909 CE21692 Queuine-tRNA-ribosyltransferase	ORX92687.1 tRNA-guanine transglycosylase [Basidiobolus meristosporus CBS 931.73]	Queuine tRNA-ribosyltransferase OS=Symbiobacterium thermophilum (strain T / IAM 14863) OX=292459 GN=tgt PE=3 SV=1
A2447	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	KOG1624 At2g20060 Mitochondrial/chloroplast ribosomal protein L4	KAG1468480.1 hypothetical protein G6F56_003806 [Rhizopus deleamar]	Large ribosomal subunit protein uL4 OS=Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIMB 8255 / S1) OX=269796 GN=rplD PE=3 SV=1
A2448	-	-	GO:0008233(peptidase activity)	-	-	-	-	-
A2449	-	-	-	-	-	KOG2502 HsM4507739 Tub family proteins	-	Tubby-related protein 3 OS=Mus musculus OX=10090 GN=Tulp3 PE=1 SV=1

A2450	GO:0006289(nucleotide-excision repair)	GO:0005634(nucleus)	GO:0004518(nuclease activity),GO:0003697(single-stranded DNA binding),GO:0004519(endonuclease activity),GO:0016788(hydrolase activity, acting on ester bonds),GO:0003677(DNA binding),GO:0003824(catalytic activity)	K10846 ERCC5, XPG, RAD2; DNA excision repair protein ERCC-5	map03420 Nucleotide excision repair	KOG2520 At3g28030 5'-3' exonuclease	EPS30246.1 hypothetical protein PDE_05196 [Penicillium oxalicum 114-2]	DNA repair protein UVH3 OS=Arabidopsis thaliana OX=3702 GN=UVH3 PE=2 SV=1
A2451	-	-	-	-	-	-	-	-
A2452	-	-	GO:000049(tRNA binding)	K15437 AIMP1, ARC1; aminoacyl tRNA synthase complex-interacting multifunctional protein 1	-	KOG2241 At2g40660 tRNA-binding protein	RKP14899.1 hypothetical protein BJ684DRAFT_7888, partial [Piptocephalis cylindrospora]	Methionine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana OX=3702 GN=At4g13780 PE=2 SV=1
A2453	GO:0006629(lipid metabolic process)	GO:0016021(integral component of membrane)	GO:0000166(nucleotide binding),GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K05853 ATP2A; P-type Ca2+ transporter type 2A [EC:7.2.2.10]	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05415 Diabetic cardiomyopathy;map05414 Dilated cardiomyopathy;map05410 Hypertrophic cardiomyopathy;map05412 Arrhythmogenic right ventricular cardiomyopathy;map04919 Thyroid hormone signaling pathway;map04380 Osteoclast differentiation;map04261 Adrenergic	KOG0202 Hs4885077 Ca2+ transporting ATPase	KAF9207519.1 hypothetical protein BGZ49_000257 [Haplosporangium sp. Z 27]	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens OX=9606 GN=ATP2A3 PE=1 SV=3
A2454	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0006813(potassium ion transport)	GO:0016020(membrane)	GO:0005216(ion channel activity),GO:0005249(voltage-gated potassium channel activity)	K10273 FBXL7; F-box and leucine-rich repeat protein 7	-	KOG0498 Hs21359848 K+-channel ERG and related proteins, contain PAS/PAC sensor domain	KNE70337.1 hypothetical protein AMAG_14476 [Allomyces macrogynus ATCC 38327]	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1 OS=Mus musculus OX=10090 GN=Hcn1 PE=1 SV=1
A2455	-	-	-	-	-	-	-	-
A2456	-	-	-	-	-	KOG0557 At3g52200 Dihydrolipoamide acetyltransferase	OEJ90492.1 Dihydrolipoalysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondria [Hanseniaspora uvarum]	Dihydrolipoalysine-residue acetyltransferase component of pyruvate dehydrogenase complex OS=Corynebacterium glutamicum (strain ATCC 13032 / DSM 20300 / BCRC 11384 / JCM 1318 / LMG 3730 / NCIMB 10025) OX=196627 GN=aceF PE=1 SV=1

A2457	-	-	-	-	-	KOG4464 Hs20127603 Signaling protein RIC-8/synembryn (regulates neurotransmitter secretion)	-	-
A2458	GO:0000398(mRNA splicing, via spliceosome)	-	GO:0003676(nucleic acid binding)	-	-	KOG4315 Hs15811782 G-patch nucleic acid binding protein	EPZ35066.1 DExH-box splicing factor binding site domain-containing protein [Rozella allomycis CSF55]	Pre-mRNA-splicing factor SPP2 OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=SPP2 PE=3 SV=1
A2459	-	-	-	-	-	-	-	-
A2460	GO:0016126(sterol biosynthetic process), GO:0016579(protein deubiquitination), GO:0006511(ubiquitin-dependent protein catabolic process)	GO:0016020(membrane)	GO:0016628(oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor), GO:004843(thiol-dependent deubiquitinase)	K11858 USP48; ubiquitin carboxyl-terminal hydrolase 48 [EC:3.4.19.12]	-	KOG1863 Hs18860907_1 Ubiquitin carboxyl-terminal hydrolase	ORY45172.1 hypothetical protein BCR33DRAFT_716499, partial [Rhizoclostium globosum]	Ubiquitin carboxyl-terminal hydrolase 48 OS=Mus musculus OX=10090 GN=Usp48 PE=1 SV=2
A2461	GO:0006508(proteolysis)	GO:0016020(membrane)	GO:0005044(scarvenger receptor activity), GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption; map04972 Pancreatic secretion; map04080 Neuroactive ligand-receptor interaction; map05164 Influenza A	KOG3627 730109 Trypsin	KFH43498.1 Trypsin-like protein [Acremonium chrysogenum ATCC 11550]	Trypsin-4 OS=Anopheles gambiae OX=7165 GN=TRYP4 PE=2 SV=2
A2462	-	-	-	-	-	KOG1505 Hs1427110 Lysophosphatidic acid acyltransferase LPAAT and related acyltransferases	QDS70043.1 hypothetical protein FKW77_004037 [Venturia effusa]	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon OS=Mus musculus OX=10090 GN=Agpat5 PE=1 SV=2
A2463	-	-	-	K24611 AMMECR1, AMMECR1L; AMME syndrome candidate gene 1 protein	-	KOG3274 CE03582 Uncharacterized conserved protein, AMMECR1	XP_006680893.1 uncharacterized protein BATDEDRAFT_90717 [Batrachochytrium dendrobatidis JAM81]	Uncharacterized protein R166.3 OS=Caenorhabditis elegans OX=6239 GN=R166.3 PE=4 SV=1
A2464	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K09568 FKBP1; FK506-binding protein 1 [EC:5.2.1.8]	-	KOG0544 7302498 FKBP-type peptidyl-prolyl cis-trans isomerase	ORZ16354.1 FK506-binding protein 1 [Absidia repens]	Peptidyl-prolyl cis-trans isomerase Fkbp12 OS=Drosophila melanogaster OX=7227 GN=Fkbp12 PE=3 SV=2

A2465	GO:0016485(protein processing)	GO:0016021(integral component of membrane)	GO:0004190(serine-type endopeptidase activity)	-	-	KOG2736 At2g29900 Presenilin	XP_025171193.1 hypothetical protein GLOIN_2v1463170, partial [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Presenilin-B OS=Dictyostelium discoideum OX=44689 GN=psenB PE=3 SV=1
A2466	-	-	-	-	-	-	-	-
A2467	-	-	-	-	-	-	-	-
A2468	-	-	-	-	-	-	-	-
A2469	-	-	-	-	-	-	-	-
A2470	-	-	GO:0005515(protein binding)	-	-	KOG4619 CE26908 Uncharacterized conserved protein	TPX56453.1 hypothetical protein PhCBS80983_g04533 [Powellomyces hirtus]	Transmembrane protein 65 OS=Mus musculus OX=10090 GN=Tmem65 PE=1 SV=1
A2471	-	-	GO:0016787(hydrolase activity)	K07252 DOLPP1; dolichyldiphosphatase [EC:3.6.1.43]	map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG3146 Hs2046120 Dolichyl pyrophosphate phosphatase and related acid phosphatases	KAG4095995.1 PAP2-domain-containing protein [Neocallimastix sp. JGI-2020a]	Dolichyldiphosphatase 1 OS=Mus musculus OX=10090 GN=Dolpp1 PE=2 SV=1
A2472	GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds),GO:0003824(catalytic activity),GO:0030246(carbohydrate binding)	-	-	KOG1066 HsM7661898 Glucosidase II catalytic (alpha) subunit and related enzymes, glycosyl hydrolase family 31	XP_031025232.1 uncharacterized protein SmJEL517_g02847 [Synchytrium microbalum]	Alpha-glucosidase 2 OS=Bacillus thermoamyloliquefaciens OX=1425 PE=3 SV=1
A2473	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2474	-	-	-	-	-	-	OQD78941.1 hypothetical protein PENANT_c071G03670 [Penicillium antarcticum]	-
A2475	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A2476	-	-	-	-	-	-	OMJ15326.1 hypothetical protein AYI69_g8231 [Smittium culicis]	-
A2477	-	-	-	-	-	-	-	-
A2478	-	-	-	-	-	-	-	-
A2479	-	GO:0005737(cytoplasm)	GO:0005515(protein binding)	K04705 STAM; signal transducing adaptor molecule	map04144 Endocytosis;map04630 JAK-STAT signaling pathway	KOG3601 CE01784 Adaptor protein GRB2, contains SH2 and SH3 domains	KAG0365135.1 class II myosin [Gamsiella multivaricata]	P47(GAG-CRK) protein OS=Avian sarcoma virus CT10 OX=11878 PE=4 SV=1
A2480	-	-	-	-	-	-	-	-

A2481	GO:0044237(cellular metabolic process)	-	GO:0003824(catalytic activity)	-	-	-	-	-
A2482	GO:0046168(glycerol-3-phosphate catabolic process)	-	GO:0016491(oxidoreductase activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0051287(NAD binding)	-	-	-	-	Opine dehydrogenase OS=Haliotis discus hannai OX=42344 GN=tadh PE=2 SV=1
A2483	-	-	-	-	-	-	-	-
A2484	GO:0048193(Golgi vesicle transport)	GO:0030008(TRAPP complex)	-	K20302 TRAPPC3, BET3; trafficking protein particle complex subunit 3	-	KOG3330 At5g54750 Transport protein particle (TRAPP) complex subunit	ORX50414.1 TRAPP I complex [Piromyces finnis]	Trafficking protein particle complex subunit 3 OS=Gallus gallus OX=9031 GN=TRAPPC3 PE=2 SV=1
A2485	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K08139 HXT; MFS transporter, SP family, sugar:H+ symporter	map04113 Meiosis - yeast	KOG0254 At1g11260 Predicted transporter (major facilitator superfamily)	KAG0735666.1 hypothetical protein G6F23_01143.1 [Rhizopus oryzae]	Sugar transport protein 1 OS=Arabidopsis thaliana OX=3702 GN=STP1 PE=1 SV=2
A2486	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K08139 HXT; MFS transporter, SP family, sugar:H+ symporter	map04113 Meiosis - yeast	KOG0254 At1g11260 Predicted transporter (major facilitator superfamily)	KAG0735666.1 hypothetical protein G6F23_01143.1 [Rhizopus oryzae]	Sugar transport protein 1 OS=Arabidopsis thaliana OX=3702 GN=STP1 PE=1 SV=2
A2487	-	-	GO:0016746(acyltransferase activity)	K13507 GAT; glycerol-3-phosphate O-acyltransferase / dihydroxyacetone phosphate acyltransferase [EC:2.3.1.15 2.3.1.42]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	-	ODQ74991.1 hypothetical protein LIPSTDRAFT_235628 [Lipomyces starkeyi NRRL Y-11557]	Glycerol-3-phosphate O-acyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCT1 PE=1 SV=3
A2488	-	-	-	-	-	-	-	-
A2489	-	-	-	-	-	-	-	-
A2490	GO:0006457(protein folding)	-	GO:0051082(unfolded protein binding),GO:0030544(Hsp70 protein binding)	K09503 DNAJA2; DnaJ homolog subfamily A member 2	map04141 Protein processing in endoplasmic reticulum	KOG0712 Hs5031741 Molecular chaperone (DnaJ) superfamily)	XP_01661272.7.1 chaperone DnaJ [Spizellomyces punctatus DAOM BR117]	DnaJ homolog subfamily A member 2 OS=Mus musculus OX=10090 GN=DnaJ2 PE=1 SV=1
A2491	-	-	GO:0046872(metal ion binding)	-	-	KOG3266 Hs8923431 Predicted glycine cleavage system H protein	PVU90748.1 hypothetical protein BB561_00473.1 [Smittium simulii]	Protein Abitram OS=Gallus gallus OX=9031 GN=ABITRAM PE=2 SV=1

A2492	GO:0007165(signal transduction)	-	GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity),GO:0008081(phosphoric diester hydrolase activity)	-	-	KOG3689 CE02038 Cyclic nucleotide phosphodiesterase	KXS20315.1 HD-domain/PDEase-like protein [Gonapodya prolifera JEL478]	3',5'-cyclic-AMP phosphodiesterase 4C (Fragment) OS=Rattus norvegicus OX=10116 GN=Pde4c PE=2 SV=2
A2493	GO:005085(transmembrane transport)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG0254 At1g11260 Predicted transporter (major facilitator superfamily)	GAM39555.1 glucose transporter [Talaromyces cellulolyticus]	Sugar transport protein 1 OS=Arabidopsis thaliana OX=3702 GN=STP1 PE=1 SV=2
A2494	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity)	-	-	-	-	-
A2495	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	KOG0113 Hs2050771 U1 small nuclear ribonucleoprotein (RRM superfamily)	KAG0231209.1 hypothetical protein BGW41_002237 [Actinomortella wolfii]	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens OX=9606 GN=SNRNP70 PE=1 SV=2
A2496	-	GO:0016021(integral component of membrane)	-	K13348 MPV17; protein Mpv17	map04146 Peroxisome	KOG1944 YLR251w Peroxisomal membrane protein MPV17 and related proteins	XP_02466455.4.1 Protein SYM1 [Wickerhamia lilasorbophila]	Protein SYM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SYM1 PE=1 SV=1
A2497	-	-	-	-	-	-	-	cGMP-dependent 3',5'-cGMP phosphodiesterase A OS=Dictyostelium discoideum OX=44689 GN=pdeD PE=1 SV=1
A2498	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K01205 NAGLU; alpha-N-acetylglucosaminidase [EC:3.2.1.50]	map04142 Lysosome;map00531 Glycosaminoglycan degradation;map01100 Metabolic pathways	KOG2233 Hs4505327 Alpha-N-acetylglucosaminidase	GU88610.1 hypothetical protein Asppvi_007534 [Aspergillus pseudoviridutans]	Alpha-N-acetylglucosaminidase OS=Homo sapiens OX=9606 GN=NAGLU PE=1 SV=2
A2499	GO:0006788(heme oxidation)	-	GO:0004392(heme oxygenase (decyclizing) activity)	K21480 HO, pbsA1, hmuO; heme oxygenase (biliverdin-producing, ferredoxin) [EC:1.14.15.20]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01100 Metabolic pathways	KOG4480 Hs4504437 Heme oxygenase	KAG0259876.1 Heme oxygenase 2 [Mortierella polycephala]	Heme oxygenase OS=Takifugu rubripes OX=31033 GN=hmoX PE=3 SV=1
A2500	-	-	GO:0016787(hydrolase activity)	-	-	KOG1515 At3g48700 Arylacetamide deacetylase	KAF1982210.1 alpha/beta-hydrolase [Aulographum hederæ CBS 113979]	Esterase FPSE_08126 OS=Fusarium pseudograminearum (strain CS3096) OX=1028729 GN=FPSE_08126 PE=2 SV=1
A2501	-	-	-	-	-	-	-	-
A2502	GO:0006355(regulation of transcription, DNA-templated)	GO:0016592(mediator complex)	GO:0003712(transcription coregulator activity)	-	-	KOG4086 At5g19910 Transcriptional regulator SOH1	ORY98612.1 SOH1-domain-containing protein [Syncephalaster racemosum]	Mediator of RNA polymerase II transcription subunit 31 OS=Arabidopsis thaliana OX=3702 GN=MED31 PE=1 SV=1

A2503	-	-	GO:0005515(protein binding)	-	-	KOG0167 At5g13060 FOG: Armadillo/beta-catenin-like repeats	-	-
A2504	-	-	GO:0009916(alternative oxidase activity)	-	-	-	RKP10927.1 alternative oxidase-domain-containing protein [Thamnocephalus sphaerospora]	Ubiquinol oxidase, mitochondrial OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) OX=684364 GN=AOX PE=3 SV=1
A2505	GO:0006281(DNA repair)	-	GO:0003824(catalytic activity),GO:0004518(nuclease activity),GO:0003677(DNA binding),GO:0004519(endonuclease activity)	K10772 APEX2; AP endonuclease 2 [EC:3.1.11.2]	-	KOG1294 Hs18375507 Apurinic/apyrimidinic endonuclease and related enzymes	KXS11820.1 DNase I-like protein [Gonapodya prolifera JEL478]	DNA-(apurinic or apyrimidinic site) endonuclease OS=Mus musculus OX=10090 GN=Apex1 PE=1 SV=2
A2506	GO:0006486(protein glycosylation)	GO:0016020(membrane)	GO:0000030(mannosyltransferase activity)	-	-	KOG4472 ECU04g1130 Glycolipid 2-alpha-mannosyltransferase (alpha-1,2-mannosyltransferase)	ODV91426.1 glycosyltransferase family 15 protein, partial [Tortispora caseinolytica NRRL Y-17796]	Glycolipid 2-alpha-mannosyltransferase 2 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MNT2 PE=3 SV=4
A2507	-	-	-	-	-	-	-	-
A2508	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K11498 CENPE, KIF10; centromeric protein E	map04814 Motor proteins	KOG4280 CE27986 Kinesin-like protein	THW62788.1 kinesin-domain-containing protein [Aureobasidium pullulans]	Chromosome-associated kinesin KIF4 OS=Xenopus laevis OX=8355 GN=kif4 PE=2 SV=1
A2509	-	-	-	-	-	-	-	-
A2510	-	-	-	-	-	-	-	-
A2511	-	-	GO:0005458(GDP-mannose transmembrane transporter activity)	-	-	-	KAG5362916.1 GDP-mannose transporter [Yarrowia sp. B02]	GDP-mannose transporter OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=VRG4 PE=3 SV=1
A2512	GO:0006511(ubiquitin-dependent protein catabolic process)	GO:0031461(cullin-RING ubiquitin ligase complex)	GO:0031625(ubiquitin protein ligase binding)	K03869 CUL3; cullin 3	map04340 Hedgehog signaling pathway;map04341 Hedgehog signaling pathway - fly;map04120 Ubiquitin mediated proteolysis	KOG2166 At1g26830 Cullins	GBB95576.1 hypothetical protein RclHR1_02570010 [Rhizophagus clarus]	Cullin-3A OS=Arabidopsis thaliana OX=3702 GN=CUL3A PE=1 SV=1
A2513	-	-	-	-	-	-	-	-
A2514	-	-	-	-	-	-	-	-
A2515	GO:0007099(centriole replication),GO:0010457(centriole-centriole cohesion)	-	-	-	-	-	TPX64074.1 hypothetical protein SpCBS45565g06173 [Spizellomyces sp. 'palustris']	Centrosomal protein of 135 kDa OS=Danio rerio OX=7955 GN=cep135 PE=1 SV=2

A2516	-	-	GO:0000030(mannosyltransferase activity),GO:0016757(glycosyltransferase activity)	K03846 ALG9; alpha-1,2-mannosyltransferase [EC:2.4.1.259-2.4.1.261]	map00513 Various types of N-glycan biosynthesis;map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG2515[Hs13376062 Mannosyltransferase	XP_007676998.1 glycosyltransferase family 22 protein [Baudoinia panamERICANA UAMH 10762]	Alpha-1,2-mannosyltransferase ALG9 OS=Mus musculus OX=10090 GN=Alg9 PE=2 SV=1
A2517	-	-	-	-	-	-	ORY50313.1 hypothetical protein BCR33DRAFT_762690 [Rhizoclostium globosum]	-
A2518	-	-	GO:0070006(metalloaminopeptidase activity),GO:0016787(hydrolase activity)	K01262 pepP; Xaa-Pro aminopeptidase [EC:3.4.11.9]	-	KOG2413[At4g36760 Xaa-Pro aminopeptidase	TPX58919.1 hypothetical protein SpCBS45565_g07872 [Spizellomyces sp. 'palustris']	Probable Xaa-Pro aminopeptidase P OS=Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) OX=486041 GN=AMPP PE=3 SV=1
A2519	-	-	-	-	-	KOG2283[7297635 Clathrin coat dissociation kinase GAK/PTEN/Auxilin and related tyrosine phosphatases	RKO87251.1 hypothetical protein BDK51DRAFT_38882, partial [Blyttomyces helicus]	Formin-like protein 3 OS=Oryza sativa subsp. japonica OX=39947 GN=FH3 PE=2 SV=2
A2520	-	-	-	-	-	KOG3193[CE18570 K+ channel subunit	KNE72136.1 hypothetical protein AMAG_16628 [Allomyces macrogynus ATCC 38327]	-
A2521	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity),GO:0004965(G protein-coupled GABA receptor activity)	-	-	KOG1055[7296172 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	TPX74488.1 hypothetical protein CcCBS67573_g04237 [Chytridiomycetes confervae]	Metabotropic glutamate receptor-like protein E OS=Dictyostelium discoideum OX=44689 GN=grlE PE=2 SV=2
A2522	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2523	-	-	GO:0051015(actin filament binding)	-	-	KOG0443[7296888 Actin regulatory proteins (gelsolin/villin family)	KAF9289892.1 hypothetical protein BGZ68_008376 [Mortierella alpina]	Gelsolin-like protein 1 OS=Lumbricus terrestris OX=6398 GN=AM PE=1 SV=1
A2524	-	-	GO:0008767(UDP-galactopyranose mutase activity)	-	-	-	KAG4097258.1 UDP-galactopyranose mutase [Neocallimastix sp. JGI-2020a]	UDP-galactopyranose mutase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=glf PE=3 SV=1

A2525	-	-	-	-	-	KOG0800 CE00866 FOG: Predicted E3 ubiquitin ligase	KAG0073483.1 hypothetical protein BGZ92_003836 [Podila epicladia]	RING finger protein 11 OS=Bos taurus OX=9913 GN=RNf11 PE=2 SV=1
A2526	GO:0019464(glycine decarboxylation via glycine cleavage system)	GO:0005960(glycine cleavage complex)	-	K02437 gcvH; GCSH; glycine cleavage system H protein	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map00630 Glyoxylate and dicarboxylate metabolism	KOG3373 At2g35120 Glycine cleavage system H protein (lipoate-binding)	KAG1133139.1 hypothetical protein G6F42_001715 [Rhizopus oryzae]	Glycine cleavage system H protein OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=gcvH PE=1 SV=1
A2527	GO:0006352(DNA-templated transcription, initiation), GO:0044237(cellular metabolic process)	GO:0030880(RNA polymerase complex)	GO:0000166(nucleotide binding)	K03012 RPB4; POLR2D; DNA-directed RNA polymerase II subunit RPB4	map03420 Nucleotide excision repair;map03020 RNA polymerase;map05016 Huntington disease	KOG2351 Hs4758574 RNA polymerase II, fourth largest subunit	PIA19764.1 hypothetical protein COEREDRAFT_5570 [Coemansia reversa NRRL 1564]	DNA-directed RNA polymerase II subunit RPB4 OS=Homo sapiens OX=9606 GN=POLR2D PE=1 SV=1
A2528	-	-	GO:0005515(protein binding)	-	-	-	ORX47608.1 hypothetical protein BCR36DRAFT_413548 [Piromyces finnis]	Bardet-Biedl syndrome 7 protein homolog OS=Mus musculus OX=10090 GN=Bbs7 PE=1 SV=1
A2529	-	-	-	-	-	-	-	-
A2530	-	-	-	-	-	-	-	-
A2531	-	-	GO:0003824(catalytic activity)	-	-	KOG3957 7300628 Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	KXS13549.1 CoA-transferase family III [Gonapodya prolifera JEL478]	Acyl-CoA transferase FPSE_08120 OS=Fusarium pseudograminearum (strain CS3096) OX=1028729 GN=FPSE_08120 PE=2 SV=1
A2532	-	-	-	-	-	-	-	-
A2533	-	-	-	-	-	-	-	-
A2534	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	PIG85102.1 hypothetical protein AARAC_000702 [Aspergillus arachidicola]	E3 ubiquitin-protein ligase SspH1 OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=sspH1 PE=1 SV=1
A2535	-	-	GO:0016491(oxidoreductase activity)	K00387 SUOX; sulfite oxidase [EC:1.8.3.1]	map01120 Microbial metabolism in diverse environments;map00920 Sulfur metabolism;map01100 Metabolic pathways	KOG0535 Hs4557867.2 Sulfite oxidase, molybdopterin-binding component	PSS36913.1 hypothetical protein PHLCE_N_2v1231 [Phlebia centrifuga]	Sulfite oxidase, mitochondrial OS=Macaca fascicularis OX=9541 GN=SUOX PE=2 SV=3

A2536	-	-	-	-	-	-	ORX76358.1 putative 13 KDA deflagellation-inducible protein [Anaeromyxos robustus]	Microtubule nucleation factor SSNA1 OS=Chlamydomonas reinhardtii OX=3055 GN=SSNA1 PE=1 SV=1
A2537	GO:0006417(regulation of translation)	-	GO:0003676(nucleic acid binding),GO:0003723(RNA binding),GO:0003729(mRNA binding)	-	-	-	-	RNA-binding protein FXR2 OS=Homo sapiens OX=9606 GN=FXR2 PE=1 SV=2
A2538	GO:0006298(mismatch repair)	-	GO:0005524(ATP binding),GO:0030983(mismatched DNA binding)	-	-	-	KAG0420552.1 DNA mismatch repair protein MutS, partial [Dictyococcoides roeselii]	DNA mismatch repair protein MutS OS=Chelativorans sp. (strain BNC1) OX=266779 GN=mutS PE=3 SV=1
A2539	-	-	-	-	-	-	-	-
A2540	-	-	-	-	-	KOG4308[Hs11436853 LRR-containing protein]	-	Ribonuclease inhibitor OS=Rattus norvegicus OX=10116 GN=Rnh1 PE=1 SV=2
A2541	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1336[Hs14318424 Monodehydroascorbate/ferredoxin reductase]	XP_007868239.1 amid-like NADH oxidoreductase [Gloeophyllum trabeum ATCC 11539]	Ferroptosis suppressor protein 1 OS=Xenopus laevis OX=8355 GN=aifm2 PE=2 SV=1
A2542	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG2495[At3g44190 NADH-dehydrogenase (ubiquinone)]	TFK51270.1 FAD/NAD(P)-binding domain-containing protein [Heliocybe sulcata]	Ferroptosis suppressor protein 1 OS=Xenopus tropicalis OX=8364 GN=aifm2 PE=2 SV=1
A2544	-	-	-	-	-	-	-	-
A2545	-	-	-	-	-	-	-	-
A2546	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K12196 VPS4; vacuolar protein-sorting-associated protein 4	map04144 Endocytosis;map03250 Viral life cycle - HIV-1;map04217 Necroptosis	KOG0738[Hs5901990 AAA+-type ATPase]	XP_006676377.1 uncharacterized protein BATDEDRAFT_84945 [Batrachochytrium dendrobatidis JAM81]	Katanin p60 ATPase-containing subunit A-like 1 OS=Sorex araneus OX=42254 GN=KATNAL1 PE=3 SV=1
A2547	-	-	GO:0003824(catalytic activity),GO:0008270(zinc ion binding),GO:0016787(hydrolase activity)	-	-	-	XP_013021353.1 cytosine deaminase [Schizosaccharomyces cryophilus OY26]	Probable cytosine deaminase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC965.14c PE=3 SV=1
A2548	-	-	GO:0005515(protein binding)	-	-	KOG0531[Hs18597149 Protein phosphatase 1, regulatory subunit, and related proteins]	TPX57737.1 hypothetical protein PhCBS80983g03605 [Powellomyces hirtus]	Leucine-rich repeat-containing protein 9 OS=Homo sapiens OX=9606 GN=LRRC9 PE=2 SV=2

A2549	-	-	-	-	-	-	XP_001588867.1 hypothetical protein SS1G_10415 [Sclerotinia sclerotiorum 1980 UF-70]	8-demethyl-8-(2,3-dimethoxy-alpha-L-rhamnosyl)-tetracenomycin-C 4'-O-methyltransferase OS=Streptomyces olivaceus OX=47716 GN=elmMIII PE=1 SV=1
A2550	-	-	-	-	-	KOG3017 Hs13899332 Defense-related protein containing SCP domain	EUC53808.1 LCCL domain protein [Rhizoctonia solani AG-3 Rh51AP]	Cysteine-rich secretory protein LCCL domain-containing 2 OS=Bos taurus OX=9913 GN=CRISPLD2 PE=2 SV=1
A2551	GO:0006457(protein folding)	-	GO:0005515(protein binding),GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding)	K12274 SEC72; translocation protein SEC72	-	-	EPZ35927.1 hypothetical protein O9G_005386 [Rozella allomyces CSF55]	Translocation protein sec72 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=sec72 PE=3 SV=1
A2552	GO:0007165(signal transduction),GO:0006355(regulation of transcription, DNA-templated)	-	GO:0005515(protein binding)	K11341 YEATS4, GAS41, YAF9; YEATS domain-containing protein 4	map03082 ATP-dependent chromatin remodeling	KOG3149 At5g45600 Transcription initiation factor IIF, auxiliary subunit	KAF9976713.1 NuA4 histone H4 acetyltransferase complex and the SWR1 complex subunit [Actinomortierella ambigua]	Transcription initiation factor TFIID subunit 14b OS=Arabidopsis thaliana OX=3702 GN=TAF14B PE=1 SV=1
A2553	-	-	-	-	-	KOG0048 Hs4505293.1 Transcription factor, Myb superfamily	KAF8940947.1 DNA binding transcription coactivator transcription factor [Dissophora ornata]	Transcriptional activator Myb OS=Xenopus laevis OX=8355 GN=myb PE=2 SV=1
A2554	-	-	-	-	-	-	-	-
A2555	-	-	-	-	-	-	-	-
A2556	-	-	-	-	-	-	-	-
A2557	GO:0006725(cellular aromatic compound metabolic process)	-	GO:0005506(iron ion binding),GO:0016702(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen),GO:0003824(catalytic activity),GO:0008199(ferric iron binding)	-	-	-	XP_024737051.1 aromatic compound dioxygenase [Hyaloscypha bicolor E]	-

A2558	GO:0006725 (cellular aromatic compound metabolic process)	-	GO:0005506 (iron ion binding), GO:0016702 (oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen), GO:0003824 (catalytic activity), GO:0008199 (ferric iron binding)	-	-	-	RPB29052.1 aromatic compound dioxygenase [Terfezia boudieri ATCC MYA-4762]	-
A2559	-	-	-	-	-	-	-	-
A2560	GO:0018216 (peptidyl-arginine methylation), GO:0000463 (maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA))	GO:0022625 (cytosolic large ribosomal subunit)	GO:0016274 (protein-arginine N-methyltransferase activity), GO:0003735 (structural constituent of ribosome)	K02516 PRMT5, HSL7, type II protein arginine methyltransferase [EC:2.1.1.320]	map04011 MAPK signaling pathway - yeast; map04111 Cell cycle - yeast	KOG0822 [Hs20070220 Protein kinase inhibitor]	RUS20150.1 PRMT5 arginine-N-methyltransferase - domain-containing protein [Endogone sp. FLAS-F59071]	Protein arginine N-methyltransferase 1.5 OS=Arabidopsis thaliana OX=3702 GN=PMRT15 PE=1 SV=2
A2561	-	-	-	-	-	-	-	-
A2562	GO:0006457 (protein folding)	-	GO:0003755 (peptidyl-prolyl cis-trans isomerase activity)	K09568 FKBP1; FK506-binding protein 1 [EC:5.2.1.8]	-	-	KAG0920853.1 hypothetical protein G6F32_015386 [Rhizopus oryzae]	Macrophage infectivity potentiator OS=Trypanosoma cruzi OX=5693 GN=MIP PE=1 SV=1
A2563	-	-	-	-	-	-	ORZ31233.1 hint-domain-domain-containing protein [Catenaria anguillulae PL171]	-
A2564	-	-	-	-	-	-	-	-
A2565	GO:0036211 (protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2158 [7301565 Tubulin-tyrosine ligase-related protein]	ORY38770.1 TTL-domain-containing protein [Rhizoclostium globosum]	Tubulin polyglutamylase ttl6 OS=Danio rerio OX=7955 GN=ttl6 PE=2 SV=1
A2566	-	-	-	-	-	-	-	-
A2567	GO:0006508 (proteolysis), GO:0006511 (ubiquitin-dependent protein catabolic process), GO:0016579 (protein deubiquitination), GO:0016311 (dephosphorylation)	-	GO:0004198 (calcium-dependent cysteine-type endopeptidase activity), GO:0005509 (calcium ion binding), GO:0004843 (thiol-dependent deubiquitinase), GO:0016791 (phosphatase activity)	K18045 SIW14, OCA3; tyrosine-protein phosphatase SIW14 [EC:3.1.3.48]	-	KOG1572 [At1g05000 Predicted protein tyrosine phosphatase]	RKP00882.1 hypothetical protein CXG81DRAFT_2796, partial [Caulochytrium protostelioides]	Tyrosine-protein phosphatase DSP1 OS=Arabidopsis thaliana OX=3702 GN=DSP1 PE=1 SV=1

A2568	GO:000045(autophagosome assembly)	-	GO:0005515(protein binding)	K14818 SQT1; ribosome assembly protein SQT1	-	KOG0288 At5g50230 WD40 repeat protein TipD	RUS17762.1 autophagy protein 16 [Endogone sp. FLAS-F59071]	Protein tipD OS=Dictyostelium discoideum OX=44689 GN=tipD PE=3 SV=1
A2569	-	-	-	-	-	-	-	-
A2570	GO:0006468(protein phosphorylation),GO:0006914(autophagy)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding),GO:0004674(protein serine/threonine kinase activity)	-	-	-	ORY46275.1 kinase-like protein [Neocallimastix californiae]	RasGEF domain-containing serine/threonine-protein kinase X OS=Dictyostelium discoideum OX=44689 GN=gefX PE=2 SV=1
A2571	-	-	GO:0020037(heme binding)	K00326 CYB5R; cytochrome-b5 reductase [EC:1.6.2.2]	map00520 Amino sugar and nucleotide sugar metabolism	KOG0537 At2g32720 Cytochrome b5	KAF9149403.1 hypothetical protein BG015_008810 [Linnemannia schmuckeri]	Cytochrome b5 isoform B OS=Arabidopsis thaliana OX=3702 GN=CYTb5-B PE=1 SV=1
A2572	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG0240 At3g54870 Kinesin (SMY1 subfamily)	ORZ36448.1 P-loop containing nucleoside triphosphate hydrolase protein [Catenaria anguillulae PL171]	Kinesin-like protein KIN-UC OS=Arabidopsis thaliana OX=3702 GN=KINUC PE=1 SV=2
A2573	-	-	-	-	-	-	-	-
A2574	-	-	-	-	-	-	-	-
A2575	GO:0006813(potassium ion transport)	GO:0008076(voltage-gated potassium channel complex)	GO:0005249(voltage-gated potassium channel activity)	-	-	KOG1420 CE24409 Ca2+-activated K+ channel Slowpoke, alpha subunit	KAF8156567.1 hypothetical protein B0H34DRAFT_466692 [Crassisporium funariophilum]	Calcium-gated potassium channel TvoK OS=Thermoplasma volcanium (strain ATCC 51530 / DSM 4299 / JCM 9571 / NBRC 15438 / GSS1) OX=273116 GN=tvoK PE=1 SV=1
A2576	-	-	-	-	-	-	-	-

A2577	-	-	GO:0005515(protein binding)	K03350 APC3, CDC27; anaphase-promoting complex subunit 3	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG1174 At2g39090 Anaphase-promoting complex (APC), subunit 7	RUS34734.1 hypothetical protein BC938DRAFT_478855 [Jimgerdennia flammicorona]	Anaphase-promoting complex subunit 7 OS=Arabidopsis thaliana OX=3702 GN=APC7 PE=2 SV=1
A2578	-	-	-	-	-	-	-	-
A2579	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2580	-	-	-	-	-	-	-	-
A2581	GO:0006914(autophagy)	-	-	K17907 ATG9; autophagy-related protein 9	map04140 Autophagy - animal;map04138 Autophagy - yeast;map04137 Mitophagy - animal;map04136 Autophagy - other	KOG2173 At2g31260 Integral membrane protein	OAD05509.1 hypothetical protein MUCCIDRAFT_116964, partial [Mucor lusitanicus CBS 277.49]	Autophagy-related protein 9 OS=Arabidopsis thaliana OX=3702 GN=ATG9 PE=1 SV=1
A2582	-	-	GO:0008289(lipid binding)	-	-	-	-	-
A2583	-	-	-	K13350 PXMP4, PMP24; peroxisomal membrane protein 4	map04146 Peroxisome	-	TPX61066.1 hypothetical protein PhCBS80983_g01396 [Powellomyces hirtus]	Peroxisomal membrane protein 4 OS=Bos taurus OX=9913 GN=PXMP4 PE=2 SV=1
A2584	GO:0006812(cation transport), GO:0055085(transmembrane transport), GO:0006814(sodium ion transport), GO:0006885(regulation of pH)	GO:0016021(integral component of membrane)	GO:0015299(solute:proton antiporter activity), GO:0015385(sodium:proton antiporter activity)	K12041 SLC9A6_7, NHE6_7; solute carrier family 9 (sodium/hydrogen exchanger), member 6/7	map04260 Cardiac muscle contraction	KOG1965 Hs22062123 Sodium/hydrogen exchanger protein	TPX60708.1 hypothetical protein PhCBS80983_g01591 [Powellomyces hirtus]	Sodium/hydrogen exchanger 5 OS=Arabidopsis thaliana OX=3702 GN=NHX5 PE=2 SV=2
A2585	GO:0006091(generation of precursor metabolites and energy)	-	GO:0016836(hydro-lyase activity), GO:0016829(lyase activity), GO:0004333(fumarate hydratase activity), GO:0003824(catalytic activity)	-	-	-	KAG1717052.1 hypothetical protein ID866_26 [Astraeus odoratus]	Fumarate hydratase class I, aerobic OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) OX=199310 GN=fumA PE=3 SV=2

A2586	-	-	GO:0005458(GDP-mannose transmembrane transporter activity)	K15356 GONST1_2, VRG4; GDP-mannose transporter	-	-	KAG2202790.1 hypothetical protein INT47_004814 [Mucor saturninus]	GDP-mannose transporter GONST1 OS=Arabidopsis thaliana OX=3702 GN=GONST1 PE=1 SV=2
A2587	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE24887 FOG: Reverse transcriptase	OMJ13590.1 Transposon TX1 protein [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A2588	-	-	-	K23114 ARMT1; damage-control phosphatase, subfamily III [EC:3.1.3.-]	-	KOG3870 7291365 Uncharacterized conserved protein	RKP26516.1 hypothetical protein SYNPS1DRAFT_14088 [Syncephalis pseudoplumi galeata]	Damage-control phosphatase ARMT1 OS=Danio rerio OX=7955 GN=arnt1 PE=2 SV=1
A2589	-	-	-	-	-	-	KGQ13354.1 Exopolyphosphatase [Beauveria bassiana D1-5]	-
A2590	-	-	GO:0003779(actin binding),GO:0051015(actin filament binding)	-	-	KOG3655 7294461 Drebrins and related actin binding proteins	XP_016605345.1 hypothetical protein SPPG_07234 [Spizellomyces punctatus DAOM BR117]	Drebrin-like protein OS=Drosophila melanogaster OX=7227 GN=Abp1 PE=1 SV=1
A2591	-	-	-	-	-	-	-	-
A2592	-	-	GO:0005515(protein binding)	K11493 RCC1; regulator of chromosome condensation	-	KOG1426 Hs4557445 FOG: RCC1 domain	PWW77216.1 hypothetical protein C7212DRAFT_277797 [Tuber magnatum]	RCC1 and BTB domain-containing protein 2 OS=Homo sapiens OX=9606 GN=RCBTB2 PE=1 SV=1
A2593	-	-	GO:0016803(ether hydrolase activity),GO:0003824(catalytic activity)	-	-	KOG2565 Hs4503583 Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	XP_031022021.1 microsomal epoxide hydrolase [Synchytrium microbalum]	Putative epoxide hydrolase OS=Stigmatella aurantiaca (strain DW4/3-1) OX=378806 GN=STAU_4299 PE=3 SV=2
A2594	GO:0006526(arginine biosynthetic process)	-	GO:0004055(argininosuccinate synthase activity),GO:0005524(ATP binding)	K01940 argG, ASS1; argininosuccinate synthase [EC:6.3.4.5]	map01110 Biosynthesis of secondary metabolites;map05418 Fluid shear stress and atherosclerosis; map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map00220 Arginine biosynthesis;map01100 Metabolic pathways	KOG1706 Hs16950633 Argininosuccinate synthase	XP_031022629.1 argininosuccinate synthase [Synchytrium microbalum]	Argininosuccinate synthase OS=Thermotoga sp. (strain RQ2) OX=126740 GN=argG PE=3 SV=1

A2595	-	-	-	-	-	-	-	-
A2596	-	-	GO:0003824(catalytic activity),GO:0016740(transferase activity)	-	-	KOG3275 At1g31160 Zinc-binding protein of the histidine triad (HIT) family	KAG1716110.1 hypothetical protein ID866_1014 [Astraeus odoratus]	14 kDa zinc-binding protein OS=Zea mays OX=4577 GN=ZBP14 PE=1 SV=1
A2597	GO:0009086(methionine biosynthetic process), GO:0006633(fatty acid biosynthetic process)	-	GO:0016491(oxidoreductase activity),GO:0016740(transferase activity),GO:0016746(acyltransferase activity),GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups),GO:0003871(5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity),GO:0008270(zinc ion binding),GO:0004315(3-oxoacyl-[acyl-carrier-protein] synthase activity)	-	-	KOG1202 Hs21618359 Animal-type fatty acid synthase and related proteins	KAG0288047.1 hypothetical protein BGZ97_006924, partial [Linnemannia gamsii]	6-deoxyerythronolide-B synthase EryA3, modules 5 and 6 OS=Saccharopolyspora erythraea OX=1836 GN=eryA PE=1 SV=4
A2598	GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	K07407 E3.2.1.22B, galA, rafA; alpha-galactosidase [EC:3.2.1.22]	map00603 Glycosphingolipid biosynthesis - globo and isoglobo series;map00600 Sphingolipid metabolism;map00052 Galactose metabolism;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	KOG2366 At5g08380 Alpha-D-galactosidase (melibiase)	TFK41875.1 glycoside hydrolase family 27 protein [Crucibulum laeve]	Alpha-galactosidase OS=Oryza sativa subsp. japonica OX=39947 GN=Os10g0493600 PE=1 SV=1
A2599	GO:0009098(leucine biosynthetic process)	GO:0009316(3-isopropylmalate dehydratase complex)	GO:0003861(3-isopropylmalate dehydratase activity),GO:0051539(4 iron, 4 sulfur cluster binding)	K01702 LEU1; 3-isopropylmalate dehydratase [EC:4.2.1.33]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	-	NP_594576.1 putative 3-isopropylmalate dehydratase Leu2 [Schizosaccharomyces pombe]	3-isopropylmalate dehydratase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=leu2 PE=1 SV=1
A2600	-	-	-	-	-	-	-	-

A2601	-	-	-	-	-	KOG4580 EC U06g1420i_2 Component of vacuolar transporter chaperone (Vtc) involved in vacuole fusion	AJA32468.1 vacuolar transporter chaperone 4 [Nosema pernyi]	Vacuolar transporter chaperone complex subunit 1 OS=Trypanosoma brucei brucei (strain 927/4 GUTat10.1) OX=185431 GN=VTC1 PE=3 SV=1
A2602	GO:0016485(protein processing)	GO:0005777(peroxisome)	GO:0004252(serine-type endopeptidase activity)	-	-	-	XP_021884759.1 trypsin-like cysteine/serine peptidase domain-containing protein [Lobosporangium transversale]	Glyoxysomal processing protease, glyoxysomal OS=Arabidopsis thaliana OX=3702 GN=DEG15 PE=1 SV=2
A2603	-	-	-	-	-	-	-	-
A2604	-	-	GO:0005515(protein binding)	-	-	-	XP_016612029.1 hypothetical protein SPPG_01438 [Spizellomyces punctatus DAOM BR117]	-
A2605	-	-	GO:0016787(hydrolase activity)	-	-	-	XP_016760209.1 Brefeldin A esterase [Sphaerulina musiva SO2202]	Ethyl acetate hydrolase OS=Pseudomonas putida OX=303 GN=estZ PE=1 SV=1
A2606	-	-	GO:0016787(hydrolase activity)	-	-	KOG1515 At3g48700 Arylacetamide deacetylase	KAF7189930.1 Carboxylesterase NihH [Pseudocercospora fuligena]	Arylesterase OS=Saccharolobus solfataricus OX=2287 GN=are PE=1 SV=1
A2607	-	-	GO:0016491(oxidoreductase activity)	K00344 qor, CRYZ; NADPH:quinone reductase [EC:1.6.5.5]	-	KOG1198 At3g56460 Zinc-binding oxidoreductase	RIA84971.1 hypothetical protein C1645_782924 [Glomus cerebriforme]	Quinone oxidoreductase-like protein 2 homolog OS=Nematostella vectensis OX=45351 GN=v1g238856 PE=3 SV=1
A2608	GO:0006508(proteolysis)	-	GO:0005515(protein binding),GO:0004190(aspartic-type endopeptidase activity)	K11885 DDI1; DNA damage-inducible protein 1	-	KOG0012 7293232 DNA damage inducible protein	GEM09332.1 DNA damage-inducible v-SNARE binding protein Ddi1 [Rhodotorula toruloides]	Protein DNA-DAMAGE INDUCIBLE 1 OS=Arabidopsis thaliana OX=3702 GN=DDI1 PE=1 SV=1
A2609	-	-	-	-	-	-	-	-
A2610	-	-	-	-	-	KOG4108 Hs2042346 Dynein light chain	ORX88842.1 Tctex-1, partial [Basidiobolus meristosporus CBS 931.73]	Dynein light chain Tctex-type 5 OS=Danio rerio OX=7955 GN=dyntl5 PE=2 SV=1
A2611	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	KAG2098817.1 capsule polysaccharide biosynthesis [Colletotrichum camelliae]	Glycosyltransferase afumC OS=Aspergillus fumigatus (strain CBS 144.89 / FGSC A1163 / CEA10) OX=451804 GN=afumC PE=1 SV=1
A2612	-	-	-	-	-	-	-	-

A2613	-	-	-	K26544 SEC14, SEC14L; phosphatidyli nositol/phosp hatidylcholin e transfer protein	-	KOG1471 At4 g34580 Phosphatidyl nositol transfer protein SEC14 and related proteins	ORX94477.1 hypothetical protein K493DRAFT_ 315461 [Basidiobolus meristosporu s CBS 931.73]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH12 OS=Arabidopsis thaliana OX=3702 GN=SFH12 PE=2 SV=1
A2614	-	-	-	K26544 SEC14, SEC14L; phosphatidyli nositol/phosp hatidylcholin e transfer protein	-	KOG1471 At1 g55840 Phosphatidyl nositol transfer protein SEC14 and related proteins	OWB54998.1 hypothetical protein B5S28_g861 [[Candida] boidinii]	SEC14-like protein 4 OS=Homo sapiens OX=9606 GN=SEC14L4 PE=1 SV=1
A2615	-	-	-	-	-	-	KXS22149.1 hypothetical protein M427DRAFT_ 50507 [Gonapodya prolifera JEL478]	-
A2616	-	-	GO:0022857(tra nsmembrane transporter activity)	-	-	-	KAG1107679. 1 hypothetical protein G6F42_01628 1 [Rhizopus oryzae]	-
A2617	GO:00066 29(lipid metabolic process)	-	-	-	-	-	ORX84903.1 hypothetical protein BCR32DRAFT_ 291062 [Anaeromyce s robustus]	-
A2618	-	-	GO:0003676(nu cleic acid binding),GO:000 5524(ATP binding),GO:000 3723(RNA binding),GO:000 4386(helicase activity)	K12823 DDX5, DBP2; ATP- dependent RNA helicase DDX5/DBP2 [EC:3.6.4.13]	map03040 Spliceosome;ma p05202 Transcriptional misregulation in cancer;map0520 5 Proteoglycans in cancer	KOG0331 Hs1 3787209 ATP- dependent RNA helicase	RKP05367.1 P-loop containing nucleoside triphosphate hydrolase protein [Thamnoceph alis sphaerospora]	Nucleolar RNA helicase 2 OS=Rattus norvegicus OX=10116 GN=Ddx21 PE=2 SV=1
A2619	-	-	GO:0005509(cal cium ion binding),GO:000 5515(protein binding)	-	-	-	-	-
A2620	-	-	GO:0003676(nu cleic acid binding),GO:000 5524(ATP binding)	K14809 DDX55, SPB4; ATP- dependent RNA helicase DDX55/SPB4 [EC:3.6.4.13]	-	KOG0345 At5 g05450 ATP- dependent RNA helicase	XP_01661139 6.1 hypothetical protein SPPG_02400 [Spizellomyce s punctatus DAOM BR117]	ATP-dependent RNA helicase DDX55 OS=Homo sapiens OX=9606 GN=DDX55 PE=1 SV=3
A2621	-	-	GO:0051087(cha perone binding)	-	-	-	-	-

A2622	GO:0006886 (intracellular protein transport)	GO:0005784 (Sec61 translocation complex)	-	K09481 SEC61B, SBH2; protein transport protein SEC61 subunit beta	map04145 Phagosome; map04141 Protein processing in endoplasmic reticulum; map03060 Protein export; map05110 Vibrio cholerae infection	KOG3457 At5g60460 Sec61 protein translocation complex, beta subunit	RHZ82858.1 hypothetical protein Glove_103g1 [Diversispora epigaea]	Protein transport protein Sec61 subunit beta OS=Arabidopsis thaliana OX=3702 GN=At2g45070 PE=1 SV=1
A2623	GO:0005975 (carbohydrate metabolic process)	-	GO:0004553 (hydrolase activity, hydrolyzing O-glycosyl compounds)	K07407 E3.2.1.22B, galA, rafA; alpha-galactosidase [EC:3.2.1.22]	map00603 Glycosphingolipid biosynthesis - globo and isogloboseries; map00600 Sphingolipid metabolism; map00052 Galactose metabolism; map00561 Glycerolipid metabolism; map01100 Metabolic pathways	KOG2366 At3g56310 Alpha-D-galactosidase (melibiase)	KAF5230090.1 hypothetical protein FANTH_13972 [Fusarium anthophilum]	Alpha-galactosidase OS=Oryza sativa subsp. japonica OX=39947 GN=Os10g0493600 PE=1 SV=1
A2624	-	-	GO:0005506 (iron ion binding); GO:0016491 (oxidoreductase activity)	-	-	-	GBC41945.1 peroxidase [Rhizophagus irregularis DAOM 181602=DAOM 197198]	-
A2625	-	GO:0016021 (integral component of membrane)	-	-	-	-	-	-
A2626	-	-	GO:0005515 (protein binding)	-	-	-	-	-
A2627	-	-	GO:0016491 (oxidoreductase activity)	-	-	-	XP_026600600.1 Uncharacterized protein DSM5745_08571 [Aspergillus mulundensis]	-
A2628	-	-	GO:0020037 (heme binding)	K23490 CYB5; cytochrome b5	-	KOG0537 At5g48810 Cytochrome b5	RLV89994.1 Cytochrome b5 [Spathaspora sp. JA1]	Cytochrome B5 isoform D OS=Arabidopsis thaliana OX=3702 GN=CYTB5-D PE=1 SV=1
A2629	-	-	-	K03676 grxC, GLRX, GLRX2; glutaredoxin 3	-	-	KXS11117.1 hypothetical protein M427DRAFT_138648 [Gonapodya prolifera JEL478]	Uncharacterized protein ycf45 OS=Porphyra purpurea OX=2787 GN=ycf45 PE=3 SV=1

A2630	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0601 CE14884_1 Cyclin-dependent kinase WEE1	KAF9976048.1 hypothetical protein BGZ73_009207 [Actinomortierella ambigua]	Mitogen-activated protein kinase kinase kinase 17 OS=Arabidopsis thaliana OX=3702 GN=MAPKKK17 PE=1 SV=1
A2631	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0601 CE14884_1 Cyclin-dependent kinase WEE1	XP_016612360.1 CAMK protein kinase [Spizellomyces punctatus DAOM BR117]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei brucei OX=5702 GN=CRK2 PE=3 SV=1
A2632	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0019773(proteasome core complex, alpha-subunit complex), GO:0005839(proteasome core complex)	-	K02726 PSMA2; 20S proteasome subunit alpha 2 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0181 At1g16470 20S proteasome, regulatory subunit alpha type PSMA2/PREB	ORY06978.1 20S proteasome alpha subunit B [Basidiobolus meristosporus CBS 931.73]	Proteasome subunit alpha type-2 OS=Oryza sativa subsp. indica OX=39946 GN=PAB1 PE=2 SV=2
A2633	-	-	-	-	-	-	-	-
A2634	-	-	-	-	-	-	-	-
A2635	-	-	-	-	-	KOG1179 Hs4503653 Very long-chain acyl-CoA synthetase/fatty acid transporter	KAG0343168.1 hypothetical protein BG004_005456 [Podila humilis]	Long-chain fatty acid transport protein 4 OS=Homo sapiens OX=9606 GN=SLC27A4 PE=1 SV=1
A2636	GO:0007094(mitotic spindle assembly checkpoint signaling)	-	-	K06679 MAD1; mitotic spindle assembly checkpoint protein MAD1	map04914 Progesterone-mediated oocyte maturation;map05203 Viral carcinogenesis; map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG4593 Hs22062407 Mitotic checkpoint protein MAD1	ORY43787.1 MAD-domain-containing protein [Rhizoclostium globosum]	Mitotic spindle assembly checkpoint protein MAD1 OS=Homo sapiens OX=9606 GN=MAD1L1 PE=1 SV=2
A2637	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-

A2638	GO:0006629(lipid metabolic process)	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors)	-	-	KOG4650 At1g18180 Predicted steroid reductase	RUS16916.1 hypothetical protein BC937DRAFT_90654 [Endogone sp. FLAS-F59071]	-
A2639	-	-	-	-	-	-	-	-
A2640	GO:0008652(cellular amino acid biosynthetic process)	-	GO:0004072(aspartate kinase activity)	K00928 lysC; aspartate kinase [EC:2.7.2.4]	map00300 Lysine biosynthesis;map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00261 Monobactam biosynthesis;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism;map00270 Cysteine and methionine metabolism	KOG0456 At5g14060 Aspartate kinase	KAG1462599.1 hypothetical protein G6F57_013920 [Rhizopus oryzae]	Lysine-sensitive aspartokinase 3 OS=Escherichia coli (strain K12) OX=83333 GN=lysC PE=1 SV=2
A2641	-	-	GO:0016758(hexosyltransferase activity)	-	-	KOG3349 At4g16710 Predicted glycosyltransferase	TRM61861.1 glycosyltransferase family 1 protein, partial [Auriculariopsis amplaj]	UDP-N-acetylglucosamine transferase subunit ALG13 homolog OS=Rattus norvegicus OX=10116 GN=Alg13 PE=1 SV=1
A2642	-	-	GO:0016409(palmitoyltransferase activity)	-	-	KOG1311 At5g41060 DHHC-type Zn-finger proteins	KAF7759371.1 hypothetical protein DSO57_011168 [Entomophthora muscae]	Palmitoyltransferase app OS=Drosophila melanogaster OX=7227 GN=app PE=1 SV=1
A2643	GO:0006457(protein folding)	-	GO:0051082(unfolded protein binding)	K09510 DNAJB4; DnaJ homolog subfamily B member 4	-	KOG0714 Hs6631085 Molecular chaperone (DnaJ superfamily)	KXN73140.1 putative heat shock protein [Conidiobolus coronatus NRRL 28638]	DnaJ homolog subfamily B member 4 OS=Homo sapiens OX=9606 GN=DNAJB4 PE=1 SV=1
A2644	-	-	-	-	-	-	-	-
A2645	GO:0006508(proteolysis)	-	GO:0008237(metallopeptidase activity),GO:0004222(metalloendopeptidase activity)	-	-	KOG3607 Hs11496994 Meltrins, fertilins and related Zn-dependent metalloproteinases of the ADAMs family	RZR60946.1 ADAM 8 precursor [Pochonia chlamydosporia 123]	Zinc metalloproteinase-disintegrin-like EoVMP2 OS=Echis ocellatus OX=99586 GN=Svmp3-Eoc22 PE=1 SV=1
A2646	-	-	GO:0005516(calmodulin binding)	-	-	-	-	-

A2647	GO:0006623(protein targeting to vacuole), GO:0006886(intracellular protein transport), GO:0016192(vesicle-mediated transport)	-	GO:0005515(protein binding)	K20184 VPS41; vacuolar protein sorting-associated protein 41	map04140 Autophagy - animal;map05132 Salmonella infection;map04138 Autophagy - yeast	KOG2066 At1g08190 Vacuolar assembly/sorting protein VPS41	KAG0281653.1 Vacuolar protein sorting-associated protein 41 [Linnemannia exigua]	Vacuolar protein sorting-associated protein 41 homolog OS=Solanium lycopersicum OX=4081 GN=VPS41 PE=2 SV=1
A2648	-	-	-	K01881 PARS, proS; prolyl-tRNA synthetase [EC:6.1.1.15]	map00970 Aminoacyl-tRNA biosynthesis	KOG4163 At5g52520 Prolyl-tRNA synthetase	TIB78557.1 hypothetical protein E3Q23_00686 [Wallemia mellicola]	Proline--tRNA ligase OS=Sulfurisphaera tokodaii (strain DSM 16993 / JCM 10545 / NBRC 100140 / 7) OX=273063 GN=proS PE=3 SV=1
A2649	-	-	-	-	-	KOG3012 At2g15240 Uncharacterized conserved protein	ORX84333.1 UNC-50 protein [Anaeromyces robustus]	Protein unc-50 homolog OS=Dictyostelium discoideum OX=44689 GN=DDB_G0292320 PE=3 SV=1
A2650	-	-	-	-	-	-	-	-
A2651	-	-	-	-	-	-	-	-
A2652	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2653	-	-	-	-	-	-	-	-
A2654	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2655	-	-	-	-	-	-	-	-
A2656	GO:0006457(protein folding)	-	GO:0005515(protein binding),GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding)	-	-	KOG0548 Hs5803181 Molecular co-chaperone ST11	XP_013937006.1 Heat shock protein ST11 [Ogataea parapolymorpha DL-1]	Stress-induced-phosphoprotein 1 OS=Macaca fascicularis OX=9541 GN=STIP1 PE=2 SV=1
A2657	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02962 RP-S17e, RPS17; small subunit ribosomal protein S17e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0187 Hs4506693 40S ribosomal protein S17	CDS12245.1 Putative 40S ribosomal protein S17-B [Lichtheimia ramosa]	Small ribosomal subunit protein eS17 OS=Theileria parva OX=5875 GN=RPS17 PE=3 SV=3
A2658	-	-	GO:0016491(oxidoreductase activity)	K17738 ARD; D-arabinitol 2-dehydrogenase [EC:1.1.1.250]	map00040 Pentose and glucuronate interconversions;map01100 Metabolic pathways	KOG0725 7295487 Reductases with broad range of substrate specificities	CCA70935.1 related to D-arabinitol 2-dehydrogenase [Serendipita indica DSM 11827]	NAD-dependent glycerol dehydrogenase OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) OX=272626 GN=golD PE=1 SV=1
A2659	GO:0006298(mismatch repair)	-	GO:0005524(ATP binding),GO:0030983(mismatched DNA binding),GO:0005515(protein binding)	K08740 MSH4; DNA mismatch repair protein MSH4	-	KOG0220 Hs20535615 Mismatch repair ATPase MSH4 (MutS family)	XP_033414576.1 mutS protein homolog 4 [Aspergillus lentulus]	DNA mismatch repair protein MSH4 OS=Arabidopsis thaliana OX=3702 GN=MSH4 PE=2 SV=1
A2660	-	-	GO:0030246(carbohydrate binding),GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	-	-	KOG3587 CE18468 Galectin, galactose-binding lectin	-	32 kDa beta-galactoside-binding lectin OS=Haemonchus contortus OX=6289 GN=GAL-1 PE=1 SV=1

A2661	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding);GO:0005515(protein binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	CAE6505588.1 unnamed protein product [Rhizoctonia solani]	PAS domain-containing serine/threonine-protein kinase OS=Mus musculus OX=10090 GN=Pask PE=1 SV=3
A2662	GO:0006457(protein folding)	-	GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity);GO:0051082(unfolded protein binding)	K04079 HSP90A, htpG; molecular chaperone HtpG	map05417 Lipid and atherosclerosis; map04141 Protein processing in endoplasmic reticulum;map05132 Salmonella infection;map04217 Necroptosis;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05418 Fluid shear stress and atherosclerosis; map04657 IL-17 signaling pathway;map04659 Th17 cell differentiation;map05215 Prostate cancer;map0461	KOG0019 At5g56030 Molecular chaperone (HSP90 family)	TPX78387.1 hypothetical protein CcCBS67573_g00357 [Chytridiomycetes confervae]	Heat shock protein 81-1 OS=Oryza sativa subsp. indica OX=39946 GN=HSP81-1 PE=2 SV=1
A2663	-	-	GO:0035091(phosphatidylinositol binding);GO:0005515(protein binding)	K03361 CDC4; F-box and WD-40 domain protein CDC4	map04120 Ubiquitin mediated proteolysis;map04111 Cell cycle - yeast	KOG0288 At5g50230 WD40 repeat protein TipD	KAE9397398.1 WD40 repeat-like protein, partial [Gymnopus androsaceus JB14]	Autophagy-related protein 16 OS=Arabidopsis thaliana OX=3702 GN=ATG16 PE=1 SV=1
A2664	GO:0019354(siroheme biosynthetic process)	-	GO:0008168(methyltransferase activity)	K00589 MET1; uroporphyrin-III C-methyltransferase [EC:2.1.1.107]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG1527 At5g40850 Uroporphyrin III methyltransferase	KGQ13438.1 Siroheme synthase [Beauveria bassiana D1-5]	Uroporphyrinogen-III C-methyltransferase OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=cobA PE=3 SV=2

A2665	GO:0007018(microtubule-based movement)	-	GO:0003824(catalytic activity),GO:0005515(protein binding),GO:0008483(transaminase activity),GO:0030170(pyridoxal phosphate binding),GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K00823 puuE; 4-aminobutyrate aminotransferase [EC:2.6.1.19]	map00410 beta-Alanine metabolism;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00250 Alanine, aspartate and glutamate metabolism;map00650 Butanoate metabolism;map01100 Metabolic pathways	KOG0239 At5g27550 Kinesin (KAR3 subfamily)	XP_007729511.1 4-aminobutyrate aminotransferase [Capronia epimyces CBS 606.96]	5-aminovalerate aminotransferase DavT OS=Pseudomonas putida (strain ATCC 47054 / DSM 6125 / CFBP 8728 / NCIMB 11950 / KT2440) OX=160488 GN=davT PE=1 SV=1
A2666	-	-	-	-	-	-	XP_031024706.1 uncharacterized protein SmJEL517_g03347 [Synchytrium microbalum]	Beta-lactamase domain-containing protein 2 OS=Caenorhabditis elegans OX=6239 GN=lact-2 PE=4 SV=1
A2667	-	-	-	-	-	-	-	-
A2668	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K03695 clpB; ATP-dependent Clp protease ATP-binding subunit ClpB	map04213 Longevity regulating pathway - multiple species	KOG1051 At1g74310 Chaperone HSP104 and related ATP-dependent Clp proteases	XP_031026708.1 uncharacterized protein SmJEL517_g01312 [Synchytrium microbalum]	Chaperone protein ClpB1 OS=Arabidopsis thaliana OX=3702 GN=CLP1 PE=1 SV=2
A2669	-	-	-	-	-	-	-	-
A2670	GO:0006730(one-carbon metabolic process),GO:0006231(dTMP biosynthetic process),GO:0046654(tetrahydrofolate biosynthetic process)	-	GO:0004146(dihydrofolate reductase activity),GO:0004799(thymidylate synthase activity),GO:0016741(transferase activity, transferring one-carbon groups)	K00560 thya, TYMS; thymidylate synthase [EC:2.1.1.45]	map00670 One carbon pool by folate;map01523 Antifolate resistance;map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG0673 At4g34570.2 Thymidylate synthase	KAG2206813.1 hypothetical protein INT47_007569 [Mucor saturnus]	Bifunctional dihydrofolate reductase-thymidylate synthase OS=Glycine max OX=3847 PE=1 SV=1
A2671	-	-	GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	-	XP_002175972.1 calmodulin Cam1 [Schizosaccharomyces japonicus yFS275]	Calmodulin OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=cam1 PE=1 SV=1

A2672	-	-	-	-	-	-	-	-
A2673	GO:0030001(metal ion transport);GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	-	-	KOG2474 At3g08650 Zinc transporter and related ZIP domain-containing proteins	-	Putative zinc transporter At3g08650 OS=Arabidopsis thaliana OX=3702 GN=At3g08650 PE=2 SV=2
A2674	-	-	GO:0016491(oxidoreductase activity)	-	-	-	KAG1454789.1 hypothetical protein G6F57_015427 [Rhizopus oryzae]	D-amino acid dehydrogenase OS=Cereibacter sphaeroides (strain ATCC 17023 / DSM 158 / JCM 6121 / CCUG 31486 / LMG 2827 / NBRC 12203 / NCIMB 8253 / ATH 2.4.1.) OX=272943 GN=dadA PE=3 SV=1
A2675	GO:0030001(metal ion transport);GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	-	-	KOG2474 At3g08650 Zinc transporter and related ZIP domain-containing proteins	-	Putative zinc transporter At3g08650 OS=Arabidopsis thaliana OX=3702 GN=At3g08650 PE=2 SV=2
A2676	GO:0006811(ion transport);GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005216(ion channel activity)	-	-	-	KAF9195036.1 hypothetical protein BGZ51_006000 [Haplosporangium sp. Z 767]	-
A2677	-	-	-	-	-	-	-	-
A2678	GO:0042558(pteridine-containing compound metabolic process);GO:0044237(cellular metabolic process);GO:0009396(folic acid-containing compound biosynthetic process)	-	GO:0003848(2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase activity);GO:0004156(dihydropterotate synthase activity)	K13939 FOL1; dihydroneopterin aldolase / 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase / dihydropterotate synthase [EC:4.1.2.25 2.7.6.3 2.5.1.15]	map01240 Biosynthesis of cofactors;map01100 Metabolic pathways;map00790 Folate biosynthesis	KOG2544 At4g30000 Dihydropterotate synthase/7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase/Dihydropteroneopterin aldolase	GBB94879.1 hypothetical protein RclHR1_02430020 [Rhizophagus clarus]	Folate synthesis bifunctional protein, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MitHPPK/DHPS PE=2 SV=1
A2679	-	-	-	K07200 PRKAG; 5'-AMP-activated protein kinase, regulatory gamma subunit	map05410 Hypertrophic cardiomyopathy; map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map04910 Insulin signaling pathway;map04714 Thermogenesis; map04710 Circadian rhythm;map04530 Tight junction;map04371 Apelin signaling pathway;map04931 Insulin resistance;map04932 Non-alcoholic fatty liver	KOG1764 Hs4506061 5'-AMP-activated protein kinase, gamma subunit	XP_018292781.1 hypothetical protein PHYBLDRAFT_132891 [Phycomyces blakesleeanus NRRL 1555(-)]	5'-AMP-activated protein kinase subunit gamma-1 OS=Sus scrofa OX=9823 GN=PRKAG1 PE=1 SV=2
A2680	GO:0006281(DNA repair)	GO:0005634(nucleus);GO:0030915(Smc5-Smc6 complex)	-	K22825 NSMCE4, NSE4; non-structural maintenance of chromosome element 4	-	KOG2866 7297703 Uncharacterized conserved protein	RHZ44827.1 hypothetical protein Glove_709g6 [Diversispora epigaea]	Non-structural maintenance of chromosomes element 4 homolog A OS=Bos taurus OX=9913 GN=NSMCE4A PE=2 SV=1

A2681	-	GO:0016020(membrane)	-	-	-	-	-	-
A2682	-	-	-	-	-	KOG2130[Hs14769286 Phosphatidyserine-specific receptor PtdSerR, contains JmjC domain	OZI03333.1 hypothetical protein BZG36_04224 [Bifiguratus adelaidae]	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Danio rerio OX=7955 GN=jmjd6 PE=2 SV=2
A2683	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A2684	-	-	-	-	-	-	ORX47283.1 hypothetical protein BCR36DRAFT_295736 [Piromyces finnis]	Protein MFI OS=Mus musculus OX=10090 GN=Mfi PE=1 SV=1
A2685	-	-	GO:0005515(protein binding)	-	-	-	TPX72852.1 hypothetical protein SpCBS45565_g00042 [Spizellomyces sp. 'palustris']	-
A2686	-	-	-	-	-	-	-	-
A2687	-	-	GO:0016491(oxidoreductase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	K00135 gabD; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]	map01120 Microbial metabolism in diverse environments;map00760 Nicotinate and nicotinamide metabolism;map00250 Alanine, aspartate and glutamate metabolism;map00650 Butanoate metabolism;map00310 Lysine degradation;map00350 Tyrosine metabolism;map01100 Metabolic pathways	-	XP_038739079.1 succinate-semialdehyde dehydrogenase [Colletotrichum karstii]	Succinate-semialdehyde dehydrogenase [NADP(+)] GabD OS=Escherichia coli (strain K12) OX=83333 GN=gabD PE=1 SV=1
A2688	-	-	-	-	-	-	TPX74414.1 hypothetical protein CcCBS67573_g04325 [Chytridiomycetes confervae]	-
A2689	-	-	-	-	-	-	-	-
A2690	GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004842(ubiquitin-protein transferase activity),GO:0061630(ubiquitin protein ligase activity)	K10590 TRIP12; E3 ubiquitin-protein ligase TRIP12 [EC:2.3.2.26]	map04120 Ubiquitin mediated proteolysis	KOG4276[Hs15300020 Predicted hormone receptor interactor	KAF3985009.1 hypothetical protein FT663_05464 [[Candida haemulonii var. vulnereis]	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens OX=9606 GN=HECTD1 PE=1 SV=4

A2691	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	-	-	KOG4598 7295436 Putative ubiquitin-specific protease	KAF9938245.1 hypothetical protein BGZ67_000390 [Mortierella alpina]	Ubiquitin carboxyl-terminal hydrolase 47 OS=Xenopus tropicalis OX=8364 GN=usp47 PE=2 SV=1
A2692	GO:0006418(tRNA aminoacylation for protein translation),GO:0006428(isoleucyl-tRNA aminoacylation)	-	GO:0004812(aminoacyl-tRNA ligase activity),GO:0000166(nucleotide binding),GO:0004822(isoleucine-tRNA ligase activity),GO:0005524(ATP binding),GO:0002161(aminoacyl-tRNA editing activity),GO:0000049(tRNA binding)	K01870 IARS, ileS; isoleucyl-tRNA synthetase [EC:6.1.1.5]	map00970 Aminoacyl-tRNA biosynthesis	KOG0434 At4g10320 Isoleucyl-tRNA synthetase	ORX56468.1 isoleucyl-tRNA synthetase [Piromyces finnis]	Isoleucine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana OX=3702 GN=At4g10320 PE=2 SV=1
A2693	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map04972 Pancreatic secretion;map04080 Neuroactive ligand-receptor interaction;map05164 Influenza A	KOG3627 7303605 Trypsin	PBP24814.1 serine endopeptidase [Diplocarpon rosae]	Trypsin delta OS=Drosophila melanogaster OX=7227 GN=deltaTry PE=2 SV=1
A2694	-	-	-	-	-	-	-	-
A2695	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At4g28710 Myosin class V heavy chain	KAF2861957.1 hypothetical protein K470DRAFT_275820 [Piedraia hortae CBS 480.64]	Myosin-13 OS=Arabidopsis thaliana OX=3702 GN=XI-G PE=3 SV=1
A2696	-	-	-	K21804 METTL21A; protein N-lysine methyltransferase METTL21A [EC:2.1.1.-]	-	KOG2793 CE26910 Putative N2,N2-dimethylguanosine tRNA methyltransferase	EUC66678.1 ribosomal protein L11 methyltransferase [Rhizoctonia solani AG-3 Rhs1AP]	Secreted RxLR effector protein 48 OS=Plasmopara viticola OX=143451 GN=RXLR48 PE=2 SV=1
A2697	GO:0006468(protein phosphorylation)	-	GO:0035091(phosphatidylinositol binding),GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0690 CE05274 Serine/threonine protein kinase	XP_016612967.1 AGC/AKT protein kinase [Spizellomyces punctatus DAOM BR117]	Protein kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pkgB PE=1 SV=2

A2698	GO:0000737(DNA catabolic process, endonucleolytic),GO:0006302(double-strand break repair)	-	GO:0008821(crossover junction endonuclease activity),GO:0003677(DNA binding),GO:0004518(nuclease activity)	K08991 MUS81; crossover junction endonuclease MUS81 [EC:3.1.22.-]	map03440 Homologous recombination; map03460 Fanconi anemia pathway	KOG2379[Hs1.3376707 Endonuclease MUS81	KAF7754229.1 Crossover junction endonuclease mus81 [Entomophthora muscae]	Crossover junction endonuclease MUS81 OS=Xenopus tropicalis OX=8364 GN=mus81 PE=2 SV=1
A2699	GO:0000724(double-strand break repair via homologous recombination),GO:0006281(DNA repair)	GO:0030915(Smc5-Smc6 complex)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K22804 SMC6; structural maintenance of chromosome protein 6	-	KOG0250[At5g61460 DNA repair protein RAD18 (SMC family protein)	XP_033532949.1 DNA repair protein Rad18 [Eremomyces bilateralis CBS 781.70]	Structural maintenance of chromosomes protein 6B OS=Arabidopsis thaliana OX=3702 GN=SMC6B PE=2 SV=1
A2700	GO:0007062(sister chromatid cohesion)	GO:0008278(cohesin complex)	GO:0005515(protein binding)	K06670 SCC1, MCD1, RAD21; cohesin complex subunit SCC1	map04111 Cell cycle - yeast;map04110 Cell cycle	KOG1213[7289833 Sister chromatid cohesion complex Cohesin, subunit RAD21/SCC1	ORX65574.1 hypothetical protein K493DRAFT_294493 [Basidiobolus meristosporus CBS 931.73]	Double-strand-break repair protein rad21 homolog OS=Xenopus laevis OX=8355 GN=rad21 PE=1 SV=1
A2701	-	-	-	-	-	-	-	-
A2702	-	-	-	-	-	KOG4609[CE02024 Predicted phosphoglycerate mutase	-	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Danio rerio OX=7955 GN=pgam5 PE=2 SV=2
A2703	-	-	GO:0016422(mRNA (2'-O-methyladenosine-N6-)-methyltransferase activity),GO:0099122(RNA polymerase II C-terminal domain binding)	-	-	-	TPX75241.1 hypothetical protein CcCBS67573_g03506 [Chytridiomycota confervae]	mRNA (2'-O-methyladenosine-N(6)-)-methyltransferase OS=Danio rerio OX=7955 GN=pcif1 PE=1 SV=1
A2704	-	-	-	-	-	-	-	-
A2705	GO:0042276(error-prone translesion synthesis)	-	GO:0003887(DNA-directed DNA polymerase activity),GO:0003896(DNA primase activity)	-	-	-	-	-
A2706	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2707	-	-	-	-	-	-	-	-
A2708	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2709	-	-	GO:0005509(calcium ion binding),GO:0005515(protein binding)	-	-	KOG1029[Hs2.0544596 Endocytic adaptor protein intersectin	KAF8137291.1 hypothetical protein EV363DRAFT_1394838 [Boletus edulis]	SH3 domain-containing kinase-binding protein 1 OS=Homo sapiens OX=9606 GN=SH3KBP1 PE=1 SV=2
A2710	GO:0006812(cation transport),GO:00055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015299(solute:proton antiporter activity)	-	-	KOG1650[At1g64170 Predicted K+/H+-antiporter	EJD52857.1 Sodium/hydrogen exchanger [Auricularia subglabra TFB-10046 SS5]	Na(+)/H(+) antiporter OS=Enterococcus hirae OX=1354 GN=napA PE=1 SV=1

A2711	-	GO:0016020(membrane)	-	-	-	-	KAG0369522.1 hypothetical protein BGZ54_009665 [Gamsiella multivaricata]	-
A2712	-	-	-	-	-	-	-	-
A2713	-	-	GO:0000981(DNA-binding transcription factor activity, RNA polymerase II-specific)	K09425 K09425; Myb-like DNA-binding protein FlbD	-	KOG0048[Hs13641706.1 Transcription factor, Myb superfamily	EPZ36294.1 Homeo-like domain-containing protein [Rozella allomyces CSF55]	Transforming protein Myb OS=Avian myeloblastosis virus OX=11866 GN=V-MYB PE=1 SV=2
A2714	-	-	-	K18066 TYW5; tRNA wybutosine-synthesizing protein 5 [EC:1.14.11.4.2]	-	KOG2132[Hs14741442 Uncharacterized conserved protein, contains JmjC domain	ORX72375.1 Clavaminase synthase-like protein [Linderina pennisporea]	Hypoxia-inducible factor 1-alpha inhibitor OS=Mus musculus OX=10090 GN=Hif1an PE=1 SV=2
A2715	-	-	GO:0008237(metallopeptidase activity)	-	-	-	-	-
A2716	-	-	-	-	-	-	-	-
A2717	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2718	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192[At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	XP_011271262.1 hypothetical protein BN7_6474 [Wickerhamomyces ciferrii]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei OX=5702 GN=CRK2 PE=3 SV=1
A2719	-	-	-	-	-	-	-	-
A2720	-	-	-	-	-	KOG3223[At1g16210 Uncharacterized conserved protein	ORZ33520.1 hypothetical protein BCR44DRAFT_127808 [Catenaria anguillulalae PL171]	Coiled-coil domain-containing protein 124 homolog OS=Dictyostelium discoideum OX=44689 GN=DDb_G0289893 PE=3 SV=1
A2721	-	-	-	-	-	-	-	-
A2722	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867[Hs4557333 Sulfatase	GFZ52310.1 Uncharacterized sulfatase [Saitozyma sp. JCM 24511]	Arylsulfatase B OS=Rattus norvegicus OX=10116 GN=Arspb PE=2 SV=2
A2723	GO:0006633(fatty acid biosynthetic process)	-	GO:0004318(enoyl-[acyl-carrier-protein] reductase (NADH) activity)	-	-	KOG0725[At2g05990 Reductases with broad range of substrate specificities	KXS20796.1 short-chain dehydrogenase/reductase SDR [Gonapodya prolifera JEL478]	Enoyl-[acyl-carrier-protein] reductase [NADH] 1 OS=Rhizobium meliloti (strain 1021) OX=266834 GN=fabI1 PE=3 SV=1
A2724	-	-	-	-	-	-	-	-
A2725	-	-	GO:0061630(ubiquitin protein ligase activity)	-	-	KOG0800[At3g19910 FOG: Predicted E3 ubiquitin ligase	EPZ32396.1 hypothetical protein O9G_001298 [Rozella allomyces CSF55]	E3 ubiquitin-protein ligase BIG BROTHER OS=Arabidopsis thaliana OX=3702 GN=BB PE=1 SV=1

A2726	-	-	-	K12272 SRPRB, SRP102; signal recognition particle receptor subunit beta	map03060 Protein export	KOG0090 At2g18770 Signal recognition particle receptor, beta subunit (small G protein superfamily)	CDS07076.1 hypothetical protein LRAMOSA09599 [Lichtheimia ramosa]	Signal recognition particle receptor subunit beta OS=Mus musculus OX=10090 GN=Srprb PE=1 SV=1
A2727	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K02677 PRKCA; classical protein kinase C alpha type [EC:2.7.11.13]	map04360 Axon guidance;map04020 Calcium signaling pathway;map05415 Diabetic cardiomyopathy;map05417 Lipid and atherosclerosis;map04730 Long-term depression;map05223 Non-small cell lung cancer;map04510 Focal adhesion;map04933 AGE-RAGE signaling pathway in diabetic complications;map04070 Phosphatidylinositol signaling system;map04071 Sphingolipid signaling pathway;map04	KOG0603 Hs19923570 Ribosomal protein S6 kinase	CDS11010.1 hypothetical protein LRAMOSA03274 [Lichtheimia ramosa]	Ribosomal protein S6 kinase beta-2 OS=Mus musculus OX=10090 GN=Rps6kb2 PE=1 SV=1
A2728	GO:0006457(protein folding)	-	GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding),GO:0005515(protein binding)	-	-	-	RKO90553.1 hypothetical protein BDK51DRAFT_17541, partial [Blyttomyces helicus]	-
A2729	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	EPZ37081.1 Adenylyl cyclase class-3/4/guanylyl cyclase domain-containing protein [Rozella allomycis CSF55]	Adenylate cyclase type 10 OS=Mus musculus OX=10090 GN=Adcy10 PE=1 SV=2
A2730	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	-
A2731	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity)	-	-	-	CDS07880.1 hypothetical protein LRAMOSA01829 [Lichtheimia ramosa]	Acyl-CoA dehydrogenase family member 10 OS=Homo sapiens OX=9606 GN=ACAD10 PE=1 SV=1
A2732	-	-	-	K00856 ADK, adok; adenosine kinase [EC:2.7.1.20]	map00230 Purine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG2854 7304245 Possible pfkB family carbohydrate kinase	ORY91483.1 carbohydrate kinase PrkB [Leucosporidium creatinivorum]	Uncharacterized sugar kinase AF_0356 OS=Archaeoglobus fulgidus (strain ATCC 49558 / DSM 4304 / JCM 9628 / NBRC 100126 / VC-16) OX=224325 GN=AF_0356 PE=3 SV=1
A2733	-	-	-	-	-	-	-	-

A2734	GO:0006520 (cellular amino acid metabolic process)	-	GO:0030170 (pyridoxal phosphate binding)	-	-	KOG1250 7299166 Threonine/serine dehydratases	KJK63819.1 Pyridoxal-phosphate dependent enzyme [Aspergillus parasiticus SU-1]	L-threonine ammonia-lyase OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=TM_0356 PE=1 SV=1
A2735	-	-	GO:0008289 (lipid binding)	-	-	-	-	Protein ENHANCED DISEASE RESISTANCE 2 OS=Arabidopsis thaliana OX=3702 GN=EDR2 PE=2 SV=1
A2736	-	-	GO:0005515 (protein binding)	K11407 HDAC6; histone deacetylase 6 [EC:3.5.1.98]	map05014 Amyotrophic lateral sclerosis; map04613 Neutrophil extracellular trap formation; map05034 Alcoholism; map05203 Viral carcinogenesis	KOG1343 At3g18520 Histone deacetylase complex, catalytic component HDA1	KAG0165639.1 hypothetical protein DFQ30_008192 [Apophysomycetes sp. BC1015]	Type-2 histone deacetylase 2 OS=Dictyostelium discoideum OX=44689 GN=hdaC PE=2 SV=1
A2737	-	-	-	-	-	-	-	-
A2738	-	-	-	K20291 COG4, COD1; conserved oligomeric Golgi complex subunit 4	-	KOG0412 At4g01400.2 Golgi transport complex COD1 protein	KAF9973616.1 Golgi transport complex subunit 4 [Actinomyces rella ambigua]	Conserved oligomeric Golgi complex subunit 4 OS=Danio rerio OX=7955 GN=cog4 PE=1 SV=1
A2739	-	-	-	-	-	KOG2743 At1g80480 Cobalamin synthesis protein	KAG2228067.1 hypothetical protein INT45_009113 [Mucor circinatus]	Zinc chaperone YjiA OS=Escherichia coli (strain K12) OX=83333 GN=yjiA PE=1 SV=3
A2740	-	-	-	-	-	-	KKY18544.1 putative short chain dehydrogenase reductase family superfamily [Phaeomonella chlamydospora]	1-hydroxy-2-glutathionyl-2-methyl-3-butene dehydrogenase OS=Rhodococcus sp. (strain AD45) OX=103808 GN=isoH PE=1 SV=1
A2741	-	-	-	-	-	-	-	-
A2742	-	-	-	-	-	-	-	-
A2743	-	-	-	-	-	-	-	-
A2744	-	-	GO:0005515 (protein binding)	K16794 PAFAH1B1, LIS1; platelet-activating factor acetylhydrolase IB subunit alpha	map00565 Ether lipid metabolism; map01100 Metabolic pathways	-	-	-
A2745	GO:0006629 (lipid metabolic process)	-	GO:0016491 (oxidoreductase activity)	K13076 SLD; sphingolipid 8-(E)-desaturase [EC:1.14.19.18]	-	KOG4232 At2g46210 Delta 6-fatty acid desaturase/delta-8 sphingolipid desaturase	ORZ39923.1 fatty acid desaturase-domain-containing protein [Catenaria anguillulae PL171]	Delta(8)-fatty-acid desaturase 2 OS=Arabidopsis thaliana OX=3702 GN=SLD2 PE=1 SV=1
A2746	GO:0015693 (magnesium ion transport)	GO:0016021 (integral component of membrane)	GO:0015095 (magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	RHZ79634.1 hypothetical protein Glove_143g61 [Diversispora epigaea]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1

A2747	-	-	-	K12589 RRP42, EXOSC7; exosome complex component RRP42	map03018 RNA degradation	KOG1612 7303006 Exosomal 3'-5' exoribonuclease complex, subunit Rrp42	KAG2221675.1 hypothetical protein INT45_002713 [Mucor circinatus]	Putative exosome complex exonuclease RRP42 OS=Dictyostelium discoideum OX=44689 GN=exosc7 PE=3 SV=1
A2748	-	-	-	K15110 SLC25A21, ODC; solute carrier family 25 (mitochondrial 2-oxodicarboxylate transporter), member 21	-	-	KXS22404.1 mitochondria l carrier [Gonapodya prolifera JEL478]	Probable mitochondrial 2-oxodicarboxylate carrier OS=Dictyostelium discoideum OX=44689 GN=mcT PE=3 SV=1
A2749	-	-	-	-	-	-	-	-
A2750	GO:0006629(lipid metabolic process)	-	-	K01052 LIPA; lysosomal acid lipase/cholesterol ester hydrolase [EC:3.1.1.13]	map04142 Lysosome;map04979 Cholesterol metabolism;map00100 Steroid biosynthesis	KOG2624 At1g18460 Triglyceride lipase-cholesterol esterase	KAF4994395.1 hypothetical protein FGRMN_5814 [Fusarium gramineum]	Gastric triacylglycerol lipase OS=Rattus norvegicus OX=10116 GN=Lipf PE=1 SV=1
A2751	-	-	-	-	-	-	-	-
A2752	GO:0006629(lipid metabolic process)	-	-	-	-	KOG2088 Hs21040277 Predicted lipase/calmodulin-binding heat-shock protein	TPX57557.1 hypothetical protein SpCBS45565_g08181 [Spizellomyces sp. 'palustris']	Diacylglycerol lipase-beta OS=Homo sapiens OX=9606 GN=DAGLB PE=1 SV=2
A2753	GO:0035556(intracellular signal transduction),GO:006629(lipid metabolic process),GO:0007165(signal transduction)	-	GO:0008081(phosphoric diester hydrolase activity),GO:0004435(phosphatidylinositol phospholipase C activity)	K05857 PLCD; phosphatidylinositol phospholipase C, delta [EC:3.1.4.11]	map04020 Calcium signaling pathway;map05131 Shigellosis;map04933 AGE-RAGE signaling pathway in diabetic complications;map04070 Phosphatidylinositol signaling system;map04919 Thyroid hormone signaling pathway;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	-	XP_016608873.1 hypothetical protein SPPG_03939 [Spizellomyces punctatus DAOM BR117]	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1 OS=Rattus norvegicus OX=10116 GN=Plce1 PE=1 SV=1

A2754	-	-	GO:0016491(oxidoreductase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	K00128 ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]	map00410 beta-Alanine metabolism;map00981 Insect hormone biosynthesis;map00770 Pantothenate and CoA biosynthesis;map00340 Histidine metabolism;map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map00903 Limonene degradation;map01240 Biosynthesis of cofactors;map00330 Arginine and proline metabolism;map01120 Microbial metabolism in	KOG2450[Hs1436533 Aldehyde dehydrogenase	CAE6388437.1 unnamed protein product [Rhizoctonia solani]	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH2 PE=1 SV=2
A2755	-	-	-	-	-	-	-	-
A2756	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0003924(GTPase activity),GO:0019001(guanyl nucleotide binding),GO:0031683(G-protein beta/gamma-subunit complex binding)	-	-	KOG0082[CE27889 G-protein alpha subunit (small G protein superfamily)]	KAG1151564.1 hypothetical protein G6F38_001184 [Rhizopus oryzae]	Guanine nucleotide-binding protein subunit alpha-15 OS=Rattus norvegicus OX=10116 GN=Gna15 PE=2 SV=1
A2757	GO:0006096(glycolytic process)	-	GO:0000287(magnesium ion binding),GO:0004743(pyruvate kinase activity),GO:0030955(potassium ion binding),GO:0003824(catalytic activity)	K00873 PK, pyk; pyruvate kinase [EC:2.7.1.40]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map05203 Viral carcinogenesis;map04930 Type II diabetes mellitus;map00620 Pyruvate metabolism;map05230 Central carbon metabolism in cancer;map01100 Metabolic	KOG2323[CE15898 Pyruvate kinase	RKP00935.1 hypothetical protein CXG81DRAFT_26381 [Caulochytrium protostelioides]	Pyruvate kinase I OS=Escherichia coli O157:H7 OX=83334 GN=pykF PE=3 SV=1
A2758	-	-	-	-	-	-	-	-
A2759	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2760	-	-	-	-	-	-	OUM60759.1 hypothetical protein PIROE2DRAFT_45959 [Piromyces sp. E2]	-

A2761	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0008569(minus-end-directed microtubule motor activity)	K10413 DYNC1H1; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map041814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595[7300687 Dyneins, heavy chain	TPX75780.1 hypothetical protein CcCBS67573_g02949 [Chytridiomycota confervae]	Dynein beta chain, flagellar outer arm OS=Chlamydomonas reinhardtii OX=3055 GN=ODA4 PE=3 SV=1
A2762	-	-	GO:0016787(hydrolase activity)	K15423 PPP4C; serine/threonine-protein phosphatase 4 catalytic subunit [EC:3.1.3.16]	map04922 Glucagon signaling pathway	KOG0372[CE23041 Serine/threonine specific protein phosphatase involved in glycogen accumulation, PP2A-related	XP_031022776.1 uncharacterized protein SmJEL517_g05348 [Synchytrium microbalum]	Serine/threonine-protein phosphatase 4 catalytic subunit OS=Dictyostelium discoideum OX=44689 GN=ppp4c PE=1 SV=1
A2763	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity),GO:0008138(protein tyrosine/serine/threonine phosphatase activity)	-	-	KOG2836[Hs14589856 Protein tyrosine phosphatase IVA1	KAF9936821.1 Protein tyrosine phosphatase type IVA 1 [Mortierella alpina]	Probable protein tyrosine phosphatase type IVA A OS=Dictyostelium discoideum OX=44689 GN=DDB_G0292024 PE=3 SV=1
A2764	-	-	-	-	-	-	-	-
A2765	-	GO:0005856(cytoskeleton)	GO:0005515(protein binding)	-	-	KOG4229[Hs4505307 Myosin VII, myosin IXB and related myosins	KXS20836.1 hypothetical protein M427DRAFT_51790 [Gonapodya prolifera JEL478]	Unconventional myosin-VIIb OS=Homo sapiens OX=9606 GN=MYO7B PE=1 SV=2
A2766	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04563 CDC28, CDC2; cyclin-dependent kinase [EC:2.7.11.22]	map04011 MAPK signaling pathway - yeast;map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0593[Hs4507281 Predicted protein kinase KKIAMRE	KNE64097.1 CMGC/CDKL protein kinase [Allomyces macrogynus ATCC 38327]	Cyclin-dependent kinase-like 5 OS=Mus musculus OX=10090 GN=Cdkl5 PE=1 SV=1
A2767	-	-	-	-	-	-	-	-
A2768	-	-	-	-	-	-	-	-
A2769	-	-	-	-	-	-	-	-
A2770	GO:0006952(defense response), GO:0019441(tryptophan catabolic process to kynurenine)	-	GO:0003824(catalytic activity),GO:0020037(heme binding),GO:0046872(metal ion binding)	-	-	-	-	-
A2771	-	-	GO:0005515(protein binding)	-	-	-	-	-

A2772	-	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups);GO:0016746(acyltransferase activity)	K00626 ACAT, atoB; acetyl-CoA C-acyltransferase [EC:2.3.1.9]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00900 Terpenoid backbone biosynthesis;map01120 Microbial metabolism in diverse environments;map00720 Carbon fixation pathways in prokaryotes;map04975 Fat digestion and absorption;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00620 Pyruvate metabolism;map	KOG1390 At5g47720 Acetyl-CoA acetyltransferase	XP_021879187.1 Thiolase, N-terminal domain-containing protein [Lobosporangium transversale]	Acetyl-CoA acetyltransferase B, mitochondrial OS=Xenopus laevis OX=8355 GN=acat1-b PE=2 SV=1
A2773	-	-	GO:0005515(protein binding)	K17262 TBCB, CKAP1, ALF1; tubulin-specific chaperone B	-	KOG3206 At3g10220 Alpha-tubulin folding cofactor B	TFL05188.1 tubulin-folding cofactor B [Pterula gracilis]	Tubulin-folding cofactor B OS=Arabidopsis thaliana OX=3702 GN=TFCB PE=1 SV=1
A2774	GO:0032509(endosome transport via multivesicular body sorting pathway)	GO:000814(ESCRT II complex)	GO:0043130(ubiquitin binding);GO:0032266(phosphatidylinositol-3-phosphate binding)	K12190 VPS36, EAP45; ESCRT-II complex subunit VPS36	map04144 Endocytosis	KOG2760 At5g04920 Vacuolar sorting protein VPS36	RIB15412.1 EAP30/Vps36 family-domain-containing protein [Gigaspora rosea]	Vacuolar protein sorting-associated protein 36 OS=Arabidopsis thaliana OX=3702 GN=VPS36 PE=1 SV=1
A2775	-	-	-	-	-	-	-	-
A2776	GO:0017186(peptidyl-pyroglutamic acid biosynthetic process, using glutaminyll-peptide cyclotransferase)	-	GO:0016603(glutaminyll-peptide cyclotransferase activity)	-	-	-	-	-
A2777	-	-	-	-	-	-	-	-
A2778	-	-	-	-	-	KOG2132 Hs20562348 Uncharacterized conserved protein, contains JmjC domain	KAG0320327.1 hypothetical protein BGZ99_004571 [Dissophora globulifera]	JmjC domain-containing protein F OS=Dictyostelium discoideum OX=44689 GN=jcdF PE=4 SV=1
A2779	-	-	-	-	-	KOG1701 7292937 Focal adhesion adaptor protein Paxillin and related LIM proteins	ORX85427.1 LIM-domain-containing protein [Anaeromyces robustus]	LIM domain-containing protein 1 OS=Xenopus tropicalis OX=8364 GN=limd1 PE=2 SV=1
A2780	GO:0036211(protein modification process)	-	-	-	-	-	-	-
A2781	-	-	-	-	-	-	-	-

A2782	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	-	-	-	PPQ96894.1 hypothetical protein CVT26_005880 [Gymnopilus dilepis]	-
A2783	-	-	-	K20291 COG4, COD1; conserved oligomeric Golgi complex subunit 4	-	-	TPX54007.1 hypothetical protein PhCBS80983_g06083 [Powellomyces hirtus]	Conserved oligomeric Golgi complex subunit 4 OS=Danio rerio OX=7955 GN=cog4 PE=1 SV=1
A2784	GO:0000462(maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA))	GO:0005730(nucleolus),GO:0030686(90S preribosome),GO:0030688(preribosome, small subunit precursor)	-	-	-	-	-	-
A2785	-	-	GO:0005515(protein binding)	K06694 PSMD10; 26S proteasome non-ATPase regulatory subunit 10	-	KOG0504[Hs22062923 FOG: Ankyrin repeat	XP_013329066.1 Proteasome regulatory particle subunit (Nas6) [Rasamsonia emersonii CBS 393.64]	Rabankyrin-5 OS=Mus musculus OX=10090 GN=Ankfy1 PE=1 SV=2
A2786	GO:0007165(signal transduction)	-	-	-	-	-	-	-
A2787	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	ROW08264.1 hypothetical protein VMCG_03137 [Valsa malicola]	-
A2788	GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	KOG1482[At2g46800 Zn2+ transporter	TPX57968.1 hypothetical protein PhCBS80983_g03446 [Powellomyces hirtus]	Probable zinc transporter protein DDB_G0283629 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0283629 PE=3 SV=1
A2789	GO:0030001(metal ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	-	-	KOG2662[At5g22830 Magnesium transporters: CorA family	PVU94786.1 hypothetical protein BB561_002252 [Smittium simulii]	Magnesium transporter MRS2-11, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=MRS2-11 PE=1 SV=1

A2790	GO:0009082(branch ed-chain amino acid biosynthetic process)	-	GO:0016836(hydro-lyase activity),GO:0003824(catalytic activity),GO:0004160(dihydroxy-acid dehydratase activity)	K01687 ilvD; dihydroxy-acid dehydratase [EC:4.2.1.9]	map00770 Pantothenate and CoA biosynthesis;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	-	KAG0223853.1 hypothetical protein BGW42_0055.11 [Actinomortierella wolffii]	Dihydroxy-acid dehydratase OS=Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) OX=243090 GN=ilvD PE=3 SV=2
A2791	-	-	-	-	-	-	-	-
A2792	-	-	GO:0005515(protein binding)	K25866 NUDC; nuclear migration protein NudC	-	KOG2265[At4g27890 Nuclear distribution protein NUDC	KAF9167401.1 hypothetical protein DFQ26_004730 [Actinomortierella ambigua]	Protein BOBBER 2 OS=Arabidopsis thaliana OX=3702 GN=BOB2 PE=2 SV=1
A2793	-	-	-	-	-	-	-	-
A2794	-	-	-	K06911 PIR; quercetin 2,3-dioxygenase [EC:1.13.11.24]	-	-	ORY37950.1 hypothetical protein BCR33DRAFT_441727 [Rhizoclostium globosum]	Putative quercetin 2,3-dioxygenase PA3240 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA3240 PE=3 SV=1
A2795	-	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	-
A2796	-	-	-	K06689 UBE2D, UBC4, UBC5; ubiquitin-conjugating enzyme E2 D [EC:2.3.2.23]	map04141 Protein processing in endoplasmic reticulum;map05131 Shigellosis;map04624 Toll and Imd signaling pathway;map04120 Ubiquitin mediated proteolysis;map03083 Polycomb repressive complex;map04013 MAPK signaling pathway - fly	KOG0417[Hs5454146 Ubiquitin-protein ligase	KAG0354304.1 ubiquitin-conjugating enzyme E2 E1 [Gamsiella multidivariata]	Ubiquitin-conjugating enzyme E2 E3 OS=Bos taurus OX=9913 GN=UBE2E3 PE=2 SV=1
A2797	GO:0006470(protein dephosphorylation)	-	GO:0005515(protein binding),GO:0016787(hydrolase activity),GO:0004721(phosphoprotein phosphatase activity)	K04460 PPP5C; serine/threonine-protein phosphatase 5 [EC:3.1.3.16]	map04010 MAPK signaling pathway	KOG0376[Hs5453958 Serine-threonine phosphatase 2A, catalytic subunit	GES96794.1 serine/threonine-protein phosphatase 5 [Rhizophagus clarus]	Serine/threonine-protein phosphatase 5 OS=Homo sapiens OX=9606 GN=PPP5C PE=1 SV=1
A2798	-	-	-	-	-	-	-	-

A2799	-	-	-	K14831 MAK16; protein MAK16	-	KOG3064 Hs1 4210516 RNA-binding nuclear protein (MAK16) containing a distinct C4 Zn-finger	ORX54786.1 Mak16 protein [Piromyces finnis]	Protein MAK16 homolog A OS=Xenopus laevis OX=8355 GN=mak16-a PE=2 SV=1
A2800	-	-	-	-	-	KOG3700 Z9 3604 Predicted acyltransferas e	-	Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans OX=6239 GN=nrf-6 PE=1 SV=3
A2801	GO:00071 65(signal transducti on)	-	GO:0005515(pro tein binding)	-	-	-	ORY42063.1 hypothetical protein BCR33DRAFT _825036 [Rhizoclosma tium globosum]	-
A2802	-	-	-	-	-	-	-	-
A2803	-	-	-	-	-	-	-	-
A2804	GO:00064 68(protein phosphory lation)	-	GO:0005515(pro tein binding),GO:000 4672(protein kinase activity),GO:000 5524(ATP binding)	-	-	KOG0192 At3 g50730 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9162929. 1 hypothetical protein DFQ26_0031 07 [Actinomortie rella ambigua]	Dual specificity protein kinase shkC OS=Dictyostelium discoideum OX=44689 GN=shkC PE=3 SV=1
A2805	GO:00071 86(G protein-c oupled receptor signaling pathway)	GO:00160 21(integra l compone nt of membra ne)	GO:0004930(G protein-coupled receptor activity)	-	-	-	RUS21415.1 hypothetical protein BC937DRAFT _92750 [Endogone sp. FLAS- F59071]	Phosphate-binding protein PstS OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=pstS PE=3 SV=1
A2806	GO:00550 85(transm embrane transport)	GO:00160 21(integra l compone nt of membra ne)	GO:0003677(DN A binding),GO:002 2857(transmem brane transporter activity)	K11446 KDM5, JARID1; [histone H3]- trimethyl-L- lysine4 demethylase [EC:1.14.11.6 7]	-	KOG1246 Hs4 826968 DNA-binding protein jumonji/RBP2 /SMCY, contains JmjC domain	XP_01455876 0.1 hypothetical protein COCVIDRAFT _24723 [Bipolaris victoriae FI3]	Lysine-specific demethylase 5A OS=Homo sapiens OX=9606 GN=KDM5A PE=1 SV=3
A2807	-	-	-	K23978 IAH1; isoamyl acetate esterase [EC:3.1.1.112]	-	KOG3035 At5 g62930 Isoamyl acetate- hydrolyzing esterase	GBC06828.1 hypothetical protein RclHRI_0707 0010 [Rhizophagus clarus]	Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Mus musculus OX=10090 GN=lah1 PE=1 SV=1
A2808	-	-	-	-	-	-	-	-
A2809	GO:00063 55(regulat ion of transcripti on, DNA- templated)	-	GO:0000981(DN A-binding transcription factor activity, RNA polymerase II- specific),GO:000 8270(zinc ion binding)	-	-	-	-	-
A2810	-	-	GO:0005515(pro tein binding)	K11982 RNF115_126; E3 ubiquitin- protein ligase RNF115/126 [EC:2.3.2.27]	-	KOG0800 At4 g10150 FOG: Predicted E3 ubiquitin ligase	RIB02041.1 hypothetical protein C2G38_92325 3 [Gigaspora rosea]	RING-H2 finger protein ATL7 OS=Arabidopsis thaliana OX=3702 GN=ATL7 PE=2 SV=1
A2811	-	-	-	-	-	-	-	-

A2812	GO:0006629(lipid metabolic process), GO:0007165(signal transduction), GO:0035556(intracellular signal transduction)	-	GO:0004435(phosphatidylinositol phospholipase C activity), GO:0005509(calcium ion binding), GO:0008081(phosphoric diester hydrolase activity)	K05857 PLCD; phosphatidylinositol phospholipase C, delta [EC:3.1.4.11]	map04020 Calcium signaling pathway; map05131 Shigellosis; map04933 AGE-RAGE signaling pathway in diabetic complications; map04070 Phosphatidylinositol signaling system; map04919 Thyroid hormone signaling pathway; map00562 Inositol phosphate metabolism; map01100 Metabolic pathways	KOG0169[Hs6453910 Phosphoinositide-specific phospholipase C	KNE63737.1 hypothetical protein AMAG_08820 [Allomyces macrogynus ATCC 38327]	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Bos taurus OX=9913 GN=PLCD1 PE=2 SV=2
A2813	-	GO:0016459(myosin complex), GO:0005856(cytoskeleton)	GO:0003774(motor activity), GO:0005524(ATP binding), GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection; map04814 Motor proteins	KOG0160[At3g19960 Myosin class V heavy chain	RKO94560.1 myosin VIIA, isoform CRA_d, partial [Blyttiomycetes helicus]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1
A2814	GO:0046854(phosphatidylinositol phosphate biosynthetic process), GO:0048015(phosphatidylinositol-mediated signaling)	-	GO:0016301(kinase activity), GO:0016303(1-phosphatidylinositol-3-kinase activity)	K00914 PIK3C3, VPS34; phosphatidylinositol 3-kinase [EC:2.7.1.137]	map05014 Amyotrophic lateral sclerosis; map04145 Phagosome; map04140 Autophagy - animal; map05132 Salmonella infection; map05131 Shigellosis; map04070 Phosphatidylinositol signaling system; map04138 Autophagy - yeast; map04136 Autophagy - other; map05022 Pathways of neurodegeneration - multiple diseases; map04371 Apelin signaling pathway; map00562 Inositol phosphate	KOG0906[At1g60490 Phosphatidylinositol 3-kinase VPS34, involved in signal transduction	RPB10428.1 phosphatidylinositol 3-kinase [Morchella conica CCBAS932]	Phosphatidylinositol 3-kinase, root isoform OS=Glycine max OX=3847 PE=2 SV=1
A2815	-	-	-	-	-	-	-	-
A2816	GO:0090481(pyrimidine nucleotide-sugar transmembrane transport)	GO:0000139(Golgi membrane), GO:0016021(integral component of membrane)	GO:0015165(pyrimidine nucleotide-sugar transmembrane transporter activity)	K15272 SLC35A1_2_3; solute carrier family 35 (UDP-sugar transporter), member A1/2/3	-	KOG2234[Hs6912668 Predicted UDP-galactose transporter	XP_016240643.1 hypothetical protein PV08_01002 [Exophiala spinifera]	UDP-N-acetylglucosamine transporter OS=Rattus norvegicus OX=10116 GN=Slc35a3 PE=2 SV=1
A2817	-	-	GO:0008270(zinc ion binding)	K17808 ZIM17, DNLZ, Tim15; mitochondrial protein import protein ZIM17	-	KOG3277[Hs20539000 Uncharacterized conserved protein	KU65180.1 hypothetical protein HYDPIIDRAFT_175201 [Hydnomerulis pinastri MD-312]	DNL-type zinc finger protein OS=Xenopus laevis OX=8355 GN=dnlz PE=2 SV=1

A2818	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding);GO:0008569(minus-end-directed microtubule motor activity)	K10413 DYNC1H; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map04184 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595 7301678 Dyneins, heavy chain	XP_016612814.1 hypothetical protein SPPG_00478 [Spizellomyces punctatus DAOM BR117]	Dynein-1-alpha heavy chain, flagellar inner arm I1 complex OS=Chlamydomonas reinhardtii OX=3055 GN=DHC1 PE=1 SV=1
A2819	-	-	-	-	-	-	-	-
A2820	-	-	GO:0005515(protein binding)	K17508 PTC7, PPTC7; protein phosphatase PTC7 [EC:3.1.3.16]	-	KOG1379 7301827 Serine/threonine protein phosphatase	KAG1468564.1 hypothetical protein G6F56_003761 [Rhizopus delemar]	Protein phosphatase PTC7 homolog fig OS=Drosophila erecta OX=7220 GN=fig PE=3 SV=1
A2821	-	-	-	-	-	-	-	-
A2822	-	-	-	-	-	-	XP_019023656.1 Clavaminate synthase-like protein [Saitoella complicata NRRL Y-17804]	JmjC domain-containing protein 4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=jmj4 PE=1 SV=1
A2823	-	-	GO:0016972(thiol oxidase activity)	-	-	-	-	-
A2824	-	-	-	-	-	-	-	-
A2825	-	-	GO:0005515(protein binding);GO:0044877(protein-containing complex binding);GO:0004674(protein serine/threonine kinase activity);GO:0016301(kinase activity)	K07203 MTOR, FRAP, TOR; serine/threonine-protein kinase mTOR [EC:2.7.11.1]	map04361 Axon regeneration;map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04140 Autophagy - animal;map05131 Shigellosis;map04211 Longevity regulating pathway;map04212 Longevity regulating pathway - worm;map04213 Longevity regulating pathway - multiple species;map04218 Cellular senescence;map04072 Phospholipase D signaling	-	TPX61832.1 hypothetical protein PhCBS80983_g00770 [Powellomyces hirtus]	Serine/threonine-protein kinase tor OS=Dictyostelium discoideum OX=44689 GN=tor PE=1 SV=1
A2826	GO:0043328(protein transport to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway)	-	GO:0035091(phosphatidylinositol binding);GO:0043130(ubiquitin binding)	-	-	-	-	-
A2827	-	-	GO:0016407(acyltransferase activity)	-	-	-	-	-

A2828	-	-	GO:0005515(protein binding)	K20649 ARHGAP39; Rho GTPase-activating protein 39	-	KOG1450 Hs20558968 Predicted Rho GTPase-activating protein	-	Rho GTPase-activating protein 27 OS=Rattus norvegicus OX=10116 GN=Arhgap27 PE=1 SV=1
A2829	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A2830	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A2831	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2832	-	-	GO:0005525(GTP binding)	K06942 ychF; ribosome-binding ATPase	-	-	TPX73596.1 hypothetical protein CcCBS67573_g05145 [Chytridiomycetes confervae]	Uncharacterized GTP-binding protein C428.15 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC428.15 PE=3 SV=1
A2833	GO:0006364(rRNA processing)	-	GO:0019843(rRNA binding);GO:0042134(rRNA primary transcript binding)	K14561 IMP4; U3 small nucleolar ribonucleoprotein protein IMP4	map03008 Ribosome biogenesis in eukaryotes	KOG2781 At1g63780 U3 small nucleolar ribonucleoprotein (snoRNP) component	TPX65290.1 hypothetical protein SpCBS45565_g05271 [Spizellomyces sp. 'palustris']	U3 small nucleolar ribonucleoprotein protein IMP4 OS=Homo sapiens OX=9606 GN=IMP4 PE=1 SV=1
A2834	-	-	GO:0018580(nitronate monooxygenase activity)	-	-	-	XP_031027785.1 nitronate monooxygenase [Synchytrium microbalum]	Putative monooxygenase Rv1533 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv1533 PE=1 SV=1
A2835	GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K11863 ATXN3, MJD; Ataxin-3 [EC:3.4.22.-]	map04141 Protein processing in endoplasmic reticulum;map05022 Pathways of neurodegeneration - multiple diseases;map05017 Spinocerebellar ataxia	KOG2935 Hs13518019 Ataxin 3/Josephin	XP_031024327.1 uncharacterized protein SmJEL517_g03711 [Synchytrium microbalum]	Ataxin-3 OS=Homo sapiens OX=9606 GN=ATXN3 PE=1 SV=5
A2836	-	-	-	-	-	-	-	-
A2837	-	-	-	-	-	-	-	-
A2838	-	-	GO:0005515(protein binding);GO:0005524(ATP binding);GO:0005509(calcium ion binding)	-	-	KOG0061 At5g06530 Transporter, ABC superfamily (Breast cancer resistance protein)	RIB30631.1 P-loop containing nucleoside triphosphate hydrolase protein [Gigaspora rosea]	ABC transporter G family member 22 OS=Arabidopsis thaliana OX=3702 GN=ABCG22 PE=1 SV=1
A2839	GO:0006508(proteolysis)	GO:0005634(nucleus)	GO:0004197(cysteine-type endopeptidase activity)	K02365 ESP1; separase [EC:3.4.22.49]	map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG1849 Hs6912454 Regulator of spindle pole body duplication	KAF7755880.1 hypothetical protein DSO57_021236, partial [Entomophthora muscae]	Separin OS=Homo sapiens OX=9606 GN=ESPL1 PE=1 SV=3

A2840	-	-	GO:0005515(protein binding)	-	-	-	-	-
A2841	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A2842	-	-	-	-	-	-	-	-
A2843	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0054 At1g30400 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	TPX73118.1 hypothetical protein CcCBS67573_g05613 [Chytridiomycetes confervae]	ATP-binding cassette sub-family C member 2 OS=Rattus norvegicus OX=10116 GN=Abcc2 PE=1 SV=1
A2844	-	GO:0016021(integral component of membrane)	GO:0004190(serine-type endopeptidase activity)	K09595 HM13; minor histocompatibility antigen H13 [EC:3.4.23.-]	-	KOG2443 7296194 Uncharacterized conserved protein	KAF9933167.1 hypothetical protein FBUS0_006333 [Linnemannia zychae]	Minor histocompatibility antigen H13 OS=Homo sapiens OX=9606 GN=HM13 PE=1 SV=1
A2845	GO:0016560(protein import into peroxisome matrix, docking)	GO:0005778(peroxisomal membrane)	GO:0005515(protein binding)	K13343 PEX14; peroxin-14	map04146 Peroxisome	KOG2629 At5g62810.2 Peroxisomal membrane anchor protein (peroxin)	KAG0801248.1 hypothetical protein G6F22_001431 [Rhizopus oryzae]	Peroxisomal membrane protein PEX14 OS=Arabidopsis thaliana OX=3702 GN=PEX14 PE=1 SV=2
A2846	-	-	-	-	-	KOG1700 At1g10200 Regulatory protein MLP and related LIM proteins	KAG4103849.1 Rap/Ran-GAP [Neocallimastix sp. JGI-2020a]	Pollen-specific protein SF3 OS=Helianthus annuus OX=4232 GN=SF3 PE=2 SV=1
A2847	-	GO:0016020(membrane)	-	K10082 LMAN2, VIP36; lectin, mannose-binding 2	map04141 Protein processing in endoplasmic reticulum	KOG3839 CE23946 Lectin VIP36, involved in the transport of glycoproteins carrying high mannose-type glycans	KAF2786745.1 vesicular integral-membrane protein VIP36 precursor [Melanomma pulvis-pyrius CBS 109.77]	VIP36-like protein OS=Mus musculus OX=10090 GN=Lman2l PE=1 SV=1
A2848	-	-	GO:0018580(nitronate monooxygenase activity)	K23948 E1.6.5.9; NADH:quinone reductase (non-electrogenic) [EC:1.6.5.9]	-	-	CDH58854.1 2-nitropropane dioxygenase [Lichtheimia corymbifera JMRc:FSU:9682]	NADH:quinone reductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA1024 PE=1 SV=1
A2849	-	-	-	-	-	-	-	-
A2850	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0005515(protein binding)	K11407 HDAC6; histone deacetylase 6 [EC:3.5.1.98]	map05014 Amyotrophic lateral sclerosis;map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG1343 At5g61060 Histone deacetylase complex, catalytic component HDA1	KAG1188132.1 hypothetical protein G6F35_014320 [Rhizopus oryzae]	Type-2 histone deacetylase 2 OS=Dictyostelium discoideum OX=44689 GN=hdaC PE=2 SV=1
A2851	-	-	-	-	-	-	-	-

A2852	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02883 RP-L18e, RPL18; large subunit ribosomal protein L18e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1714 At3g05590 60s ribosomal protein L18	KAF7748587.1 60S ribosomal protein L18 [Entomophthora muscae]	Large ribosomal subunit protein eL18y OS=Arabidopsis thaliana OX=3702 GN=RPL18B PE=1 SV=2
A2853	-	-	-	K00079 CBR1; carbonyl reductase 1 [EC:1.1.1.184 1.1.1.189 1.1.1.197]	map00980 Metabolism of xenobiotics by cytochrome P450;map00590 Arachidonic acid metabolism;map05204 Chemical carcinogenesis - DNA adducts;map05208 Chemical carcinogenesis - reactive oxygen species;map01100 Metabolic pathways;map00790 Folate biosynthesis	KOG1208 Hs4g05590 60s ribosomal protein L18	XP_003658014.1 uncharacterized protein THITE_2124387 [Thermothielavioides terrestris NRRL 8126]	Carbonyl reductase [NADPH] 3 OS=Mus musculus OX=10090 GN=Cbr3 PE=1 SV=1
A2854	-	-	-	K00079 CBR1; carbonyl reductase 1 [EC:1.1.1.184 1.1.1.189 1.1.1.197]	map00980 Metabolism of xenobiotics by cytochrome P450;map00590 Arachidonic acid metabolism;map05204 Chemical carcinogenesis - DNA adducts;map05208 Chemical carcinogenesis - reactive oxygen species;map01100 Metabolic pathways;map00790 Folate biosynthesis	KOG1208 At1g01800 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	GAP82652.2 putative short-chain dehydrogenase reductase SDR [Rosellinia necatrix]	Carbonyl reductase [NADPH] 1 OS=Bos taurus OX=9913 GN=CBR1 PE=2 SV=1
A2855	-	-	-	-	-	-	-	-
A2856	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02922 RP-L37e, RPL37; large subunit ribosomal protein L37e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3475 7293042 60S ribosomal protein L37	XP_016608967.1 60S ribosomal protein L37-A [Spizellomyces punctatus DAOM BR117]	Large ribosomal subunit protein eL37A OS=Drosophila melanogaster OX=7227 GN=Rpl37-1 PE=1 SV=1
A2857	-	-	-	-	-	-	-	-
A2858	-	-	-	-	-	-	-	-
A2859	-	-	-	-	-	-	-	-
A2860	-	-	-	-	-	-	-	-
A2861	GO:0006811(ion transport);GO:0055085(transmembrane transport)	GO:0016020(membrane);GO:0016021(integral component of membrane)	GO:0005515(protein binding);GO:0005216(ion channel activity)	-	-	KOG3676 CE24256 Ca2+-permeable cation channel OSM-9 and related channels (OTRPC family)	OAA65142.1 Ankyrin repeat-containing domain protein [Akanthomyces lecanii RCEF 1005]	Ankyrin repeat domain-containing protein 46 OS=Pongo abelii OX=9601 GN=ANKRD46 PE=2 SV=1

A2862	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05658 ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:7.6.2.2]	map04976 Bile secretion;map02010 ABC transporters;map05226 Gastric cancer;map05206 MicroRNAs in cancer	KOG0055 At1g02520 Multidrug/phoromone exporter, ABC superfamily	KAF0430296.1 P-loop containing nucleoside triphosphate hydrolase protein [Gigaspora margarita]	ATP-dependent translocase ABCB1 OS=Cricetulus griseus OX=10029 GN=ABCB1 PE=1 SV=2
A2863	-	-	-	-	-	-	-	-
A2864	GO:0006508(proteolysis),GO:0030163(protein catabolic process)	-	GO:0004176(ATP-dependent peptidase activity),GO:0004252(serine-type endopeptidase activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K08675 PRSS15, PIM1; ATP-dependent Lon protease [EC:3.4.21.53]	-	KOG2004 At5g26860 Mitochondrial ATP-dependent protease PIM1/LON	KXS21509.1 ATP-dependent protease La [Gonapodya prolifera JEL478]	Lon protease homolog, mitochondrial OS=Phaeodactylum tricornutum (strain CCAP 1055/1) OX=556484 GN=PHATRDRRAFT_18202 PE=3 SV=1
A2865	GO:0009102(biotin biosynthetic process)	-	GO:0000287(magnesium ion binding),GO:0004141(dethiobiotin synthase activity),GO:0005524(ATP binding)	K19562 BIO3-BIO1; bifunctional dethiobiotin synthetase / adenosylmethionine--8-amino-7-oxononanoate aminotransferase [EC:6.3.3.3 2.6.1.62]	map00780 Biotin metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	-	KFA71312.1 hypothetical protein S40288_06702 [Stachybotrys chartarum IBT 40288]	Bifunctional dethiobiotin synthetase/adenosylmethionine-8-amino-7-oxononanoate aminotransferase OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=bioDA PE=1 SV=1
A2866	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs4502553 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORY19105.1 Pkinase-domain-containing protein [Neocallimastix californiae]	Calcium/calmodulin-dependent protein kinase type 1 OS=Macrobrachium nipponense OX=159736 GN=CaMKI PE=2 SV=1
A2867	-	-	-	-	-	-	-	-
A2868	GO:0035434(copper ion transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005375(copper ion transmembrane transporter activity)	-	-	-	-	-
A2869	GO:0006116(NADH oxidation)	-	GO:0003954(NADH dehydrogenase activity),GO:0016491(oxidoreductase activity)	K03885 ndh; NADH:quinone reductase (non-electrogenic) [EC:1.6.5.9]	map00190 Oxidative phosphorylation; map01100 Metabolic pathways	KOG2495 At1g07180 NADH-dehydrogenase (ubiquinone)	KAF8976121.1 hypothetical protein BGZ46_008561 [Entomortierella lignicola]	Probable NADH dehydrogenase OS=Dictyostelium discoideum OX=44689 GN=DDB_G0270104 PE=3 SV=2
A2870	-	-	-	-	-	-	-	Beta-arabinofuranosyltransferase RAY1 OS=Arabidopsis thaliana
A2871	GO:0006412(translation)	-	GO:0008168(methyltransferase activity)	-	-	KOG2539 Hs12232389 Mitochondrial/chloroplast ribosome small subunit component	KAG2184542.1 hypothetical protein INT43_000451, partial [Umbelopsis isabellina]	Methyltransferase-like protein 17, mitochondrial OS=Bos taurus OX=9913 GN=METTLL17 PE=2 SV=1

A2872	-	-	GO:0003824(catalytic activity)	K00167 BCKDHB, bkdA2; 2-oxoisovalerate dehydrogenase E1 component subunit beta [EC:1.2.4.4]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map00640 Propanoate metabolism;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0525 At1g55510 Branched chain alpha-keto acid dehydrogenase E1, beta subunit	ORZ33944.1 Thiamin diphosphate-binding protein [Catenaria anguillulae PL171]	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=bkdB PE=3 SV=1
A2873	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11252 H2B; histone H2B	map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG1744 YBL002w Histone H2B	ORE18420.1 histone H2b, partial [Rhizopus microsporus]	Histone H2B OS=Olisthodiscus luteus OX=83000 PE=1 SV=2
A2874	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11251 H2A; histone H2A	map04217 Necroptosis;map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map03082 ATP-dependent chromatin remodeling	KOG1756 CE05477 Histone 2A	RUO96772.1 histone-fold-containing protein [Jimgerdennia flammicorona]	Histone H2A-III OS=Volvox carteri OX=3067 PE=3 SV=1
A2875	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	-	-	-
A2876	GO:0006897(endocytosis)	GO:0016020(membrane)	-	K20069 NECAP1_2; adaptin ear-binding coat-associated protein 1/2	-	KOG2500 CE25196 Uncharacterized conserved protein	KAF7751850.1 hypothetical protein DSO57_014872 [Entomophthora muscae]	NECAP-like protein CG9132 OS=Drosophila melanogaster OX=7227 GN=CG9132 PE=2 SV=1
A2877	-	-	-	-	-	-	-	-
A2878	-	-	GO:0010181(FMN binding),GO:0003955(NAD(P)H dehydrogenase (quinone) activity),GO:0016491(oxidoreductase activity)	-	-	KOG3135 At5g54500 1,4-benzoquinone reductase-like; Trp repressor binding protein-like/protoplast-secreted protein	EIE77389.1 NAD(P)H:quinone oxidoreductase, type IV [Rhizopus delemar RA99-880]	Quinone-oxidoreductase QR2 OS=Triphysaria versicolor OX=64093 PE=1 SV=1

A2879	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding),GO:0000049(tRNA binding)	K03242 EIF2S3; translation initiation factor 2 subunit 3	-	KOG0466[Hs4503507 Translation initiation factor 2, gamma subunit (eIF-2gamma; GTPase)	KAG4087856.1 P-loop containing nucleoside triphosphate hydrolase protein [Neocallimastix sp. JGI-2020a]	Eukaryotic translation initiation factor 2 subunit 3 OS=Bos taurus OX=9913 GN=EIF2S3 PE=2 SV=1
A2880	-	-	-	-	-	-	-	-
A2881	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration;map04024 cAMP signaling pathway;map04020 Calcium signaling pathway;map05414 Dilated cardiomyopathy;map04140 Autophagy - animal;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map01522 Endocrine resistance;map04919 Thyroid hormone signaling pathway;map04918 Thyroid hormone synthesis;map04	KOG0603[Hs19923570 Ribosomal protein S6 kinase	OAG32185.1 protein kinase X [Nematocida disploclere]	Ribosomal protein S6 kinase alpha-2 OS=Homo sapiens OX=9606 GN=RPS6KA2 PE=1 SV=2
A2882	GO:0006013(mannose metabolic process), GO:0006468(protein phosphorylation),GO:0005975(carbohydrate metabolic process)	-	GO:0004559(alpha-mannosidase activity),GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0003824(catalytic activity),GO:0030246(carbohydrate binding)	-	-	KOG1958[7299177 Glycosyl hydrolase, family 38 - alpha-mannosidase	KAG0359235.1 hypothetical protein BG005_001181 [Podila minutissima]	Probable serine/threonine-protein kinase drkA OS=Dictyostelium discoideum OX=44689 GN=drkA PE=3 SV=1
A2883	-	-	-	-	-	-	-	-
A2884	-	-	GO:0016491(oxidoreductase activity),GO:0003955(NAD(P)H dehydrogenase (quinone) activity),GO:0010181(FMN binding)	K03809 wrbA; NAD(P)H dehydrogenase (quinone) [EC:1.6.5.2]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00130 Ubiquinone and other terpenoid-quinone biosynthesis;map01100 Metabolic pathways	KOG3135[At5g54500 1,4-benzoquinone reductase-like; Trp repressor binding protein-like/protoplast-secreted protein	KIY71941.1 benzoquinone reductase [Cylindrobacterium torrendii FP15055 ss-10]	Quinone-oxidoreductase QR2 OS=Triphysaria versicolor OX=64093 PE=1 SV=1

A2885	-	-	GO:0016491(oxidoreductase activity),GO:0003955(NAD(P)H dehydrogenase (quinone) activity),GO:0010181(FMN binding)	K03809 wrbA; NAD(P)H dehydrogenase (quinone) [EC:1.6.5.2]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00130 Ubiquinone and other terpenoid-quinone biosynthesis;map01100 Metabolic pathways	KOG3135 At5g54500 1,4-benzoquinone reductase-like; Trp repressor binding protein-like/protoplast-secreted protein	PVF96617.1 putative 1,4-benzoquinone reductase [Serendipita vermicifera 'subsp. bescii']	NAD(P)H dehydrogenase (quinone) FQR1 OS=Arabidopsis thaliana OX=3702 GN=FQR1 PE=1 SV=1
A2886	-	-	GO:0005544(calcium-dependent phospholipid binding)	-	-	KOG1327 Hs4503015 Copine	TPX62249.1 hypothetical protein PhCBS80983_g00457 [Powellomyces hirtus]	Copine-5 OS=Mus musculus OX=10090 GN=Cpne5 PE=1 SV=1
A2887	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08850 AURKX; aurora kinase, other [EC:2.7.11.1]	-	KOG0580 Hs4507275 Serine/threonine protein kinase	OZJ06633.1 Aurora kinase A-B [Figuratus adelaidae]	Aurora kinase A OS=Mus musculus OX=10090 GN=Aurka PE=1 SV=1
A2888	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08850 AURKX; aurora kinase, other [EC:2.7.11.1]	-	KOG0580 Hs4507275 Serine/threonine protein kinase	OON02143.1 hypothetical protein BSLG_07291, partial [Batrachochytrium salamandrivorans]	Aurora kinase A-A OS=Xenopus laevis OX=8355 GN=aurka-a PE=1 SV=1
A2889	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0580 At4g32830 Serine/threonine protein kinase	ORX60879.1 AGC family protein kinase [Piromyces finnis]	Aurora kinase A-B OS=Xenopus laevis OX=8355 GN=aurka-b PE=2 SV=3
A2890	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0580 Hs4759178 Serine/threonine protein kinase	RKP10390.1 kinase-like domain-containing protein [Thamnocephalus sphaerospora]	Aurora kinase A-B OS=Xenopus laevis OX=8355 GN=aurka-b PE=2 SV=3
A2891	-	-	-	-	-	-	XP_031026442.1 uncharacterized protein SmJEL517_g01472 [Synchytrium microbalum]	-
A2892	-	-	-	-	-	-	-	-
A2893	-	-	-	-	-	-	-	-
A2894	-	-	-	K20242 EVI5; ecotropic viral integration site 5 protein	-	KOG4436 CE07531 Predicted GTPase activator NB4S/EVI5 (contains TBC domain)/Calmodulin-binding protein Pollux (contains PTB and TBC domains)	CDS10054.1 hypothetical protein LRAMOSA02731 [Lichtheimia ramosa]	Rab GTPase-activating protein eat-17 OS=Caenorhabditis elegans OX=6239 GN=eat-17 PE=1 SV=1

A2895	-	-	GO:0050661(NADP binding);GO:0051287(NAD binding);GO:0016491(oxidoreductase activity);GO:0008442(3-hydroxyisobutyrate dehydrogenase activity)	-	-	KOG0409 Hs20539653 Predicted dehydrogenase	ORX84405.13-hydroxyisobutyrate dehydrogenase [Basidiobolus meristosporus CBS 931.73]	Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=hibA PE=3 SV=1
A2896	GO:0031204(posttranslational protein targeting to membrane, translocation)	-	-	K09540 SEC63, DNAJC23; translocation protein SEC63	map04141 Protein processing in endoplasmic reticulum;map03060 Protein export	KOG0721 Hs6005872.1 Molecular chaperone (DnaJ superfamily)	KAG4093916.1 hypothetical protein H8356DRAFT_999457 [Neocallimastix sp. JGI-2020a]	DnaJ protein ERDJ2A OS=Arabidopsis thaliana OX=3702 GN=ERDJ2A PE=1 SV=1
A2897	-	-	-	-	-	-	-	-
A2898	-	-	GO:0005524(ATP binding);GO:0046872(metal ion binding);GO:0016874(ligase activity)	-	-	KOG0369 Hs4505627 Pyruvate carboxylase	XP_016605259.1 hypothetical protein SPPG_07606 [Spizellomyces punctatus DAOM BR117]	Pyruvate carboxylase subunit A OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=pycA PE=1 SV=1
A2899	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity)	-	-	-	ORZ35749.1 periplasmic binding protein-like I [Catenaria anguillulae PL171]	-
A2900	-	-	-	-	-	-	-	-
A2901	GO:0055085(transmembrane transport);GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	K07300 chaA, CAX; Ca2+:H+ antiporter	-	KOG1397 At1g55730 Ca2+/H+ antiporter VCX1 and related proteins	KJA22895.1 hypothetical protein HYP5UDRAFT_87039 [Hypholoma sublateritium FD-334 SS-4]	Vacuolar cation/proton exchanger 2 OS=Oryza sativa subsp. japonica OX=39947 GN=CAX2 PE=2 SV=2
A2902	-	-	-	-	-	-	-	-
A2903	-	-	-	-	-	-	-	Leishmanolysin homolog OS=Crithidia fasciculata OX=5656 GN=gp63
A2904	-	-	-	K01113 phoD; alkaline phosphatase D [EC:3.1.3.1]	map01240 Biosynthesis of cofactors;map02020 Two-component system;map01100 Metabolic pathways;map00790 Folate biosynthesis	-	TPX65929.1 hypothetical protein SpCBS45565_g04833 [Spizellomyces sp. 'palustris']	Phospholipase D OS=Streptomyces chromofuscus OX=42881 GN=pld PE=1 SV=2
A2905	-	-	-	-	-	-	-	-
A2906	-	-	GO:0008270(zinc ion binding);GO:0016491(oxidoreductase activity)	-	-	KOG0023 At4g37980 Alcohol dehydrogenase, class V	KAF9139747.1 hypothetical protein BGX30_007546 [Mortierella sp. GBA39]	Probable formaldehyde dehydrogenase AdhA OS=Bacillus subtilis (strain 168) OX=224308 GN=adhA PE=2 SV=1
A2907	-	-	GO:0008168(methyltransferase activity)	-	-	-	-	Lovastatin diketide synthase lovF OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) OX=341663 GN=lovF PE=1 SV=1

A2908	-	-	-	-	-	-	KAG4087738.1 hypothetical protein H8356DRAFT_1727824 [Neocallimastix sp. JGI-2020a]	-
A2909	GO:0008654(phospholipid biosynthetic process)	-	GO:0004609(phosphatidylserine decarboxylase activity)	K01613 psd, PISD; phosphatidylserine decarboxylase [EC:4.1.1.65]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG2419 At5g57190 Phosphatidylserine decarboxylase	XP_007383415.1 hypothetical protein PUNSTDRAFT_102181 [Puntularia strigosozonata HHB-11173 SS5]	Phosphatidylserine decarboxylase proenzyme 2 OS=Oryza sativa subsp. japonica OX=39947 GN=PSD2 PE=3 SV=3
A2910	GO:0006891(intra-Golgi vesicle-mediated transport)	GO:001719(Golgi transport complex)	-	K20292 COG5; conserved oligomeric Golgi complex subunit 5	-	KOG2211 Hs5453670 Predicted Golgi transport complex 1 protein	TPX77103.1 hypothetical protein CcCBS67573.g01595 [Chytridiomycetes confervae]	Conserved oligomeric Golgi complex subunit 5 OS=Mus musculus OX=10090 GN=Cog5 PE=1 SV=3
A2911	GO:0006886(intracellular protein transport) GO:0016192(vesicle-mediated transport)	GO:003017(membrane coat)	GO:0005198(structural molecule activity),GO:0005515(protein binding)	K17302 COPB2, SEC27; coatomer subunit beta'	-	KOG0276 At1g79990 Vesicle coat complex COPI, beta' subunit	OAJ42349.1 hypothetical protein BDEG_25808 [Batrachochytrium dendrobatidis JEL423]	Coatomer subunit beta'-1 OS=Arabidopsis thaliana OX=3702 GN=At1g79990 PE=2 SV=2
A2912	-	-	-	K10355 ACTF, actin, other eukaryote	map04814 Motor proteins	KOG0679 At1g18450 Actin-related protein - Arp4p/Act3p	KAG0245645.1 Actin-like 6A [Mortierella sp. GBA43]	Actin-related protein 4 OS=Arabidopsis thaliana OX=3702 GN=ARP4 PE=1 SV=1
A2913	-	-	-	-	-	KOG1632 7291045 Uncharacterized PHD Zn-finger protein	KAF9965992.1 hypothetical protein BGZ70_003605 [Mortierella alpina]	-
A2914	-	-	GO:0005096(GTPase activator activity)	K12488 ASAP; Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein	map04144 Endocytosis;map04666 Fc gamma R-mediated phagocytosis	KOG0521 Hs17977656 Putative GTPase activating proteins (GAPs)	EPZ35948.1 Arf-GAP-like with coiled-coil, ANK repeat and PH domain-containing protein [Rozella allomyces CSF55]	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Oryctolagus cuniculus OX=9986 GN=ACAP2 PE=2 SV=1

A2915	GO:0006525(arginine metabolic process)	-	GO:0046872(metal ion binding);GO:0004053(arginase activity);GO:0016813(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides)	K01476 E3.5.3.1, rocF; arg; arginase [EC:3.5.3.1]	map01110 Biosynthesis of secondary metabolites;map00330 Arginine and proline metabolism;map01230 Biosynthesis of amino acids;map05146 Amoebiasis;map00220 Arginine biosynthesis;map01100 Metabolic pathways	KOG2965[Hs10947139 Arginase	CDI55474.1 probable arginase [Melanopsichium pennsylvanicum 4]	Arginase OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=agaA PE=3 SV=2
A2916	-	-	GO:0005515(protein binding)	K14018 PLAA, DOA1, UFD3; phospholipase A-2-activating protein	map04141 Protein processing in endoplasmic reticulum	-	XP_022582813.1 hypothetical protein ASPZODRAFT_62655 [Penicillium zonata CBS 506.65]	Ubiquitin homeostasis protein lub1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=lub1 PE=1 SV=2
A2917	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0725[At3g29250 Reductases with broad range of substrate specificities	KAF9127961.1 hypothetical protein BGX30_014519 [Mortierella sp. GBA39]	Uncharacterized oxidoreductase YuxG OS=Bacillus subtilis (strain 168) OX=224308 GN=yuxG PE=3 SV=2
A2918	-	-	-	K13102 KIN; DNA/RNA-binding protein KIN17	-	KOG2837[Hs13124883 Protein containing a U1-type Zn-finger and implicated in RNA splicing or processing	GJH88890.1 hypothetical protein NliqN6_5292 [Naganishia liquefaciens]	DNA/RNA-binding protein KIN17 OS=Mus musculus OX=10090 GN=Kin PE=1 SV=1
A2919	-	-	GO:0016409(palmitoyltransferase activity)	K20031 ZDHHC6; palmitoyltransferase ZDHHC6 [EC:2.3.1.225]	-	KOG1311[7303015 DHHC-type Zn-finger proteins	KAF8481638.1 zf-DHHC-domain-containing protein [Russula ochroleuca]	Palmitoyltransferase ZDHHC7 OS=Mus musculus OX=10090 GN=Zdhhc7 PE=1 SV=1
A2920	-	-	GO:0008641(ubiquitin-like modifier activating enzyme activity)	-	-	KOG2017[CE28320 Molybdopterin synthase sulfurylase	KGQ13963.1 Molybdopterin molybdenum transferase [Beauveria bassiana D1-5]	Molybdopterin-synthase adenyllyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=moeB PE=3 SV=2

A2921	GO:0006099(tricarboxylic acid cycle)	-	GO:0016624(oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor),GO:0004591(oxoglutarate dehydrogenase (succinyl-transferring) activity),GO:0030976(thiamine pyrophosphate binding)	K00164 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0450 At5g65750 2-oxoglutarate dehydrogenase, E1 subunit	CDS04572.1 hypothetical protein LRAMOSA07203 [Lichtheimia ramosa]	2-oxoglutarate dehydrogenase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=ogdh PE=3 SV=1
A2922	GO:0006508(proteolysis)	-	GO:0004181(metalloprotease activity),GO:0008270(zinc ion binding)	K08783 ECM14; extracellular matrix protein 14 [EC:3.4.17.-]	-	KOG2650 YHR132c Zinc carboxypeptidase	ORY87504.1 hypothetical protein BCR35DRAFT_277408 [Leucosporidium creatinivorum]	Inactive metalloprotease ecm14 OS=Emmericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=ecm14 PE=3 SV=2
A2923	-	-	GO:0005515(protein binding)	K14546 UTP5, WDR43; U3 small nucleolar RNA-associated protein 5	map03008 Ribosome biogenesis in eukaryotes	KOG4547 Hs20535866 WD40 repeat-containing protein	KAF9984994.1 WD repeat-containing protein 43 [Mortierella antarctica]	U3 small nucleolar RNA-associated protein 5 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=utp5 PE=3 SV=2
A2924	GO:0055085(transmembrane transport)	-	-	K15114 ORT1; mitochondrial ornithine carrier protein	-	KOG0758 YOR130c Mitochondrial carnitine-acylcarnitine carrier protein	ORX60869.1 mitochondrial carrier [Pirromyces finnis]	Mitochondrial substrate carrier family protein S OS=Dictyostelium discoideum OX=44689 GN=mcfs PE=3 SV=1
A2925	-	-	-	-	-	-	XP_016613135.1 carrier protein [Spizellomyces punctatus DAOM BR117]	-
A2926	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K12823 DDX5, DBP2; ATP-dependent RNA helicase DDX5/DBP2 [EC:3.6.4.13]	map03040 Spliceosome;map05202 Transcriptional misregulation in cancer;map05205 Proteoglycans in cancer	KOG0331 YNL112w ATP-dependent RNA helicase	ODV96010.1 hypothetical protein PACTADRAFT_49432 [Pachysolen tannophilus NRRL Y-2460]	ATP-dependent RNA helicase DBP2 OS=Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) OX=322104 GN=DBP2 PE=3 SV=1
A2927	-	-	-	-	-	-	-	-
A2928	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K12811 DDX46, PRP5; ATP-dependent RNA helicase DDX46/PRP5 [EC:3.6.4.13]	map03040 Spliceosome	KOG0334 At1g20920 RNA helicase	RGB32634.1 P-loop containing nucleoside triphosphate hydrolase protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	DEAD-box ATP-dependent RNA helicase 42 OS=Arabidopsis thaliana OX=3702 GN=RH42 PE=1 SV=2
A2929	-	-	-	-	-	-	-	-

A2930	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity),GO:0004965(G protein-coupled GABA receptor activity)	-	-	KOG1055[Hs20127671 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	TPX54710.1 hypothetical protein PhCBS80983_g05811 [Powellomyces hirtus]	Gamma-aminobutyric acid type B receptor subunit 2 OS=Caenorhabditis elegans OX=6239 GN=gbb-2 PE=1 SV=1
A2931	-	-	-	-	-	-	-	-
A2932	GO:0034553(mitochondrial respiratory chain complex II assembly)	-	-	K18167 SDHAF1: succinate dehydrogenase assembly factor 1	-	KOG4620[Hs18591128 Uncharacterized conserved protein	XP_016612093.1 hypothetical protein SPPG_01499 [Spizellomyces punctatus DAOM BR117]	Succinate dehydrogenase assembly factor 1A, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=sdhaf1A PE=3 SV=1
A2933	-	-	-	-	-	-	OON05628.1 hypothetical protein BSLG_04537 [Batrachochytrium salamandrivorans]	-
A2934	GO:0019343(cysteine biosynthetic process via cystathionine)	GO:0005737(cytoplasm)	GO:0004122(cystathionine beta-synthase activity)	K01697 CBS; cystathionine beta-synthase [EC:4.2.1.22]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG1252[Hs4557415 Cystathionine beta-synthase and related enzymes	ORX88472.1 cystathionine beta-synthase [Basidiobolus meristosporus CBS 931.73]	Cystathionine beta-synthase OS=Oryctolagus cuniculus OX=9986 GN=CBS PE=2 SV=3
A2935	-	-	GO:0005515(protein binding)	-	-	-	RUS14401.1 6-phosphogluconolactonase [Endogone sp. FLAS-F59071]	6-phosphogluconolactonase OS=Bacillus subtilis (strain 168) OX=224308 GN=pgl PE=1 SV=1
A2936	-	-	-	-	-	-	KAG0269463.1 hypothetical protein DFQ27_003375 [Actinomortierella ambigua]	-
A2937	-	GO:0016021(integral component of membrane)	-	K06199 crcB, FEX; fluoride exporter	-	-	XP_016610223.1 hypothetical protein SPPG_09047 [Spizellomyces punctatus DAOM BR117]	Fluoride export protein 1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=FEX1 PE=3 SV=1

A2938	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0003924(GTPase activity),GO:0019001(guanylnucleotide binding),GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04730 Long-term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082(CE08571 G-protein alpha subunit (small G protein superfamily))	KAG4089144.1 guanine nucleotide-binding protein alpha-17 subunit [Neocallimastix sp. JGI-2020a]	Guanine nucleotide-binding protein alpha-17 subunit OS=Caenorhabditis elegans OX=6239 GN=odr-3 PE=1 SV=1
A2939	GO:0000160(phosphorelay signal transduction system),GO:0016310(phosphorylation)	-	GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	-	SMR41597.1 unnamed protein product [Zymoseptoria tritici ST99CH_1E4]	Hybrid signal transduction histidine kinase K OS=Dictyostelium discoideum OX=44689 GN=dhkk PE=1 SV=1
A2940	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	-	-	KOG0239[At5g27550 Kinesin (KAR3 subfamily)]	RKO98564.1 hypothetical protein CXG81DRAFT_6275, partial [Caulochytrium protostelioides]	Kinesin-like protein KIN-14R OS=Arabidopsis thaliana OX=3702 GN=KIN14R PE=3 SV=1
A2941	-	-	-	-	-	-	-	-
A2942	GO:0009089(lysine biosynthetic process via diaminopimelate)	-	GO:0016829(lyase activity),GO:0008840(4-hydroxy-tetrahydrodipicolinate synthase activity)	-	-	-	KAG0321908.1 hypothetical protein BGZ97_009767 [Linnemannia gamsii]	4-hydroxy-tetrahydrodipicolinate synthase OS=Endomicrobium trichonymphae OX=1408204 GN=dapA PE=3 SV=1
A2943	GO:0008299(isoprenoid biosynthetic process)	-	-	K05355 hexPS, COQ1: hexaprenyldiphosphate synthase [EC:2.5.1.82 2.5.1.83]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis	KOG0776[7302032 Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase]	GBB85948.1 hypothetical protein RclHR1_12390010 [Rhizophagus clarus]	Probable hexaprenyl pyrophosphate synthase, mitochondrial OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=NCU02305 PE=3 SV=1
A2944	-	-	-	-	-	-	-	-
A2945	-	-	-	-	-	-	-	-
A2946	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	XP_031025646.1 uncharacterized protein SmJEL517_g02373 [Synchytrium microbalum]	-
A2947	-	-	GO:0003824(catalytic activity)	-	-	KOG1075(CE04575 FOG: Reverse transcriptase)	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A2948	-	-	-	-	-	-	-	-
A2949	-	-	-	-	-	-	-	-

A2950	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity)	-	-	KOG1055[Hs20127671 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	RUS24755.1 hypothetical protein BC938DRAFT_473115 [Jimgerdennia flammicorona]	Gamma-aminobutyric acid type B receptor subunit 2 OS=Mus musculus OX=10090 GN=Gabbr2 PE=1 SV=2
A2951	GO:0055085(transmembrane transport)	-	GO:0005509(calcium ion binding),GO:0022857(transmembrane transporter activity)	-	-	-	KXS12741.1 MFS general substrate transporter [Gonapodya prolifera JEL478]	Uncharacterized MFS-type transporter MJ1560 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ1560 PE=3 SV=1
A2952	GO:0030163(protein catabolic process)	GO:0005737(cytoplasm)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0036402(proteasome-activating activity)	-	-	KOG0652[At3g05530 26S proteasome regulatory complex, ATPase RPT5	XP_018291570.1 hypothetical protein PHYBLDRAFT_125125 [Phycomyces blakesleeanus NRRL 1555(-)]	26S proteasome regulatory subunit 6A homolog OS=Brassica campestris OX=3711 GN=TBP1 PE=2 SV=1
A2953	-	-	GO:0019239(deaminase activity)	-	-	KOG1097[7299138 Adenine deaminase/adenosine deaminase	XP_016291508.1 hypothetical protein PSEUBRA_SC AF3g04037 [Kalmanozyma brasiliensis GHG001]	Adenosine deaminase-like protein OS=Drosophila melanogaster OX=7227 GN=Ada PE=2 SV=1
A2954	GO:0006099(tricarboxylic acid cycle)	-	GO:0004450(isocitrate dehydrogenase (NADP+) activity),GO:0000287(magnesium ion binding),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0051287(NAD binding)	K00030 IDH3; isocitrate dehydrogenase (NAD+) [EC:1.1.1.41]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00020 Citrate cycle (TCA cycle);map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0785[7293593 Isocitrate dehydrogenase, alpha subunit	KAF9133883.1 hypothetical protein BGX30_012115 [Mortierella sp. GBA39]	Isocitrate dehydrogenase [NADP] OS=Bacillus subtilis (strain 168) OX=224308 GN=icd PE=1 SV=1
A2955	-	-	-	-	-	-	-	-
A2956	-	-	-	K20360 TBC1D22, GYP1; TBC1 domain family member 2	-	-	OAQ26535.1 RabGAP/TBC [Linnemannia elongata AG-77]	GTPase-activating protein gyp1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=gyp1 PE=3 SV=1
A2957	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07910 RAB18; Ras-related protein Rab-18	-	KOG0092[At4g19640 GTPase Rab5/YPT51 and related small G protein superfamily GTPases	KAG5351769.1 GTPase Ypt2 [Termitomyces sp. Mn162]	Ras-related protein Rab-42 OS=Mus musculus OX=10090 GN=Rab42 PE=2 SV=1
A2958	-	-	-	-	-	-	-	-

A2959	GO:0070588(calcium ion transmembrane transport),GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005262(calcium channel activity),GO:0005216(ion channel activity)	-	-	KOG3533 7296736 Inositol 1,4,5-trisphosphate receptor	KAF1806889.1 hypothetical protein FB192DRAFT_1352816 [Mucor lusitanicus]	Inositol 1,4,5-trisphosphate receptor OS=Drosophila melanogaster OX=7227 GN=Itpr PE=2 SV=3
A2960	-	-	-	-	-	-	CDH50673.1 cobyrinic acid-diamide mitochondrial-like [Lichtheimia corymbifera JMRC.FSU:9682]	Corrinoid adenosyltransferase MMAB OS=Mus musculus OX=10090 GN=Mmab PE=1 SV=1
A2961	GO:0006629(lipid metabolic process)	-	-	-	-	-	KXS19429.1 hypothetical protein M427DRAFT_450463 [Gonapodya prolifera JEL478]	-
A2962	-	-	GO:0022857(transmembrane transporter activity)	K17794 TIM23; mitochondrial import inner membrane translocase subunit TIM23	map04212 Longevity regulating pathway - worm	KOG3324 At1g72750 Mitochondrial import inner membrane translocase, subunit TIM23	CAF990881.1 hypothetical protein GOMPHAMP_RED_006321 [Gomphillus americanus]	Mitochondrial import inner membrane translocase subunit TIM23-2 OS=Arabidopsis thaliana OX=3702 GN=TIM23-2 PE=1 SV=1
A2963	-	-	-	-	-	-	-	-
A2964	GO:0006520(cellular amino acid metabolic process),GO:0009097(isoleucine biosynthetic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0004794(L-threonine ammonia-lyase activity)	K01754 E4.3.1.19, ilvA, tdcB; threonine dehydratase [EC:4.3.1.19]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways	-	ORY42543.1 threonine ammonia-lyase [Rhizoclostium globosum]	L-threonine dehydratase biosynthetic IlvA OS=Burkholderia multivorans (strain ATCC 17616 / 249) OX=395019 GN=ilvA PE=3 SV=1
A2965	GO:0000079(regulation of cyclin-dependent protein serine/threonine kinase activity)	-	GO:0019901(protein kinase binding)	-	-	KOG1674 At2g44740 Cyclin	ORX46575.1 cyclin-domain-containing protein [Hesseltinella vesiculosa]	Cyclin-U4-1 OS=Arabidopsis thaliana OX=3702 GN=CYCU4-1 PE=1 SV=1
A2966	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0051082(unfolded protein binding)	K09498 CCT6; T-complex protein 1 subunit zeta	-	KOG0359 Hs4502643 Chaperonin complex component, TCP-1 zeta subunit (CCT6)	KAG4107596.1 T-complex protein 1 zeta subunit [Neocallimastix sp. JGI-2020a]	T-complex protein 1 subunit zeta OS=Mus musculus OX=10090 GN=Cct6a PE=1 SV=3

A2967	-	-	-	-	-	-	TPX55401.1 hypothetical protein PhCBS80983.g05341 [Powellomyces hirtus]	-
A2968	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1198[Hs4758912 Zinc-binding oxidoreductase	TPX59572.1 hypothetical protein SpCBS45565.g07696 [Spizellomyces sp. 'palustris']	Quinone oxidoreductase PIG3 OS=Homo sapiens OX=9606 GN=TP5313 PE=1 SV=2
A2969	-	-	GO:0008641(ubiquitin-like modifier activating enzyme activity)	-	-	KOG2336[Hs13376212 Molybdopterin biosynthesis-related protein	KFX51507.1 Ubiquitin-activating enzyme E1-like, partial [Talaromyces marneffei PM1]	Ubiquitin-like modifier-activating enzyme 5 OS=Xenopus laevis OX=8355 GN=uba5 PE=2 SV=1
A2971	-	-	-	-	-	-	-	-
A2972	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K02213 CDC6; cell division control protein 6	map05207 Chemical carcinogenesis - receptor activation;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG2227[At1g07270 Pre-initiation complex, subunit CDC6, AAA+ superfamily ATPase	KAG0327949, 1 AAA ATPase [Podila humilis]	Cell division control protein 6 homolog OS=Mus musculus OX=10090 GN=Cdc6 PE=1 SV=2
A2973	GO:0006886(intracellular protein transport)	GO:0005783(endoplasmic reticulum),GO:0016021(integral component of membrane)	-	-	-	-	-	-
A2974	-	-	-	-	-	-	-	-
A2975	-	-	-	-	-	-	-	-
A2976	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	-	-	KOG0256[At2g22810 1-aminocyclopropane-1-carboxylate synthase, and related proteins	KAG4100947, 1 pyridoxal phosphate-dependent transferase [Neocallimastix sp. JGI-2020a]	1-aminocyclopropane-1-carboxylate synthase 4 OS=Arabidopsis thaliana OX=3702 GN=ACS4 PE=1 SV=1
A2977	-	-	GO:0046983(protein dimerization activity)	-	-	-	-	-

A2978	GO:0019427(acetyl-CoA biosynthetic process from acetate)	-	GO:0003987(acetate-CoA ligase activity),GO:0016208(AMP binding)	K01895 ACSS1.2, acs; acetyl-CoA synthetase [EC:6.2.1.1]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00720 Carbon fixation pathways in prokaryotes;map00680 Methane metabolism;map00620 Pyruvate metabolism;map01100 Metabolic pathways;map00630 Glyoxylate and dicarboxylate	KOG1175 YLR153c Acyl-CoA synthetase	RIA95660.1 hypothetical protein C1645_816355 [Glomus cerebriforme]	Acetyl-coenzyme A synthetase OS=Alkaliimnicola ehrlichii (strain ATCC BAA-1101 / DSM 17681 / MLHE-1) OX=187272 GN=acsA PE=3 SV=1
A2979	GO:0006367(transcription initiation from RNA polymerase II promoter)	GO:0005673(transcription factor TFIIIE complex)	-	-	-	-	-	-
A2980	GO:0006303(double-strand break repair via nonhomologous end joining)	GO:0005634(nucleus)	GO:0005515(protein binding)	K07203 MTOR, FRAP, TOR; serine/threonine-protein kinase mTOR [EC:2.7.11.1]	map04361 Axon regeneration;map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map04140 Autophagy - animal;map05131 Shigellosis;map04211 Longevity regulating pathway;map04212 Longevity regulating pathway - worm;map04213 Longevity regulating pathway - multiple species;map04218 Cellular senescence;map04072 Phospholipase D signaling	KOG0891 Hs13654237 DNA-dependent protein kinase	RUS22723.1 hypothetical protein BC937DRAFT_87605 [Endogone sp. FLAS-F59071]	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens OX=9606 GN=PRKDC PE=1 SV=3
A2981	GO:0051252(regulation of RNA metabolic process)	-	GO:0008428(ribonuclease inhibitor activity)	-	-	-	KGQ11057.1 Regulator of ribonuclease activity A [Beauveria bassiana D1-5]	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) OX=322710 GN=Avin_23290 PE=3 SV=1
A2982	-	-	GO:0016757(glycosyltransferase activity)	-	-	KOG1950 At1g60450 Glycosyl transferase, family 8 - glycogenin	RSH88874.1 hypothetical protein EHS25_002536 [Saitozyma podzolica]	Galactinol synthase 7 OS=Arabidopsis thaliana OX=3702 GN=GOLS7 PE=2 SV=1
A2983	-	-	-	-	-	-	-	-
A2984	-	-	-	-	-	-	-	-

A2985	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K07937 ARF1_2; ADP-ribosylation factor 1/2	map04144 Endocytosis;map05134 Legionellosis;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04072 Phospholipase D signaling pathway;map05110 Vibrio cholerae infection	KOG0070 Hs14149815 GTP-binding ADP-ribosylation factor Arf1	XP_006682559.1 uncharacterized protein BATDEDRAFT_14608 [Batrachochytrium dendrobatidis JAM81]	ADP-ribosylation factor-like protein 6 OS=Mus musculus OX=10090 GN=Arl6 PE=1 SV=1
A2986	GO:003042(actin filament depolymerization)	GO:0015629(actin cytoskeleton)	GO:0003779(actin binding)	K05765 CFL; cofilin	map04360 Axon guidance;map05133 Pertussis;map04810 Regulation of actin cytoskeleton;map05170 Human immunodeficiency virus 1 infection;map04666 Fc gamma R-mediated phagocytosis	-	XP_031013529.1 uncharacterized protein FIESC28_08236 [Fusarium coffeatum]	Actophorin OS=Acanthamoeba castellanii OX=5755 PE=1 SV=2
A2987	-	-	-	K09518 DNAJB12; DnaJ homolog subfamily B member 12	map04141 Protein processing in endoplasmic reticulum	KOG0714 Hs8923030 Molecular chaperone (DnaJ superfamily)	KAG4102661.1 DnaJ-domain-containing protein [Neocallimastix sp. JGI-2020a]	DnaJ homolog subfamily B member 12 OS=Bos taurus OX=9913 GN=DNAJB12 PE=2 SV=1
A2988	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	GO:0016746(acyltransferase activity)	-	-	-	RKP21311.1 adenylyl cyclase, partial [Rozella allomycis CSF55]	Adenylate cyclase type 10 OS=Rattus norvegicus OX=10116 GN=Adcy10 PE=1 SV=1
A2989	-	GO:0005634(nucleus)	-	K13119 FAM50, XAP5; protein FAM50	-	KOG2894 Hs6912326 Uncharacterized conserved protein XAP-5	KAF9646374.1 XAP5-domain-containing protein [Thelephora ganbajun]	Protein XAP5 CIRCADIAN TIMEKEEPER OS=Oryza sativa subsp. indica OX=39946 GN=XCT PE=3 SV=1
A2990	-	-	-	-	-	-	-	-
A2991	-	-	-	-	-	-	-	-
A2992	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	-	-	KOG0244 At5g47820 Kinesin-like protein	KAF9294989.1 Kinesin-like protein kif21b, partial [Linnemannia elongata]	Kinesin-like protein KIN-4A OS=Gossypium hirsutum OX=3635 GN=KIN4A PE=2 SV=1
A2993	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-

A2994	-	-	GO:0003756(protein disulfide isomerase activity)	K13996 EPS1; protein disulfide-isomerase [EC:5.3.4.1]	map04141 Protein processing in endoplasmic reticulum	KOG0191 7301255 Thioredoxin/protein disulfide isomerase	KAG2195285.1 hypothetical protein INT47_005060 [Mucor saturninus]	Thioredoxin domain-containing protein OS=Theileria parva OX=5875 GN=TP02_0602 PE=1 SV=1
A2995	-	-	GO:0016746(acyltransferase activity)	K00624 E2.3.1.7; carnitine O-acetyltransferase [EC:2.3.1.7]	map04146 Peroxisome	KOG3719 YAR035w Carnitine O-acetyltransferase CPT2/YAT1	ORY95364.1 acyltransferase ChoActase/COT/CPT [Syncephalaster racemosum]	Putative mitochondrial carnitine O-acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YAT1 PE=1 SV=2
A2996	-	-	GO:0051015(actin filament binding)	-	-	KOG1700 At3g55770 Regulatory protein MLP and related LIM proteins	XP_031027538.1 uncharacterized protein SmJEL517_g00699 [Synchytrium microbalum]	LIM domain-containing protein WLIM2b OS=Arabidopsis thaliana OX=3702 GN=WLIM2B PE=1 SV=1
A2997	-	-	GO:0003723(RNA binding);GO:0003676(nucleic acid binding)	K14838 NOP15; nucleolar protein 15	-	KOG4208 At5g04600 Nucleolar RNA-binding protein NIFK	XP_018297549.1 hypothetical protein PHYBLDRAFT_14704, partial [Phycomyces blakesleeanus NRRL 1555(-)]	MKI67 FHA domain-interacting nucleolar phosphoprotein-like OS=Xenopus tropicalis OX=8364 GN=nifk PE=2 SV=1
A2998	-	-	-	K20360 TBC1D22, GYP1; TBC1 domain family member 2	-	KOG1092 Hs18594431 Ypt/Rab-specific GTPase-activating protein GYP1	KAG2185054.1 hypothetical protein INT43_000967, partial [Umbelopsis isabellina]	TBC1 domain family member 22A OS=Homo sapiens OX=9606 GN=TBC1D22A PE=1 SV=2
A2999	GO:0006097(glyoxylate cycle)	-	GO:0004474(malate synthase activity);GO:0003824(catalytic activity)	K01638 aceB; glcB; malate synthase [EC:2.3.3.9]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00620 Pyruvate metabolism;map01100 Metabolic pathways;map00630 Glyoxylate and dicarboxylate metabolism	-	XP_006683310.1 uncharacterized protein BATDEDRAFT_93074 [Batrachochytrium dendrobatidis JAM81]	Malate synthase G OS=Agrobacterium fabrum (strain C58 / ATCC 33970) OX=176299 GN=glcB PE=3 SV=2

A3000	-	-	GO:0003924(GTPase activity);GO:0005525(GTP binding)	K07889 RAB5C; Ras-related protein Rab-5C	map04144 Endocytosis;map04145 Phagosome;map05132 Salmonella infection;map05146 Amoebiasis;map04014 Ras signaling pathway;map05152 Tuberculosis;map04962 Vasopressin-regulated water reabsorption	KOG0092 7295967 GTPase Rab5/YPT51 and related small G protein superfamily GTPases	ABS00941.1 GTP-binding protein RAB5 [Lentiniula edodes]	Ras-related protein RABF1 OS=Arabidopsis thaliana OX=3702 GN=RABF1 PE=1 SV=1
A3001	-	-	GO:0016787(hydrolase activity)	K03574 mutT, NUDT15, MTH2; 8-oxo-dGTP diphosphatase [EC:3.6.1.55]	-	KOG0648 At5g47240 Predicted NUDIX hydrolase FGF-2 and related proteins	OTA06785.1 hypothetical protein A9Z42_0075610 [Trichoderma parareesei]	Nudix hydrolase 8 OS=Arabidopsis thaliana OX=3702 GN=NUDT8 PE=2 SV=2
A3002	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K12761 SNF1; carbon catabolite-derepressing protein kinase [EC:2.7.11.1]	map04138 Autophagy - yeast;map04113 Meiosis - yeast	KOG0583 At2g26980 Serine/threonine protein kinase	ODV90381.1 hypothetical protein CANCADRAFT_24132 [Tortispora caseinolytica NRRL Y-17796]	CBL-interacting protein kinase 23 OS=Oryza sativa subsp. japonica OX=39947 GN=CIPK23 PE=2 SV=1
A3003	GO:0015743(malate transport)	-	-	-	-	-	-	-
A3004	GO:0000103(sulfate assimilation);GO:007034(vacuolar transport)	-	GO:0004781(sulfate adenyllyltransferase (ATP) activity)	K00958 sat, met3; sulfate adenyllyltransferase [EC:2.7.7.4]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map00261 Monobactam biosynthesis;map00920 Sulfur metabolism;map01100 Metabolic pathways;map00450 Selenocompound metabolism	KOG0636 YJR010w ATP sulfurylase (sulfate adenyllyltransferase)	GBB83334.1 hypothetical protein RclHR1_10060007 [Rhizophagus clarus]	Sulfate adenyllyltransferase OS=Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) OX=321614 GN=MET3 PE=3 SV=1
A3005	GO:0015689(molybdate ion transport)	GO:0016021(integral component of membrane)	GO:0015098(molybdate ion transmembrane transporter activity)	K24175 MFSD5; MFS transporter, MFS domain-containing protein family, molybdate-anion transporter	-	KOG4332 At1g64650 Predicted sugar transporter	TPX62511.1 hypothetical protein PhCBS80983g00239 [Powellomyces hirtus]	Molybdate-anion transporter OS=Mus musculus OX=10090 GN=Mfsd5 PE=2 SV=1
A3006	-	-	-	-	-	-	-	-

A3007	-	-	-	-	-	-	TPX57151.1 hypothetical protein PhCBS80983. g04032 [Powellomyces hirtus]	Coiled-coil domain-containing protein 42 homolog OS=Nematostella vectensis OX=45351 GN=v1g187067 PE=3 SV=1
A3008	-	-	-	-	-	-	KAF9118842. 1 hypothetical protein BGX30_004263, partial [Mortierella sp. GBA39]	Putative nickel insertion protein OS=Roseiflexus castenholzii (strain DSM 13941 / HLO8) OX=383372 GN=Rcas_1165 PE=3 SV=1
A3009	GO:0006520(cellular amino acid metabolic process)	-	GO:0016491(oxidoreductase activity)	K15371 GDH2; glutamate dehydrogenase [EC:1.4.1.2]	map00910 Nitrogen metabolism;map01120 Microbial metabolism in diverse environments;map00250 Alanine, aspartate and glutamate metabolism;map00430 Taurine and hypotaurine metabolism;map00220 Arginine biosynthesis;map01100 Metabolic pathways	KOG2250 YDL215c Glutamate/leucine/phenylalanine/valine dehydrogenases	XP_007729983.1 NAD-specific glutamate dehydrogenase [Capronia epimyces CBS 606.96]	Glutamate dehydrogenase 2 OS=Dictyostelium discoideum OX=44689 GN=glud2 PE=1 SV=2
A3010	-	-	GO:0046983(protein dimerization activity)	-	-	-	-	-
A3011	GO:0019243(methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione)	-	GO:0004416(hydroxyacylglutathione hydrolase activity)	K01069 gloB, gloC, HAGH; hydroxyacylglutathione hydrolase [EC:3.1.2.6]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG0813 At3g10850 Glyoxylase	RUS17088.1 beta-lactamase-like protein [Endogone sp. FLAS-F59071]	Hydroxyacylglutathione hydrolase cytoplasmic OS=Arabidopsis thaliana OX=3702 GN=GLX2-2 PE=1 SV=2
A3012	GO:0036211(protein modification process)	-	GO:0004719(protein-L-isoaspartate (D-aspartate) O-methyltransferase activity)	K00573 E2.1.1.77, pcm; protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77]	-	KOG1661 Hs4885539 Protein-L-isoaspartate(D-aspartate) O-methyltransferase	OTB12485.1 hypothetical protein K445DRAFT_66122 [Daldinia sp. EC12]	Protein-L-isoaspartate O-methyltransferase 1 OS=Arabidopsis thaliana OX=3702 GN=PIMT1 PE=1 SV=3
A3013	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity);GO:0004965(G protein-coupled GABA receptor activity)	-	-	-	TPX54710.1 hypothetical protein PhCBS80983. g05811 [Powellomyces hirtus]	Metabotropic glutamate receptor-like protein F OS=Dictyostelium discoideum OX=44689 GN=grIF PE=2 SV=1
A3014	GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0031625(ubiquitin protein ligase binding)	-	-	KOG2166 At1g43140 Cullins	OON05698.1 hypothetical protein BSLG_04477 [Batrachochytrium salamandrivorans]	Cullin-1 OS=Arabidopsis thaliana OX=3702 GN=CUL1 PE=1 SV=1

A3015	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	KOG1023 7293749 Natriuretic peptide receptor, guanylate cyclase	EPZ34615.1 Adenylyl cyclase class-3/4/guanylyl cyclase domain-containing protein, partial [Rozella allomycis CSF55]	Adenylate cyclase 1 OS=Rhizobium meliloti (strain 1021) OX=266834 GN=cya1 PE=3 SV=2
A3016	-	-	GO:0051879(Hsp90 protein binding),GO:0005515(protein binding)	-	-	KOG0551 Hs14729151 Hsp90 co-chaperone CNS1 (contains TPR repeats)	TPX72699.1 hypothetical protein SpCBS45565_g00019 [Spizellomyces sp. 'palustris']	Tetratricopeptide repeat protein 4 homolog OS=Dictyostelium discoideum OX=44689 GN=ttc4 PE=3 SV=1
A3017	-	-	-	-	-	-	KAG0357396.1 hypothetical protein BG005_003594 [Podila minutissima]	-
A3018	-	-	-	-	-	-	-	-
A3019	-	-	-	-	-	-	-	-
A3020	GO:0002098(tRNA wobble uridine modification)	-	GO:0043828(tRNA 2-selenouridine synthase activity)	-	-	-	KAG1716250.1 hypothetical protein ID866_908 [Astraeus odoratus]	tRNA 2-selenouridine synthase OS=Cupriavidus taiwanensis (strain DSM 17343 / BCRC 17206 / CCUG 44338 / CIP 107171 / LMG 19424 / R1) OX=977880 GN=selu PE=3 SV=1
A3021	GO:0070940(dephosphorylation of RNA polymerase II C-terminal domain)	GO:0005634(nucleus)	GO:0008420(RNA polymerase II CTD heptapeptide repeat phosphatase activity),GO:0004721(phosphoprotein phosphatase activity)	K15732 CTDPI, FCP1; RNA polymerase II subunit A C-terminal domain phosphatase [EC:3.1.3.16]	-	-	EPB87679.1 hypothetical protein HMPREF1544_05562, partial [Mucor circinelloides 1006PhL]	RNA polymerase II subunit A C-terminal domain phosphatase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=fcp1 PE=1 SV=1
A3022	-	-	-	-	-	-	KAG1445995.1 hypothetical protein G6F57_017434 [Rhizopus oryzae]	CBS domain-containing protein CBSX3, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=CBSX3 PE=1 SV=1
A3023	-	-	GO:0005515(protein binding),GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG2080 Hs20558056 Uncharacterized conserved protein, contains DENN and RUN domains	OON10322.1 hypothetical protein BSLG_00838 [Batrachochytrium salamandrivorans]	C-myc promoter-binding protein OS=Homo sapiens OX=9606 GN=DENND4A PE=1 SV=2
A3024	GO:0042254(ribosome biogenesis)	-	-	K02941 RP-LP0, RPLP0; large subunit ribosomal protein LP0	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0815 Hs4506667 60S acidic ribosomal protein P0	ORX87912.1 hypothetical protein BCR32DRAFT_324251 [Anaeromyces robustus]	Large ribosomal subunit protein uL10 OS=Lithobates sylvaticus OX=45438 GN=RPLP0 PE=2 SV=1
A3025	-	-	-	-	-	KOG4356 7304153 Uncharacterized conserved protein	ORX58615.1 PIH1-domain-containing protein [Piromyces finnis]	Protein kintoun OS=Anopheles gambiae OX=7165 GN=AGAP005250 PE=3 SV=4
A3026	-	-	-	-	-	-	-	-
A3027	-	-	-	-	-	-	-	-

A3028	-	-	GO:0005509(cal cium ion binding)	-	-	-	-	-
A3029	-	-	-	-	-	KOG2502 At1 g25280 Tub family proteins	RUS19378.1 tubby C- terminal-like domain- containing protein [Endogone sp. FLAS- F59071]	Tubby-like F-box protein 13 OS=Oryza sativa subsp. japonica OX=39947 GN=TULP13 PE=2 SV=1
A3030	GO:00064 06(mRNA export from nucleus)	-	GO:0005515(pro tein binding)	K12880 THOC3; THO complex subunit 3	map03040 Spliceosome;ma p03013 Nucleocytoplas mic transport	KOG1407 At5 g56130 WD40 repeat protein	ORX51467.1 WD40 repeat-like protein [Piromyces finnis]	THO complex subunit 3 OS=Arabidopsis thaliana OX=3702 GN=THO3 PE=1 SV=1
A3031	-	-	GO:0003924(GT Pase activity),GO:000 5525(GTP binding)	-	-	KOG2037 Hs1 4735497 Guanylate- binding protein	KNE64433.1 hypothetical protein AMAG_09455 [Allomyces macrogynus ATCC 38327]	Guanylate-binding protein 1 OS=Chlorocebus aethiops OX=9534 GN=GBP1 PE=2 SV=1
A3032	GO:00002 26(microt ubule cytoskelet on organizati on),GO:00 07020(mic rotubule nucleatio n)	GO:00009 22(spindle pole),GO: 0005815(m icrotubule organizin g center)	GO:0043015(ga mma-tubulin binding)	-	-	KOG4344 Hs1 6161844 Uncharacteriz ed conserved protein	CCO28449.1 Spindle pole body component alp6 AltName: Full=Altered polarity protein 6 [Rhizoctonia solani AG-1 IB]	Gamma-tubulin complex component 5 (Fragment) OS=Macaca fascicularis OX=9541 GN=TUBGCP5 PE=2 SV=2
A3033	-	-	-	-	-	KOG1726 729 1641 HVA22/DP1 gene product- related proteins	-	-
A3034	-	-	-	-	-	-	-	-
A3035	GO:00064 14(transla tional elongatio n)	-	GO:0003746(tran slation elongation factor activity),GO:000 5515(protein binding)	K02357 tsf, TSFM; elongation factor Ts	-	KOG1071 At4 g11120 Mitochondria l translation elongation factor EF- Tsmt, catalyzes nucleotide exchange on EF-Tumt	KAG0771903. 1 hypothetical protein G6F22_01611 1 [Rhizopus oryzae]	Elongation factor Ts OS=Rhodospirillum centenum (strain ATCC 51521 / SW) OX=414684 GN=tsf PE=3 SV=1
A3036	-	-	-	K15559 RTT103; regulator of Ty1 transposition protein 103	-	KOG2669 At3 g26990 Regulator of nuclear mRNA	RLV86384.1 hypothetical protein JA9_004391 [Meyerozyma sp. JA9]	CID domain-containing protein 1 OS=Caenorhabditis elegans OX=6239 GN=cids-1 PE=4 SV=2
A3037	-	-	-	-	-	-	-	-
A3038	-	-	-	K09008 NDUFAF3; NADH dehydrogena se [ubiquinone] 1 alpha subcomplex assembly factor 3	map04714 Thermogenesis	KOG3363 CE 12554 Uncharacteriz ed conserved nuclear protein	RPD66840.1 DUF498- domain- containing protein [Lentinus tigrinus ALCF2SS1-6]	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Rattus norvegicus OX=10116 GN=Ndufaf3 PE=2 SV=1

A3039	-	-	GO:0003824(catalytic activity),GO:0016833(oxo-acid-lyase activity)	K01640 HMGCL, hmgL; hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]	map04146 Peroxisome;map00907 Pinene, camphor and geraniol degradation;map01120 Microbial metabolism in diverse environments;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map01100 Metabolic pathways	KOG2368 Hs4504427 Hydroxymethylglutaryl-CoA lyase	KNZ51084.1 hypothetical protein VP01_40g8 [Puccinia sorghi]	3-hydroxy-3-methylglutaryl-CoA lyase, cytoplasmic OS=Danio rerio OX=7955 GN=hmgcl1 PE=2 SV=1
A3040	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02906 RP-L3, MRPL3, rplC; large subunit ribosomal protein L3	map03010 Ribosome	KOG3141 At3g17465 Mitochondria l/chloroplast ribosomal protein L3	XP_021885591.1 translation protein [Lobosporangium transversale]	Large ribosomal subunit protein uL3m OS=Arabidopsis thaliana OX=3702 GN=RPL3B PE=1 SV=1
A3041	GO:0006511(ubiquitin-dependent protein catabolic process)	-	-	-	-	KOG1816 At2g21270 Ubiquitin fusion-degradation protein	KFX42033.1 Ubiquitin fusion degradation protein 1 [Talaromyces marneffei PM1]	Ubiquitin recognition factor in ER-associated degradation protein 1 OS=Homo sapiens OX=9606 GN=UFD1 PE=1 SV=3
A3042	GO:0006508(proteolysis)	-	GO:0008233(peptidase activity)	-	-	-	XP_033568736.1 M6 metalloprotease [Mytilinidion resinicola]	-
A3043	-	-	-	K26066 XYRB; D-xylose/L-arabinose reductase (NADPH) [EC:1.1.1.431 1.1.1.-]	map00040 Pentose and glucuronate interconversions	KOG1201 CE28011 Hydroxysteroid 17-beta dehydrogenase 11	KXH33648.1 short chain dehydrogenase [Colletotrichum simmondsii]	Putative oxidoreductase SadH OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=sadH PE=3 SV=1
A3044	-	-	-	-	-	KOG1201 Hs20373187 Hydroxysteroid 17-beta dehydrogenase 11	KAF1988495.1 NAD(P)-binding protein [Aulographum hederarum CBS 113979]	Putative oxidoreductase SadH OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=sadH PE=3 SV=1
A3045	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3046	-	-	-	-	-	-	-	-
A3047	-	GO:0016021(integral component of membrane)	-	-	-	KOG2568 At1g72480 Predicted membrane protein	KAF9911269.1 hypothetical protein EC991_004167 [Linnemannia zychae]	Transmembrane protein 87B OS=Mus musculus OX=10090 GN=Tmem87b PE=2 SV=1

A3048	-	-	-	K17260 ACTR2, ARP2; actin-related protein 2	map04144 Endocytosis;map 05135 Yersinia infection;map05 132 Salmonella infection;map05 130 Pathogenic Escherichia coli infection;map05 131 Shigellosis;map0 4810 Regulation of actin cytoskeleton;ma p04138 Autophagy - yeast;map05100 Bacterial invasion of epithelial cells;map04666 Fc gamma R- mediated phagocytosis;ma p04530 Tight junction	KOG0677[Hs5 031571 Actin-related protein Arp2/3 complex, subunit Arp2	XP_01829273 7.1 hypothetical protein PHYBLDRAFT _180921 [Phycomyces blakesleeanu s NRRL 1555(-)]	Actin-related protein 2 OS=Gallus gallus OX=9031 GN=ACTR2 PE=2 SV=1
A3049	-	-	-	-	-	-	-	-
A3050	-	-	-	-	-	-	-	-
A3051	-	-	-	-	-	-	-	-
A3052	-	-	-	-	-	-	RIB12910.1 BRO1 domain- containing protein [Gigaspora rosea]	-
A3053	-	-	-	-	-	-	-	-
A3054	-	-	-	-	-	-	-	-
A3055	-	-	GO:0035091(ph osphatidylinosit ol binding)	-	-	-	-	-
A3056	-	-	-	-	-	-	-	-
A3057	GO:00322 59(methyl ation)	-	GO:0008168(me thyltransferase activity),GO:000 3676(nucleic acid binding)	K15430 TRMT11; tRNA (guanine10- N2)- methyltransfe rase [EC:2.1.1.214]	-	KOG2671[At3 g26410 Putative RNA methylase	RIB14870.1 S-adenosyl- L- methionine- dependent methyltransfe rase [Gigaspora rosea]	tRNA (guanine(10)-N2)-methyltransferase homolog OS=Homo sapiens OX=9606 GN=TRMT11 PE=1 SV=1
A3058	-	-	GO:0050660(flav in adenine dinucleotide binding),GO:001 6614(oxidoredu ctase activity, acting on CH- OH group of donors)	-	-	KOG1238[729 3012 Glucose dehydrogena se/choline dehydrogena se/mandelon trile lyase (GMC oxidoreducta se family)	XP_01661142 4.1 hypothetical protein SPPG_00874 [Spizellomyce s punctatus DAOM BR117]	L-sorbose 1-dehydrogenase OS=Gluconobacter oxydans OX=442 PE=3 SV=1
A3059	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding),GO:000 5515(protein binding)	K08286 E2.7.11.-; protein- serine/threon ine kinase [EC:2.7.11.-]	-	KOG0601[CE 14884_1 Cyclin- dependent kinase WEE1	OJT05228.1 MAP kinase kinase kinase mkh1 [Trametes pubescens]	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase wee-1.3 OS=Caenorhabditis elegans OX=6239 GN=wee-1.3 PE=1 SV=1
A3060	GO:00067 96(phosp hate- containin g compoun d metaboli c process)	GO:00057 37(cytopl asm)	GO:0000287(ma gnesium ion binding),GO:000 4427(inorganic diphosphatase activity)	-	-	KOG1626[At1 g01050 Inorganic pyrophospha tase/Nucleos ome remodeling factor, subunit NURF38	KAG1538272. 1 hypothetical protein G6F50_01469 5 [Rhizopus delemar]	Inorganic pyrophosphatase OS=Saccharolobus solfataricus (strain ATCC 35092 / DSM 1617 / JCM 11322 / P2) OX=273057 GN=ppa PE=3 SV=1

A3061	-	-	GO:0050660(flavin adenine dinucleotide binding),GO:0016614(oxidoreductase activity, acting on CH-OH group of donors)	-	-	KOG1238 Z93019 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	XP_016611424.1 hypothetical protein SPPG_00874 [Spizellomyces punctatus DAOM BR117]	L-sorbose 1-dehydrogenase OS=Gluconobacter oxydans OX=442 PE=3 SV=1
A3062	GO:0018343(protein farnesylation)	GO:0005965(protein farnesyltransferase complex)	GO:0008318(protein prenyltransferase activity),GO:0003824(catalytic activity)	K05954 FNTB; protein farnesyltransferase subunit beta [EC:2.5.1.58]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis	KOG0365 Hs10835059 Beta subunit of farnesyltransferase	TPX55794.1 protein farnesyltransferase [Powellomyces hirtus]	Protein farnesyltransferase subunit beta OS=Mus musculus OX=10090 GN=Fntb PE=1 SV=1
A3063	-	-	GO:0003824(catalytic activity),GO:0016803(ether hydrolase activity)	-	-	KOG2565 Hs4503583 Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	XP_031023986.1 microsomal epoxide hydrolase [Synchytrium microbalum]	Putative epoxide hydrolase OS=Stigmatella aurantiaca (strain DW4/3-1) OX=378806 GN=STAU_R_4299 PE=3 SV=2
A3064	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	-	-	KOG2037 At5g46070 Guanylate-binding protein	KNE64433.1 hypothetical protein AMAG_09455 [Allomyces macrogynus ATCC 38327]	Guanylate-binding protein 1 OS=Mus musculus OX=10090 GN=Gbp1 PE=1 SV=1
A3065	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0051082(unfolded protein binding)	K04079 HSP90A, htpG; molecular chaperone HtpG	map05417 Lipid and atherosclerosis; map04141 Protein processing in endoplasmic reticulum;map05132 Salmonella infection;map04217 Necroptosis;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05418 Fluid shear stress and atherosclerosis; map04657 IL-17 signaling pathway;map04659 Th17 cell differentiation;map05215 Prostate cancer;map0461	KOG0019 7302271 Molecular chaperone (HSP90 family)	KAF8933368.1 TNF receptor-associated protein 1, mitochondrial [Dissophora ornata]	TNF receptor-associated protein 1 homolog, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=trap1 PE=2 SV=1
A3066	-	-	-	-	-	-	-	-
A3067	-	-	GO:0008168(methyltransferase activity)	-	-	-	PBK99471.1 UbiE family methyltransferase [Armillaria gallica]	Uncharacterized methyltransferase C1B3.06c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC1B3.06c PE=3 SV=1
A3068	GO:0016036(cellular response to phosphate starvation)	-	-	K06653 PHO81; CDK inhibitor PHO81	map04111 Cell cycle - yeast	KOG1161 At2g26660 Protein involved in vacuolar polyphosphate accumulation, contains SPX domain	XP_024664010.1 Ankyrin repeat protein nuc-2 [Wickerhamia sorbophila]	SPX domain-containing protein 2 OS=Arabidopsis thaliana OX=3702 GN=SPX2 PE=2 SV=1

A3069	GO:0000398(mRNA splicing, via spliceosome)	GO:0046540(U4/U6 x U5 tri-snRNP complex)	-	K12843 PRPF3, PRP3; U4/U6 small nuclear ribonucleoprotein PRP3	map03040 Spliceosome	KOG2769 7293728 Putative u4/u6 small nuclear ribonucleoprotein	XP_02346784.4.1 Pre-mRNA-splicing factor 3, partial [Rhizopus microsporus ATCC 52813]	U4/U6 small nuclear ribonucleoprotein Prp3 OS=Gallus gallus OX=9031 GN=PRPF3 PE=2 SV=1
A3070	-	-	-	K14347 SLC10A7, P7; solute carrier family 10 (sodium/bile acid cotransporter), member 7	-	KOG4821 At3g56160 Predicted Na+-dependent cotransporter	EPB86687.1 hypothetical protein HMPREF1544_06473 [Mucor circinelloides 1006PhL]	Probable sodium/metabolite cotransporter BASS4, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=BASS4 PE=3 SV=1
A3071	-	-	GO:0005515(protein binding)	-	-	KOG2699 Hs13376854 Predicted ubiquitin regulatory protein	ORY04516.1 hypothetical protein K493DRAFT_311361 [Basidiobolus meristosporus CBS 931.73]	UBX domain-containing protein 6 OS=Mus musculus OX=10090 GN=Ubx6 PE=1 SV=1
A3072	-	GO:0005739(mitochondrion)	-	K03963 NDUFB7; NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 7	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG3468 At2g02050 NADH:ubiquinone oxidoreductase, NDUFB7/B18 subunit	KFH46633.1 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit-like protein [Acremonium chrysogenum ATCC 11550]	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Dictyostelium discoideum OX=44689 GN=ndufb7 PE=3 SV=1
A3073	GO:0055085(transmembrane transport)	-	-	K14684 SLC25A23S; solute carrier family 25 (mitochondrial phosphate transporter), member 23/24/25/41	-	KOG0752 At4g01100 Mitochondrial solute carrier protein	KAG4305782.1 hypothetical protein PORY_000692 [Pneumocystis oryctolagi]	ADP/ATP translocase 4 OS=Bos taurus OX=9913 GN=SLC25A31 PE=2 SV=1
A3074	-	-	-	-	-	-	-	-
A3075	-	-	-	-	-	-	-	-
A3076	GO:0006357(regulation of transcription by RNA polymerase II)	GO:0016592(mediator complex)	GO:0003712(transcription coregulator activity)	K15128 MED6; mediator of RNA polymerase II transcription subunit 6	-	KOG3169 Hs4885481 RNA polymerase II transcriptional regulation mediator	KAF9110096.1 Mediator of RNA polymerase II transcription subunit 6 [Mortierella sp. AM989]	Mediator of RNA polymerase II transcription subunit 6 OS=Bos taurus OX=9913 GN=MED6 PE=2 SV=1

A3077	-	-	GO:0003677(DNA binding),GO:0004518(nuclease activity)	K10848 ERCC4, XPF; DNA excision repair protein ERCC-4 [EC:3.1.-.-]	map03420 Nucleotide excision repair;map03460 Fanconi anemia pathway	KOG0442 Hs4885217 Structure-specific endonuclease ERCC1-XPF, catalytic component XPF/ERCC4	KAF9327086.1 hypothetical protein BG006_009579 [Podila minutissima]	DNA repair endonuclease XPF OS=Cricetulus griseus OX=10029 GN=ERCC4 PE=2 SV=3
A3078	-	-	GO:0043130(ubiquitin binding),GO:0005515(protein binding)	-	-	-	KAG2214411.1 hypothetical protein INT47_000967 [Mucor saturninus]	-
A3079	GO:0006508(proteolysis)	-	GO:0004222(metalloendopeptidase activity),GO:0008237(metalloproteinase activity)	K01410 MIPEP; mitochondria l intermediate peptidase [EC:3.4.24.59]	-	KOG2090 At5g51540 Metalloendopeptidase family - mitochondria l intermediate peptidase	ORY05442.1 zincin [Basidiobolus meristosporus CBS 931.73]	Mitochondrial intermediate peptidase, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=OCT1 PE=3 SV=1
A3080	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0725 At3g51680 Reductases with broad range of substrate specificities	KAF5343924.1 hypothetical protein D9758_012122 [Tetrapyrgos nigripes]	Levodione reductase OS=Leifsonia aquatica OX=144185 GN=lvr PE=1 SV=1
A3081	-	-	-	-	-	-	-	-
A3082	-	-	-	-	-	KOG2743 At1g15730 Cobalamin synthesis protein	KAG1467349.1 hypothetical protein G6F57_013057 [Rhizopus oryzae]	Zinc chaperone YciC OS=Bacillus subtilis (strain 168) OX=224308 GN=yciC PE=2 SV=1
A3083	-	-	-	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1235 At5g24810 Predicted unusual protein kinase	ORY42369.1 ABC1-domain-containing protein [Rhizoclosmatium globosum]	Protein ACTIVITY OF BC1 COMPLEX KINASE 8, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ABC1K8 PE=2 SV=1
A3084	GO:0006520(cellular amino acid metabolic process)	-	GO:0003824(catalytic activity),GO:0016829(lyase activity)	-	-	KOG1368 At3g04520 Threonine aldolase	KAG0779781.1 hypothetical protein G6F22_010445 [Rhizopus oryzae]	Probable low-specificity L-threonine aldolase 2 OS=Arabidopsis thaliana OX=3702 GN=THA2 PE=1 SV=1
A3085	GO:0007165(signal transduction)	-	-	-	-	KOG0619 7300644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A3086	-	-	-	-	-	KOG0619 7300644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase roco5 OS=Dictyostelium discoideum OX=44689 GN=roco5 PE=3 SV=1
A3087	-	GO:0016459(myosin complex), GO:0005856(cytoskeleton)	GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At3g19960 Myosin class V heavy chain	XP_031027609.1 uncharacterized protein SmJEL517_g00731 [Synchytrium microbalum]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1

A3088	-	-	-	-	-	-	TPX46521.1 hypothetical protein SeLEV6574_g 03192 [Synchytrium endobioticu m]	Spindle assembly abnormal protein 6 homolog OS=Gallus gallus OX=9031 GN=SASS6 PE=2 SV=1
A3089	-	-	-	-	-	-	-	-
A3090	GO:00060 06(glucose metabolic process)	-	GO:0016620(oxi doreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor),GO:00 51287(NAD binding),GO:005 0661(NADP binding)	K00134 GAPDH, gapA; glyceraldehy de 3- phosphate dehydrogena se (phosphoryla ting) [EC:1.2.1.12]	map05415 Diabetic cardiomyopathy; map05132 Salmonella infection;map05 130 Pathogenic Escherichia coli infection;map01 110 Biosynthesis of secondary metabolites;map 01200 Carbon metabolism;map 00010 Glycolysis / Gluconeogenesi s;map01120 Microbial metabolism in diverse environments;m ap01230 Biosynthesis of amino acids;map00710 Carbon fixation in photosynthetic organisms;map0	-	XP_00217132 8.1 glyceraldehy de-3- phosphate dehydrogena se Tdh1 [Schizosacch aromyces japonicus yFS275]	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=tdh1 PE=1 SV=1
A3091	-	-	-	-	-	-	-	-
A3092	-	-	-	K14304 NUP85; nuclear pore complex protein Nup85	map05014 Amyotrophic lateral sclerosis;map030 13 Nucleocytoplas mic transport	KOG2271 730 2655 Nuclear pore complex component (sc Nup85)	RUP45641.1 hypothetical protein BC936DRAFT _147911 [Jimgerdema nnia flammicorona]	Nuclear pore complex protein Nup75 OS=Drosophila melanogaster OX=7227 GN=Nup75 PE=2 SV=1
A3093	GO:00033 41(cilium movement),GO:003 6158(outer dynein arm assembly)	GO:00059 29(cilium)	-	-	-	-	TPX58773.1 hypothetical protein SpCBS45565_ g07915 [Spizellomyces sp. 'palustris']	Outer dynein arm-docking complex subunit 3 OS=Mus musculus OX=10090 GN=ODAD3 PE=2 SV=2
A3094	-	GO:00056 34(nucleu s)	-	-	-	KOG3404 At4 g21110 G10 protein/predi cted nuclear transcription regulator	OMJ28544.1 Protein BUD31-like protein [Smittium culicis]	Protein BUD31 homolog 2 OS=Oryza sativa subsp. japonica OX=39947 GN=Os05g0446300 PE=2 SV=1
A3095	GO:00070 18(microt ubule- based movement)	-	GO:0003777(mi crotubule motor activity),GO:000 5524(ATP binding),GO:000 8017(microtubul e binding)	K10392 KIF1; kinesin family member 1	map04814 Motor proteins	KOG4280 Hs9 910266_1 Kinesin-like protein	PJF16795.1 Kinesin, motor region domain- containing protein, partial [Paramicrosp oridium saccamoebae]	Kinesin-like protein KIF15-B OS=Xenopus laevis OX=8355 GN=kif15-b PE=1 SV=1
A3096	GO:00481 93(Golgi vesicle transport)	GO:19900 71(TRAPP I protein complex)	-	K20307 TRAPPC10, TRS130; trafficking protein particle complex subunit 10	-	KOG1931 At5 g54440 Putative transmembra ne protein	KAF8503619. 1 trafficking protein particle complex subunit 10 [Russula emetica]	Trafficking protein particle complex subunit 10 OS=Dictyostelium discoideum OX=44689 GN=trapcc10-1 PE=3 SV=1

A3097	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity)	-	-	-	OJJ35810.1 hypothetical protein ASPWEDRAFT_41052 [Aspergillus wentii DTO 134E9]	FAD synthase OS=Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANA E) OX=304371 GN=ribL PE=3 SV=1
A3098	-	-	-	-	-	-	-	-
A3099	-	-	-	-	-	-	-	-
A3100	GO:0016192(vesicle-mediated transport)	GO:0035658(Mon1-Ccz1 complex)	-	-	-	-	-	-
A3101	GO:0006887(exocytosis)	GO:000145(exocyst),GO:0016021(integral component of membrane)	GO:0005546(phosphatidylinositol-4,5-bisphosphate binding),GO:0004252(serine-type endopeptidase activity)	-	-	KOG2980 YGR101w Integral membrane protease of the rhomboid family involved in different forms of regulated intramembrane proteolysis	XP_00303684.1.1 uncharacterized protein SCHCODRAFT_47819 [Schizophyllum commune H4-8]	RHOMBROID-like protein 12, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=RBL12 PE=2 SV=1
A3102	-	-	GO:0003676(nucleic acid binding)	-	-	-	RYN73534.1 hypothetical protein AA0120_g12601 [Alternaria tenuissima]	MFS-type transporter clz9 OS=Cochliobolus lunatus OX=5503 GN=clz9 PE=3 SV=1
A3103	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	KOG4171 J299962 Adenylate/guanylate kinase	ACS49835.1 guanylyl cyclase 3, partial [Blastocladiella emersonii]	Soluble guanylate cyclase 88E OS=Drosophila melanogaster OX=7227 GN=Gyc88E PE=1 SV=4
A3104	-	-	-	-	-	-	-	-
A3105	-	-	-	-	-	-	TPX62756.1 hypothetical protein CcCBS67573_g08805 [Chytridiomycota confervae]	Rlla domain-containing protein 1 OS=Bos taurus OX=9913 GN=RIIAD1 PE=4 SV=1
A3106	-	-	-	-	-	-	-	-
A3107	GO:0055085(transmembrane transport)	-	GO:0005509(calcium ion binding)	K15084 SLC25A16, GDA, LEU5; solute carrier family 25 (mitochondrial carrier protein), member 16	-	KOG0752 CE10358 Mitochondrial solute carrier protein	XP_025181442.1 mitochondrial carrier domain-containing protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Mitochondrial coenzyme A transporter SLC25A42 OS=Mus musculus OX=10090 GN=Slc25a42 PE=1 SV=1
A3108	-	-	-	K14775 UTP30, RSL1D1; ribosome biogenesis protein UTP30	-	KOG1685 At3g58660 Uncharacterized conserved protein	ORX89530.1 ribosomal protein L1 [Basidiobolus meristosporus CBS 931.73]	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RSL1D1 PE=1 SV=3

A3109	-	-	GO:0003824(catalytic activity)	-	-	KOG1680 7303265 Enoyl-CoA hydratase	OSD00596.1 enoyl-CoA hydratase [Trametes coccinea BRFM310]	1,2-epoxyphenylacetyl-CoA isomerase OS=Escherichia coli (strain K12) OX=83333 GN=paaG PE=1 SV=1
A3110	-	-	-	-	-	-	-	-
A3111	GO:0009073(aromatic amino acid family biosynthetic process)	-	GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups),GO:0003866(3-phosphoshikimate 1-carboxyvinyltransferase activity),GO:0003824(catalytic activity)	K13830 ARO1; pentafunctional AROM polypeptide [EC:4.2.3.4 4.2.1.10 1.1.1.25 2.7.1.71 2.5.1.19]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map00999 Biosynthesis of various plant secondary metabolites;map01100 Metabolic pathways	KOG0692 At2g45300 Pentafunctional AROM protein	KGQ11427.1 3-phosphoshikimate 1-carboxyvinyltransferase [Beauveria bassiana D1-5]	3-phosphoshikimate 1-carboxyvinyltransferase OS=Nostoc punctiforme (strain ATCC 29133 / PCC 73102) OX=63737 GN=aroA PE=3 SV=1
A3112	-	-	GO:0016409(palmitoyltransferase activity)	K20031 ZDHHC6; palmitoyltransferase ZDHHC6 [EC:2.3.1.225]	-	KOG1315 At4g22750.2 Predicted DHHC-type Zn-finger protein	RKP20707.1 zf-DHHC-domain-containing protein, partial [Rozella allomyces CSF55]	Probable protein S-acyltransferase 13 OS=Arabidopsis thaliana OX=3702 GN=PAT13 PE=2 SV=1
A3113	-	-	GO:0003677(DNA binding),GO:0008270(zinc ion binding)	-	-	KOG1037 Hs4501955 NAD+ ADP-ribosyltransferase Parp, required for poly-ADP ribosylation of nuclear proteins	-	Poly [ADP-ribose] polymerase 1 OS=Danio rerio OX=7955 GN=parp1 PE=2 SV=1
A3114	GO:0006511(ubiquitin-dependent protein catabolic process),GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K11853 USP34; ubiquitin carboxyl-terminal hydrolase 34 [EC:3.4.19.12]	-	KOG1866 Hs11641423 Ubiquitin carboxyl-terminal hydrolase	KAF9905687.1 hypothetical protein EC991_00136.1 [Linnemannia zychae]	Ubiquitin carboxyl-terminal hydrolase 9Y OS=Mus musculus OX=10090 GN=Usp9y PE=2 SV=1
A3115	-	GO:0016020(membrane)	-	-	-	-	-	-
A3116	-	-	GO:0016491(oxidoreductase activity)	K00101 lldD; L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG0538 YML054c.2 Glycolate oxidase	KXS13117.1 hypothetical protein M427DRAFT_59013 [Gonapodya prolifera JEL478]	L-lactate dehydrogenase (cytochrome) OS=Wickerhamomyces anomalus OX=4927 GN=CYB2 PE=1 SV=2
A3117	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3118	-	-	-	-	-	-	-	-
A3119	GO:0006851(mitochondrial calcium ion transmembrane transport)	-	GO:0005509(calcium ion binding)	-	-	KOG2643 At4g32060 Ca2+ binding protein, contains EF-hand motifs	RKP01639.1 hypothetical protein CXG81DRAFT_25674 [Caulochytrium protostelioides]	Calcium uptake protein, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MICU PE=2 SV=1

A3120	-	-	GO:0010945(Co A pyrophosphatase activity)	-	-	KOG3069 CE07570 Peroxisomal NUDIX hydrolase	XP_031021989.1 uncharacterized protein SmJEL517_g06112 [Synchytrium microbalum]	Uncharacterized Nudix hydrolase NudL OS=Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) OX=218491 GN=nudL PE=3 SV=1
A3121	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K11226 STE7; mitogen-activated protein kinase kinase [EC:2.7.12.2]	map04011 MAPK signaling pathway - yeast	KOG0192 At3g24720 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	ORX86810.1 kinase-like protein [Anaeromyces robustus]	Mitogen-activated protein kinase kinase 1b OS=Physcomitrium patens OX=3218 GN=MKK1b PE=2 SV=2
A3122	-	-	-	-	-	-	ORZ35457.1 hypothetical protein BCR44DRAFT_1499651 [Catenaria anguillulae PL171]	Protein psiH OS=Dictyostelium discoideum OX=44689 GN=psiH PE=2 SV=1
A3123	-	-	-	-	-	-	ORZ35457.1 hypothetical protein BCR44DRAFT_1499651 [Catenaria anguillulae PL171]	Protein psiG OS=Dictyostelium discoideum OX=44689 GN=psiG-1 PE=3 SV=1
A3124	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At2g31500 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	TGZ78921.1 Pkinase-domain-containing protein [Ascodesmis nigricans]	Calcium-dependent protein kinase 8 OS=Oryza sativa subsp. japonica OX=39947 GN=CPK8 PE=2 SV=1
A3125	GO:0071985(multivesicular body sorting pathway)	GO:0000814(ESCRT II complex)	-	K12188 SNF8, EAP30; ESCRT-II complex subunit VPS22	map04144 Endocytosis	KOG3341 Hs21361380 RNA polymerase II transcription factor complex subunit	XP_016612566.1 hypothetical protein SPPG_00255 [Spizellomyces punctatus DAOM BR117]	Vacuolar-sorting protein SNF8 OS=Dictyostelium discoideum OX=44689 GN=snf8 PE=3 SV=1
A3126	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A3127	-	-	GO:0005525(GTP binding)	-	-	-	-	-
A3128	-	-	-	-	-	-	ORZ34157.1 hypothetical protein BCR44DRAFT_1514141 [Catenaria anguillulae PL171]	-
A3129	GO:0006812(cation transport), GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	-	-	-

A3130	GO:0006812(cation transport), GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	-	-	-
A3131	GO:0006812(cation transport), GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	-	-	-
A3132	GO:0042273(ribosomal large subunit biogenesis)	GO:0005730(nucleolus)	GO:0005515(protein binding)	-	-	KOG3881 Hs8922422 Uncharacterized conserved protein	TPX43186.1 hypothetical protein SeLEV6574_g05197 [Synchytrium endobioticum]	WD repeat-containing protein 74 OS=Bos taurus OX=9913 GN=WDR74 PE=2 SV=1
A3133	GO:0036211(protein modification process)	-	-	-	-	KOG2158 7301565 Tubulin-tyrosine ligase-related protein	XP_006680310.1 uncharacterized protein BATDEDRAFT_26123 [Batrachochytrium dendrobatidis JAM81]	Probable beta-tubulin polyglutamylase OS=Tetrahymena thermophila (strain SB210) OX=312017 GN=Ttlf6a PE=3 SV=2
A3134	-	-	GO:0046872(metal ion binding),GO:0003676(nucleic acid binding),GO:0004527(exonuclease activity)	K12619 XRN2, RAT1; 5'-3' exoribonuclease 2 [EC:3.1.13.-]	map03018 RNA degradation;map03008 Ribosome biogenesis in eukaryotes	KOG2044 YOR048c 5'-3' exonuclease HKE1/RAT1	XP_022467040.1 hypothetical protein KNAG_0L01770 [Kazachstania naganishii CBS 8797]	5'-3' exoribonuclease 2 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / BCRC 21394 / JCM 1990 / NBRC 0083 / IGC 2968) OX=284592 GN=RAT1 PE=3 SV=4
A3135	-	-	GO:0003824(catalytic activity)	-	-	KOG1549 At1g08490 Cysteine desulfurase NFS1	KAF9123275.1 hypothetical protein BGX30_001532 [Mortierella sp. GBA39]	Uncharacterized aminotransferase YcbU OS=Bacillus subtilis (strain 168) OX=224308 GN=ycbU PE=3 SV=3
A3136	-	-	GO:0003824(catalytic activity)	K20247 EGT2; mercaptopyruvate S-oxalyltransferase [EC:4.4.1.36]	map00340 Histidine metabolism;map01100 Metabolic pathways	KOG1549 At1g08490 Cysteine desulfurase NFS1	KAG5421749.1 hypothetical protein I9W82_000841 [Candida metapsilosis]	Cysteine desulfurase OS=Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) OX=309800 GN=sufS PE=1 SV=2
A3137	-	GO:0005680(anaphase-promoting complex)	-	K03352 APC5, ANAPC5; anaphase-promoting complex subunit 5	map04914 Progesterone-mediated oocyte maturation;map04657 IL-17 signaling pathway;map04120 Ubiquitin-mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG4322 Hs20127553 Anaphase-promoting complex (APC), subunit 5	KAF0538292.1 anaphase-promoting complex subunit 5-like isoform X2 [Gigaspora margarita]	Anaphase-promoting complex subunit 5 OS=Arabidopsis thaliana OX=3702 GN=APC5 PE=1 SV=1

A3138	-	-	GO:0005515(protein binding)	K20121 FNBP1; formin-binding protein 1	map05131 Shigellosis	KOG4348[Hs2 2060285 Adaptor protein CMS/SETA	CEJ01578.1 hypothetical protein RMCBS34429_2_15601 [Rhizopus microsporus]	SH3 domain-containing kinase-binding protein 1 OS=Homo sapiens OX=9606 GN=SH3KBP1 PE=1 SV=2
A3139	-	-	-	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1235[At2 g40090 Predicted unusual protein kinase	KAG0290050.1 hypothetical protein BGZ96_006489 [Linnemannia gamsii]	Uncharacterized aarF domain-containing protein kinase 5 OS=Mus musculus OX=10090 GN=Adck5 PE=2 SV=2
A3140	-	-	-	-	-	-	-	-
A3141	GO:0006412(translation),GO:0007165(signal transduction)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome),GO:0005515(protein binding)	K02915 RP-L34e, RPL34; large subunit ribosomal protein L34e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1790[YL052c 60s ribosomal protein L34	XP_007802254.1 60S ribosomal protein L34-B [Endocarpon pusillum Z07020]	Large ribosomal subunit protein eL34 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=RPL34B PE=1 SV=1
A3142	-	-	-	-	-	KOG0498[Hs1 5150797 K+-channel ERG and related proteins, contain PAS/PAC sensor domain	KNE66921.1 hypothetical protein AMAG_11395 [Allomyces macrogynus ATCC 38327]	Potassium voltage-gated channel subfamily H member 7 OS=Mus musculus OX=10090 GN=Kcnh7 PE=1 SV=2
A3143	GO:0006508(proteolysis)	-	GO:0004181(metalloprotease activity),GO:0008270(zinc ion binding)	-	-	KOG2649[CE18294 Zinc carboxypeptidase	-	Carboxypeptidase D OS=Mus musculus OX=10090 GN=Cpd PE=1 SV=2
A3144	-	-	-	-	-	KOG2430[729 8014 Glycosyl hydrolase, family 47	XP_016610502.1 hypothetical protein SPPG_02926 [Spizellomyces punctatus DAOM BR117]	-
A3145	-	-	-	-	-	-	-	tRNA/tmRNA (uracil-C(5))-methyltransferase OS=Chromohalobacter salexigens (strain ATCC BAA-138 / DSM 3043 / CIP 106854 / NCIMB
A3146	-	-	-	-	-	-	-	-
A3147	-	-	-	-	-	-	-	-
A3148	-	-	-	-	-	-	-	-
A3149	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3150	GO:0006470(protein dephosphorylation),GO:0016311(dephosphorylation)	-	GO:0008138(protein tyrosine/serine/threonine phosphatase activity),GO:0016791(phosphatase activity)	K14819 DUSP12, YVH1; dual specificity phosphatase 12 [EC:3.1.3.16 3.1.3.48]	-	KOG1716[729 4466 Dual specificity phosphatase	KAF8916541.1 phosphatases II [Mucidula mucida]	MAP kinase phosphatase with leucine-rich repeats protein 3 OS=Dictyostelium discoideum OX=44689 GN=mpl3 PE=3 SV=1
A3151	-	-	-	-	-	-	-	-
A3152	-	-	-	-	-	-	-	-
A3153	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3154	-	-	-	-	-	-	-	-

A3155	-	-	-	K07200 PRKAG; 5'-AMP-activated protein kinase, regulatory gamma subunit	map05410 Hypertrophic cardiomyopathy; map04211 Longevity regulating pathway; map04213 Longevity regulating pathway - multiple species; map04910 Insulin signaling pathway; map04714 Thermogenesis; map04710 Circadian rhythm; map04530 Tight junction; map04371 Apelin signaling pathway; map04931 Insulin resistance; map04932 Non-alcoholic fatty liver	-	ORX85046.1 cystathionine beta-synthase [Basidiobolus meristosporus CBS 931.73]	-
A3156	GO:0071562(nucleus-vacuole junction assembly)	-	GO:0005515(protein binding); GO:0043495(protein-membrane adaptor activity)	-	-	KOG4350 7291183 Uncharacterized conserved protein, contains BTB/POZ domain	-	-
A3157	-	-	-	-	-	-	-	-
A3158	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02995 RPS8; small subunit ribosomal protein S8e	map05171 Coronavirus disease - COVID-19; map03010 Ribosome	KOG3283 Hs4506743 40S ribosomal protein S8	EPZ31448.1 40S ribosomal protein S8-B [Rozella allomycis CSF55]	Small ribosomal subunit protein eS8 OS=Ictalurus punctatus OX=7998 GN=rps8 PE=2 SV=3
A3159	-	-	-	-	-	-	-	-
A3160	-	GO:0005815(microtubule organizing center)	-	-	-	-	-	-
A3161	GO:0006139(nucleobase-containing compound metabolic process)	GO:0005634(nucleus)	GO:0003676(nucleic acid binding); GO:0004527(exonuclease activity); GO:0004534(5'-3' exoribonuclease activity)	K12619 XRN2, RAT1; 5'-3' exoribonuclease 2 [EC:3.1.13.-]	map03018 RNA degradation; map03008 Ribosome biogenesis in eukaryotes	KOG2044 At1g75660 5'-3' exonuclease HKE1/RAT1	TPX68689.1 hypothetical protein SpCBS45565_g02905 [Spizellomyces sp. 'palustris']	5'-3' exoribonuclease 2 OS=Mus musculus OX=10090 GN=Xrn2 PE=1 SV=1
A3162	GO:0016192(vesicle-mediated transport)	GO:0016021(integral component of membrane)	-	K08516 YKT6; synaptobrevin homolog YKT6	map04140 Autophagy - animal; map04138 Autophagy - yeast; map04130 SNARE interactions in vesicular transport	KOG0859 Hs5032137 Synaptobrevin/VAMP-like protein	ORX43374.1 vesicle-associated membrane protein [Piromyces finnis]	Vesicle-associated membrane protein 7 OS=Mus musculus OX=10090 GN=Vamp7 PE=1 SV=1
A3163	GO:0007051(spindle organization); GO:0030951(establishment or maintenance of microtubule cytoskeleton polarity); GO:0046785(microtubule polymerization)	-	GO:0051010(microtubule plus-end binding); GO:0061863(microtubule plus end polymerase); GO:0005515(protein binding)	K16803 CKAP5; cytoskeleton-associated protein 5	-	KOG1820 At2g35630 Microtubule-associated protein	XP_031026872.1 uncharacterized protein SmJEL517_g01345 [Synchytrium microbalum]	Cytoskeleton-associated protein 5 OS=Homo sapiens OX=9606 GN=CKAP5 PE=1 SV=3

A3164	-	-	GO:0003839(gamma-glutamylcyclotransferase activity)	-	-	KOG4059 7293898 Uncharacterized conserved protein	-	-
A3165	-	-	-	-	-	-	-	-
A3166	GO:0006465(signal peptide processing)	GO:0005787(signal peptidase complex), GO:0016020(membrane)	GO:0008236(serine-type peptidase activity), GO:0008233(peptidase activity), GO:0004252(serine-type endopeptidase activity)	K13280 SEC11, sipW; signal peptidase I [EC:3.4.21.89]	map03060 Protein export	KOG3342 Hs7657609 Signal peptidase I	OZJ03777.1 Signal peptidase complex catalytic subunit SEC11C [Bifiguratus adalaidae]	Signal peptidase complex catalytic subunit SEC11A OS=Bos taurus OX=9913 GN=SEC11A PE=2 SV=1
A3167	-	-	GO:0005524(ATP binding)	K15628 PXA; ATP-binding cassette, subfamily D (ALD), peroxisomal long-chain fatty acid import protein [EC:7.6.2.4]	map04146 Peroxisome:map02010 ABC transporters	KOG0060 Hs10947129 Long-chain acyl-CoA transporter, ABC superfamily (involved in peroxisome organization and biogenesis)	KAF3008834.1 hypothetical protein E8E13_010794 [Curvularia kusanoi]	Lysosomal cobalamin transporter ABCD4 OS=Homo sapiens OX=9606 GN=ABCD4 PE=1 SV=1
A3168	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity), GO:0005524(ATP binding), GO:0005509(calcium ion binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway, map05214 Glioma; map04921 Oxytocin signaling pathway, map04925 Aldosterone synthesis and secretion	KOG0032 At5g23580 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KAG0779655.1 hypothetical protein G6F22_010514 [Rhizopus oryzae]	Calcium and calcium/calmodulin-dependent serine/threonine-protein kinase OS=Oryza sativa subsp. japonica OX=39947 GN=CCAMK PE=2 SV=1
A3169	-	-	-	-	-	-	-	-
A3170	GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	-	-	-	OBZ90155.1 Alpha-glucosidase YihQ [Choanephora cucurbitarum]	Sulfoquinovosidase OS=Agrobacterium fabrum (strain C58 / ATCC 33970) OX=176299 GN=smol PE=1 SV=1
A3171	-	-	GO:0046983(protein dimerization activity)	-	-	-	-	-
A3172	-	-	-	-	-	-	-	Transmembrane protein 138 OS=Danio rerio OX=7955 GN=tmem138
A3173	GO:0006470(protein dephosphorylation)	-	GO:0043169(cation binding), GO:0004722(protein serine/threonine phosphatase activity)	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698 At5g53140 Serine/threonine protein phosphatase	XP_006675023.1 uncharacterized protein BATDEDRAFT_8550 [Batrachochytrium dendrobatidis JAM81]	Probable protein phosphatase 2C 56 OS=Oryza sativa subsp. japonica OX=39947 GN=Os06g0526800 PE=3 SV=2

A3174	GO:0006468(protein phosphorylation)	GO:0005675(transcription factor TFIIF holo complex), GO:0070985(transcription factor TFIIF complex)	GO:0008353(RNA polymerase II CTD heptapeptide repeat kinase activity), GO:0004672(protein kinase activity), GO:0005524(ATP binding)	K02202 CDK7; cyclin-dependent kinase 7 [EC:2.7.11.22 2.7.11.23]	map03420 Nucleotide excision repair;map03022 Basal transcription factors;map04110 Cell cycle	KOG0659[Hs4502743 Cdk activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIF/TFIIF, kinase subunit CDK7	SPO24105.1 probable KIN28 - cyclin-dependent ser/thr protein kinase [Ustilago trichophora]	Cyclin-dependent kinase 7 OS=Dictyostelium discoideum OX=44689 GN=cdk7 PE=2 SV=2
A3175	GO:0006555(methionine metabolic process)	-	GO:0004489(methylenetetrahydrofolate reductase (NAD(P)H) activity)	K25004 MTHFR; methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.53]	map00670 One carbon pool by folate;map01523 Antifolate resistance;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG0564[At3g59970 5,10-methylenetetrahydrofolate reductase	KXN68030.1 methylenetetrahydrofolate reductase [Conidiobolus coronatus NRRL 28638]	Probable methylenetetrahydrofolate reductase (NADH) OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0815200 PE=2 SV=1
A3176	GO:0019674(NAD metabolic process)	-	GO:0003951(NAD+ kinase activity)	-	-	KOG4180[CE25616 Predicted kinase	-	NAD kinase 2, mitochondrial OS=Xenopus tropicalis OX=8364 GN=nadk2 PE=2 SV=1
A3177	-	-	-	-	-	-	ORX81185.1 hypothetical protein K493DRAFT_308154 [Basidiobolus meristosporus CBS 931.73]	-
A3178	-	-	-	-	-	-	-	-
A3179	-	-	-	-	-	-	-	-
A3180	-	-	-	-	-	-	TPX51081.1 hypothetical protein SeLEV6574_g00511 [Synchytrium endobioticum]	-
A3181	-	-	-	-	-	-	-	-
A3182	-	-	-	-	-	-	-	-
A3183	-	-	-	-	-	-	-	-
A3184	-	-	GO:0003676(nucleic acid binding), GO:0005524(ATP binding), GO:0003724(RNA helicase activity)	K17679 MSS116; ATP-dependent RNA helicase MSS116, mitochondria I [EC:3.6.4.13]	-	KOG0342[At5g63630 ATP-dependent RNA helicase pitchoune	RKO91655.1 P-loop containing nucleoside triphosphate hydrolase protein [Blyttomyces helicus]	DEAD-box ATP-dependent RNA helicase 26 OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0618500 PE=2 SV=1
A3185	-	-	GO:0005515(protein binding)	K10415 DYNC1L1, DNCL; dynein cytoplasmic 1 intermediate chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG1587[7291215 Cytoplasmic dynein intermediate chain	XP_016610566.1 hypothetical protein SPPG_02986 [Spizellomyces punctatus DAOM BR117]	Dynein axonemal intermediate chain 4 OS=Xenopus laevis OX=8355 GN=dnai4 PE=2 SV=1

A3186	-	-	-	-	-	-	-	-
A3187	GO:0006122(mitochondrial electron transport, ubiquinol to cytochrome c)	GO:0005750(mitochondrial respiratory chain complex III),GO:0070469(respirasome)	-	-	-	-	-	Probable cytochrome b-c1 complex subunit 8 OS=Dictyostelium discoideum OX=44689 GN=DDb_G0280569 PE=3 SV=1
A3188	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	-	-
A3189	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	TPX76941.1 hypothetical protein CcCBS67573_g01807 [Chytridiomycetes confervae]	-
A3190	-	-	-	-	-	-	KZM27989.1 hypothetical protein ST47_g860 [Ascochyta rabiei]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A3191	-	-	-	-	-	-	-	-
A3192	-	-	-	-	-	-	-	-
A3193	-	GO:0016021(integral component of membrane)	GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K14802 DRS2, ATP8A; phospholipid -transporting ATPase [EC:7.6.2.1]	-	KOG0206[Hs17978471 P-type ATPase	RPB02219.1 phospholipid -translocating P-type ATPase [Choiromyces venosus 120613-1]	Phospholipid-transporting ATPase IA OS=Mus musculus OX=10090 GN=Atp8a1 PE=1 SV=2
A3194	-	-	-	-	-	-	-	-
A3195	-	-	GO:0003824(catalytic activity)	-	-	KOG1075[CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A3196	-	-	-	K17818 ARD1; D-arabinitol dehydrogenase (NADP+) [EC:1.1.1.287]	map00040 Pentose and glucuronate interconversions; map01100 Metabolic pathways	-	THV07110.1 GroES-like protein [Dendrothele bispora CBS 962.96]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A3197	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclosmatium globosum]	-
A3198	-	-	-	-	-	-	-	-
A3199	-	-	-	-	-	-	-	-
A3200	-	-	-	-	-	KOG1950[At1g56600 Glycosyl transferase, family 8 - glycogenin	RSH88875.1 hypothetical protein EHS25_002537 [Saitozyma podzolica]	Galactinol synthase 2 OS=Arabidopsis thaliana OX=3702 GN=GOLS2 PE=1 SV=1
A3201	-	-	-	-	-	-	-	-
A3202	-	-	GO:0005515(protein binding)	-	-	-	-	Anthrax toxin receptor 2 OS=Mus musculus OX=10090 GN=Antrx2 PE=1 SV=1

A3203	-	-	GO:0051015(actin filament binding)	K05768 GSN; gelsolin	map04810 Regulation of actin cytoskeleton;map04666 Fc gamma R-mediated phagocytosis;map05203 Viral carcinogenesis	KOG0443 7296888 Actin regulatory proteins (gelsolin/villin family)	RKO89939.1 hypothetical protein BDK51DRAFT_36402 [Blyttomyces helicus]	Severin OS=Dictyostelium discoideum OX=44689 GN=sevA PE=1 SV=1
A3204	-	GO:0005737(cytoplasm)	GO:0005515(protein binding);GO:0035091(phosphatidylinositol binding)	K17917 SNX1_2; sorting nexin-1/2	map04144 Endocytosis	KOG2273 At5g06140 Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	CEP08160.1 hypothetical protein [Parasitella parasitica]	Hydroxylysine kinase OS=Mus musculus OX=10090 GN=Hykk PE=1 SV=2
A3205	-	-	-	-	-	-	-	-
A3206	-	-	-	-	-	-	-	-
A3207	-	-	-	-	-	-	-	-
A3208	GO:0006508(proteolysis)	-	GO:0004185(serine-type carboxypeptidase activity)	K13289 CTSA, CPY; cathepsin A (carboxypeptidase C) [EC:3.4.16.5]	map04142 Lysosome;map04614 Renin-angiotensin system	KOG1282 HsM13786125 Serine carboxypeptidases (lysosomal cathepsin A)	TPX58515.1 hypothetical protein PhCBS80983_g03085 [Powellomyces hirtus]	Venom serine carboxypeptidase OS=Apis mellifera OX=7460 PE=2 SV=1
A3209	GO:0030150(protein import into mitochondrial matrix)	GO:0005744(TIM23 mitochondrial import inner membrane translocase complex)	-	-	-	KOG4836 Hs7661810 Uncharacterized conserved protein	CEP07540.1 hypothetical protein [Parasitella parasitica]	Mitochondrial import inner membrane translocase subunit Tim21 OS=Xenopus laevis OX=8355 GN=tim21 PE=2 SV=1
A3210	-	-	GO:0005515(protein binding)	-	-	KOG4340 Hs18550554 Uncharacterized conserved protein	KAG4090475.1 TPR-like protein [Neocallimastix sp. JGI-2020a]	Intraflagellar transport protein 70A OS=Xenopus tropicalis OX=8364 GN=ift70a PE=2 SV=1
A3211	-	-	-	-	-	-	-	-
A3212	GO:0006113(fermentation)	GO:0016021(integral component of membrane)	-	K24965 CSF1; protein CSF1	-	KOG3596 YLR087c Uncharacterized conserved protein	ORX46568.1 hypothetical protein DM01DRAFT_1364417 [Hesseltinella vesiculosa]	Protein CSF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CSF1 PE=1 SV=1
A3213	GO:0006457(protein folding);GO:0000413(protein peptidyl-prolyl isomerization)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	-	-	KOG0865 Hs10863927 Cyclophilin type peptidyl-prolyl cis-trans isomerase	KAG1179671.1 hypothetical protein G6F71_000801 [Rhizopus microsporus]	Peptidyl-prolyl cis-trans isomerase OS=Hemicentrotus pulcherrimus OX=7650 PE=2 SV=1
A3214	-	-	GO:0003924(GTPase activity);GO:0005525(GTP binding)	K03267 ERF3, GSPT; peptide chain release factor subunit 3	map03015 mRNA surveillance pathway	KOG0459 At1g18070 Polypeptide release factor 3	RUP15912.1 hypothetical protein BC936DRAFT_139568 [Jimgerdemannia flammicorona]	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens OX=9606 GN=GSPT1 PE=1 SV=1

A3215	-	-	-	-	-	-	RUS14599.1 hypothetical protein BC937DRAFT_93574 [Endogone sp. FLAS- F59071]	-
A3216	-	-	-	-	-	KOG2504[CE 20478 Monocarboxy late transporter	RYP57755.1 hypothetical protein DL771_01142 0 [Monosporas cus sp. 5C6A]	L-lactate transporter OS=Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB) OX=335543 GN=Sfum_3364 PE=1 SV=1
A3217	-	-	GO:0005515(pro tein binding)	-	-	-	-	-
A3218	GO:00062 81(DNA repair)	-	GO:0003677(DN A binding),GO:000 5524(ATP binding)	K10871 RAD51L3, RAD51D; RAD51-like protein 3	map03440 Homologous recombination	KOG1433[Hs1 9924119 DNA repair protein RAD51/RHP5 5	XP_01661317 3.1 hypothetical protein SPPG_00804 [Spizellomyce s punctatus DAOM BR117]	DNA repair protein RAD51 homolog 4 OS=Homo sapiens OX=9606 GN=RAD51D PE=1 SV=1
A3219	-	-	-	-	-	-	KAF7320199. 1 RIC1 domain- containing protein [Mycena kentingensis]	-
A3220	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	K08838 STK24_25_MS T4; serine/threon ine-protein kinase 24/25/MST4 [EC:2.7.11.1]	-	KOG0574[CE 27082 STE20-like serine/threon ine kinase MST	TPX60491.1 hypothetical protein SpCBS45565_ g07484 [Spizellomyce s sp. 'palustris']	Serine/threonine-protein kinase 3/4 OS=Squalus acanthias OX=7797 GN=STK4 PE=2 SV=1
A3221	GO:00003 87(spliceo somal snRNP assembly) ,GO:0000 398(mRN A splicing, via spliceoso me)	GO:00056 81(spliceo somal complex)	-	K11098 SNRPF, SMF; small nuclear ribonucleopr oteins F	map03040 Spliceosome	KOG3482[At4 g30220 Small nuclear ribonucleo protein (snRNP) SMF	ORX81975.1 small nuclear ribonucleo protein SmF [Anaeromyce s robustus]	Probable small nuclear ribonucleoprotein F OS=Arabidopsis thaliana OX=3702 GN=At4g30220 PE=3 SV=1
A3222	-	-	GO:0043023(rib osomal large subunit binding)	K07562 NMD3; 60S ribosomal export protein NMD3	map03013 Nucleocytoplas mic transport;map03 008 Ribosome biogenesis in eukaryotes	KOG2613[729 0283 NMD protein affecting ribosome stability and mRNA decay	CDS10222.1 hypothetical protein LRAMOSAO2 898 [Lichtheimia ramosa]	60S ribosomal export protein NMD3 OS=Dictyostelium discoideum OX=44689 GN=nmd3 PE=3 SV=1
A3223	-	-	-	-	-	KOG1305[Hs1 5723370 Amino acid transporter protein	KZT10163.1 hypothetical protein LAESUDRAFT_741706 [Laetiporus sulphureus 93-53]	Sodium-coupled neutral amino acid transporter 5 OS=Mus musculus OX=10090 GN=Slc38a5 PE=1 SV=1
A3224	-	-	-	K10355 ACTF, actin, other eukaryote	map04814 Motor proteins	KOG0676[CE 12358 Actin and related proteins	CDS10215.1 Putative Actin (Fragment) [Lichtheimia ramosa]	Actin-1 OS=Schistosoma mansoni OX=6183 PE=2 SV=1

A3225	GO:0006355(regulation of transcription, DNA-templated)	GO:0016602(CCAAT-binding factor complex)	GO:0046982(protein heterodimerization activity),GO:0001228(DNA-binding transcription activator activity, RNA polymerase II-specific)	K08065 NFYB, HAP3; nuclear transcription Y subunit beta	map04612 Antigen processing and presentation;map05152 Tuberculosis;map05166 Human T-cell leukemia virus 1 infection	KOG0869 At2g38880 CCAAT-binding factor, subunit A (HAP3)	ORX66846.1 nuclear transcription factor Y subunit B-3 [Linderina pennisporea]	Nuclear transcription factor Y subunit B-1 OS=Arabidopsis thaliana OX=3702 GN=NFYB1 PE=1 SV=2
A3226	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1200 CE19130 Mitochondrial/plastidial beta-ketoacyl-ACP reductase	KAG1257408.1 hypothetical protein G6F65_015928 [Rhizopus oryzae]	(3R)-3-hydroxyacyl-CoA dehydrogenase OS=Canis lupus familiaris OX=9615 GN=HSD17B8 PE=3 SV=1
A3227	GO:0051568(histone H3-K4 methylation)	-	GO:0005515(protein binding),GO:0042800(histone methyltransferase activity (H3-K4 specific))	-	-	KOG1080 7289568 Histone H3 (Lys4) methyltransferase complex, subunit SET1 and related methyltransferases	ORY55818.1 SET domain-containing protein, partial [Neocallimastix californiae]	Histone-lysine N-methyltransferase ATXR7 OS=Arabidopsis thaliana OX=3702 GN=ATXR7 PE=2 SV=1
A3228	-	-	-	-	-	-	-	-
A3229	-	-	-	-	-	-	-	-
A3230	-	-	-	-	-	-	OAL42787.1 hypothetical protein IQ07DRAFT_668727 [Pyrenochaeta sp. DS3sAY3a]	-
A3231	GO:0071704(organic substance metabolic process), GO:0005975(carbohydrate metabolic process)	-	GO:0016868(intramolecular transferase activity, phosphotransferases),GO:0004610(phosphoacetylglucosamine mutase activity),GO:0000287(magnesium ion binding)	-	-	KOG2537 Hs7661568 Phosphoglucosomutase/phosphomannomutase	PIA15670.1 n-acetylglucosamine-phosphate mutase [Coemansia reversa NRRL 1564]	Phosphoacetylglucosamine mutase OS=Sus scrofa OX=9823 GN=PGM3 PE=1 SV=2
A3232	-	-	-	-	-	KOG4308 Hs21450705 LRR-containing protein	OAJ37754.1 hypothetical protein BDEG_21746 [Batrachochytrium dendrobatidis JEL423]	Leucine-rich repeat-containing protein 45 OS=Homo sapiens OX=9606 GN=LRRC45 PE=1 SV=1
A3233	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG0252 At5g43350 Inorganic phosphate transporter	EQL32025.1 hypothetical protein BDFG_05746 [Blastomyces dermatitidis ATCC 26199]	Low affinity inorganic phosphate transporter 4 OS=Lotus japonicus OX=34305 GN=PT4 PE=1 SV=1
A3234	-	-	GO:0016787(hydrolase activity)	-	-	KOG1378 Hs14775287 Purple acid phosphatase	-	Serine/threonine-protein phosphatase CPPED1 OS=Xenopus tropicalis OX=8364 GN=cpped1 PE=2 SV=1

A3235	GO:0006364(rRNA processing)	-	-	-	-	KOG4484 At5g43720 Uncharacterized conserved protein	KAG2187089.1 hypothetical protein INT44_004759 [Umbelopsis vinacea]	rRNA-processing protein efg1 OS=Botryotinia fuckeliana (strain B05.10) OX=332648 GN=efg1 PE=3 SV=1
A3236	-	-	-	-	-	-	-	-
A3237	-	-	-	K09425 K09425; Myb-like DNA-binding protein FlbD	-	KOG0048 Hs13641706_1 Transcription factor, Myb superfamily	KAF8940947.1 DNA binding transcription coactivator transcription factor [Dissophora ornata]	Transcription factor MYB3R-2 OS=Oryza sativa subsp. japonica OX=39947 GN=MYB3R-2 PE=2 SV=1
A3238	GO:0009113(purine nucleobase biosynthetic process)	-	GO:0004044(amidophosphoribosyltransferase activity)	K00764 purF, PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG0572 YMR300c Glutamine phosphoribosylpyrophosphate amidotransferase	RKP07641.1 phosphoribosyltransferase-like protein [Thamnocephalusphaerosporalis]	Amidophosphoribosyltransferase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=purF PE=3 SV=3
A3239	-	-	-	-	-	-	-	-
A3240	-	-	-	-	-	-	-	-
A3241	-	-	-	-	-	-	-	-
A3242	-	-	-	-	-	-	-	-
A3243	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors)	-	-	KOG0137 CE19166 Very-long-chain acyl-CoA dehydrogenase	ORZ40466.1 hypothetical protein BCR44DRAFT_1386096 [Catenaria anguillulae PL171]	Acyl-CoA dehydrogenase family member 11 OS=Caenorhabditis elegans OX=6239 GN=acdH-11 PE=1 SV=1
A3244	-	-	-	-	-	-	-	-
A3245	GO:0032324(molybdopterin cofactor biosynthetic process), GO:0006777(Mo-molybdopterin cofactor biosynthetic process)	-	-	K15376 GPHN; geophyrin [EC:2.10.1.1 2.7.7.75]	map01240 Biosynthesis of cofactors;map04727 GABAergic synapse;map01100 Metabolic pathways;map00790 Folate biosynthesis	KOG2371 At5g20990 Molybdopterin biosynthesis protein	XP_022461213.1 uncharacterized protein KUCA_T00005213001 [Kuraishia capsulata CBS 1993]	Molybdopterin biosynthesis protein CNX1 OS=Arabidopsis thaliana OX=3702 GN=CNX1 PE=1 SV=2
A3246	-	-	GO:0004518(nuclease activity)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518 YOR033c 5'-3' exonuclease	PNY27590.1 Exodeoxyribonuclease 1 [Tolypocladium capitatum]	Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EXO1 PE=1 SV=2
A3247	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K14430 PHO87_91; phosphate transporter	-	KOG1281 At5g47560 Na+/dicarboxylate, Na+/tricarboxylate and phosphate transporters	SGZ20031.1 BQ5605_C02.1g09242 [Microbotryum silenes-dioicae]	Sodium-dependent dicarboxylate transporter SdcS OS=Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229 / NCIMB 8711 / NCTC 7292 / S-41) OX=342451 GN=sdcs PE=3 SV=1

A3248	GO:0006979(response to oxidative stress)	-	GO:0004602(glutathione peroxidase activity)	K23856 GPX; peroxiredoxin [EC:1.11.1.24]	-	KOG1651 CE09696 Glutathione peroxidase	KAF5327770.1 hypothetical protein D9619_004554 [Psilocybe cf. subviscida]	Probable phospholipid hydroperoxide glutathione peroxidase OS=Citrus sinensis OX=2711 GN=CSA PE=1 SV=1
A3249	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K14430 PHO87_91; phosphate transporter	-	KOG1281 At5g47560 Na+/dicarboxylate, Na+/tricarboxylate and phosphate transporters	SGZ20031.1 BQ5605_C021g09242 [Microbotryum silenes-dioicae]	Sodium-dependent dicarboxylate transporter SdcS OS=Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229 / NCIMB 8711 / NCTC 7292 / S-41) OX=342451 GN=sdcs PE=3 SV=1
A3250	-	-	GO:0005515(protein binding)	-	-	-	TEB30231.1 hypothetical protein FA13DRAFT_1859201 [Coprinellus micaceus]	-
A3251	GO:0001522(pseudouridine synthesis), GO:0009451(RNA modification)	-	GO:0003723(RNA binding),GO:0009982(pseudouridine synthase activity)	K14655 RIB2, PUS8; tRNA pseudouridine synthase / 2,5-diamino-6-(5-phosphoribitylamino)-pyrimidin-4(3H)-one deaminase [EC:5.4.99.28]	map01240 Biosynthesis of cofactors;map00740 Riboflavin metabolism;map01100 Metabolic pathways	KOG1919 At4g21770 RNA pseudouridylate synthases	RKP08180.1 pseudouridine synthase, partial [Thamnocephalis sphaerospora]	RNA pseudouridine synthase 6, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0660400 PE=2 SV=1
A3252	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239 At5g27550 Kinesin (KAR3 subfamily)	KXN69631.1 kinesin-domain-containing protein, partial [Conidiobolus coronatus NRRL 28638]	Kinesin-like protein KIN-14E OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14E PE=2 SV=1
A3253	-	-	-	-	-	-	-	-
A3254	-	-	GO:0016491(oxidoreductase activity),GO:0008270(zinc ion binding)	-	-	KOG0023 At4g37990 Alcohol dehydrogenase, class V	KAF9139747.1 hypothetical protein BGX30_007546 [Mortierella sp. GBA39]	NADP-dependent alcohol dehydrogenase C 1 OS=Mycolicibacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=adhc1 PE=1 SV=1
A3255	-	-	GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG0023 At4g37990 Alcohol dehydrogenase, class V	KAF9139747.1 hypothetical protein BGX30_007546 [Mortierella sp. GBA39]	NADP-dependent alcohol dehydrogenase C 1 OS=Mycolicibacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=adhc1 PE=1 SV=1
A3256	-	-	GO:0016491(oxidoreductase activity),GO:0008270(zinc ion binding)	-	-	KOG0023 At4g37980 Alcohol dehydrogenase, class V	KAF9139747.1 hypothetical protein BGX30_007546 [Mortierella sp. GBA39]	NADP-dependent alcohol dehydrogenase C 1 OS=Mycolicibacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=adhc1 PE=1 SV=1

A3257	-	-	GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG0023 At4g37990 Alcohol dehydrogenase, class V	KAF9139747.1 hypothetical protein BGX30_007546 [Mortierella sp. GBA39]	NADP-dependent alcohol dehydrogenase C 1 OS=Mycolicibacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=adhC1 PE=1 SV=1
A3258	-	-	GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG0023 At4g37990 Alcohol dehydrogenase, class V	KAF9139747.1 hypothetical protein BGX30_007546 [Mortierella sp. GBA39]	Probable formaldehyde dehydrogenase AdhA OS=Bacillus subtilis (strain 168) OX=224308 GN=adhA PE=2 SV=1
A3259	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A3260	-	-	-	-	-	KOG0023 At4g37970 Alcohol dehydrogenase, class V	KAF9139747.1 hypothetical protein BGX30_007546 [Mortierella sp. GBA39]	NADP-dependent alcohol dehydrogenase C 1 OS=Mycolicibacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=adhC1 PE=1 SV=1
A3261	-	-	GO:0002161(aminoacyl-tRNA editing activity)	-	-	-	RPB04535.1 putative proline--tRNA ligase C19C7.06 [Choiromyces venosus 120613-1]	Putative prolyl-tRNA synthetase associated domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PRORS1P PE=5 SV=3
A3262	-	-	-	-	-	-	TPX58572.1 hypothetical protein PhCBS80983_g03051 [Powellomyces hirtus]	-
A3263	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005509(calcium ion binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At4g04720 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORX54885.1 calcium/calmodulin-dependent protein kinase I delta short [Piromyces finnis]	Calcium and calcium/calmodulin-dependent serine/threonine-protein kinase OS=Lilium longiflorum OX=4690 GN=CCAMK PE=1 SV=1
A3264	-	-	-	-	-	KOG1502 CE04390 Flavonol reductase/cinnamoyl-CoA reductase	KIM99747.1 hypothetical protein OIADMADRAFT_126280 [Oidiodendron maius Zn]	Tetraketide alpha-pyrone reductase 1 OS=Arabidopsis thaliana OX=3702 GN=TKPR1 PE=1 SV=1
A3265	-	-	-	K09518 DnaJ B12; DnaJ homolog subfamily B member 12	map04141 Protein processing in endoplasmic reticulum	KOG0521 CE25223 Putative GTPase activating proteins (GAPs)	KAA8913063.1 hypothetical protein TRICI_003292 [Trichomonas ciferrii]	Chaperone protein DnaJ OS=Malacoplasma penetrans (strain HF-2) OX=272633 GN=dnaJ PE=3 SV=1

A3266	GO:0006814(sodium ion transport), GO:0006885(regulation of pH), GO:0055085(transmembrane transport), GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0015385(sodium:proton antiporter activity), GO:0015299(solute:proton antiporter activity)	K12041 SLC9A6_7, NHE6_7; solute carrier family 9 (sodium/hydrogen exchanger), member 6/7	map04260 Cardiac muscle contraction	KOG1965[7296268 Sodium/hydrogen exchanger protein	ORX55681.1 sodium/hydrogen exchanger [Hesseltinella vesiculosa]	Sodium/hydrogen exchanger 8 OS=Homo sapiens OX=9606 GN=SLC9A8 PE=1 SV=4
A3267	-	-	-	K01897 ACSL fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway; map04146 Peroxisome; map04216 Ferroptosis; map04714 Thermogenesis; map00061 Fatty acid biosynthesis; map02024 Quorum sensing; map01100 Metabolic pathways; map01212 Fatty acid metabolism; map00071 Fatty acid degradation; map04920 Adipocytokine signaling pathway	KOG1256[At5g27600 Long-chain acyl-CoA synthetases (AMP-forming)	XP_016606276.1 hypothetical protein SPPG_06636 [Spizellomyces punctatus DAOM BR117]	Fatty acyl-CoA synthetase A OS=Dictyostelium discoideum OX=44689 GN=fcsA PE=1 SV=1
A3268	-	-	GO:0016787(hydrolyase activity)	-	-	-	RUP44363.1 Metallo-dependent phosphatase-like protein [Dimgerdennia flammicorona]	Bis(5'-nucleosyl)-tetrakisphosphatase, symmetrical OS=Psychromonas ingrahamii (strain DSM 17664 / CCUG 51855 / 37) OX=357804 GN=apaH PE=3 SV=1
A3269	-	-	GO:0005515(protein binding)	K03456 PPP2R1; serine/threonine-protein phosphatase 2A regulatory subunit A	map04391 Hippo signaling pathway - fly; map04390 Hippo signaling pathway; map04730 Long-term depression; map04350 TGF-beta signaling pathway; map04071 Sphingolipid signaling pathway; map04728 Dopaminergic synapse; map04660 T cell receptor signaling pathway; map04261 Adrenergic signaling in cardiomyocytes; map05142 Chagas disease; map04530 Tight junction; map03015 mRNA	KOG0211[Hs21361399 Protein phosphatase 2A regulatory subunit A and related proteins	KAF9305847.1 Polyamine N-acetyltransferase 1 [Mortierella antarctica]	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Bos taurus OX=9913 GN=PPP2R1A PE=1 SV=1
A3270	GO:0000413(protein peptidyl-prolyl isomerization), GO:0006457(protein folding)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K01802 E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]	-	KOG0865[At2g16600 Cyclophilin type peptidyl-prolyl cis-trans isomerase	XP_001941476.1 peptidyl-prolyl cis-trans isomerase [Pyrenophora tritici-repentis Pt-1C-BFP]	Peptidyl-prolyl cis-trans isomerase 1 OS=Glycine max OX=3847 GN=Cyp1 PE=2 SV=1
A3271	-	-	GO:0005515(protein binding)	-	-	-	-	-

A3272	-	-	-	K24083 ABHD13; abhydrolase domain- containing protein 13 [EC:3.-.-.-]	-	KOG4391 729 5869 Predicted alpha/beta hydrolase BEM46	VBB71772.1 Putative protein similar to protein bem46 of Schizosaccha romyces pombe [Podospora comata]	Protein ABHD13 OS=Danio rerio OX=7955 GN=abhd13 PE=2 SV=1
A3273	GO:00550 85(transm embrane transport)	GO:00160 20(memb rane)	GO:0015267(cha nnel activity)	K09885 AQPf; aquaporin rerated protein, other eukaryote	-	KOG0223 Hs4 502177 Aquaporin (major intrinsic protein family)	XP_01821919 2.1 hypothetical protein DI49_5636 [Saccharomy ces eubayanus]	Aquaporin-1 OS=Homo sapiens OX=9606 GN=AQP1 PE=1 SV=3
A3274	GO:00550 85(transm embrane transport)	GO:00160 20(memb rane)	GO:0015267(cha nnel activity)	K09885 AQPf; aquaporin rerated protein, other eukaryote	-	KOG0223 Hs4 502177 Aquaporin (major intrinsic protein family)	ORY02492.1 major intrinsic protein, partial [Basidiobolus meristosporu s CBS 931.73]	Aquaporin-1 OS=Rattus norvegicus OX=10116 GN=Aqp1 PE=1 SV=4
A3275	-	-	-	-	-	KOG1430 At4 g00560 C-3 sterol dehydrogena se/3-beta- hydroxysteroid dehydrogena se and related dehydrogena ses	XP_01623355 1.1 dTDP-4- dehydrorham nose reductase [Exophiala spinifera]	Probable low-salt glycan biosynthesis reductase Agl14 OS=Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) OX=309800 GN=agl14 PE=3 SV=1
A3276	-	-	-	-	-	-	-	-
A3277	-	-	-	-	-	-	-	-
A3278	GO:00069 79(respon se to oxidative stress),GO :0030091(protein repair)	-	GO:0016671(oxi doreductase activity, acting on a sulfur group of donors, disulfide as acceptor),GO:00 33743(peptide- methionine (R)- S-oxide reductase activity)	K07305 msrB; peptide- methionine (R)-S-oxide reductase [EC:1.8.4.12]	-	KOG0856 At4 g04830 Predicted pilin-like transcription factor	KAF2227385. 1 putative peptide methionine sulfoxide reductase B3 [Elsinoe ampelina]	Peptide methionine sulfoxide reductase B5 OS=Oryza sativa subsp. japonica OX=39947 GN=MSRB5 PE=2 SV=1
A3279	GO:00065 08(proteo lysis)	-	GO:0004181(me tallocalcarboxypep tidase activity),GO:000 8270(zinc ion binding)	-	-	KOG2650 729 5241 Zinc carboxypepti dase	ORZ37181.1 hypothetical protein BCR44DRAFT _1430632 [Catenaria anguillulae PL171]	Carboxypeptidase B OS=Helicoverpa zea OX=7113 GN=CPB PE=1 SV=1
A3280	GO:00063 64(rRNA processin g)	-	GO:0003676(nu cleic acid binding)	K14792 RRP5, PDCD11; rRNA biogenesis protein RRP5	-	KOG1070 Hs2 0544347 rRNA processing protein Rrp5	ORX90106.1 nucleic acid- binding protein [Basidiobolus meristosporu s CBS 931.73]	rRNA biogenesis protein RRP5 OS=Arabidopsis thaliana OX=3702 GN=RRP5 PE=2 SV=2
A3281	-	-	GO:0016491(oxi doreductase activity)	-	-	-	KXS14584.1 nadh- dependent fmn reductase [Gonapodya prolifera JEL478]	FMN-dependent NADPH-azoreductase OS=Bacillus subtilis (strain 168) OX=224308 GN=azr PE=1 SV=1

A3282	GO:0019379(sulfate assimilation, phosphoadenylyl sulfate reduction by phosphoadenylyl-sulfate reductase (thioredoxin))	-	GO:0004604(phosphoadenylyl-sulfate reductase (thioredoxin) activity),GO:0003824(catalytic activity)	K00390 cysH; phosphoadenosine phosphosulfate reductase [EC:1.8.4.8 1.8.4.10]	map01120 Microbial metabolism in diverse environments;map00920 Sulfur metabolism;map01100 Metabolic pathways	-	KAG1716685.1 hypothetical protein ID866_480 [Astraeus odoratus]	Phosphoadenosine 5'-phosphosulfate reductase OS=Synechococcus elongatus (strain ATCC 33912 / PCC 7942 / FACHB-805) OX=1140 GN=cysH PE=3 SV=2
A3283	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0030131(clathrin adaptor complex)	-	-	-	-	-	-
A3284	GO:0016567(protein ubiquitination)	-	GO:0005515(protein binding)	-	-	KOG1832 Hs7662316 HIV-1 Vpr-binding protein	RUS17149.1 hypothetical protein BC937DRAFT_90367 [Endogone sp. FLAS-F59071]	DDB1- and CUL4-associated factor 1 OS=Homo sapiens OX=9606 GN=DCAF1 PE=1 SV=3
A3285	-	-	GO:0005515(protein binding)	-	-	-	KAG0167483.1 hypothetical protein DFQ30_006018 [Apophysomycetes sp. BC1015]	Phosphate-binding protein PstS OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=pstS PE=3 SV=1
A3286	GO:0009058(biosynthetic process)	GO:0005737(cytoplasm)	GO:0008676(3-deoxy-8-phosphooctulonate synthase activity)	-	-	-	KAF9396987.1 hypothetical protein CPC16_000023 [Podila verticillata]	2-dehydro-3-deoxyphosphooctonate aldolase 1 OS=Arabidopsis thaliana OX=3702 GN=KDSA1 PE=1 SV=2
A3287	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A3288	-	-	-	-	-	-	-	-
A3289	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map04972 Pancreatic secretion;map04080 Neuroactive ligand-receptor interaction;map05164 Influenza A	KOG3627 7295397 Trypsin	KAF1957862.1 insect inhibitor with A fungal trypsin [Byssoshectium circinans]	Chymotrypsinogen A OS=Bos taurus OX=9913 PE=1 SV=1

A3290	GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds),GO:0004563(beta-N-acetylhexosaminidase activity)	K12373 HEXA_B; hexosaminidase [EC:3.2.1.52]	map04142 Lysosome;map00513 Various types of N-glycan biosynthesis;map00511 Other glycan degradation;map00603 Glycosphingolipid biosynthesis - globo and isogloboseries;map00600 Sphingolipid metabolism;map00604 Glycosphingolipid biosynthesis - ganglioseries;map00531 Glycosaminoglycan degradation;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic	KOG2499[Hs4504373 Beta-N-acetylhexosaminidase	KAF9189309.1 hypothetical protein BGZ51_009703 [Haplosporangium sp. Z 767]	Beta-hexosaminidase 3 OS=Arabidopsis thaliana OX=3702 GN=HEXO3 PE=1 SV=1
A3291	-	-	GO:0003824(catalytic activity)	-	-	KOG1680[Hs303265 Enoyl-CoA hydratase	RKU44598.1 hypothetical protein DL546_005942 [Coniochaeta pulveracea]	Enoyl-CoA hydratase ACTT3 OS=Alternaria alternata OX=5599 GN=ACTT3 PE=3 SV=1
A3292	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08793 STK32, YANK; serine/threonine kinase 32 [EC:2.7.11.1]	-	KOG0603[Hs20149547 Ribosomal protein S6 kinase	RKP20702.1 kinase-like protein [Rozeella allomyces CSF55]	Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens OX=9606 GN=RPS6KA1 PE=1 SV=2
A3293	-	-	-	-	-	-	-	-
A3294	-	-	-	-	-	-	-	-
A3295	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0005524(ATP binding),GO:0019205(nucleobase-containing compound kinase activity)	K13800 CMPK1, UMPK; UMP-CMP kinase [EC:2.7.4.14]	map00983 Drug metabolism - other enzymes;map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3079[Hs7706497 Uridylate kinase/adenylate kinase	KXN72281.1 UMP-CMP kinase [Conidiobolus coronatus NRRL 28638]	UMP-CMP kinase OS=Mus musculus OX=10090 GN=Cmpk1 PE=1 SV=1
A3296	-	-	GO:0016409(palmitoyltransferase activity)	-	-	KOG1311[Hs14761406 DHHC-type Zn-finger proteins	XP_007385471.1 zf-DHHC-domain-containing protein [Punctularia strigosozonata HHB-11173 SS5]	Palmitoyltransferase ZDHHC9 OS=Danio rerio OX=7955 GN=zdhhc9 PE=2 SV=2
A3297	GO:0000226(microtubule cytoskeleton organization),GO:0007020(microtubule nucleation)	GO:0000922(spindle pole),GO:0005815(microtubule organizing center)	GO:0043015(gamma-tubulin binding)	K16569 TUBGCP2, GCP2; gamma-tubulin complex component 2	-	KOG2001[Hs5729840 Gamma-tubulin complex, DGRIP84/SPC97 component	KAF9406891.1 hypothetical protein BGZ94_002913 [Podila epigama]	Gamma-tubulin complex component 2 OS=Homo sapiens OX=9606 GN=TUBGCP2 PE=1 SV=2

A3298	GO:0006006(glucose metabolic process)	-	GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor),GO:0050661(NADP binding),GO:0051287(NAD binding)	K00134 GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]	map05415 Diabetic cardiomyopathy; map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00710 Carbon fixation in photosynthetic organisms;map0	KOG0657 At1g13440 Glyceraldehyde 3-phosphate dehydrogenase	XP_016610677.1 glyceraldehyde-3-phosphate dehydrogenase, type I [Spizellomyces punctatus DAOM BR117]	Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) OX=103690 GN=gap3 PE=2 SV=1
A3299	GO:0006629(lipid metabolic process)	-	-	-	-	KOG2088 At2g42450 Predicted lipase/calmodulin-binding heat-shock protein	ORX82928.1 hypothetical protein BCR32DRAFT_278479 [Anaeromyces robustus]	Diacylglycerol lipase-beta OS=Rattus norvegicus OX=10116 GN=Daglb PE=1 SV=1
A3300	GO:0016575(histone deacetylation)	-	GO:0004407(histone deacetylase activity)	K06067 HDAC1_2; histone deacetylase 1/2 [EC:3.5.1.98]	map04350 TGF-beta signaling pathway;map04213 Longevity regulating pathway - multiple species;map04919 Thyroid hormone signaling pathway;map05031 Amphetamine addiction;map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map03082 ATP-dependent chromatin remodeling;map03083 Polycomb repressive complex;map05200 Pathways in cancer;map05202 Transcriptional	KOG1342 Hs20551695 Histone deacetylase complex, catalytic component RPD3	ORX87828.1 histone deacetylase [Basidiobolus meristosporus CBS 931.73]	Histone deacetylase 2 OS=Homo sapiens OX=9606 GN=HDAC2 PE=1 SV=2
A3301	-	-	-	-	-	-	OAJ43330.1 hypothetical protein BDEG_26697 [Batrachochytrium dendrobatidis JEL423]	Outer dynein arm protein 1 OS=Chlamydomonas reinhardtii OX=3055 GN=ODA1 PE=1 SV=1

A3302	-	-	GO:0003824(catalytic activity)	K01834 PGAM, gpmA; 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00680 Methane metabolism;map00260 Glycine, serine and threonine metabolism;map05230 Central carbon metabolism in cancer;map01100 Metabolic pathways;map04	-	TPX71853.1 hypothetical protein SpCBS45565.g00846 [Spizellomyces sp. 'palustris']	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase OS=Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831 / NBRC 15690 / NCIMB 10815 / 0-1) OX=426355 GN=gpmA PE=3 SV=1
A3303	-	-	-	K01897 ACSL fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04146 Peroxisome;map04216 Ferroptosis;map04714 Thermogenesis;map00061 Fatty acid biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation;map04920 Adipocytokine signaling pathway	KOG1256[HsM13569883 Long-chain acyl-CoA synthetases (AMP-forming)	ORZ30659.1 long-chain-fatty-acid-CoA ligase [Catenaria anguillulae PL171]	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Gallus gallus OX=9031 GN=ACSBG2 PE=2 SV=2
A3304	-	-	-	-	-	-	-	-
A3305	-	-	-	-	-	-	-	-
A3306	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A3307	-	-	-	-	-	-	-	-
A3308	GO:0006260(DNA replication)	GO:0000808(origin recognition complex), GO:0005634(nucleus)	-	K02604 ORC2; origin recognition complex subunit 2	map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG2928[At2g37560 Origin recognition complex, subunit 2	XP_018285462.1 hypothetical protein PHYBLDRAFT_118265 [Phycomyces blakesleeana NRRL 1555(-)]	Origin of replication complex subunit 2 OS=Arabidopsis thaliana OX=3702 GN=ORC2 PE=1 SV=1
A3309	-	-	-	-	-	-	-	-

A3310	GO:0006914 (autophagy)	-	-	K08334 BECN, VPS30, ATG6; beclin	map05014 Amyotrophic lateral sclerosis; map04140 Autophagy - animal; map05131 Shigellosis; map04215 Apoptosis - multiple species; map04138 Autophagy - yeast; map04137 Mitophagy - animal; map04136 Autophagy - other; map05022 Pathways of neurodegeneration - multiple diseases; map04371 Apelin signaling pathway; map05010 Alzheimer disease; map05017 Spinocerebellar ataxia; map05016 Huntington	KOG2751 Hs4502395 Beclin-like protein	KAG1109886.1 hypothetical protein G6F42_015509 [Rhizopus oryzae]	Beclin-1-like protein B OS=Dictyostelium discoideum OX=44689 GN=atg6B PE=3 SV=1
A3311	-	-	GO:0008237 (metallopeptidase activity)	-	-	-	-	-
A3312	-	-	GO:0005515 (protein binding)	K09527 DNAJC7; DnaJ homolog subfamily C member 7	-	-	NP_596790.1 DNAJ/TPR domain protein DNAJC7 family [Schizosaccharomyces pombe]	DnaJ homolog subfamily C member 7 homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC543.02c PE=4 SV=1
A3313	-	-	GO:0003676 (nucleic acid binding)	-	-	-	-	Stage V sporulation protein S OS=Bacillus subtilis (strain 168) OX=224308 GN=spoVS PE=1 SV=1
A3314	-	-	GO:0070403 (NAD+ binding)	-	-	KOG2684 CE06302 Sirtuin 5 and related class III sirtuins (SIR2 family)	RIB24917.1 DHS-like NAD/FAD-binding domain-containing protein [Gigaspora rosea]	NAD-dependent protein deacetylase sir-2.1 OS=Caenorhabditis elegans OX=6239 GN=sir-2.1 PE=1 SV=1
A3315	GO:0007165 (signal transduction)	-	-	-	-	-	KAG5358030.1 GTPase-activating protein [Yarrowia sp. B02]	-
A3316	-	-	GO:0016491 (oxidoreductase activity)	-	-	-	KXS17967.1 thioredoxin-like protein [Gonapodya prolifera JEL478]	2-hydroxychromene-2-carboxylate isomerase OS=Sphingobium xenophagum OX=121428 GN=nsaD PE=1 SV=1
A3317	-	-	GO:0005515 (protein binding)	K03128 TAF2; transcription initiation factor TFIID subunit 2	map03022 Basal transcription factors	KOG1472 7295327 Histone acetyltransferase SAGA/ADA, catalytic subunit PCAF/GCN5 and related proteins	XP_017990768.1 taf2-component of tfiid complex [Malassezia pachydermatis]	SWR1 complex bromodomain subunit bdf1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=bdf1 PE=1 SV=1
A3318	-	-	-	-	-	-	-	-
A3319	-	-	GO:0003724 (RNA helicase activity); GO:0005524 (ATP binding); GO:0003676 (nucleic acid binding)	K11594 DDX3X, bel; ATP-dependent RNA helicase DDX3X [EC:3.6.4.13]	map04622 RIG-I-like receptor signaling pathway; map05203 Viral carcinogenesis; map05161 Hepatitis B	KOG0335 YPL119c ATP-dependent RNA helicase	RKP27673.1 P-loop containing nucleoside triphosphate hydrolase protein [Syncephalis pseudoplumigaleata]	ATP-dependent RNA helicase DED1 OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=DED1 PE=3 SV=1

A3320	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A3321	-	-	-	-	-	-	-	-
A3322	-	-	-	-	-	-	KAG0281992.1 hypothetical protein BGZ97_009190 [Linnemannia gamsii]	-
A3323	-	-	-	-	-	-	-	-
A3324	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A3325	-	-	-	-	-	-	XP_002144403.1 SNARE domain protein [Talaromyces marneffei ATCC 18224]	Syntaxin pep12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=pep12 PE=1 SV=2
A3326	-	-	GO:0005515(protein binding)	-	-	KOG4226[CE29645 Adaptor protein NCK/Dock, contains SH2 and SH3 domains	OWB51227.1 hypothetical protein B5S27_g2786 [[Candida] boidinii]	Unconventional myosin-le OS=Mus musculus OX=10090 GN=Myo1e PE=1 SV=1
A3327	-	-	GO:0005096(GTPase activator activity)	K12488 ASAP; Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein	map04144 Endocytosis;map04666 Fc gamma R-mediated phagocytosis	KOG0521[Hs17977656 Putative GTPase activating proteins (GAPs)	RUS17252.1 hypothetical protein BC937/DRAFT_90211 [Endogone sp. FLAS-F59071]	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Gallus gallus OX=9031 GN=ACAP2 PE=2 SV=1
A3328	GO:0016070(RNA metabolic process)	-	GO:0043565(sequence-specific DNA binding),GO:0003697(single-stranded DNA binding),GO:0003723(RNA binding)	-	-	KOG3067[Hs4759270 Translin family protein	XP_007288365.1 putative recombination hotspot-binding protein (Translin) [Marssonina brunnea f. sp. 'multigermtu bi' MB_m1]	Translin OS=Gallus gallus OX=9031 GN=TSN PE=1 SV=1
A3329	-	-	GO:0005515(protein binding)	-	-	KOG0046[Hs7549809 Ca2+-binding actin-bundling protein (fimbrin/plastin), EF-Hand protein superfamily	-	Plastin-3 OS=Bos taurus OX=9913 GN=PLS3 PE=2 SV=1

A3330	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K02216 CHEK1; serine/threonine-protein kinase CHEK1 [EC:2.7.11.1]	map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map05203 Viral carcinogenesis; map04115 p53 signaling pathway;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG0583 At2g26980 Serine/threonine protein kinase	KAG4083587.1 Pkinase-domain-containing protein [Neocallimastix sp. JGI-2020a]	CBL-interacting serine/threonine-protein kinase 26 OS=Arabidopsis thaliana OX=3702 GN=CIPK26 PE=1 SV=2
A3331	GO:0006559(L-phenylalanine catabolic process), GO:0006570(tyrosine metabolic process)	-	GO:0004411(homogentisate 1,2-dioxygenase activity)	K00451 HGD; hmgA; homogentisate 1,2-dioxygenase [EC:1.13.11.5]	map01120 Microbial metabolism in diverse environments;map00643 Styrene degradation;map00350 Tyrosine metabolism;map01100 Metabolic pathways	KOG1417 Hs4504381 Homogentisate 1,2-dioxygenase	PIA19684.1 Homogentisate 1,2-dioxygenase [Coemansia reversa NRRL 1564]	Homogentisate 1,2-dioxygenase OS=Dictyostelium discoideum OX=44689 GN=hgd PE=2 SV=1
A3332	-	-	-	-	-	-	-	Pleckstrin homology domain-containing family D member 1 OS=Homo sapiens OX=9606 GN=PLEKHD1 PE=2 SV=3
A3333	GO:0007264(small GTPase mediated signal transduction)	-	GO:0005085(guananyl-nucleotide exchange factor activity)	K03099 SOS; son of sevenless	map04810 Regulation of actin cytoskeleton;map05223 Non-small cell lung cancer;map04722 Neurotrophin signaling pathway;map04320 Dorso-ventral axis formation;map04510 Focal adhesion;map04072 Phospholipase D signaling pathway;map01521 EGFR tyrosine kinase inhibitor resistance;map01522 Endocrine resistance;map04917 Prolactin signaling pathway;map04915 Estrogen signaling	KOG3417 YLR310c Ras1 guanine nucleotide exchange factor	XP_025535725.1 guanine nucleotide exchange factor [Aspergillus costaricensis CBS 115574]	Ras guanine nucleotide exchange factor K OS=Dictyostelium discoideum OX=44689 GN=gefK PE=2 SV=1
A3334	-	-	-	K20367 ERGIC3, ERV46; endoplasmic reticulum-Golgi intermediate compartment protein 3	-	KOG2667 At1g22200 COP1 vesicle protein	KLU81334.1 endoplasmic reticulum-Golgi intermediate compartment protein 3 [Magnaporthe oryzae ATCC 64411]	Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Homo sapiens OX=9606 GN=ERGIC3 PE=1 SV=1

A3335	GO:007185(multivesicular body sorting pathway)	GO:0000814(ESCRT-II complex)	-	K12189 VPS25, EAP20; ESCRT-II complex subunit VPS25	map04144 Endocytosis	KOG4068 Hs14150155 Uncharacterized conserved protein	KAG4094128.1 ESCRT-II complex, vps25 subunit [Neocallimastix sp. JGI-2020a]	Vacuolar protein-sorting-associated protein 25 OS=Xenopus laevis OX=8355 GN=vps25 PE=2 SV=1
A3336	-	-	GO:0008270(zinc ion binding)	K10601 SYVN1, HRD1; E3 ubiquitin-protein ligase synoviolin [EC:2.3.2.27]	map04141 Protein processing in endoplasmic reticulum;map04120 Ubiquitin mediated proteolysis	KOG0802 At3g16090 E3 ubiquitin ligase	RHZ88591.1 hypothetical protein Glove_22g103 [Diversispora epigaea]	ERAD-associated E3 ubiquitin-protein ligase HRD1 OS=Oryza sativa subsp. japonica OX=39947 GN=HRD1 PE=2 SV=1
A3337	GO:0006606(protein import into nucleus)	GO:0005737(cytoplasm)	GO:0005515(protein binding);GO:0061608(nuclear import signal receptor activity)	K15042 KPNA5_6; importin subunit alpha-6/7	map03013 Nucleocytoplasmic transport;map05207 Chemical carcinogenesis - receptor activation;map05164 Influenza A	KOG0166 At3g06720 Karyopherin (importin) alpha	RKO85499.1 armadillo-type protein [Blyttiomycetes helicus]	Importin subunit alpha-1a OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0253300 PE=2 SV=2
A3338	-	-	-	-	-	-	-	-
A3339	-	-	GO:0003723(RNA binding);GO:0005515(protein binding)	K17583 NOM1; nucleolar MIF4G domain-containing protein 1	-	-	EPZ35014.1 Initiation factor eIF-4 gamma, MA3 domain-containing protein [Rozella allomyces CSF55]	Nucleolar MIF4G domain-containing protein 1 OS=Mus musculus OX=10090 GN=Nom1 PE=1 SV=2
A3340	-	-	GO:0005515(protein binding);GO:0003676(nucleic acid binding);GO:0005524(ATP binding)	K14807 DDX51, DBP6; ATP-dependent RNA helicase DDX51/DBP6 [EC:3.6.4.13]	-	KOG0350 At4g15850 DEAD-box ATP-dependent RNA helicase	RUS34572.1 P-loop containing nucleoside triphosphate hydrolase protein [Jimgerdennia flammicorona]	DEAD-box ATP-dependent RNA helicase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0795900 PE=2 SV=1
A3341	-	-	-	-	-	-	-	-
A3342	-	-	GO:0005515(protein binding)	K12857 SNRNP40, PRP8BP; Prp8 binding protein	map03040 Spliceosome	KOG0265 CE18578 U5 snRNP-specific protein-like factor and related proteins	KLJ06695.1 hypothetical protein EMPG_17806 [Blastomyces silverae]	U5 small nuclear ribonucleoprotein 40 kDa protein OS=Bos taurus OX=9913 GN=SNRNP40 PE=2 SV=1
A3343	GO:0006355(regulation of transcription, DNA-templated)	-	-	-	-	KOG1513 Hs7662410 Nuclear helicase MOP-3/SNO (DEAD-box superfamily)	RKP28182.1 putative methylase/helicase [Syncephalis pseudoplumigaleata]	Protein strawberry notch homolog 2 OS=Bos taurus OX=9913 GN=SBNO2 PE=2 SV=1
A3344	-	-	-	-	-	-	-	-
A3345	-	-	GO:0016787(hydrolase activity)	-	-	KOG1515 At2g45600 Arylacetamide deacetylase	THH03607.1 hypothetical protein EW145_g6146 [Phellinidium pouzarii]	Lipase 2 OS=Moraxella sp. (strain TA144) OX=77152 GN=lip2 PE=1 SV=1

A3346	GO:0005975(carbohydrate metabolic process)	-	GO:0004563(beta-N-acetylhexosaminidase activity),GO:0018580(nitronate monooxygenase activity),GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	-	-	KOG2499 At3g55260 Beta-N-acetylhexosaminidase	ORY45234.1 2-nitropropane dioxygenase [Rhizoclostium globosum]	Beta-hexosaminidase 1 OS=Arabidopsis thaliana OX=3702 GN=HEXO1 PE=1 SV=1
A3347	-	-	-	-	-	-	TPX72939.1 hypothetical protein SpC8S45565_g00253 [Spizellomyces sp. 'palustris']	Dynein regulatory complex protein 9 OS=Chlamydomonas reinhardtii OX=3055 GN=DRC9 PE=1 SV=1
A3348	-	GO:0016021(integral component of membrane)	-	K26753 TVP38; golgi apparatus membrane protein TVP38	-	KOG3140 At1g22850 Predicted membrane protein	KAF9348962.1 hypothetical protein BGX26_01265 [Mortierella sp. AD094]	TVP38/TMEM64 family membrane protein slr0305 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=slr0305 PE=3 SV=1
A3349	-	-	-	-	-	-	-	-
A3350	-	-	GO:0035091(phosphatidylinositol binding)	-	-	KOG2527 Hs7019539 Sorting nexin SNX11	-	Sorting nexin-11 OS=Homo sapiens OX=9606 GN=SNX11 PE=1 SV=2
A3351	-	-	GO:0010181(FMN binding),GO:0016491(oxidoreductase activity)	K00327 POR; NADPH-ferrihemoprotein reductase [EC:1.6.2.4]	-	KOG1158 Hs4505279 NADP/FAD dependent oxidoreductase	KAG0373513.1 hypothetical protein BGX24_011605 [Mortierella sp. AD032]	Methionine synthase reductase OS=Rattus norvegicus OX=10116 GN=Mtrr PE=2 SV=2
A3352	GO:0006862(nucleotide transport),GO:0055085(transmembrane transport)	-	-	K15115 SLC25A32, MFT; solute carrier family 25 (mitochondrial folate transporter), member 32	-	KOG0764 YEL006w Mitochondrial FAD carrier protein	CDH58404.1 mitochondrial nad transporter [Lichtheimia corymbifera JMRC:FSU:9682]	Mitochondrial nicotinamide adenine dinucleotide transporter 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YEA6 PE=1 SV=1
A3353	-	-	-	-	-	-	-	-
A3354	GO:0000244(spliceosomal tri-snRNP complex assembly),GO:0000398(mRNA splicing, via spliceosome)	GO:0046540(U4/U6 x U5 tri-snRNP complex)	-	-	-	KOG2574 At1g60170 mRNA splicing factor PRP31	ORY03530.1 Nop domain-containing protein [Basidiobolus meristosporus CBS 931.73]	U4/U6 small nuclear ribonucleoprotein Prp31 homolog OS=Arabidopsis thaliana OX=3702 GN=PRP31 PE=1 SV=1
A3355	-	-	-	K14403 CPSF3, YSH1; cleavage and polyadenylation specificity factor subunit 3 [EC:3.1.27.-]	map03015 mRNA surveillance pathway	KOG1137 Hs706427 mRNA cleavage and polyadenylation factor II complex, BRR5 (CPSF subunit)	KAF9974539.1 Cleavage and polyadenylation specificity factor subunit 3 [Actinomyces rella ambigua]	Cleavage and polyadenylation specificity factor subunit 3 OS=Bos taurus OX=9913 GN=CPSF3 PE=1 SV=1

A3356	-	-	GO:0003723(RNA binding)	K14790 NOP9; nucleolar protein 9	-	KOG2188[7304224 Predicted RNA-binding protein, contains Pumilio domains	ORX93043.1 ARM repeat-containing protein [Basidiobolus meristosporus CBS 931.73]	-
A3357	-	-	GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding)	K07178 RIOK1; RIO kinase 1 [EC:2.7.11.1]	map03008 Ribosome biogenesis in eukaryotes	KOG2269[7295659 Serine/threonine protein kinase	XP_01826770.0.1 uncharacterized protein RHOBADRAFT_56485 [Rhodotorula graminis WP1]	Serine/threonine-protein kinase RIO3 OS=Bos taurus OX=9913 GN=RIOK3 PE=2 SV=1
A3358	GO:0071704(organic substance metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	-	-	-	RKP18466.1 glycoside hydrolase [Rozella allomyces CSF55]	Glucosylceramidase OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) OX=246409 GN=ERC1 PE=1 SV=1
A3359	-	-	GO:0005515(protein binding),GO:0005525(GTP binding),GO:0046872(metal ion binding),GO:0005509(calcium ion binding)	K12182 HGS, HRS, VPS27; hepatocyte growth factor-regulated tyrosine kinase substrate	map04144 Endocytosis;map04145 Phagosome;map03250 Viral life cycle - HIV-1	KOG1954[CE28509 Endocytosis/signaling protein EHD1	TPX57961.1 hypothetical protein PhCBS80983_g03471 [Powellomyces hirtus]	EH domain-containing protein 1 OS=Bos taurus OX=9913 GN=EHD1 PE=1 SV=1
A3360	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map04972 Pancreatic secretion;map04080 Neuroactive ligand-receptor interaction;map05164 Influenza A	KOG3627[7295981 Trypsin	PBP24291.1 serine endopeptidase [Diplocarpon rosae]	Urokinase-type plasminogen activator OS=Gallus gallus OX=9031 GN=PLAU PE=2 SV=1
A3361	-	-	GO:0030246(carbohydrate binding)	-	-	-	KNE61759.1 fibro-slime domain-containing protein [Allomyces macrogynus ATCC 38327]	Protein psiD OS=Dictyostelium discoideum OX=44689 GN=psiD PE=3 SV=1
A3362	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map04972 Pancreatic secretion;map04080 Neuroactive ligand-receptor interaction;map05164 Influenza A	KOG3627[7303605 Trypsin	KXN67069.1 putative trypsin-like serine protease precursor [Conidiobolus coronatus NRRL 28638]	Trypsin-1 OS=Astacus astacus OX=6715 PE=1 SV=1

A3363	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K12761 SNF1; carbon catabolite-repressing protein kinase [EC:2.7.11.1]	map04138 Autophagy - yeast;map04113 Meiosis - yeast	KOG0583 At3g01090 Serine/threonine protein kinase	CDH54751.1 snf1-like protein kinase ssp2 [Lichtheimia corymbifera JMRC:FSU:9682]	SNF1-related protein kinase catalytic subunit alpha KIN10 OS=Arabidopsis thaliana OX=3702 GN=KIN10 PE=1 SV=3
A3364	-	-	-	-	-	-	-	-
A3365	-	-	-	K06685 MOB1, Mats; MOB kinase activator 1	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04392 Hippo signaling pathway - multiple species;map04111 Cell cycle - yeast	KOG0440 Hs8922671 Cell cycle-associated protein Mob1-1	XP_031026532.1 uncharacterized protein SmJEL517_g01560 [Synchytrium microbalum]	MOB kinase activator-like 1 homolog B OS=Dictyostelium discoideum OX=44689 GN=mobB PE=3 SV=1
A3366	GO:0006508(proteolysis)	GO:0005576(extracellular region)	GO:0005515(protein binding)	-	-	-	-	-
A3367	-	-	GO:0005509(calcium ion binding)	K16466 CETN3, CDC31; centrin-3	-	KOG0027 CE01908 Calmodulin and related proteins (EF-Hand superfamily)	PSK77794.1 cell division control protein 31 [[Candida] auris]	Polcalcin Cup a 4 OS=Hesperocyparis arizonica OX=49011 PE=1 SV=1
A3368	-	-	-	-	-	-	-	-
A3369	GO:0016226(iron-sulfur cluster assembly)	GO:0097361(CIA complex)	GO:0005515(protein binding)	K24730 CIAO1, CIA1; cytosolic iron-sulfur protein assembly protein CIAO1	-	KOG0645 CE21405 WD40 repeat protein	PVG04639.1 WD40 repeat-like protein [Serendipita vermifera 'subsp. besicii']	Probable cytosolic iron-sulfur protein assembly protein 1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CIA1 PE=3 SV=2
A3370	-	-	-	-	-	-	RSH88874.1 hypothetical protein EHS25_002536 [Saitozyma podzolica]	-
A3371	-	-	-	-	-	-	-	-
A3372	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity)	K18083 MTMR6_7_8; myotubularin-related protein 6/7/8 [EC:3.1.3.64 3.1.3.95]	map04070 Phosphatidylinositol signaling system;map04138 Autophagy - yeast;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG4471 Hs2055421 Phosphatidylinositol 3-phosphate 3-phosphatase myotubularin MTM1	KIM30967.1 hypothetical protein M408DRAFT_327880 [Serendipita vermifera MAFF 305830]	Myotubularin-related protein 8 OS=Gallus gallus OX=9031 GN=MTMR8 PE=2 SV=1
A3373	GO:0007205(protein kinase C-activating G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0016301(kinase activity),GO:0004143(diacylglycerol kinase activity)	-	-	KOG0782 Z290991 Predicted diacylglycerol kinase	TPX62063.1 diacylglycerol kinase (ATP) [Powellomyces hirtus]	Diacylglycerol kinase zeta OS=Mus musculus OX=10090 GN=Dgkz PE=1 SV=2

A3374	GO:0007165(signal transduction),GO:007205(protein kinase C-activating G protein-coupled receptor signaling pathway)	-	GO:0004143(diacylglycerol kinase activity),GO:0016301(kinase activity)	-	-	KOG0782 Hs4758156 Predicted diacylglycerol kinase	TPX62063.1 diacylglycerol kinase (ATP) [Powellomyces hirtus]	Diacylglycerol kinase iota OS=Homo sapiens OX=9606 GN=DGKI PE=1 SV=1
A3375	-	-	GO:0008168(methyltransferase activity)	K14850 RRP8; ribosomal RNA-processing protein 8 [EC:2.1.1.287]	-	-	XP_023466792.1 hypothetical protein RHIMIDRAFT_202104, partial [Rhizopus microsporus ATCC 52813]	25S rRNA (adenine(645)-N(1))-methyltransferase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rrp8 PE=3 SV=1
A3376	GO:0051603(proteolysis involved in cellular protein catabolic process), GO:0006511(ubiquitin-dependent protein catabolic process)	GO:0005839(proteasome complex), GO:0019773(proteasome complex, alpha-subunit complex)	-	K02728 PSMA4; 20S proteasome subunit alpha 3 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0178 At3g22110 20S proteasome, regulatory subunit alpha type PSMA4/PRE9	RIB13494.1 nucleophile aminohydrolase [Gigasporarosea]	Proteasome subunit alpha type-4-A OS=Arabidopsis thaliana OX=3702 GN=PAC1 PE=1 SV=1
A3377	-	-	-	-	-	-	-	-
A3378	-	-	-	-	-	KOG3260 Hs7656952 Calcyclin-binding protein CacyBP	-	Calcyclin-binding protein OS=Mus musculus OX=10090 GN=Cacybp PE=1 SV=1
A3379	-	-	-	-	-	-	-	-
A3380	-	-	-	-	-	-	-	-
A3381	-	-	-	K00750 GYG1, GYG2; glycogenin [EC:2.4.1.186]	map01110 Biosynthesis of secondary metabolites;map00500 Starch and sucrose metabolism;map01100 Metabolic pathways	-	RSH88874.1 hypothetical protein EHS25_002536 [Saitozyma podzolica]	-
A3382	GO:0030001(metal ion transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	K12346 SMF; metal ion transporter	-	KOG1291 At5g67330 Mn2+ and Fe2+ transporters of the NRAMP family	XP_018289384.1 hypothetical protein PHYBLRAFT_134855 [Phycomyces blakesleeanus NRRL 1555(-)]	Metal transporter nramp1 homolog OS=Dictyostelium discoideum OX=44689 GN=nramp1 PE=2 SV=1

A3383	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding);GO:0005515(protein binding)	K06276 PDPK1; 3-phosphoinositide dependent protein kinase-1 [EC:2.7.11.1]	map04360 Axon guidance;map03320 PPAR signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map05223 Non-small cell lung cancer;map04722 Neurotrophin signaling pathway;map04510 Focal adhesion;map04210 Apoptosis;map04071 Sphingolipid signaling pathway;map01524 Platinum drug resistance;map04919 Thyroid hormone signaling	KOG0592 At3g10540 3-phosphoinositide-dependent protein kinase (PDK1)	OAD06126.1 hypothetical protein MUCCIDRAFT_137721, partial [Mucor lusitanicus CBS 277.49]	3-phosphoinositide-dependent protein kinase 2 OS=Arabidopsis thaliana OX=3702 GN=PDPK2 PE=1 SV=1
A3384	GO:0006099(tricarboxylic acid cycle)	GO:0045252(oxoglutarate dehydrogenase complex)	GO:0016746(acyltransferase activity);GO:0004149(dihydrolipooyllysine-residue succinyltransferase activity)	K00658 DLST, sucB; 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00310 Lysine degradation;map00380 Tryptophan metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0559 YDR148c Dihydrolipoamide succinyltransferase (2-oxoglutarate dehydrogenase, E2 subunit)	CEP11388.1 hypothetical protein [Parasitella parasitica]	Dihydrolipooyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=odhB PE=1 SV=1
A3385	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	-	-
A3386	-	-	GO:0016757(glycosyltransferase activity)	-	-	KOG1950 At1g60450 Glycosyltransferase, family 8 - glycogenin	RSH88874.1 hypothetical protein EHS25_002536 [Saitozyma podzolica]	Galactinol synthase 7 OS=Arabidopsis thaliana OX=3702 GN=GOLS7 PE=2 SV=1
A3387	-	-	-	-	-	-	-	-
A3388	-	-	GO:0003677(DNA binding);GO:0005515(protein binding)	K06062 PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]	map03250 Viral life cycle - HIV-1;map04919 Thyroid hormone signaling pathway;map05203 Viral carcinogenesis; map04330 Notch signaling pathway;map05166 Human T-cell leukemia virus 1 infection	KOG1474 7290870 Transcription initiation factor TFIIID, subunit BDF1 and related bromodomain proteins	RKO92683.1 Bromodomain-containing protein [Blytiomyces helicus]	Homeotic protein female sterile OS=Drosophila melanogaster OX=7227 GN=fs(1)h PE=1 SV=2

A3389	-	-	GO:0005515(protein binding)	K05864 PPID, CYPD; peptidyl-prolyl isomerase D [EC:5.2.1.8]	map05131 Shigellosis;map04217 Necroptosis;map04218 Cellular senescence;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease	KOG0543[Hs4503729 FKBP-type peptidyl-prolyl cis-trans isomerase	KXS22446.1 TPR-like protein [Gonapodya prolifera JEL478]	70 kDa peptidyl-prolyl isomerase OS=Triticum aestivum OX=4565 GN=FKBP70 PE=1 SV=1
A3390	-	-	-	-	-	-	-	-
A3391	-	-	GO:0030246(carbohydrate binding)	-	-	-	KNE61759.1 fibro-slime domain-containing protein [Allomyces macrogynus ATCC 38327]	Protein psiD OS=Dictyostelium discoideum OX=44689 GN=psiD PE=3 SV=1
A3392	-	-	-	-	-	KOG2774[7296317 NAD dependent epimerase	ORX91412.1 L-threonine dehydrogenase [Basidiobolus meristosporus CBS 931.73]	L-threonine 3-dehydrogenase, mitochondrial OS=Bos taurus OX=9913 GN=TDH PE=2 SV=1
A3393	-	-	GO:0005515(protein binding);GO:0016407(acetyltransferase activity);GO:0004402(histone acetyltransferase activity)	K06062 PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]	map03250 Viral life cycle - HIV-1;map04919 Thyroid hormone signaling pathway;map05203 Viral carcinogenesis; map04330 Notch signaling pathway;map05166 Human T-cell leukemia virus 1 infection	-	OUM68377.1 hypothetical protein PIROE2DRAFT_39260, partial [Piromyces sp. E2]	Histone acetyltransferase GCN5 OS=Oryza sativa subsp. japonica OX=39947 GN=GCN5 PE=1 SV=1
A3394	-	-	-	-	-	-	-	-
A3395	-	-	-	-	-	-	-	-
A3396	-	-	-	-	-	-	-	-
A3397	GO:0007165(signal transduction)	-	-	-	-	-	XP_031022346.1 uncharacterized protein SmJEL517_g05739 [Synchytrium microbalum]	-
A3398	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003723(RNA binding);GO:0003735(structural constituent of ribosome)	K02875 RP-L14e, RPL14; large subunit ribosomal protein L14e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3421[At4g27090 60S ribosomal protein L14	ORY21583.1 putative 60S ribosomal protein L14 [Rhizoclostridium globosum]	Large ribosomal subunit protein eL14 OS=Pisum sativum OX=3888 PE=2 SV=1
A3399	-	-	-	-	-	-	-	-

A3400	GO:0000462(maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA))	GO:0030686(90S preribosome)	GO:0005515(protein binding)	K14548 UTP4, CIRH1A; U3 small nucleolar RNA-associated protein 4	map03008 Ribosome biogenesis in eukaryotes	KOG2048 Hs14249536 WD40 repeat protein	EPB86306.1 hypothetical protein HMPREF1544_06948 [Mucor circinelloides 1006PhL]	U3 small nucleolar RNA-associated protein 4 homolog OS=Mus musculus OX=10090 GN=Utp4 PE=2 SV=3
A3401	-	GO:0016020(membrane)	-	-	-	KOG4267 At3g20510 Predicted membrane protein	XP_018279690.1 TMEM14-domain-containing protein [Cutaneotrichosporon oleaginosum]	Protein FATTY ACID EXPORT 6 OS=Arabidopsis thaliana OX=3702 GN=FAX6 PE=3 SV=1
A3402	-	-	-	-	-	-	-	-
A3403	-	-	-	-	-	-	-	-
A3404	-	-	-	-	-	KOG1207 7293522 Diacetyl reductase/L-xylulose reductase	KAF8605265.1 CsgA protein [Ceratobasidium sp. AG-I]	1-hydroxy-2-glutathionyl-2-methyl-3-butene dehydrogenase OS=Rhodococcus sp. (strain AD45) OX=103808 GN=isoH PE=1 SV=1
A3405	GO:0006468(protein phosphorylation),GO:0000911(cytokinesis by cell plate formation),GO:0000914(phragmoplast assembly)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity),GO:0008017(microtubule binding)	K08838 STK24_25_MST4; serine/threonine-protein kinase 24/25/MST4 [EC:2.7.11.1]	-	KOG0597 At5g18700 Serine-threonine protein kinase FUSED	PIA18358.1 fused serine/threonine kinase-like protein [Coemansia reversa NRRL 1564]	Serine/threonine-protein kinase RUNKEL OS=Arabidopsis thaliana OX=3702 GN=RUK PE=1 SV=1
A3406	-	-	-	-	-	-	-	-
A3407	-	-	-	-	-	-	-	-
A3408	GO:0035556(intracellular signal transduction)	-	-	-	-	KOG1032 Hs2052111 Uncharacterized conserved protein, contains GRAM domain	-	-
A3409	-	-	-	-	-	-	-	-
A3410	-	-	-	-	-	-	-	-
A3411	GO:0006370(7-methylguanosine mRNA capping)	-	GO:0004484(mRNA guanylyltransferase activity),GO:0005524(ATP binding)	K00987 CEG1; mRNA guanylyltransferase [EC:2.7.7.50]	-	-	PQE32274.1 hypothetical protein CJF32_00001016 [Rutstroemia sp. NJR-2017a WRK4]	mRNA-capping enzyme subunit alpha OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ceg1 PE=1 SV=1
A3412	-	-	-	-	-	KOG1441 At3g17430 Glucose-6-phosphate/phosphate and phosphoenolpyruvate/phosphate antiporter	KAF8800577.1 TPT-domain-containing protein [Cortinarius glaucopus]	Probable sugar phosphate/phosphate translocator At3g17430 OS=Arabidopsis thaliana OX=3702 GN=At3g17430 PE=1 SV=1
A3413	GO:0006508(proteolysis)	-	GO:0004185(serine-type carboxypeptidase activity)	K13289 CTSA, CPY; cathepsin A (carboxypeptidase C) [EC:3.4.16.5]	map04142 Lysosome;map04614 Renin-angiotensin system	-	KAG0244091.1 hypothetical protein BGX31_009889 [Mortierella sp. GBA43]	Carboxypeptidase Y OS=Komagataella phaffii (strain GS115 / ATCC 20864) OX=644223 GN=PRC1 PE=1 SV=1

A3414	-	-	-	K17498 SPN1, IWS1; transcription factor SPN1	-	KOG1793 Hs2 2043544 Uncharacteriz ed conserved protein	ORX99011.1 hypothetical protein K493DRAFT_ 335964 [Basidiobolus meristosporu s CBS 931.73]	Protein IWS1 homolog OS=Rattus norvegicus OX=10116 GN=lws1 PE=1 SV=1
A3415	GO:00192 64(glycine biosynthe tic process from serine),G O:003599 9(tetrahyd rofolate interconv ersion)	-	GO:0003824(cat alytic activity),GO:003 0170(pyridoxal phosphate binding),GO:000 4372(glycine hydroxymethyltr ansferase activity)	K00600 glyA, SHMT; glycine hydroxymeth yltransferase [EC:2.1.2.1]	map00670 One carbon pool by folate;map01110 Biosynthesis of secondary metabolites;map 00460 Cyanoamino acid metabolism;map 01200 Carbon metabolism;map 01523 Antifolate resistance;map0 1240 Biosynthesis of cofactors;map01 120 Microbial metabolism in diverse environments;m ap01230 Biosynthesis of amino acids;map00680 Methane metabolism;map 00260 Glycine, serine and threonine	KOG2467 At4 g13890 Glycine/serin e hydroxymeth yltransferase	ORX90469.1 serine hydroxymeth yltransferase [Basidiobolus meristosporu s CBS 931.73]	Serine hydroxymethyltransferase 5 OS=Arabidopsis thaliana OX=3702 GN=SHM5 PE=3 SV=1
A3416	-	-	-	-	-	-	-	-
A3417	-	GO:00160 20(membr ane)	GO:0003885(D- arabinono-1,4- lactone oxidase activity),GO:001 6899(oxidoredu ctase activity, acting on the CH-OH group of donors, oxygen as acceptor),GO:00 71949(FAD binding),GO:005 0660(flavin adenine dinucleotide binding)	K00103 GULO; L- gulonolacton e oxidase [EC:1.1.3.8]	map01240 Biosynthesis of cofactors;map00 053 Ascorbate and aldarate metabolism;map 01100 Metabolic pathways	KOG4730 At3 g47930 D- arabinono-1, 4-lactone oxidase	KXS16522.1 FAD-binding domain- containing protein [Gonapodya prolifera JEL478]	L-galactono-1,4-lactone dehydrogenase, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=GLDH PE=1 SV=1
A3418	-	-	-	-	-	-	-	-
A3419	-	-	-	-	-	-	-	-
A3420	-	-	GO:0005515(pro tein binding)	-	-	KOG0506 Hs2 0336214 Glutaminase (contains ankyrin repeat)	TLD27614.1 serine/threon ine-protein phosphatase 6 regulatory ankyrin repeat subunit B- like [Venturia nashicola]	Glutaminase liver isoform, mitochondrial OS=Mus musculus OX=10090 GN=Gls2 PE=1 SV=2
A3421	-	GO:00160 21(integra l compo nent of membran e)	-	-	-	KOG3664 Hs1 7448847 Predicted patched transmembra ne receptor	-	Protein dispatched homolog 3 OS=Gallus gallus OX=9031 GN=DISP3 PE=1 SV=1
A3422	-	-	-	-	-	-	-	-
A3423	-	-	-	-	-	-	-	-
A3424	-	-	-	-	-	-	-	-

A3425	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	-	-	-	GAN06780.1 conserved hypothetical protein [Mucor ambiguus]	Branchpoint-bridging protein OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=bbp-1 PE=3 SV=1
A3426	-	-	-	-	-	-	-	-
A3427	GO:0006281(DNA repair),GO:0006310(DNA recombination),GO:0071897(DNA biosynthetic process)	-	GO:0003677(DNA binding),GO:0003910(DNA ligase (ATP) activity),GO:0005524(ATP binding),GO:0003909(DNA ligase activity)	K10747 LIG1; DNA ligase 1 [EC:6.5.1.1 6.5.1.6 6.5.1.7]	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03430 Mismatch repair	KOG0967 At1g66730.2 ATP-dependent DNA ligase I	ORY94104.1 ATP-dependent DNA ligase [Syncephalastrium racemosum]	DNA ligase 6 OS=Arabidopsis thaliana OX=3702 GN=LIG6 PE=2 SV=1
A3428	-	-	-	K01013 TSTD1; thiosulfate:glutathione sulfurtransferase [EC:2.8.1.-]	-	KOG1530 7301095 Rhodanese-related sulfurtransferase	KAB5572356.1 Rhodanese-like domain-containing protein [Coniochaeta sp. 2T2.1]	Putative thiosulfate sulfurtransferase, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC4H3.07c PE=3 SV=2
A3429	-	-	-	-	-	-	-	-
A3430	-	-	-	-	-	-	-	-
A3431	-	-	-	-	-	-	-	-
A3432	-	-	-	-	-	-	-	-
A3433	GO:0008615(pyridoxine biosynthetic process)	-	GO:0004733(pyridoxamine-phosphate oxidase activity),GO:0010181(FMN binding)	-	-	KOG2586 At5g49970.2 Pyridoxamine-phosphate oxidase	KAE8230161.1 hypothetical protein CF326_g4844 [Tilletia indica]	Pyridoxine/pyridoxamine 5'-phosphate oxidase OS=Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB 9086 / R18194 / 383) OX=482957 GN=pdxH PE=3 SV=1
A3434	-	-	-	-	-	-	-	-
A3435	GO:0008615(pyridoxine biosynthetic process)	-	GO:0004733(pyridoxamine-phosphate oxidase activity),GO:0010181(FMN binding)	K00275 pdxH, PNPO; pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]	map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map00750 Vitamin B6 metabolism;map01100 Metabolic pathways	KOG4558 At2g46580 Uncharacterized conserved protein	TPX70134.1 pyridoxal 5'-phosphate synthase [Spizellomyces sp. 'palustris']	Pyridoxine/pyridoxamine 5'-phosphate oxidase 2 OS=Arabidopsis thaliana OX=3702 GN=PPOX2 PE=3 SV=2
A3436	-	-	GO:0005515(protein binding)	-	-	KOG3689 7298454 Cyclic nucleotide phosphodiesterase	TPX54411.1 hypothetical protein CcBS67573_g09575 [Chytridiomycota confervae]	Probable 3',5'-cyclic phosphodiesterase pde-5 OS=Caenorhabditis elegans OX=6239 GN=pde-5 PE=3 SV=3

A3437	-	-	-	-	-	-	SCZ89766.1 BZ3500_Mvs of-1268-A1- R1_Chr1- 3g01565 [Microbotryu m saponariae]	Transmembrane emp24 domain-containing protein A OS=Dictyostelium discoideum OX=44689 GN=empA PE=3 SV=1
A3438	-	-	-	-	-	-	-	-
A3439	-	-	-	-	-	KOG1502 At1 g09480 Flavonol reductase/cin namoyl-CoA reductase	CEL57895.1 NADPH- dependent aldehyde reductase ARI1 OS=Saccharo myces cerevisiae (strain ATCC 204508 / S288c) GN=ARI1 PE=1 SV=1 [Rhizoctonia solani AG-1 IB]	Cinnamoyl-CoA reductase 1 OS=Arabidopsis thaliana OX=3702 GN=CCR1 PE=1 SV=1
A3440	-	-	-	-	-	-	-	-
A3441	GO:00001 05(histidin e biosynthe tic process)	GO:00057 37(cytopl asm)	GO:0000287(ma gnesium ion binding),GO:000 3879(ATP phosphoribosylt ransferase activity)	K00765 hisG; ATP phosphoribos yltransferase [EC:2.4.2.17]	map00340 Histidine metabolism;map 01110 Biosynthesis of secondary metabolites;map 01230 Biosynthesis of amino acids;map01100 Metabolic pathways	KOG2831 YER 055c ATP phosphoribos yltransferase	KAG4096339. 1 HisG- domain- containing protein [Neocallimast ix sp. JGI- 2020a]	ATP phosphoribosyltransferase OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=HIS1 PE=3 SV=1
A3442	GO:00068 11(ion transport), GO:00550 85(transm embrane transport)	GO:00160 20(memb rane)	GO:0005216(ion channel activity)	-	-	-	-	-
A3443	GO:00063 96(RNA processin g)	-	-	K11088 SNRPD3, SMD3; small nuclear ribonucleopr oteins D3	map03040 Spliceosome;ma p04139 Mitophagy - yeast;map05322 Systemic lupus erythematosus	KOG3172 730 3511 Small nuclear ribonucleopr oteins Sm D3	XP_03186109 0.1 uncharacteriz ed protein C1109_00345 0 [Kwoniella shandongens is]	Small nuclear ribonucleoprotein Sm D3 OS=Drosophila melanogaster OX=7227 GN=SmD3 PE=1 SV=1
A3444	-	-	-	-	-	-	-	Uncharacterized protein TP_0851 OS=Treponema pallidum (strain Nichols) OX=243276 GN=TP_0851 PE=4 SV=1
A3445	-	-	-	-	-	-	-	-
A3446	GO:00064 70(protein dephosph orylation), GO:00163 11(depho sphorylati on)	-	GO:0008138(pro tein tyrosine/serine/t hreonine phosphatase activity),GO:001 6791(phosphata se activity)	-	-	KOG1716 Hs1 8254478 Dual specificity phosphatase	EJD42233.1 phosphatases II [Auricularia subglabra TFB-10046 SS5]	Protein-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana OX=3702 GN=MKP1 PE=1 SV=1
A3447	-	-	-	-	-	-	TPX59501.1 hypothetical protein PhCBS80983_ g02426 [Powellomyce s hirtus]	Cilia- and flagella-associated protein 73 OS=Chlamydomonas reinhardtii OX=3055 GN=FAP73 PE=1 SV=1

A3448	-	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups),GO:0016746(acyltransferase activity)	K08764 SCP2, SCPX; sterol carrier protein 2 [EC:2.3.1.176]	map03320 PPAR signaling pathway;map04146 Peroxisome;map00120 Primary bile acid biosynthesis;map01040 Biosynthesis of unsaturated fatty acids;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG1406[Hs19923233_1 Peroxisomal 3-ketoacyl-CoA-thiolase P-44/SCP2	KAF9414138.1 sterol carrier protein 2 [Podila epigama]	Sterol carrier protein 2 OS=Mus musculus OX=10090 GN=Scp2 PE=1 SV=3
A3449	-	-	-	-	-	-	-	-
A3450	-	-	GO:0016874(ligase activity),GO:0016884(carbon-nitrogen ligase activity, with glutamine as amido-N-donor),GO:0003824(catalytic activity)	K02434 gatB, PET112; aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B [EC:6.3.5.6 6.3.5.7]	map00970 Aminoacyl-tRNA biosynthesis;map01100 Metabolic pathways	KOG2438[Hs4758894 Glutamyl-tRNA amidotransferase subunit B	PKY53072.1 glutamyl-tRNA amidotransferase chain B [Rhizophagus irregularis]	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial OS=Phytophthora infestans (strain T30-4) OX=403677 GN=PITG_07062 PE=3 SV=1
A3451	-	-	GO:0070403(NAD+ binding)	K11412 SIRT2, SIR2L2; NAD-dependent protein deacetylase sirtuin 2 [EC:2.3.1.286]	map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	KOG2682[Hs6912660 NAD-dependent histone deacetylases and class I sirtuins (SIR2 family)	RIA98697.1 DHS-like NAD/FAD-binding domain-containing protein [Glomus cerebriforme]	NAD-dependent protein deacetylase sirtuin-3, mitochondrial OS=Homo sapiens OX=9606 GN=SIRT3 PE=1 SV=2
A3452	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K21157 SAK1; SNF1-activating kinase 1 [EC:2.7.11.1]	map04138 Autophagy - yeast	-	KAG0657700.1 hypothetical protein C6P46_006256 [Rhodotorula mucilaginosa]	Serine/threonine-protein kinase ssp1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ssp1 PE=1 SV=1
A3453	-	-	-	-	-	-	-	-
A3454	GO:0030488(tRNA methylation),GO:006396(RNA processing)	-	GO:0008168(methyltransferase activity),GO:0009020(tRNA (guanosine-2'-O-)-methyltransferase activity),GO:0003723(RNA binding),GO:0008173(RNA methyltransferase activity)	-	-	KOG0838[At5g15390 RNA Methylase, SpoU family	KGQ11029.1 Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [Beauveria bassiana D1-5]	tRNA (guanosine(18)-2'-O)-methyltransferase OS=Escherichia coli O157:H7 OX=83334 GN=trmH PE=3 SV=1
A3455	-	-	GO:0005515(protein binding)	-	-	-	-	-

A3456	GO:0016236(macroautophagy),GO:0045324(late endosome to vacuole transport)	-	GO:0004674(protein serine/threonine kinase activity)	K08333 PIK3R4, VPS15; phosphoinositide-3-kinase, regulatory subunit 4 [EC:2.7.11.1]	map05014 Amyotrophic lateral sclerosis;map04140 Autophagy - animal;map05131 Shigellosis;map04138 Autophagy - yeast;map04136 Autophagy - other;map05022 Pathways of neurodegeneration - multiple diseases;map04371 Apelin signaling pathway;map05010 Alzheimer disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG1240 Hs14728229 Protein kinase containing WD40 repeats	KAF9937293.1 Serine/threonine-protein kinase [Mortierella alpina]	Phosphoinositide 3-kinase regulatory subunit 4 OS=Mus musculus OX=10090 GN=Pik3r4 PE=1 SV=3
A3457	-	-	-	-	-	-	-	-
A3458	-	-	-	-	-	-	-	-
A3459	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003899(DNA-directed 5'-3' RNA polymerase activity)	K03006 RPB1, POLR2A; DNA-directed RNA polymerase II subunit RPB1 [EC:2.7.7.6]	map03420 Nucleotide excision repair;map03020 RNA polymerase;map05016 Huntington disease	KOG0260 At4g35800 RNA polymerase II, large subunit	KAG2210041.1 hypothetical protein INT47_003477 [Mucor saturninus]	DNA-directed RNA polymerase II subunit RPB1 OS=Arabidopsis thaliana OX=3702 GN=NRPB1 PE=1 SV=3
A3460	-	-	GO:0051537(2 iron, 2 sulfur cluster binding),GO:0016491(oxidoreductase activity)	-	-	-	KAF3403245.1 NADH-cytochrome b5 reductase 2 [Talaromyces pinophilus]	-
A3461	-	-	-	-	-	-	-	-
A3462	-	-	-	-	-	-	-	-
A3463	-	-	-	-	-	-	KAF1982336.1 HSP20-like chaperone [Aulographum hederarum CBS 113979]	18 kDa heat shock protein OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) OX=272562 GN=hsp18 PE=2 SV=1
A3464	-	-	-	K06911 PIR; quercetin 2,3-dioxygenase [EC:1.13.11.24]	-	-	GES81613.1 RmlC-like cupin [Rhizophagus clarus]	Putative quercetin 2,3-dioxygenase sli1773 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=sli1773 PE=3 SV=1
A3465	GO:0006672(ceramide metabolic process)	GO:0016021(integral component of membrane)	GO:0016811(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides)	K04711 ACER3, YDC1; dihydroceramidase [EC:3.5.1.-]	map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG2329 7298654 Alkaline ceramidase	KAG2175303.1 hypothetical protein INT44_007791 [Umbelopsis vinacea]	Alkaline ceramidase 2 OS=Mus musculus OX=10090 GN=Acer2 PE=1 SV=1
A3466	-	-	-	-	-	KOG4568 Hs18378735 Cytoskeleton-associated protein and related proteins	-	Centrosome-associated protein 350 OS=Mus musculus OX=10090 GN=Cep350 PE=1 SV=1

A3467	-	-	-	K14819 DUSP12, YVH1; dual specificity phosphatase 12 [EC:3.1.3.16 3.1.3.48]	-	KOG1716 YR 026c Dual specificity phosphatase	PIA14308.1 dual specificity phosphatase 12 [Coemansia reversa NRRL 1564]	Tyrosine-protein phosphatase YVH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YVH1 PE=1 SV=1
A3468	GO:00064 12(transla tion)	GO:00058 40(riboso me)	GO:0003735(str uctural constituent of ribosome),GO:0 008097(5S rRNA binding)	K02932 RP- L5e, RPL5; large subunit ribosomal protein L5e	map05171 Coronavirus disease - COVID- 19;map03010 Ribosome	KOG0875 YPL 131w 60S ribosomal protein L5	ESK88438.1 60s ribosomal protein l5 [Moniliophth ora roreri MCA 2997]	Large ribosomal subunit protein uL18 OS=Bombyx mori OX=7091 GN=RpL5 PE=2 SV=1
A3469	-	-	-	-	-	-	-	-
A3470	GO:00469 07(intracel lular transport)	-	-	-	-	-	-	-
A3471	GO:00420 26(protein refolding)	-	GO:0005524(AT P binding)	-	-	KOG0356 At3 g23990 Mitochondria l chaperonin, Cpn60/Hsp60 p	XP_02536560 0.1 chaperonin GroL [Jaminaea rosea]	Chaperonin CPN60-2, mitochondrial OS=Zea mays OX=4577 GN=CPN60II PE=2 SV=1
A3472	-	-	GO:0004364(glu tathione transferase activity)	K07393 ECM4, yqjG; glutathionyl- hydroquinone reductase [EC:1.8.5.7]	-	KOG2903 At5 g44000 Predicted glutathione S-transferase	KAG0036094. 1 S- glutathionyl- (chloro)hydro quinone reductase [Podila clonocystis]	Glutathionyl-hydroquinone reductase YqjG OS=Escherichia coli (strain K12) OX=83333 GN=yqjG PE=1 SV=1
A3473	-	-	-	-	-	-	-	-
A3474	-	-	-	K19323 ATXN10; ataxin-10	map05017 Spinocerebellar ataxia	KOG2676 Hs7 106299 Uncharacteriz ed conserved protein	TPX71477.1 hypothetical protein SpCBS45565_ g01103 [Spizellomyces sp. 'palustris']	Ataxin-10 homolog OS=Dictyostelium discoideum OX=44689 GN=atxn10 PE=3 SV=1
A3475	-	-	-	-	-	-	-	-
A3476	-	-	-	-	-	-	KAF8315361. 1 hypothetical protein DL93DRAFT_ 2166733 [Clavulina sp. PML_390]	-
A3477	GO:00165 39(intein- mediated protein splicing),G O:001654 0(protein autoproces sing)	-	-	-	-	-	-	Sonic hedgehog protein OS=Rattus norvegicus OX=10116 GN=Shh PE=1 SV=1
A3478	-	-	GO:0008767(UD P- galactopyranose mutase activity)	-	-	-	KAG4097258. 1 UDP- galactopyran ose mutase [Neocallimast ix sp. JGI- 2020a]	UDP-galactopyranose mutase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=glf PE=3 SV=1
A3479	-	-	GO:0005515(pro tein binding)	K13886 CORO1B_1C_ 6; coronin- 1B/1C/6	-	KOG1445 Hs1 3375690 Tumor- specific antigen (contains WD repeats)	TPX60891.1 hypothetical protein PhCBS80983_ g01502 [Powellomyces hirtus]	Coronin-7 OS=Rattus norvegicus OX=10116 GN=Coro7 PE=1 SV=2
A3480	-	-	-	-	-	-	-	-

A3481	-	-	GO:0003723(RNA binding)	-	-	KOG2049 At1g22240 Translational repressor MPT5/PUF4 and related RNA-binding proteins (Puf superfamily)	KNZ71768.1 Pumilio like protein [Termitomyces sp. J132]	Putative pumilio homolog 8, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=APUM8 PE=3 SV=2
A3482	GO:0006511(ubiquitin-dependent protein catabolic process)	-	-	K03094 SKP1, CBF3D; S-phase kinase-associated protein 1	map04141 Protein processing in endoplasmic reticulum;map05132 Salmonella infection;map05131 Shigellosis;map04350 TGF-beta signaling pathway;map05170 Human immunodeficiency virus 1 infection;map04310 Wnt signaling pathway;map04341 Hedgehog signaling pathway - fly;map04710 Circadian rhythm;map04120 Ubiquitin mediated proteolysis;map03083 Polycomb repressive	KOG1724 Hs4507387 SCF ubiquitin ligase, Skp1 component	XP_02517741.1.1 E3 ubiquitin ligase complex SCF subunit sconeC [Rhizophagus irregularis DAOM 181602=DAOM 197198]	S-phase kinase-associated protein 1 homolog OS=Tetrahymena thermophila (strain SB210) OX=312017 GN=SKP1 PE=2 SV=1
A3483	GO:0006511(ubiquitin-dependent protein catabolic process)	-	-	K03094 SKP1, CBF3D; S-phase kinase-associated protein 1	map04141 Protein processing in endoplasmic reticulum;map05132 Salmonella infection;map05131 Shigellosis;map04350 TGF-beta signaling pathway;map05170 Human immunodeficiency virus 1 infection;map04310 Wnt signaling pathway;map04341 Hedgehog signaling pathway - fly;map04710 Circadian rhythm;map04120 Ubiquitin mediated proteolysis;map03083 Polycomb repressive	KOG1724 Hs4507387 SCF ubiquitin ligase, Skp1 component	XP_00695710.1.1 SconCp [Wallemia mellicola CBS 633.66]	S-phase kinase-associated protein 1 homolog OS=Tetrahymena thermophila (strain SB210) OX=312017 GN=SKP1 PE=2 SV=1
A3484	-	-	-	-	-	-	XP_01822743.2.1 hypothetical protein T552_00548 [Pneumocystis carinii B80]	-
A3485	-	-	GO:0005509(calcium ion binding)	-	-	KOG0044 7290875 Ca2+ sensor (EF-Hand superfamily)	-	-
A3486	-	-	GO:0010181(FMN binding);GO:0016491(oxidoreductase activity)	K00354 E1.6.99.1; NADPH2 dehydrogenase [EC:1.6.99.1]	-	KOG0134 At2g06050 NADH:flavin oxidoreductase/12-oxophytodienoate reductase	XP_01660618.4.1 hypothetical protein SPPG_06548 [Spizellomyces punctatus DAOM BR117]	Putative 12-oxophytodienoate reductase 11 OS=Oryza sativa subsp. japonica OX=39947 GN=OPR11 PE=2 SV=1
A3487	-	-	-	-	-	-	-	-

A3488	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3489	GO:0000027(ribosomal large subunit assembly)	-	-	K14815 MRT4; mRNA turnover protein 4	-	KOG0816[Hs18490987 Protein involved in mRNA turnover	KAG4097124.1 ribosomal protein L10-domain-containing protein [Neocallimastix sp. JGI-2020a]	mRNA turnover protein 4 homolog OS=Bos taurus OX=9913 GN=MRTO4 PE=2 SV=1
A3490	-	-	-	-	-	-	-	-
A3491	GO:0009086(methionine biosynthetic process), GO:0009088(threonine biosynthetic process), GO:0009089(lysine biosynthetic process via diaminopimelate), GO:0009097(isoleucine biosynthetic process), GO:0008652(cellular amino acid	-	GO:0004073(aspartate-semialdehyde dehydrogenase activity), GO:0050661(NADP binding), GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor), GO:0046983(protein dimerization activity), GO:0051287(NAD binding)	K00133 asd; aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	map00300 Lysine biosynthesis;map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00261 Monobactam biosynthesis;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism;map00270 Cysteine and methionine metabolism	KOG4777[At1g14810 Aspartate-semialdehyde dehydrogenase	KAG1453884.1 hypothetical protein G6F57_015629 [Rhizopus oryzae]	Aspartate-semialdehyde dehydrogenase OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=asd PE=3 SV=2
A3492	GO:0006633(fatty acid biosynthetic process)	GO:0005835(fatty acid synthase complex)	GO:0016740(transferase activity), GO:0000287(magnesium ion binding), GO:0008897(holo-[acyl-carrier-protein] synthase activity), GO:0004312(fatty acid synthase activity), GO:0004318(enoyl-[acyl-carrier-protein] reductase (NADH) activity), GO:0016746(acyltransferase activity), GO:0004315(3-oxoacyl-[acyl-carrier-protein] synthase activity)	K00667 FAS2; fatty acid synthase subunit alpha, fungi type [EC:2.3.1.86]	map00061 Fatty acid biosynthesis;map01100 Metabolic pathways;map01212 Fatty acid metabolism	-	CDS12520.1 hypothetical protein LRAMOSA04714 [Lichtheimia ramosa]	Fatty acid synthase 2 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=fas2 PE=2 SV=1
A3493	-	-	GO:0003924(GTPase activity), GO:0005525(GTP binding)	-	-	KOG0464[Hs19923640 Elongation factor G	GBB93390.1 hypothetical protein RclHR1_02160016 [Rhizophagus clarus]	Elongation factor G OS=Trichlorobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ) OX=398767 GN=fusA PE=3 SV=1
A3494	-	-	GO:0003723(RNA binding), GO:0003729(mRNA binding)	-	-	KOG3934[7301755 Histone mRNA stem-loop binding protein	TPX65576.1 hypothetical protein SpCBS45565_g05092 [Spizellomyces sp. 'palustris']	Oocyte-specific histone RNA stem-loop-binding protein 2 OS=Xenopus laevis OX=8355 GN=slbp2 PE=2 SV=1

A3495	-	-	-	-	-	-	KAF7727829.1 hypothetical protein EC973_006942 [Apophysomyces ossiformis]	Putative hydrolase C777.06c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC777.06c PE=4 SV=1
A3496	GO:000079(regulation of cyclin-dependent protein serine/threonine kinase activity)	-	GO:0019901(protein kinase binding)	-	-	KOG1674 At3g21870 Cyclin	ORZ19531.1 cyclin-domain-containing protein [Absidia repens]	Cyclin-P3-1 OS=Oryza sativa subsp. japonica OX=39947 GN=CYCP3-1 PE=3 SV=1
A3497	GO:0030433(ubiquitin-dependent ERAD pathway)	-	GO:0005515(protein binding)	-	-	KOG1550 At1g18260 Extracellular protein SEL-1 and related proteins	-	ERAD-associated E3 ubiquitin-protein ligase component HRD3 OS=Oryza sativa subsp. japonica OX=39947 GN=HRD3 PE=2 SV=1
A3498	-	-	-	-	-	-	-	-
A3499	-	-	GO:0016491(oxidoreductase activity),GO:0008270(zinc ion binding)	-	-	KOG1198 At1g23740 Zinc-binding oxidoreductase	ORY26433.1 alcohol dehydrogenase [Rhizoclostium globosum]	2-methylene-furan-3-one reductase OS=Fragaria ananassa OX=3747 GN=EO PE=1 SV=1
A3500	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1198 Hs14249346 Zinc-binding oxidoreductase	XP_017990789.1 nadph:quinone reductase [Malassezia pachydermatis]	Reticulon-4-interacting protein 1 homolog, mitochondrial OS=Danio rerio OX=7955 GN=rtn4ip1 PE=2 SV=2
A3501	-	-	GO:0003824(catalytic activity)	K05607 AUH; methylglutaryl-CoA hydratase [EC:4.2.1.18]	map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG1679 Hs4502327 Enoyl-CoA hydratase	RKP27912.1 methylglutaryl-CoA hydratase [Syncephalis pseudoplumigaleata]	Putative enoyl-CoA hydratase OS=Thermus thermophilus (strain ATCC 27634 / DSM 579 / HB8) OX=300852 GN=TTHA0550 PE=1 SV=1
A3502	-	-	-	K14842 NSA2; ribosome biogenesis protein NSA2	-	KOG3163 Hs7662677 Uncharacterized conserved protein related to ribosomal protein S8E	ORZ01752.1 30S ribosomal protein S8e [Syncephalastrium racemosum]	Ribosome biogenesis protein NSA2 homolog OS=Dictyostelium discoideum OX=44689 GN=nsa2 PE=3 SV=1
A3503	-	-	GO:0005515(protein binding)	K16794 PAFAH1B1, LIS1; platelet-activating factor acetylhydrolase IB subunit alpha	map00565 Ether lipid metabolism;map01100 Metabolic pathways	KOG0295 CE29339 WD40 repeat-containing protein	QSL66845.1 hypothetical protein MERGE_001232 [Pneumocystis wakefieldiae]	Nuclear distribution protein PAC1 OS=Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) OX=447093 GN=PAC1 PE=3 SV=1
A3504	-	-	-	-	-	-	-	-
A3505	-	-	GO:0008270(zinc ion binding)	-	-	KOG1609 Hs7706043 Protein involved in mRNA turnover and stability	KAF2748110.1 hypothetical protein M011DRAFT_467159 [Sporormia fimetaria CBS 119925]	E3 ubiquitin-protein ligase MARCHF2 OS=Bos taurus OX=9913 GN=MARCHF2 PE=2 SV=1

A3506	-	-	GO:0005515(protein binding)	K20285 RABEPK; Rab9 effector protein with kelch motifs	-	KOG0379 At3g05420_2 Kelch repeat-containing proteins	KAG0245016.1 hypothetical protein BGX31_008109 [Mortierella sp. GBA43]	Protein GLUTELIN PRECURSOR ACCUMULATION 3 OS=Oryza sativa subsp. japonica OX=39947 GN=GPA3 PE=1 SV=1
A3507	GO:0006101(citrate metabolic process)	-	GO:0046912(acyltransferase, acyl groups converted into alkyl on transfer),GO:0004108(citrate (Si)-synthase activity)	K01647 CS, gltA; citrate synthase [EC:2.3.3.1]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00020 Citrate cycle (TCA cycle);map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism;map00630 Glyoxylate and dicarboxylate metabolism	KOG2617 Hs4758076 Citrate synthase	KAA8914207.1 hypothetical protein TRICL_002964 [Trichomonas cucumerii]	Citrate synthase, mitochondrial OS=Iguana iguana OX=8517 GN=CS PE=2 SV=1
A3508	-	-	GO:0003713(transcription coactivator activity)	-	-	KOG3294 At5g11680 WW domain binding protein WBP-2, contains GRAM domain	NP_594988.1 WW domain-binding protein [Schizosaccharomyces pombe]	UPF0664 stress-induced protein C29B12.11c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC29B12.11c PE=2 SV=1
A3509	-	-	GO:0005515(protein binding)	-	-	-	OON06774.1 hypothetical protein BSLG_03628 [Batrachochytrium salamandrivorans]	Zinc finger MYND domain-containing protein 12 OS=Homo sapiens OX=9606 GN=ZMYND12 PE=1 SV=3
A3510	-	-	GO:0005509(calcium ion binding),GO:0005515(protein binding),GO:0003824(catalytic activity)	-	-	KOG0001 Hs22064818 Ubiquitin and ubiquitin-like proteins	KAG1101879.1 hypothetical protein G6F42_017444 [Rhizopus oryzae]	Polyubiquitin (Fragment) OS=Xenopus laevis OX=8355 PE=1 SV=2
A3511	-	-	-	-	-	-	-	-
A3512	GO:0006520(cellular amino acid metabolic process)	-	GO:0016491(oxidoreductase activity),GO:0016639(oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor)	-	-	KOG2250 At5g07440 Glutamate/leucine/phenylalanine/valine dehydrogenases	KAF0432779.1 NADP-binding protein [Gigaspora margarita]	Leucine dehydrogenase OS=Bacillus licheniformis OX=1402 GN=ldh PE=1 SV=1
A3513	-	-	-	-	-	-	-	-
A3514	-	-	GO:0005524(ATP binding)	K06185 ABCF2; ATP-binding cassette, subfamily F, member 2	map05130 Pathogenic Escherichia coli infection	KOG0927 Hs10947137 Predicted transporter (ABC superfamily)	TPX58272.1 hypothetical protein PhCBS80983_g03243 [Powellomyces hirtus]	ATP-binding cassette sub-family F member 2 OS=Homo sapiens OX=9606 GN=ABCF2 PE=1 SV=2

A3515	GO:0140647(P450-containing electron transport chain)	-	GO:0051537(2 iron, 2 sulfur cluster binding),GO:0051536(iron-sulfur cluster binding)	K22071 FDX2; ferredoxin-2; mitochondria l	-	-	KAF2403088.1 ferredoxin, partial [Trichodelisc hia bisporula]	2Fe-2S ferredoxin OS=Rickettsia conorii (strain ATCC VR-613 / Malish 7) OX=272944 GN=fdxB PE=3 SV=1
A3516	-	-	-	-	-	-	-	-
A3517	-	-	-	-	-	-	-	-
A3518	GO:0006355(regulation of transcription, DNA-templated),GO:0016570(histone modification)	-	GO:0005515(protein binding)	K15176 CTR9; RNA polymerase-associated protein CTR9	-	KOG2002 Hs7661950 TPR-containing nuclear phosphoprotein that regulates K(+) uptake	OZJ04482.1 hypothetical protein BZG36_02674 [Bifiguratus adelaidae]	RNA polymerase-associated protein CTR9 homolog OS=Homo sapiens OX=9606 GN=CTR9 PE=1 SV=1
A3519	GO:0019835(cytolysis),GO:0050829(defense response to Gram-negative bacterium)	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A3520	-	-	-	-	-	-	-	-
A3521	-	GO:0005762(mitochondrial large ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K17422 MRPL41; large subunit ribosomal protein L41	-	KOG4756 At5g39800 Mitochondrial ribosomal protein L27	ORX92721.1 hypothetical protein K493DRAFT_263152 [Basidiobolus meristosporus CBS 931.73]	-
A3522	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K07950 ARL5B; ADP-ribosylation factor-like protein 5B	-	KOG0070 At3g22950 GTP-binding ADP-ribosylation factor Arf1	RIB26550.1 ARF-like protein [Gigaspora rosea]	ADP-ribosylation factor-like protein 5A OS=Bos taurus OX=9913 GN=ARL5A PE=2 SV=1
A3523	-	-	GO:0005515(protein binding)	K21991 UNC45; protein unc-45	-	KOG4151 7298982 Myosin assembly protein/sexual cycle protein and related proteins	ORX57842.1 ARM repeat-containing protein [Piromyces finnis]	Protein unc-45 homolog A OS=Homo sapiens OX=9606 GN=UNC45A PE=1 SV=1
A3524	GO:0032259(methylation)	-	GO:0008168(methyltransferase activity)	-	-	KOG0908 Hs4759274 Thioredoxin-like protein	KXN71885.1 DUF1000-domain-containing protein [Conidiobolus coronatus NRRL 28638]	Thioredoxin-like protein 1 OS=Mus musculus OX=10090 GN=Txn1 PE=1 SV=3
A3525	GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	-	-	K20301 TRAPPC2, TRS20; trafficking protein particle complex subunit 2	-	KOG3487 Hs7657548 TRAPP 20 K subunit	KNE65144.1 hypothetical protein AMAG_10797 [Allomyces macrogynus ATCC 38327]	Trafficking protein particle complex subunit 2 OS=Dictyostelium discoideum OX=44689 GN=trappc2 PE=3 SV=1
A3526	-	-	-	-	-	-	-	-

A3527	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors);GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG0139 CE24778 Short-chain acyl-CoA dehydrogenase	RHZ54188.1 hypothetical protein Glove_429g4.2 [Diversispora epigaea]	Acyl-CoA dehydrogenase AFT10-1 OS=Alternaria alternata OX=5599 GN=AFT10-1 PE=3 SV=1
A3528	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY29231.1 hypothetical protein BCR33DRAFT_772551 [Rhizoclostium globosum]	-
A3529	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding);GO:0005515(protein binding)	K20606 ANP1; mitogen-activated protein kinase kinase ANP1 [EC:2.7.11.25]	map04016 MAPK signaling pathway - plant	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	OJT05228.1 MAP kinase kinase mkh1 [Trametes pubescens]	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase wee-1.3 OS=Caenorhabditis elegans OX=6239 GN=wee-1.3 PE=1 SV=1
A3530	-	-	-	-	-	-	-	-
A3531	-	-	-	-	-	-	KIM52504.1 hypothetical protein SCLCIDRAFT_1223705 [Scleroderma citrinum Foug A]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces ribosidificus OX=80859 GN=rbmC PE=3 SV=1
A3532	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A3533	-	-	-	-	-	-	OMJ15326.1 hypothetical protein AYI69_g8231 [Smittium culicis]	-
A3534	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3535	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9976048.1 hypothetical protein BGZ73_009207 [Actinomortierella ambigua]	Probable serine/threonine-protein kinase PkwA OS=Thermomonospora curvata OX=2020 GN=pkwa PE=1 SV=1
A3536	-	-	GO:0005515(protein binding)	-	-	-	TGZ84749.1 hypothetical protein EX30DRAFT_7016 [Ascodesmis nigricans]	-
A3537	-	-	-	-	-	-	-	-

A3538	-	-	-	K01897 ACSL fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04146 Peroxisome;map04216 Ferroptosis;map04714 Thermogenesis;map00061 Fatty acid biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation;map04920 Adipocytokine signaling pathway	KOG1180 Hs4758332 Acyl-CoA synthetase	PKK76989.1 acetyl-CoA synthetase-like protein [Rhizophagus irregularis]	Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens OX=9606 GN=ACSL4 PE=1 SV=2
A3539	GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds),GO:0008061(chitin binding)	-	-	KOG2806 Hs4502809 Chitinase	XP_01829788.1.1 glycoside hydrolase family 18 protein [Phycomyces blakesleeanus NRRL 1555(-)]	Chitotriosidase-1 OS=Mus musculus OX=10090 GN=Chit1 PE=1 SV=2
A3540	-	-	-	K06685 MOB1, Mats; MOB kinase activator 1	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04392 Hippo signaling pathway - multiple species;map04111 Cell cycle - yeast	KOG0440 Hs8922671 Cell cycle-associated protein Mob1-1	KXS17134.1 mps one binder kinase activator-like 1 protein [Gonapodya prolifera JEL478]	MOB kinase activator-like 1 homolog A OS=Dictyostelium discoideum OX=44689 GN=mobA PE=3 SV=1
A3541	-	-	-	-	-	-	-	-
A3542	-	-	-	-	-	-	-	-
A3543	-	-	-	-	-	-	-	-
A3544	GO:0055085(transmembrane transport),GO:0006862(nucleotide transport)	-	-	-	-	KOG0764 Hs21314739 Mitochondrial FAD carrier protein	KAF4303141.1 putative mitochondria l folate carrier protein [Botryosphaeria dothidea]	Folate transporter 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=FOLT1 PE=2 SV=1
A3545	GO:000668(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration;map04024 cAMP signaling pathway;map04020 Calcium signaling pathway;map05414 Dilated cardiomyopathy;map04140 Autophagy - animal;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map01522 Endocrine resistance;map04919 Thyroid hormone signaling pathway;map04918 Thyroid hormone synthesis;map04	KOG0614 Hs10835242 cGMP-dependent protein kinase	KIM58345.1 hypothetical protein SCLCIDRAFT_1218691 [Scleroderma citrinum Foug A]	cGMP-dependent protein kinase 1 OS=Homo sapiens OX=9606 GN=PRKG1 PE=1 SV=3

A3546	GO:0006801(superoxide metabolic process)	-	GO:0046872(metal ion binding)	K04565 SOD1; superoxide dismutase, Cu-Zn family [EC:1.15.1.1]	map05014 Amyotrophic lateral sclerosis;map04146 Peroxisome;map04213 Longevity regulating pathway - multiple species;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05012 Parkinson disease;map05016 Huntington disease	KOG0441 At1g08830 Cu2+/Zn2+ superoxide dismutase SOD1	KAG0039706.1 Superoxide dismutase [Cu-Zn] [Podila clonocystis]	Superoxide dismutase [Cu-Zn] 2 OS=Solanum lycopersicum OX=4081 GN=SODCC.5 PE=3 SV=3
A3547	GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	GO:0005789(endoplasmic reticulum membrane)	-	K20362 YIF1; protein transport protein YIF1	-	KOG3094 Hs20545322 Predicted membrane protein	XP_007306833.1 YIF1-domain-containing protein [Sterium hirsutum FP-91666 SS1]	Protein YIF1B-B OS=Xenopus laevis OX=8355 GN=yif1b-b PE=2 SV=1
A3548	-	-	GO:0016491(oxidoreductase activity)	-	-	-	KAF9142573.1 hypothetical protein BGX30_002635 [Mortierella sp. GBA39]	NADH dehydrogenase OS=Thermus thermophilus (strain ATCC 27634 / DSM 579 / HB8) OX=300852 GN=nox PE=1 SV=2
A3549	-	-	GO:0003824(catalytic activity)	-	-	KOG1680 7303265 Enoyl-CoA hydratase	KAG1394636.1 hypothetical protein G6F59_014148 [Rhizopus oryzae]	Short-chain-enoil-CoA hydratase OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) OX=272562 GN=crt PE=1 SV=1
A3550	-	-	-	-	-	-	-	-
A3551	-	GO:0005634(nucleus)	-	K14782 AATF, BFR2; protein AATF/BFR2	-	-	RKO92008.1 apoptosis-antagonizing transcription factor [Blyttiomycetes helicus]	Protein bfr2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=bfr2 PE=1 SV=1
A3552	-	-	-	-	-	-	ORX92017.1 NAD(P)-binding protein [Basidiobolus meristosporus CBS 931.73]	Delta(1)-pyrroline-2-carboxylate reductase OS=Bacillus cereus (strain ZK / E33L) OX=288681 GN=arcB PE=1 SV=1
A3553	GO:0007034(vacuolar transport)	-	-	K12198 CHMP5, VPS60; charged multivesicular body protein 5	map04144 Endocytosis;map04217 Necroptosis	KOG1655 At5g04850 Protein involved in vacuolar protein sorting	KAG0329885.1 hypothetical protein BG000_011899 [Podila horticola]	Vacuolar protein sorting-associated protein 60.2 OS=Arabidopsis thaliana OX=3702 GN=VPS60-2 PE=2 SV=1
A3554	-	-	GO:0005515(protein binding)	K04460 PPP5C; serine/threonine-protein phosphatase 5 [EC:3.1.3.16]	map04010 MAPK signaling pathway	KOG4648 Hs13375809 Uncharacterized conserved protein, contains LRR repeats	KAF9382308.1 hypothetical protein CPB97_007236 [Podila verticillata]	RNA polymerase II-associated protein 3 OS=Xenopus laevis OX=8355 GN=rpap3 PE=2 SV=1

A3555	GO:0044237(cellular metabolic process), GO:0006310(DNA recombination),GO:0006260(DNA replication),GO:0006281(DNA repair)	-	GO:0003676(nucleic acid binding),GO:0000166(nucleotide binding),GO:0004386(helicase activity),GO:0043138(3'-5' DNA helicase activity),GO:0005524(ATP binding)	-	-	KOG0351 At1g10930 ATP-dependent DNA helicase	RAO71919.1 hypothetical protein BHQ10_007931 [Talaromyces amestolkiae]	ATP-dependent DNA helicase Q-like 4A OS=Arabidopsis thaliana OX=3702 GN=RECQL4A PE=2 SV=1
A3556	-	-	-	-	-	-	-	-
A3557	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	EPZ37081.1 Adenylyl cyclase class-3/4/guanylyl cyclase domain-containing protein [Rozella allomyces CSF55]	Adenylate cyclase type 10 OS=Oryctolagus cuniculus OX=9986 GN=ADCY10 PE=2 SV=1
A3558	-	-	-	-	-	-	-	-
A3559	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3560	-	-	GO:0003676(nucleic acid binding),GO:0004519(endonuclease activity)	-	-	-	ORX67169.1 hypothetical protein DL89DRAFT_53940 [Linderina pennisporea]	-
A3561	-	GO:0016020(membrane)	GO:0016651(oxidoreductase activity, acting on NAD(P)H),GO:0051539(4 iron, 4 sulfur cluster binding)	K03941 NDUFS8; NADH dehydrogenase (ubiquinone) Fe-S protein 8 [EC:7.1.1.2]	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG3256 At1g16700 NADH:ubiquinone oxidoreductase, NDUFS8/23 kDa subunit	GAW23755.1 hypothetical protein ANO14919_133310 [fungal sp. No.14919]	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-B, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At1g16700 PE=1 SV=1
A3562	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K03243 EIF5B; translation initiation factor 5B	-	KOG1144 At1g76810 Translation initiation factor 5B (eIF-5B)	ORX81897.1 P-loop containing nucleoside triphosphate hydrolase protein [Anaeromyces robustus]	Eukaryotic translation initiation factor 5B OS=Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719) OX=759272 GN=CTHT_0029840 PE=1 SV=2
A3563	-	-	-	-	-	-	-	-

A3564	GO:0006259(DNA metabolic process), GO:0006281(DNA repair), GO:0006310(DNA recombination)	-	GO:0003677(DNA binding), GO:0005524(ATP binding), GO:0008094(ATPase, acting on DNA), GO:0003684(damaged DNA binding)	K10872 DMC1; meiotic recombination protein DMC1	map04113 Meiosis - yeast	KOG1434 Hs5901996 Meiotic recombination protein Dmc1	EPZ30915.1 Meiotic recombination protein DMC1/LIM15-like protein [Rozella allomyces CSF55]	Meiotic recombination protein DMC1/LIM15 homolog OS=Mus musculus OX=10090 GN=Dmc1 PE=1 SV=1
A3565	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding), GO:0016491(oxidoreductase activity)	-	-	KOG0873 7292910 C-4 sterol methyl oxidase	-	-
A3566	-	-	GO:0070569(uridylyltransferase activity)	K00972 UAP1; UDP-N-acetylglucosamine/UDP-N-acetylgalactosamine diphosphorylase [EC:2.7.7.23 2.7.7.83]	map01250 Biosynthesis of nucleotide sugars; map00520 Amino sugar and nucleotide sugar metabolism; map01100 Metabolic pathways	KOG2388 At5g52560 UDP-N-acetylglucosamine pyrophosphorylase	XP_018175935.1 UDP-N-acetylglucosamine pyrophosphorylase [Purpureocillium lilacinum]	UDP-sugar pyrophosphorylase OS=Pisum sativum OX=3888 GN=USP PE=1 SV=1
A3567	-	GO:0016459(myosin complex)	GO:0003774(motor activity), GO:0005524(ATP binding), GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection; map04814 Motor proteins	KOG0160 At4g28710 Myosin class V heavy chain	TPX57088.1 hypothetical protein SpCBS45565_g08273 [Spizellomyces sp. 'palustris']	Myosin-14 OS=Arabidopsis thaliana OX=3702 GN=XI-H PE=3 SV=1
A3568	-	-	-	-	-	-	-	-
A3569	-	-	GO:0008270(zinc ion binding)	K24512 VWA8; von Willebrand factor A domain-containing protein 8	-	KOG1808 Hs22053093 AAA ATPase containing von Willebrand factor type A (vWA) domain	KXS13469.1 hypothetical protein M427DRAFT_33874 [Gonapodya prolifera JEL478]	von Willebrand factor A domain-containing protein 8 OS=Danio rerio OX=7955 GN=sidkey-181.1 PE=3 SV=1
A3570	-	-	GO:0035091(phosphatidylinositol binding)	-	-	-	-	-
A3571	GO:0006334(nucleosome assembly)	GO:0000786(nucleosome)	GO:0003677(DNA binding), GO:0030527(structural constituent of chromatin)	-	-	-	-	-
A3572	-	-	GO:0005515(protein binding)	K11805 DCAF7, HAN11; DDB1- and CUL4-associated factor 7	map03083 Polycomb repressive complex	KOG0290 Hs5031729 Conserved WD40 repeat-containing protein AN11	KAG4099696.1 WD40-repeat-containing domain protein [Neocallimastix sp. JGI-2020a]	DDB1- and CUL4-associated factor 7 OS=Homo sapiens OX=9606 GN=DCAF7 PE=1 SV=1
A3573	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity), GO:0005524(ATP binding), GO:0008017(microtubule binding)	K10393 KIF2_24, MCAK; kinesin family member 2/24	map04361 Axon regeneration; map04814 Motor proteins	KOG0246 CE29333 Kinesin-like protein	OAD01967.1 hypothetical protein MUCCIDRAFT_144130, partial [Mucor lusitanicus CBS 277.49]	Diatom spindle kinesin-1 OS=Cylindrotheca fusiformis OX=2853 GN=DSK1 PE=2 SV=1

A3574	GO:000612(cation transport)	GO:0016021(integral component of membrane)	GO:0019829(ATPase-coupled cation transmembrane transporter activity),GO:0140358(P-type transmembrane transporter activity),GO:0001666(nucleotide binding),GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K14950 ATP13A1, SPF1; manganese-transporting P-type ATPase [EC:7.2.2.-]	-	KOG0209 At5g23630 P-type ATPase	ORX44343.1 hypothetical protein BCR36DRAFT_373362 [Piromyces finnis]	Probable manganese-transporting ATPase PDR2 OS=Arabidopsis thaliana OX=3702 GN=PDR2 PE=1 SV=1
A3575	-	-	-	-	-	-	KAG0281992.1 hypothetical protein BGX97_009190 [Linnemannia gamsii]	-
A3576	-	-	-	-	-	-	-	-
A3577	GO:0006400(tRNA modification),GO:0101030(tRNA-guanine transglycosylation)	-	GO:0016763(peptidyl transferase activity),GO:0008479(queuine tRNA-ribosyltransferase activity)	K00777 QTRT1; queuine tRNA-ribosyltransferase catalytic subunit [EC:2.4.2.64]	-	KOG3908 7296102 Queuine-tRNA ribosyltransferase	KAF9122846.1 hypothetical protein BGX30_001750 [Mortierella sp. GBA39]	Queuine tRNA-ribosyltransferase OS=Protochlamydia amoebophila (strain UWE25) OX=264201 GN=tgt PE=3 SV=1
A3578	GO:0006555(methionine metabolic process)	-	GO:0004489(methylenetetrahydrofolate reductase (NAD(P)H) activity)	K25004 MTHFR; methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.53]	map00670 One carbon pool by folate;map01523 Antifolate resistance;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG0564 At3g59970 5,10-methylenetetrahydrofolate reductase	ORX97664.1 methylenetetrahydrofolate reduct [Basidiobolus meristosporus CBS 931.73]	Methylenetetrahydrofolate reductase (NADH) 2 OS=Arabidopsis thaliana OX=3702 GN=MTHFR2 PE=1 SV=2
A3579	-	-	-	K14832 MAK21, NOC1, CEBPZ; ribosome biogenesis protein MAK21	-	KOG2038 Hs5031625 CAAT-binding transcription factor/60S ribosomal subunit biogenesis protein	ORY08287.1 CBF-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	CCAAT/enhancer-binding protein zeta OS=Mus musculus OX=10090 GN=Cebpz PE=1 SV=2
A3580	GO:0006801(superoxide metabolic process)	-	GO:0046872(metal ion binding)	-	-	-	-	-
A3581	GO:0016973(poly(A)+ mRNA export from nucleus)	-	-	K24364 CSN12; COP9 signalosome complex subunit 12	-	KOG2688 Hs8922987 Transcription-associated recombination protein - Thp1p	KAG2174209.1 hypothetical protein INT43_004230 [Umbelopsis isabellina]	PCI domain-containing protein 2 homolog OS=Dictyostelium discoideum OX=44689 GN=pcid2 PE=3 SV=1
A3582	-	-	-	-	-	-	-	-
A3583	-	-	-	-	-	-	-	-
A3584	-	-	-	-	-	-	-	-
A3585	-	-	-	-	-	-	-	-

A3586	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	KAE8378173.1 C-terminal E3 ligase [Aspergillus bertholletiae]	E3 ubiquitin-protein ligase SspH2 OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=sspH2 PE=1 SV=1
A3587	GO:0006094(gluconeogenesis)	-	GO:0004611(phosphoenolpyruvate carboxykinase activity);GO:0017076(purine nucleotide binding);GO:0004612(phosphoenolpyruvate carboxykinase (ATP) activity);GO:0005524(ATP binding)	K01610 E4.1.1.49, pckA; phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00710 Carbon fixation in photosynthetic organisms;map00620 Pyruvate metabolism;map01100 Metabolic pathways	-	ORX94628.1 ATP-utilizing phosphoenolpyruvate carboxykinase [Basidiobolus meristosporus CBS 931.73]	Phosphoenolpyruvate carboxykinase (ATP) OS=Sulfurimonas denitrificans (strain ATCC 33889 / DSM 1251) OX=326298 GN=pckA PE=3 SV=1
A3588	-	-	-	-	-	-	TPX73450.1 hypothetical protein CcCBS67573_g05280 [Chytridiomycota confervae]	Lipase 2 OS=Staphylococcus aureus (strain NCTC 8325 / PS 47) OX=93061 GN=lip2 PE=1 SV=1
A3589	-	-	GO:0005515(protein binding)	K03036 PSMD11, RPN6; 26S proteasome regulatory subunit N6	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG1463 At1g29150 26S proteasome regulatory complex, subunit RPN6/PSMD11	KAG0357212.1 26S proteasome regulatory subunit rpn6 [Gamsiella multidivariata]	26S proteasome non-ATPase regulatory subunit 11 homolog OS=Arabidopsis thaliana OX=3702 GN=RPN6 PE=1 SV=1
A3590	-	-	GO:0005515(protein binding)	-	-	-	ORY53705.1 hypothetical protein BCR33DRAFT_779054 [Rhizoclostium globosum]	IQ and ubiquitin-like domain-containing protein OS=Macaca fascicularis OX=9541 GN=IQUB PE=2 SV=2
A3591	-	-	-	-	-	-	-	-

A3592	GO:0006430(lysyl-tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation)	GO:0005737(cytoplasm)	GO:0004824(lysine-tRNA ligase activity),GO:0005524(ATP binding),GO:0001666(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0003676(nucleic acid binding)	K04567 KARS, lysyl-lysyl-tRNA synthetase, class II [EC:6.1.1.6]	map00970 Aminoacyl-tRNA biosynthesis	KOG1885 CE04861 Lysyl-tRNA synthetase (class II)	XP_016609935.1 lysine-tRNA ligase [Spizellomyces punctatus DAOM BR117]	Lysine--tRNA ligase OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0586800 PE=2 SV=1
A3593	-	-	GO:0005525(GTP binding)	-	-	-	KAF9978754.1 GTPase IMAP member 7 [Modicella reniformis]	-
A3594	-	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	KOG0941 Hs7657152 E3 ubiquitin protein ligase	RKP35922.1 hypothetical protein BJ085DRAFT_15729, partial [Dimargaris cristalligena]	Probable E3 ubiquitin-protein ligase HERC3 OS=Homo sapiens OX=9606 GN=HERC3 PE=1 SV=1
A3595	-	-	-	-	-	-	-	-
A3596	-	-	-	-	-	-	-	-
A3597	-	-	-	-	-	-	-	-
A3598	-	-	-	K03676 grxC, GLRX, GLRX2; glutaredoxin 3	-	KOG1752 7293857 Glutaredoxin and related proteins	CEG75077.1 Putative Glutaredoxin [Rhizopus microsporus]	Glutaredoxin 1 OS=Rickettsia felis (strain ATCC VR-1525 / URRWXCal2) OX=315456 GN=grxC1 PE=3 SV=1
A3599	-	GO:0000178(exosome (RNase complex))	GO:0003723(RNA binding)	K03679 RRP4, EXOSC2; exosome complex component RRP4	map03018 RNA degradation	KOG3013 Hs19923403 Exosomal 3'-5' exoribonuclease complex, subunit Rrp4	XP_016611291.1 hypothetical protein SPPG_02305 [Spizellomyces punctatus DAOM BR117]	Exosome complex component RRP4 OS=Mus musculus OX=10090 GN=Exosc2 PE=1 SV=1
A3600	GO:0016579(protein deubiquitination)	-	GO:0005515(protein binding),GO:0004843(thiol-dependent deubiquitinase)	K11853 USP34; ubiquitin carboxyl-terminal hydrolase 34 [EC:3.4.19.12]	-	KOG1866 7302097 Ubiquitin carboxyl-terminal hydrolase	KAF3924876.1 hypothetical protein ABW21_db0205556 [Drechslerella brochopaga]	Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens OX=9606 GN=USP34 PE=1 SV=2
A3601	-	-	-	-	-	-	-	-
A3602	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	K15378 SLC45A1_2_4; solute carrier family 45, member 1/2/4	-	KOG0637 At5g43610 Sucrose transporter and related proteins	KAF7723864.1 hypothetical protein DSO57_007400 [Entomophthora muscae]	Sucrose transport protein SUT2 OS=Oryza sativa subsp. indica OX=39946 GN=SUT2 PE=2 SV=2
A3603	GO:0055085(transmembrane transport)	GO:0016020(membrane)	-	-	-	-	PVV04058.1 hypothetical protein BB560_001450 [Smittium megazygosporum]	Mechanosensitive ion channel protein Msy1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=msy1 PE=1 SV=1

A3604	GO:0007017(microtubule-based process)	GO:0005874(microtubule)	GO:0005525(GTP binding);GO:0003924(GTPase activity);GO:0005200(structural constituent of cytoskeleton)	K07375 TUBB; tubulin beta	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins;map04540 Gap junction;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG1375 Hs5174735 Beta tubulin	XP_006680448.1 Alpha-Beta tubulin [Batrachochytrium dendrobatidis JAM81]	Tubulin beta chain OS=Tetrahymena thermophila OX=5911 GN=BTU1 PE=1 SV=1
A3605	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome);GO:0005506(iron ion binding);GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen);GO:0031418(L-ascorbic acid binding)	K02917 RP-L35Ae, RPL35A; large subunit ribosomal protein L35Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0887 At1g74270 60S ribosomal protein L35A/L37	XP_011121694.1 hypothetical protein AOL_s00078g129 [Orbilia oligospora ATCC 24927]	Large ribosomal subunit protein eL33 OS=Ictalurus punctatus OX=7998 GN=rpl35a PE=3 SV=1
A3606	-	-	GO:0005515(protein binding)	-	-	KOG0272 7293972 U4/U6 small nuclear ribonucleoprotein Prp4 (contains WD40 repeats)	CAE6471756.1 unnamed protein product [Rhizoctonia solani]	U4/U6 small nuclear ribonucleoprotein PRP4-like protein OS=Arabidopsis thaliana OX=3702 GN=LIS PE=2 SV=1
A3607	-	-	-	-	-	KOG1430 Hs4504509 C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	XP_018712512.1 hypothetical protein METBIDRAFT_30988 [Metschnikowia bicuspidata var. bicuspidata NRRL YB-4993]	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase OS=Canis lupus familiaris OX=9615 GN=HSD3B PE=2 SV=3
A3608	-	-	-	-	-	-	PVU98298.1 hypothetical protein BB559_001692 [Furculomyces boomerangs]	-

A3609	GO:0006351(transcription, DNA-templated)	-	GO:0046983(protein dimerization activity),GO:0003677(DNA binding),GO:0003899(DNA-directed 5'-3' RNA polymerase activity)	K03020 RPAC2, RPC19, POLR1D; DNA-directed RNA polymerases I and III subunit RPAC2	map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway	KOG3438 7298551 DNA-directed RNA polymerase, subunit L	TLD30154.1 RBP11-like subunits of RNA polymerase [Venturia nashicola]	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Bos taurus OX=9913 GN=POLR1D PE=2 SV=1
A3610	-	-	-	-	-	-	-	-
A3611	-	-	-	-	-	-	-	-
A3612	-	-	-	-	-	-	ORY49844.1 Clavaminic synthase-like protein [Rhizoclostium globosum]	-
A3613	GO:0006270(DNA replication initiation)	-	-	K06628 CDC45; cell division control protein 45	map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG2475 Hs4502713 CDC45 (cell division cycle 45)-like protein	KAG2173810.1 hypothetical protein INT43_005230 [Umbelopsis isabellina]	Cell division control protein 45 homolog OS=Homo sapiens OX=9606 GN=CDC45 PE=1 SV=1
A3614	GO:0006470(protein dephosphorylation)	-	GO:0043169(cation binding),GO:0004722(protein serine/threonine phosphatase activity)	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698 At1g09160 Serine/threonine protein phosphatase	-	Probable protein phosphatase 2C 5 OS=Arabidopsis thaliana OX=3702 GN=At1g09160 PE=2 SV=1
A3615	-	-	-	-	-	KOG4276 7297647 Predicted hormone receptor interactor	-	BTB/POZ domain-containing protein At2g30600 OS=Arabidopsis thaliana OX=3702 GN=At2g30600/At2g30610 PE=2 SV=1
A3616	GO:0042176(regulation of protein catabolic process)	GO:0000502(proteasome complex)	GO:0030234(enzyme regulator activity)	K03028 PSMD2, RPN1; 26S proteasome regulatory subunit N1	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG2005 Hs20149522 26S proteasome regulatory complex, subunit RPN1/PSMD2	PKC65115.1 26S proteasome regulatory complex, non-ATPase subcomplex, Rpn1 subunit [Rhizophagus irregularis]	26S proteasome non-ATPase regulatory subunit 2 OS=Bos taurus OX=9913 GN=PSMD2 PE=1 SV=2

A3617	-	-	-	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04 022 cGMP-PKG signaling pathway;map04 020 Calcium signaling pathway;map05 417 Lipid and atherosclerosis; map05133 Pertussis;map04 722 Neurotrophin signaling pathway;map04 218 Cellular senescence;map 04070 Phosphatidyli nitol signaling system;map0491 5 Estrogen signaling pathway;map04 912 GnRH signaling pathway;map04 910 Insulin	-	XP_00418196 2.1 hypothetical protein TBLA_0H0156 0 [Tetrapispor a blattae CBS 6284]	-
A3618	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K11835 USP4_11, UBP12; ubiquitin carboxyl- terminal hydrolase 4/11 [EC:3.4.19.12]	-	KOG1870[Hs4 507853 Ubiquitin C- terminal hydrolase	ORX96526.1 UCH- domain- containing protein [Basidiobolus meristosporus CBS 931.73]	Ubiquitin carboxyl-terminal hydrolase 4 OS=Mus musculus OX=10090 GN=Usp4 PE=1 SV=3
A3619	GO:0006260(DNA replication)	GO:0005634(nucleus),GO:0043625(delta DNA polymerase complex)	-	-	-	-	-	DNA polymerase delta subunit 3 OS=Gallus gallus OX=9031 GN=POLD3 PE=1 SV=2
A3620	-	-	-	-	-	-	-	-
A3621	-	-	-	-	-	-	-	-
A3622	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016578(histone deubiquitination),GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	-	-	KOG1867[Hs2 2065367 Ubiquitin- specific protease	KAF6013508. 1 hypothetical protein HII13_001324 [Brettanomyces bruxellensis]	Ubiquitin carboxyl-terminal hydrolase 27 OS=Homo sapiens OX=9606 GN=USP27X PE=1 SV=3
A3623	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0603[Hs2 0149547 Ribosomal protein S6 kinase	RKP20702.1 kinase-like protein [Rozella allomycis CSF55]	Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens OX=9606 GN=RPS6KA1 PE=1 SV=2
A3624	GO:0000002(mitochondrial genome maintenance)	GO:0031305(integral component of mitochondrial inner membrane)	-	-	-	-	-	Mitochondrial escape protein 2 homolog OS=Dictyostelium discoideum OX=44689 GN=yme2 PE=3 SV=1
A3625	-	-	-	-	-	-	KAF1837351. 1 hypothetical protein BDW02DRAFT_566201 [Decorospora gaudefroyi]	-

A3626	-	-	GO:0016746(acyltransferase activity),GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups)	K08764 SCP2 SCPX; sterol carrier protein 2 [EC:2.3.1.176]	map03320 PPAR signaling pathway;map04146 Peroxisome;map00120 Primary bile acid biosynthesis;map01040 Biosynthesis of unsaturated fatty acids;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG1406 7298493_1 Peroxisomal 3-ketoacyl-CoA-thiolase P-44/SCP2	KAG0232926.1 sterol carrier protein 2 [Actinomortierella wolfii]	Sterol carrier protein 2 OS=Oryctolagus cuniculus OX=9986 GN=SCP2 PE=1 SV=1
A3627	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity),GO:0004674(protein serine/threonine kinase activity),GO:0004692(cGMP-dependent protein kinase activity)	K19584 PRKX; protein kinase X [EC:2.7.11.11]	-	KOG0614 Hs10835242 cGMP-dependent protein kinase	KAF9162565.1 hypothetical protein BGX20_001681 [Mortierella sp. AD010]	cGMP-dependent protein kinase 1 OS=Bos taurus OX=9913 GN=PRKG1 PE=1 SV=2
A3628	-	-	-	-	-	-	-	-
A3629	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	RKP21311.1 adenylyl cyclase, partial [Rozella allomyces CSF55]	Adenylate cyclase type 10 OS=Rattus norvegicus OX=10116 GN=Adcy10 PE=1 SV=1
A3630	GO:0007186(G protein-coupled receptor signaling pathway), GO:0019236(response to pheromone)	-	-	-	-	KOG4290 7291350 Predicted membrane protein	-	Transmembrane protein 145 OS=Mus musculus OX=10090 GN=Tmem145 PE=1 SV=1
A3631	-	-	GO:0005515(protein binding)	K05864 PPID; CYPD; peptidyl-prolyl isomerase D [EC:5.2.1.8]	map05131 Shigellosis;map04217 Necroptosis;map04218 Cellular senescence;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease	KOG0543 At5g48570 FKBP-type peptidyl-prolyl cis-trans isomerase	XP_031027223.1 uncharacterized protein SmJEL517_g01052 [Synchytrium microbalum]	Peptidyl-prolyl cis-trans isomerase FKBP35 OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=FKBP35 PE=1 SV=1
A3632	-	-	-	-	-	-	-	-
A3633	-	-	-	-	-	KOG2819 At3g51130 Uncharacterized conserved protein	RHZ68260.1 hypothetical protein Glove_296g23 [Diversispora epigaea]	PHAF1 protein At3g51130 OS=Arabidopsis thaliana OX=3702 GN=At3g51130 PE=1 SV=2

A3634	-	-	-	-	-	-	-	-
A3635	-	-	-	-	-	-	-	-
A3636	-	-	-	-	-	-	-	-
A3637	-	-	-	-	-	-	-	-
A3638	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At5g23580 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	RKO99416.1 hypothetical protein CXG81DRAFT_30214 [Caulochytrium protostelioides]	Calcium/calmodulin-dependent protein kinase type 1 OS=Macrobrachium nipponense OX=159736 GN=CaMKI PE=2 SV=1
A3639	-	-	-	-	-	-	-	-
A3640	-	GO:0005759(mitochondrial matrix)	-	K15414 C1QBP; complement component 1 Q subcomponent-binding protein, mitochondrial	-	KOG2536 At1g15870 MAM33, mitochondrial matrix glycoprotein	KNE87806.1 hypothetical protein PSTG_18803 [Puccinia striiformis f. sp. tritici PST-78]	-
A3641	-	-	-	-	-	-	-	-
A3642	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1543 At5g60360 Cysteine proteinase Cathepsin L	KFH62689.1 hypothetical protein MVEG_12081 [Podila verticillata NRRL 6337]	Pro-cathepsin H OS=Medicago truncatula OX=3880 GN=CP PE=1 SV=1
A3643	-	-	-	K01733 thrC; threonine synthase [EC:4.2.3.1]	map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00750 Vitamin B6 metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	-	SSD60044.1 probable Threonine synthase [Saccharomyces ludwigii]	Threonine synthase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=thrc PE=1 SV=1
A3644	GO:0035025(positive regulation of Rho protein signal transduction)	-	GO:0003779(activation binding)	-	-	KOG3376 CE15975 Uncharacterized conserved protein	KXS19922.1 C6orf115 protein [Gonapodya prolifera JEL478]	Actin-binding Rho-activating protein OS=Mus musculus OX=10090 GN=Abra PE=1 SV=1
A3645	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003899(DNA-directed 5'-3' RNA polymerase activity)	K03013 RPABC1, RPB5, POLR2E; DNA-directed RNA polymerases I, II, and III subunit RPABC1	map03420 Nucleotide excision repair;map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway;map05016 Huntington disease	KOG3218 At3g22320 RNA polymerase, 25-kDa subunit (common to polymerases I, II and III)	ORX46595.1 hypothetical protein BCR36DRAFT_585066 [Piromyces finnis]	DNA-directed RNA polymerases II and IV subunit 5A OS=Arabidopsis thaliana OX=3702 GN=NRPB5A PE=1 SV=1

A3646	-	-	-	-	-	-	KAG1250098.1 hypothetical protein G6F65_018867 [Rhizopus oryzae]	-
A3647	GO:0016311(dephosphorylation),GO:0030837(negative regulation of actin filament polymerization),GO:0006470(protein dephosphorylation)	-	GO:0008138(protein tyrosine/serine/threonine phosphatase activity),GO:0016791(phosphatase activity),GO:0003779(actin binding)	-	-	KOG1716[Hs18644716_2 Dual specificity phosphatase	RKP10944.1 protein-tyrosine phosphatase-like protein [Thamnocephalis sphaerospora]	Protein phosphatase Slingshot homolog 1 OS=Homo sapiens OX=9606 GN=SSH1 PE=1 SV=2
A3648	GO:0042255(ribosome assembly)	GO:0005634(nucleus)	GO:0003723(RNA binding)	K07565 NIP7; 60S ribosome subunit biogenesis protein NIP7	-	-	KAF9972881.1 ribosome biogenesis protein nip7 [Actinomyces rella ambigua]	60S ribosome subunit biogenesis protein NIP7 homolog OS=Xenopus tropicalis OX=8364 GN=nip7 PE=2 SV=1
A3649	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K13116 DDX41, ABS; ATP-dependent RNA helicase DDX41 [EC:3.6.4.13]	-	KOG0341[At5g51280 DEAD-box protein abstract	KXS19782.1 putative ATP-dependent RNA helicase DDX41 [Gonapodya prolifera JEL478]	DEAD-box ATP-dependent RNA helicase 35 OS=Arabidopsis thaliana OX=3702 GN=RH35 PE=2 SV=1
A3650	GO:0006520(cellular amino acid metabolic process)	-	GO:0003824(catalytic activity),GO:0016829(lyase activity)	K01620 Itae; threonine aldolase [EC:4.1.2.48]	map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG3058[At3g54020 Uncharacterized conserved protein	KAG1217835.1 hypothetical protein G6F35_008815 [Rhizopus oryzae]	Low specificity L-threonine aldolase OS=Pseudomonas sp. (strain NCIMB 10558) OX=268808 GN=ItaE PE=1 SV=1
A3651	GO:0010038(response to metal ion),GO:0046938(phytochelatin biosynthetic process)	-	GO:0016756(glutathione gamma-glutamylcysteinyltransferase activity),GO:0046872(metal ion binding)	-	-	KOG0632[At1g03980 Phytochelatin synthase	KAF9354453.1 hypothetical protein BGX26_007703 [Mortierella sp. AD094]	Glutathione gamma-glutamylcysteinyltransferase 1 OS=Triticum aestivum OX=4565 GN=PCS1 PE=2 SV=1
A3652	GO:0006414(translational elongation)	-	GO:0003746(translation elongation factor activity),GO:0005525(GTP binding),GO:0003924(GTPase activity)	K03231 EEF1A; elongation factor 1-alpha	map05134 Legionellosis;map05140 Leishmaniasis;map03013 Nucleocytoplasmic transport	-	AYM47848.1 transcription elongation factor 1 [Starmerella bombicola]	Elongation factor 1- alpha 1 OS=Trypanosoma brucei brucei (strain 927/4 GUTat10.1) OX=185431 GN=TEF1 PE=1 SV=1

A3653	-	-	-	-	-	KOG4157 7293063 beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	-	WSCD family member AGAP003962 OS=Anopheles gambiae OX=7165 GN=AGAP003962 PE=3 SV=3
A3654	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239 At5g65930.2 Kinesin (KAR3 subfamily)	KXN69631.1 kinesin-domain-containing protein, partial [Conidiobolus coronatus NRRL 28638]	Kinesin-like protein KIN-14l OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14l PE=2 SV=1
A3655	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08287 E2.7.12.1; dual-specificity kinase [EC:2.7.12.1]	-	KOG0671 At4g24740 LAMMER dual specificity kinases	ORX69231.1 kinase-like protein, partial [Linderina pennisporea]	Serine/threonine-protein kinase AFC2 OS=Arabidopsis thaliana OX=3702 GN=AFC2 PE=1 SV=1
A3656	-	-	-	K14550 UTP10, HEATR1; U3 small nucleolar RNA-associated protein 10	map03008 Ribosome biogenesis in eukaryotes	KOG1837 Hs20478440 Uncharacterized conserved protein	XP_016610018.1 hypothetical protein SPPG_02486, partial [Spizellomyces punctatus DAOM BR117]	HEAT repeat-containing protein 1 OS=Danio rerio OX=7955 GN=heatr1 PE=2 SV=1
A3657	-	-	-	K13577 SLC25A10, DIC; solute carrier family 25 (mitochondrial dicarboxylate transporter), member 10	map04964 Proximal tubule bicarbonate reclamation	KOG0759 Hs21361114 Mitochondrial oxoglutarate/malate carrier proteins	OZJ04927.1 hypothetical protein BZG36_02652 [Bifiguratus adalaidae]	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus OX=10090 GN=Slc25a11 PE=1 SV=3
A3658	-	-	-	-	-	-	-	-
A3659	GO:0005975(carbohydrate metabolic process), GO:0045493(xylan catabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds),GO:0009044(xylan 1,4-beta-xylosidase activity)	K15920 XYL4; xylan 1,4-beta-xylosidase [EC:3.2.1.37]	map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	-	KIP06623.1 glycoside hydrolase family 3 protein [Phlebiopsis gigantea 11061.1 CR5-6]	Probable beta-D-xylosidase 2 OS=Arabidopsis thaliana OX=3702 GN=BXL2 PE=2 SV=1
A3660	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding),GO:0016491(oxidoreductase activity)	K07750 MESO1, ERG25; methylsterol monooxygenase [EC:1.14.18.9]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG0873 At1g07420 C-4 sterol methyl oxidase	KAF9584158.1 C-4 sterol methyl oxidase [Lunasporengiospora selenosporea]	Putative methylsterol monooxygenase DDB_G0269788 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0269788 PE=3 SV=1
A3661	-	GO:0030289(protein phosphatase 4 complex)	GO:0019888(protein phosphatase regulator activity)	K15425 PPP4R2; serine/threonine-protein phosphatase 4 regulatory subunit 2	-	KOG3175 7291160 Protein phosphatase 4 regulatory subunit 2 related protein	OON07868.1 hypothetical protein BSLG_02756 [Batrachochytrium salamandrivorans]	Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Drosophila melanogaster OX=7227 GN=PPP4R2r PE=1 SV=2

A3662	-	-	-	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis -	-	KAG2172719.1 hypothetical protein INT43_000066 [Umbelopsis isabellina]	Glutathione S-transferase 3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=gst3 PE=1 SV=3
A3663	-	-	-	-	-	-	-	-
A3664	-	-	GO:0016787(hydrolase activity)	-	-	-	XP_031024701.1 uncharacterized protein SmJEL517_g03340 [Synchytrium microbalum]	Uncharacterized protein y4mH OS=Sinorhizobium fredii (strain NBRC 101917 / NGR234) OX=394 GN=NGR_a02510 PE=3 SV=1
A3665	GO:0007062(sister chromatid cohesion), GO:0051276(chromosome organization)	GO:0008278(cohesion complex), GO:0005694(chromosome)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0005515(protein binding)	K06636 SMC1; structural maintenance of chromosome 1	map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	-	KAF8983388.1 Structural maintenance of chromosome protein 1 [Entomortiera lignicola]	Structural maintenance of chromosomes protein 1 OS=Arabidopsis thaliana OX=3702 GN=SMC1 PE=2 SV=2
A3666	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	K19932 NCS1; neuronal calcium sensor	-	KOG2106 Hs17477344 Uncharacterized conserved protein, contains HELP and WD40 domains	XP_031023021.1 uncharacterized protein SmJEL517_g05070 [Synchytrium microbalum]	Ciliary WD repeat-containing protein ctpx80 OS=Euplotoides octocarinatus OX=2716877 PE=3 SV=1
A3667	-	-	GO:0018024(histone-lysine N-methyltransferase activity)	-	-	-	-	-
A3668	-	-	GO:0005515(protein binding)	K14558 PWP2, UTP1; periodic tryptophan protein 2	map03008 Ribosome biogenesis in eukaryotes	-	KAF8935441.1 hypothetical protein BGZ58_005001 [Dissophora ornata]	Periodic tryptophan protein 2 homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC713.04c PE=1 SV=1
A3669	-	-	-	-	-	-	-	-
A3670	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	-	-
A3671	-	-	-	K09660 MPDU1; mannose-P-dolichol utilization defect 1	-	KOG3211 At5g59470 Predicted endoplasmic reticulum membrane protein Lec35/MPDU1 involved in monosaccharide-P-dolichol utilization	KAG0173527.1 hypothetical protein DFQ30_007709 [Apophysom yces sp. BC1015]	Mannose-P-dolichol utilization defect 1 protein homolog 1 OS=Arabidopsis thaliana OX=3702 GN=At5g59470 PE=2 SV=1

A3672	GO:0007010(cytoskeleton organization),GO:0030837(negative regulation of actin filament polymerization)	-	GO:0003779(actin binding)	-	-	-	CCG81398.1 Putative uncharacterized protein [Taphrina deformans PYCC 5710]	Talin-B OS=Dictyostelium discoideum OX=44689 GN=talB PE=2 SV=1
A3673	-	-	-	-	-	-	RKP25557.1 histidine phosphatase superfamily [Syncephalis pseudoplumigaleata]	-
A3674	-	-	-	-	-	-	-	-
A3675	GO:0005975(carbohydrate metabolic process)	-	GO:0004563(beta-N-acetylhexosaminidase activity),GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	K12373 HEXA_B; hexosaminidase [EC:3.2.1.52]	map04142 Lysosome;map00513 Various types of N-glycan biosynthesis;map00511 Other glycan degradation;map00603 Glycosphingolipid biosynthesis - globo and isoglobo series;map00600 Sphingolipid metabolism;map00604 Glycosphingolipid biosynthesis - ganglio series;map00531 Glycosaminoglycan degradation;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic	KOG2499 At3g55260 Beta-N-acetylhexosaminidase	KAG0349151.1 hypothetical protein BG004_001575 [Podila humilis]	Beta-hexosaminidase 3 OS=Arabidopsis thaliana OX=3702 GN=HEXO3 PE=1 SV=1
A3676	-	-	-	-	-	-	-	-
A3677	-	-	-	-	-	-	-	-
A3678	-	-	-	K24205 TMBIM, LFG; protein lifeguard	-	KOG1629 Hs14757108 Bax-mediated apoptosis inhibitor TEGT/B1-1	PKK74988.1 hypothetical protein RhiirC2_737583 [Rhizophagus irregularis]	Probable Bax inhibitor 1 OS=Paralichthys olivaceus OX=8255 GN=tmbim6 PE=2 SV=1
A3679	GO:0006644(phospholipid metabolic process)	-	-	K18693 DPP1, DPPL, PLPP4_5; diacylglycerol diphosphate phosphatase / phosphatidate phosphatase [EC:3.6.1.75 3.1.3.4]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism	KOG3030 At3g18220 Lipid phosphate phosphatase and related enzymes of the PAP2 family	KAG0068861.1 hypothetical protein BGZ89_003952 [Linnemannia elongata]	PA-phosphatase related-family protein DDB_G0284367 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0284367 PE=3 SV=1
A3680	-	-	-	-	-	-	-	-
A3681	GO:0005992(trehalose biosynthetic process)	-	GO:0003824(catalytic activity),GO:0030246(carbohydrate binding),GO:2001070(starch binding)	K16055 TPS; trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]	map01110 Biosynthesis of secondary metabolites;map00500 Starch and sucrose metabolism;map01100 Metabolic pathways	KOG1050 At1g06410 Trehalose-6-phosphate synthase component TPS1 and related subunits	XP_021876220.1 glycosyltransferase family 20-domain-containing protein [Lobosporangium transversale]	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 7 OS=Arabidopsis thaliana OX=3702 GN=TPS7 PE=1 SV=1

A3682	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02971 RP-S21e, RPS21; small subunit ribosomal protein S21e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3486 At3g53890 40S ribosomal protein S21	KAG4083099.1 30S ribosomal protein S21e [Neocallimastix sp. JGI-2020a]	Small ribosomal subunit protein eS21 OS=Cyanophora paradoxa OX=2762 GN=RPS21 PE=3 SV=1
A3683	-	-	-	-	-	KOG0715 At5g18140 Molecular chaperone (DnaJ superfamily)	XP_033434879.1 Protein tumorous imaginal discs, mitochondria I [Daldinia childiae]	Chaperone protein DnaJ OS=Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) OX=103690 GN=dnaJ PE=3 SV=1
A3684	GO:0006508(proteolysis),GO:007154(cell communication)	GO:0016021(integral component of membrane)	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1543 At1g06260 Cysteine proteinase Cathepsin L	KFH62689.1 hypothetical protein MVEG_12081 [Podila verticillata NRRL 6337]	Viral cathepsin OS=Xestia c-nigrum granulosis virus OX=51677 GN=VCATH PE=3 SV=1
A3685	-	-	-	K14839 NOP16; nucleolar protein 16	-	-	PKK73056.1 hypothetical protein RhiirC2_679582 [Rhizophagus irregularis]	Nucleolar protein 16 OS=Eremothecium gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=NOP16 PE=3 SV=1
A3686	-	-	-	-	-	-	-	-
A3687	-	-	-	K15109 SLC25A20_29, CACT, CACL, CRC1; solute carrier family 25 (mitochondrial carnitine/acyl carnitine transporter), member 20/29	map04714 Thermogenesis	KOG0763 CE02041 Mitochondrial ornithine transporter	PVU88898.1 hypothetical protein BB561_005653 [Smittium simuli]	Mitochondrial ornithine transporter 1 OS=Mus musculus OX=10090 GN=Slc25a15 PE=1 SV=1
A3688	-	-	GO:0051287(NAD binding),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)	K00058 serA, PHGDH; D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase [EC:1.1.1.95 1.1.1.399]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00680 Methane metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG0068 CE08497 D-3-phosphoglycerate dehydrogenase, D-isomer-specific 2-hydroxy acid dehydrogenase superfamily	KAF5385498.1 hypothetical protein D9757_005338 [Gymnopus confluens]	D-3-phosphoglycerate dehydrogenase OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=serA PE=3 SV=1
A3689	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At4g28710 Myosin class V heavy chain	KIK59478.1 hypothetical protein GYMLUDRAFT_169589 [Gymnopus luxurians FD-317 M1]	Myosin-6 OS=Arabidopsis thaliana OX=3702 GN=XI-2 PE=1 SV=1

A3690	GO:0006302(double-strand break repair)	-	GO:0003950(NAD+ ADP-ribosyltransferase activity)	K10798 PARP2_3_4; poly [ADP-ribose] polymerase 2/3/4 [EC:2.4.2.30]	map04210 Apoptosis;map04212 Longevity regulating pathway - worm;map03410 Base excision repair	KOG1037[Hs4885051 NAD+ ADP-ribosyltransferase Parp, required for poly-ADP ribosylation of nuclear proteins	KAF9571014.1 Poly [ADP-ribose] polymerase 2 [Mortierella alpina]	Protein mono-ADP-ribosyltransferase PARP3 OS=Homo sapiens OX=9606 GN=PARP3 PE=1 SV=4
A3691	-	-	GO:0005515(protein binding);GO:0005509(calcium ion binding)	K12472 EPS15; epidermal growth factor receptor substrate 15	map04144 Endocytosis	KOG1955[Hs13994296 Ral-GTPase effector RALBP1	XP_033548104.1 uncharacterized protein BDR25DRAFT_303326 [Lindgomyces ingoldianus]	RalBP1-associated Eps domain-containing protein 1 OS=Mus musculus OX=10090 GN=Reps1 PE=1 SV=2
A3692	-	-	-	-	-	-	EPZ35544.1 Lipoxigenase , LH2 domain-containing protein [Rozella allomyces CSF55]	-
A3693	-	-	-	-	-	-	-	-
A3694	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	-
A3695	-	-	-	-	-	-	-	-
A3696	-	-	GO:0003824(catalytic activity);GO:0051536(iron-sulfur cluster binding)	-	-	-	XP_025374467.1 radical SAM enzyme [Acaromyces ingoldii]	-
A3697	-	-	-	-	-	-	-	-
A3698	-	-	GO:0005515(protein binding)	K23563 EMC2, TTC35; ER membrane protein complex subunit 2	-	KOG3060[At3g04830 Uncharacterized conserved protein	XP_016609544.1 hypothetical protein SPPG_03303 [Spizellomyces punctatus DAOM BR117]	ER membrane protein complex subunit 2 OS=Danio rerio OX=7955 GN=emc2 PE=2 SV=1
A3699	-	-	-	-	-	-	-	-
A3700	-	-	-	-	-	-	-	-
A3701	GO:0006298(mismatch repair)	GO:0032300(mismatch repair complex)	GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity)	-	-	KOG1977[Hs7657337 DNA mismatch repair protein - MLH3 family	KAF9279863.1 DNA mismatch repair protein [Mortierella alpina]	DNA mismatch repair protein MutL OS=Methanobrevibacterium thermoautotrophicum (strain DSM 6194 / JCM 14653 / NBRC 101360 / PT) OX=349307 GN=mutL PE=3 SV=1
A3702	-	-	-	-	-	-	-	-
A3703	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding);GO:0008569(minus-end-directed microtubule motor activity)	-	-	KOG3595[Hs19115954 Dyneins, heavy chain	KNE55648.1 hypothetical protein AMAG_01535 [Allomyces macrogynus ATCC 38327]	Dynein gamma chain, flagellar outer arm OS=Chlamydomonas reinhardtii OX=3055 GN=ODA2 PE=1 SV=1
A3704	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3705	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867[Hs4557659 Sulfatase	OQO12965.1 hypothetical protein B0A48_02429 [Rachicladoprium antarcticum]	Iduronate 2-sulfatase OS=Mus musculus OX=10090 GN=Ids PE=2 SV=3

A3706	GO:0007034(vacuolar transport)	-	-	K12195 CHMP6, VPS20; charged multivesicular body protein 6	map04144 Endocytosis;map03250 Viral life cycle - HIV-1;map04217 Necroptosis	KOG2910 7291437 Uncharacterized conserved protein predicted to be involved in protein sorting	OLY83776.1 Charged multivesicular body protein 6 [Smittium mucronatum]	Charged multivesicular body protein 6-A OS=Xenopus laevis OX=8355 GN=chmp6-a PE=2 SV=3
A3707	-	-	-	-	-	-	-	-
A3708	-	GO:0016459(myosin complex), GO:0005856(cytoskeleton)	GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At4g28710 Myosin class V heavy chain	KAG1239185.1 hypothetical protein G6F35_000202 [Rhizopus oryzae]	Myosin-I heavy chain OS=Dictyostelium discoideum OX=44689 GN=myol PE=1 SV=1
A3709	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	-	-	-	TPX77683.1 hypothetical protein CcCBS67573_g01016 [Chytridiomycetes confervae]	Methylmalonic aciduria type A homolog, mitochondrial OS=Mus musculus OX=10090 GN=Mmaa PE=1 SV=1
A3710	-	-	-	-	-	KOG2861 YD L001w Uncharacterized conserved protein	XP_025172122.1 hypothetical protein GLOIN_2v1462414 [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Sporulation protein RMD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RMD1 PE=1 SV=1
A3711	GO:0006508(proteolysis)	-	GO:0016805(dipeptidase activity),GO:0070004(cysteine-type exopeptidase activity)	-	-	-	-	Secernin-2 OS=Danio rerio OX=7955 GN=scrn2 PE=2 SV=1
A3712	-	-	-	-	-	KOG2372 Hs892241 Oxidation resistance protein	ORY03105.1 TLD-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	TLD domain-containing protein 2 OS=Bos taurus OX=9913 GN=TLDC2 PE=2 SV=1
A3713	-	-	-	-	-	-	KAF9096071.1 hypothetical protein BGX29_008756 [Mortierella sp. GBA35]	Pyridoxamine 5'-phosphate oxidase family protein ustO OS=Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / IAM 13836 / NRRL 3357 / JCM 12722 / SRRC 167) OX=332952 GN=ustO PE=3 SV=1
A3714	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K18995 DHX29; ATP-dependent RNA helicase DHX29 [EC:3.6.4.13]	-	KOG0920 At2g35920 ATP-dependent RNA helicase A	KAB5571791.1 P-loop containing nucleoside triphosphate hydrolase protein [Coniochaeta sp. 2T2.1]	DExH-box ATP-dependent RNA helicase DExH1 OS=Arabidopsis thaliana OX=3702 GN=At2g35920 PE=2 SV=1
A3715	GO:0006508(proteolysis)	-	GO:0008233(peptidase activity)	-	-	-	KAG0193169.1 hypothetical protein DFO28_006177 [Apophysomyces sp. BC1034]	Na(+)/H(+) antiporter NhaA OS=Brucella abortus (strain 2308) OX=359391 GN=nhaA PE=3 SV=2
A3716	-	-	-	-	-	-	-	-

A3717	GO:0017013(protein flavinylation)	-	GO:0010181(FMN binding),GO:0016491(oxidoreductase activity)	-	-	-	KNE57146.1 flavocytochrome c [Allomyces macrogynus ATCC 38327]	Fumarate reductase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=osm1 PE=3 SV=1
A3718	GO:0051180(vitamin transport)	GO:0016021(integral component of membrane)	GO:0090482(vitamin transmembrane transporter activity)	-	-	KOG3810 CE05236 Micronutrient transporters (folate transporter family)	-	Folate transporter 1 OS=Caenorhabditis elegans OX=6239 GN=folt-1 PE=2 SV=3
A3719	-	-	-	-	-	KOG3054 730719 Uncharacterized conserved protein	-	DDRKG domain-containing protein 1 OS=Drosophila erecta OX=7220 GN=GG24454 PE=3 SV=1
A3720	GO:0006468(protein phosphorylation),GO:0007015(actin filament organization)	-	GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity),GO:0004672(protein kinase activity)	K19833 CLA4; serine/threonine-protein kinase CLA4 [EC:2.7.11.1]	map04011 MAPK signaling pathway - yeast	KOG0578 Hs4505599 p21-activated serine/threonine protein kinase	ORX93820.1 Pkinase-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Serine/threonine-protein kinase pakC OS=Dictyostelium discoideum OX=44689 GN=pakC PE=1 SV=2
A3721	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K19833 CLA4; serine/threonine-protein kinase CLA4 [EC:2.7.11.1]	map04011 MAPK signaling pathway - yeast	KOG0578 Hs4505599 p21-activated serine/threonine protein kinase	XP_01323706.2.1 Ste20-like protein [Mitosporidium daphniae]	Serine/threonine-protein kinase pakC OS=Dictyostelium discoideum OX=44689 GN=pakC PE=1 SV=2
A3722	-	-	-	-	-	-	-	-
A3723	-	-	-	-	-	-	-	-
A3724	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration;map04024 cAMP signaling pathway;map04020 Calcium signaling pathway;map05414 Dilated cardiomyopathy;map04140 Autophagy - animal;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map01522 Endocrine resistance;map04919 Thyroid hormone signaling pathway;map04918 Thyroid hormone synthesis;map04	KOG0614 Hs10835242 cGMP-dependent protein kinase	RHZ84434.1 hypothetical protein Glove_81g48 [Diversispora epigaea]	cGMP-dependent protein kinase 1 OS=Homo sapiens OX=9606 GN=PRKG1 PE=1 SV=3
A3725	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10393 KIF2_24, MCAK; kinesin family member 2/24	map04361 Axon regeneration;map04814 Motor proteins	KOG0246 At3g16060 Kinesin-like protein	ORX90795.1 kinesin-domain-containing protein, partial [Basidiobolus meristosporus CBS 931.73]	Diatom spindle kinesin-1 OS=Cylindrotheca fusiformis OX=2853 GN=DSK1 PE=2 SV=1

A3726	GO:0006520 (cellular amino acid metabolic process)	-	GO:0016743 (carboxyl- or carbamoyltransferase activity), GO:0016597 (amino acid binding)	K00611 OTC, argF, argI; ornithine carbamoyltransferase [EC:2.1.3.3]	map01110 Biosynthesis of secondary metabolites; map01230 Biosynthesis of amino acids; map00220 Arginine biosynthesis; map01100 Metabolic pathways	KOG1504 Hs9257234 Ornithine carbamoyltransferase OTC/ARG3	KAA8910418.1 ornithine carbamoyltransferase [Sphaerospora brunnea]	Ornithine transcarbamylase, mitochondrial (Fragment) OS=Sus scrofa OX=9823 GN=OTC PE=2 SV=1
A3727	-	GO:0016021 (integral component of membrane)	GO:0009922 (fatty acid elongase activity)	K10245 ELO2, fatty acid elongase 2 [EC:2.3.1.199]	map01110 Biosynthesis of secondary metabolites; map00062 Fatty acid elongation; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01212 Fatty acid metabolism	KOG3071 Hs11464975 Fatty acyl-CoA elongase/Polynunsaturated fatty acid specific elongation enzyme	ORZ40155.1 delta-6 elongase [Catenaria anguillulae PL171]	Fatty acid elongase 5 OS=Trypanosoma cruzi (strain CL Brener) OX=353153 GN=ELO5 PE=3 SV=1
A3728	-	-	-	-	-	-	-	-
A3729	-	-	-	-	-	KOG0747 At1g19690 Putative NAD+-dependent epimerases	KAG0955939.1 hypothetical protein G6F31_012743 [Rhizopus oryzae]	Protein YeeZ OS=Escherichia coli O157:H7 OX=83334 GN=yeeZ PE=3 SV=1
A3730	-	-	GO:0005227 (calcium activated cation channel activity)	-	-	-	-	-
A3731	GO:0030433 (ubiquitin-dependent ERAD pathway), GO:0030968 (endoplasmic reticulum unfolded protein response)	-	-	-	-	-	-	Protein OS-9 homolog OS=Arabidopsis thaliana OX=3702 GN=OS9 PE=1 SV=1
A3732	-	-	-	-	-	-	-	-
A3733	-	-	GO:0003924 (GTPase activity), GO:0005525 (GTP binding)	-	-	-	XP_016606274.1 hypothetical protein SPPG_06634 [Spizellomyces punctatus DAOM BR117]	Rab-like protein 3 OS=Xenopus tropicalis OX=8364 GN=rab13 PE=2 SV=1
A3734	GO:0006508 (proteolysis)	-	GO:0004222 (metalloendopeptidase activity), GO:0008237 (metallopeptidase activity), GO:0008233 (peptidase activity)	K13726 MEPB; metallopeptidase MepB [EC:3.4.24.-]	-	KOG2089 At5g65620 Metalloendopeptidase family - saccharolysin & thimet oligopeptidase	KAF9133479.1 hypothetical protein BGW39_009669 [Mortierella sp. 14UC]	Probable cytosolic oligopeptidase A OS=Arabidopsis thaliana OX=3702 GN=CYOP PE=1 SV=1

A3735	-	-	-	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis -	-	KXS16277.1 glutathione S-transferase domain-containing protein [Gonapodya prolifera JEL478]	Disulfide-bond oxidoreductase YghU OS=Escherichia coli (strain K12) OX=83333 GN=yghU PE=1 SV=2
A3736	-	-	GO:0005515(protein binding)	-	-	KOG1124(CE09867 FOG:TPR repeat	-	Protein O-mannosyl-transferase TMTC4 OS=Homo sapiens OX=9606 GN=TMTC4 PE=1 SV=2
A3737	-	-	GO:0003723(RNA binding);GO:0003676(nucleic acid binding)	-	-	-	-	Uncharacterized RNA-binding protein C902.04 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC902.04 PE=1 SV=1
A3738	-	-	-	-	-	-	-	-
A3739	-	-	-	-	-	-	-	-
A3740	GO:0017148(negative regulation of translation)	GO:0030015(CCR4-NOT core complex)	-	K12604 CNOT1, NOT1; CCR4-NOT transcription complex subunit 1	map03018 RNA degradation	KOG1831 At1g02080 Negative regulator of transcription	TPX64408.1 hypothetical protein SpCBS45565_g05897 [Spizellomyces sp. 'palustris']	CCR4-NOT transcription complex subunit 1 OS=Xenopus tropicalis OX=8364 GN=cnot1 PE=2 SV=1
A3741	-	-	-	-	-	-	-	-
A3742	GO:0070286(axonemal dynein complex assembly)	GO:0036157(outer dynein arm)	-	-	-	-	-	-
A3743	GO:0035082(axonemal assembly)	-	-	-	-	-	TPX67959.1 hypothetical protein SpCBS45565_g03525 [Spizellomyces sp. 'palustris']	Coiled-coil domain-containing protein 40 OS=Mus musculus OX=10090 GN=Ccdc40 PE=1 SV=1
A3744	-	-	-	-	-	-	-	-
A3745	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3746	-	-	-	-	-	-	-	-
A3747	-	-	GO:0005515(protein binding)	-	-	-	KAF7720927.1 hypothetical protein EC973_005773 [Apophysomyces ossiformis]	Probable assembly chaperone of rpl4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC16D10.01c PE=3 SV=2
A3748	-	-	GO:0005515(protein binding)	K15042 KPNA5_6; importin subunit alpha-6/7	map03013 Nucleocytoplasmic transport;map05207 Chemical carcinogenesis - receptor activation;map05164 Influenza A	KOG0166 At3g06720 Karyopherin (importin) alpha	RKO85499.1 armadillo-type protein [Blyttiomycetes helicis]	Importin subunit alpha-1b OS=Oryza sativa subsp. japonica OX=39947 GN=Os05g0155601 PE=1 SV=2

A3749	-	-	GO:0003677(DNA binding);GO:0016491(oxidoreductase activity);GO:0005515(protein binding)	-	-	KOG0029 7293681 Amine oxidase	KAF8456275.1 flavin-containing amine oxidoreductase-domain containing protein [Terfezia clavaryi]	Possible lysine-specific histone demethylase 1 OS=Drosophila melanogaster OX=7227 GN=Su(var)3-3 PE=1 SV=1
A3750	GO:0008652(cellular amino acid biosynthetic process), GO:0009089(lysine biosynthetic process via diaminopimelate)	-	GO:0004072(aspartate kinase activity)	K00928 lysC; aspartate kinase [EC:2.7.2.4]	map00300 Lysine biosynthesis;map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00261 Monobactam biosynthesis;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism;map00270 Cysteine and methionine metabolism	KOG0456 YER052c Aspartate kinase	KAA8912249.1 hypothetical protein TRIC_003529 [Trichomonas cucurbitis]	Aspartokinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM3 PE=1 SV=2
A3751	-	-	GO:0016491(oxidoreductase activity)	-	-	-	CDH54583.1 dsba oxidoreductase [Lichtheimia corymbifera JMRC:FSU:9682]	-
A3752	GO:0006383(transcription by RNA polymerase III)	-	GO:0005515(protein binding)	K15201 GTP3C3, TFC4; general transcription factor 3C polypeptide 3 (transcription factor C subunit 4)	-	-	KAG0123331.1 hypothetical protein HOY82DRAFT_673967 [Tuber indicum]	-
A3753	GO:1901137(carbohydrate derivative biosynthetic process), GO:1901135(carbohydrate derivative metabolic process)	-	GO:0004360(glutamine-fructose-6-phosphate transaminase (isomerizing) activity);GO:0097367(carbohydrate derivative binding)	K00820 glmS; GFPT; glutamine-fructose-6-phosphate transaminase (isomerizing) [EC:2.6.1.16]	map05415 Diabetic cardiomyopathy;map01250 Biosynthesis of nucleotide sugars;map00250 Alanine, aspartate and glutamate metabolism;map04931 Insulin resistance;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG1268 7289004 Glucosamine 6-phosphate synthetases, contain amidotransferase and phosphosugar isomerase domains	XP_025172146.1 glucosamine-fructose-6-phosphate aminotransferase [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Glutamine-fructose-6-phosphate aminotransferase [isomerizing] OS=Chlorobaculum tepidum (strain ATCC 49652 / DSM 12025 / NBRC 103806 / TLS) OX=194439 GN=glmS PE=3 SV=3
A3754	-	-	-	-	-	-	-	-

A3755	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K23481 VPS1; vacuolar protein sorting-associated protein 1	-	KOG0446[EC U10g1700i Vacuolar sorting protein VPS1, dynamin, and related proteins	CAE6410416.1 unnamed protein product [Rhizoctonia solani]	Dynammin-1-like protein OS=Danio rerio OX=7955 GN=dnm1l PE=2 SV=1
A3756	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K12196 VPS4; vacuolar protein-sorting-associated protein 4	map04144 Endocytosis;map03250 Viral life cycle - HIV-1;map04217 Necroptosis	-	XP_026610372.1 Vacuolar protein sorting-associated protein 4 [Aspergillus thermomutatus]	Suppressor protein of bem1/bed5 double mutants OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=vps4 PE=3 SV=1
A3757	GO:0000413(protein peptidyl-prolyl isomerization),GO:0016567(protein ubiquitination),GO:0006457(protein folding)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity),GO:0004842(ubiquitin-protein transferase activity)	K10598 PPIL2, CYC4, CHP60; peptidyl-prolyl cis-trans isomerase-like 2 [EC:5.2.1.8]	map04120 Ubiquitin mediated proteolysis	KOG0883[Hs7657473 Cyclophilin type, U box-containing peptidyl-prolyl cis-trans isomerase	KAF8538142.1 hypothetical protein BDD12DRAFT_806382 [Trichophaea hybrida]	Peptidyl-prolyl cis-trans isomerase cyp8 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=cyp8 PE=2 SV=3
A3758	-	-	GO:0036128(CatSper complex), GO:0097228(sperm principal piece)	-	-	-	ORY40518.1 hypothetical protein BCR33DRAFT_740348 [Rhizoclostium globosum]	Cation channel sperm-associated auxiliary subunit gamma OS=Homo sapiens OX=9606 GN=CATSPERG PE=2 SV=3
A3759	-	-	-	K14002 SCJ1; DnaJ-related protein SCJ1	map04141 Protein processing in endoplasmic reticulum	KOG0713[Hs2044388.1 Molecular chaperone (DnaJ) superfamily)	KAF4978707.1 hypothetical protein FZEAL_4949 [Fusarium zealandicum]	Chaperone protein DnaJ OS=Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562) OX=373903 GN=dnaJ PE=3 SV=1
A3760	GO:0000413(protein peptidyl-prolyl isomerization)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K09565 PPIF; peptidyl-prolyl isomerase F (cyclophilin D) [EC:5.2.1.8]	map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05415 Diabetic cardiomyopathy; map04613 Neutrophil extracellular trap formation;map05145 Toxoplasmosis; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05010 Alzheimer disease;map05012 Parkinson disease;map05017	KOG0865[CE20374 Cyclophilin type peptidyl-prolyl cis-trans isomerase	XP_028474622.1 Peptidyl-prolyl cis-trans isomerase B [Apiotrichum porosum]	Probable inactive peptidyl-prolyl cis-trans isomerase-like 6 OS=Homo sapiens OX=9606 GN=PPIL6 PE=1 SV=1
A3761	-	-	GO:0005515(protein binding)	-	-	-	EPZ32374.1 hypothetical protein O9G_002214 [Rozella allomyces CSF55]	-

A3762	GO:0009966(regulation of signal transduction),GO:0043666(regulation of phosphoprotein phosphatase activity)	-	GO:0004864(protein phosphatase inhibitor activity)	-	-	-	KNE58306.1 hypothetical protein AMAG_05114 [Allomyces macrogynus ATCC 38327]	-
A3763	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	K09831 ERG5, CYP61A; sterol 22-desaturase [EC:1.14.19.4.1]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG0157 At2g34500 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	RJE22112.1 Cytochrome p450 [Aspergillus sclerotialis]	Cytochrome P450 710A1 OS=Arabidopsis thaliana OX=3702 GN=CYP710A1 PE=1 SV=1
A3764	-	-	-	-	-	KOG3171 Hs9943842 Conserved phosducin-like protein	OA136843.1 hypothetical protein BDEG_20966 [Batrachochytrium dendrobatidis JEL423]	Phosducin-like protein 1 OS=Dictyostelium discoideum OX=44689 GN=phlp1 PE=2 SV=1
A3765	-	-	-	-	-	KOG1950 7291265 Glycosyltransferase, family 8 - glycogenin	TNY18604.1 nucleotide-diphosphosugar transferase [Rhodotorula diobovata]	Putative UDP-glucuronate:xylan alpha-glucuronosyltransferase 3 OS=Arabidopsis thaliana OX=3702 GN=GUX3 PE=2 SV=1
A3766	-	-	-	-	-	-	-	-
A3767	-	-	GO:0016491(oxidoreductase activity)	-	-	-	-	-
A3768	-	-	-	-	-	-	-	-
A3769	-	-	GO:0005525(GTP binding)	K03978 engB; GTP-binding protein	-	KOG2486 At5g11480 Predicted GTPase	CAD6439784.1 611b483f-6d13-4175-906d-8126369be18f [Sclerotinia trifoliorum]	GTP-binding protein EngB OS=Zymomonas mobilis subsp. mobilis (strain ATCC 31821 / ZM4 / CP4) OX=264203 GN=engB PE=3 SV=1
A3770	GO:0070475(rRNA base methylation)	-	GO:0070042(rRNA (uridine-N3-)-methyltransferase activity)	K19307 BMT5; 25S rRNA (uracil2634-N3)-methyltransferase [EC:2.1.1.313]	-	-	XP_03358644.5.1 uncharacterized protein BDY17DRAFT_233166, partial [Neohortaea acidophila]	Uncharacterized protein At4g26485 OS=Arabidopsis thaliana OX=3702 GN=At4g26485 PE=4 SV=1
A3771	-	-	-	K03574 mutT, NUDT15, MTH2; 8-oxo-dGTP diphosphatase [EC:3.6.1.55]	-	-	XP_00121035.2.1 nudix hydrolase 1 [Aspergillus terreus NIH2624]	Nudix hydrolase 1 OS=Arabidopsis thaliana OX=3702 GN=NUDT1 PE=1 SV=1

A3772	-	-	GO:0003924(GTPase activity);GO:0005525(GTP binding)	K07889 RAB5C; Ras-related protein Rab-5C	map04144 Endocytosis;map04145 Phagosome;map05132 Salmonella infection;map05146 Amoebiasis;map04014 Ras signaling pathway;map05152 Tuberculosis;map04962 Vasopressin-regulated water reabsorption	KOG0088[Hs7661922 GTPase Rab21, small G protein superfamily	ORX88293.1 ras-domain-containing protein [Anaeromyces robustus]	Ras-related protein Rab-21 OS=Canis lupus familiaris OX=9615 GN=RAB21 PE=3 SV=3
A3773	-	-	GO:0016407(acyltransferase activity)	-	-	-	-	-
A3774	-	-	GO:0016407(acyltransferase activity)	-	-	-	-	-
A3775	-	GO:0071203(WASH complex)	-	-	-	KOG3578[Hs20551457 Uncharacterized conserved protein	-	WASH complex subunit 4 OS=Homo sapiens OX=9606 GN=WASHC4 PE=1 SV=2
A3776	-	-	-	-	-	-	-	-
A3777	-	-	-	-	-	-	-	-
A3778	-	-	-	-	-	-	-	-
A3779	-	-	GO:0005515(protein binding);GO:0008289(lipid binding)	-	-	-	XP_018296417.1 hypothetical protein PHYBLDRAFT_107123, partial [Phycomyces blakesleeanus NRRL 1555(-)]	-
A3780	-	-	-	-	-	-	-	-
A3781	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K18670 YAK1; dual specificity protein kinase YAK1 [EC:2.7.12.1]	-	-	ORY33518.1 kinase-like domain-containing protein [Naematelia encephala]	Serine/threonine-protein kinase ppk15 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ppk15 PE=1 SV=1
A3782	-	-	-	-	-	-	-	-
A3783	-	-	-	-	-	-	-	-
A3784	-	-	-	-	-	-	-	-
A3785	GO:0006486(protein glycosylation)	GO:0016020(membrane)	GO:0008417(fucosyltransferase activity)	-	-	KOG2619[At1g49710 Fucosyltransferase	CEP17388.1 hypothetical protein [Parasitella parasitica]	Alpha-(1,3)-fucosyltransferase 11 OS=Gallus gallus OX=9031 GN=FUT11 PE=2 SV=1
A3786	-	-	-	-	-	-	-	-

A3787	GO:0006086(acetyl-CoA biosynthetic process from pyruvate)	GO:0045254(pyruvate dehydrogenase complex)	GO:0016746(acyltransferase activity)	K00627 DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoyl lysine-residue acetyltransferase) [EC:2.3.1.12]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00620 Pyruvate metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0557 Hs4505699 Dihydrolipoamide acetyltransferase	RKP40072.1 2-oxoacid dehydrogenases acyltransferase e-domain-containing protein, partial [Dimargaris cristalligena]	Pyruvate dehydrogenase protein X component, mitochondrial OS=Mus musculus OX=10090 GN=Pdhx PE=1 SV=1
A3788	-	-	-	-	-	KOG2723 7300672 Uncharacterized conserved protein, contains BTB/POZ domain	-	-
A3789	-	-	GO:0016702(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen)	-	-	KOG4281 At5g15120 Uncharacterized conserved protein	XP_031025653.1 uncharacterized protein SmJEL517_g02484 [Synchytrium microbalum]	Plant cysteine oxidase 1 OS=Arabidopsis thaliana OX=3702 GN=PCO1 PE=1 SV=1
A3790	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A3791	-	-	-	-	-	-	-	-
A3792	-	-	-	-	-	-	-	-
A3793	-	-	-	-	-	-	-	-
A3794	-	-	GO:0003676(nucleic acid binding);GO:0008270(zinc ion binding)	-	-	-	-	-
A3795	GO:0000160(phosphorelay signal transduction system),GO:0016310(phosphorylation),GO:0007165(signal transduction)	-	GO:0016772(transferase activity, transferring phosphorus-containing groups),GO:0000155(phosphorelay sensor kinase activity)	-	-	KOG0519 At1g66340 Sensory transduction histidine kinase	TPX65067.1 hypothetical protein SpCBS45565_g05465 [Spizellomyces sp. 'palustris']	Autoinducer 2 sensor kinase/phosphatase LuxQ OS=Vibrio vulnificus (strain YJ016) OX=196600 GN=luxQ PE=3 SV=1
A3796	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	-	-	-

A3797	GO:0045765(regulation of angiogenesis)	GO:0005737(cytoplasm)	-	-	-	-	TPX68872.1 hypothetical protein SpCBS45565_g02822 [Spizellomyces sp. 'palustris']	Tubuliny-Tyr carboxypeptidase 1 OS=Homo sapiens OX=9606 GN=VASH1 PE=1 SV=1
A3798	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0000981(DNA-binding transcription factor activity, RNA polymerase II-specific);GO:0008270(zinc ion binding)	-	-	-	-	-
A3799	-	-	-	-	-	-	-	-
A3800	-	-	-	-	-	-	-	-
A3801	-	-	-	-	-	-	KAF8521565.1 hypothetical protein BU17DRAFT_16058, partial [Hysterangium stoloniferum]	Transmembrane protein 163a OS=Danio rerio OX=7955 GN=tmem163a PE=2 SV=1
A3802	GO:0007165(signal transduction)	-	GO:0005515(protein binding);GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity);GO:0008081(phosphoric diester hydrolase activity)	-	-	KOG3689[Hs4505675 Cyclic nucleotide phosphodiesterase	RKP16301.1 Pde9 in complex with lbmx [Rozella allomycis CSF55]	High affinity cGMP-specific 3',5'-cyclic phosphodiesterase 9A OS=Pan troglodytes OX=9598 GN=PDE9A PE=1 SV=1
A3803	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	-	-	-	KAF9410687.1 hypothetical protein BGZ76_005483 [Entomortiera beljakovae]	-
A3804	-	-	GO:0005506(iron ion binding);GO:0016702(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen)	K00456 CDO1; cysteine dioxygenase [EC:1.13.11.20]	map00430 Taurine and hypotaurine metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG4064[Hs4502755 Cysteine dioxygenase CDO1	XP_018284359.1 hypothetical protein PHYBLDRAFT_7545, partial [Phycomyces blakesleeana NRRL 1555(-)]	Cysteine dioxygenase type 1 OS=Mus musculus OX=10090 GN=Cdo1 PE=1 SV=1
A3805	GO:0002098(tRNA wobble uridine modification)	-	GO:0016300(tRNA (uracil) methyltransferase activity);GO:0008168(methyltransferase activity)	K15444 TRM9; tRNA (uracil-5-)-methyltransferase TRM9 [EC:2.1.1.229]	-	-	RCH88930.1 tRNA methyltransferase, has a role in tRNA modification, partial [Rhizopus stolonifer]	Alkylated DNA repair protein alkB homolog 8 OS=Xenopus tropicalis OX=8364 GN=alkbh8 PE=2 SV=2
A3806	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867[Hs4502237 Sulfatase	TQV96651.1 sulfatase [Cordyceps javanica]	Steryl-sulfatase OS=Homo sapiens OX=9606 GN=STS PE=1 SV=2

A3807	GO:0051260(protein homooligomerization)	-	GO:0005525(GTP binding),GO:0005515(protein binding)	-	-	KOG2716 CE15134 Polymerase delta-interacting protein PDIP1 and related proteins, contain BTB/POZ domain	-	-
A3808	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4557333 Sulfatase	XP_024663337.1 Arylsulfatase B [Wickerhamia sorbophila]	Arylsulfatase B OS=Rattus norvegicus OX=10116 GN=ArSB PE=2 SV=2
A3809	-	GO:0005682(U5 snRNP)	GO:0005515(protein binding)	K13099 CD2BP2, PPP1R59; CD2 antigen cytoplasmic tail-binding protein 2	-	-	XP_018209750.1 uncharacterized protein OGAPODRAFT_13642 [Ogataea polymorpha]	LIN1-like protein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC83.09c PE=3 SV=1
A3810	GO:0015986(ATP synthesis coupled proton transport)	GO:0000275(mitochondrial proton-transporting ATP synthase complex, catalytic sector F(1))	GO:0046933(proton-transporting ATP synthase activity, rotational mechanism)	-	-	-	-	-
A3811	GO:0006488(dolichol-linked oligosaccharide biosynthetic process)	GO:0005788(endoplasmic reticulum lumen)	GO:0016757(glycosyltransferase activity),GO:0052917(dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichol alpha-1,6-mannosyltransferase)	K03847 ALG12; alpha-1,6-mannosyltransferase [EC:2.4.1.260]	map00513 Various types of N-glycan biosynthesis;map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG2516 7299245 Protein involved in dolichol pathway for N-glycosylation (mannosyltransferase family)	KAG0179922.1 dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichol alpha-1,6-mannosyltransferase [Apophysomycetes sp. BC1021]	Dol-P-Man:Man(7)GlcNAc(2)-PP-Dol alpha-1,6-mannosyltransferase OS=Arabidopsis thaliana OX=3702 GN=ALG12 PE=1 SV=1
A3812	GO:0016575(histone deacetylation)	-	GO:0005515(protein binding),GO:0003714(transcription corepressor activity)	K04508 TBL1; transducin (beta)-like 1	map04310 Wnt signaling pathway;map04013 MAPK signaling pathway - fly	KOG0273 Hs19913371 Beta-transducin family (WD-40 repeat) protein	ORX93815.1 WD40 repeat-like protein [Basidiobolus meristosporus CBS 931.73]	F-box-like/WD repeat-containing protein TBL1XR1 OS=Mus musculus OX=10090 GN=Tbl1xr1 PE=1 SV=1
A3813	GO:0006281(DNA repair)	GO:0030915(Smc5-Smc6 complex)	-	-	-	-	KXS18388.1 hypothetical protein M427DRAFT_53777 [Gonapodya prolifera JEL478]	-
A3814	GO:0051276(chromosome organization)	GO:0005694(chromosome)	GO:0005515(protein binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K06674 SMC2; structural maintenance of chromosome 2	map04111 Cell cycle - yeast	KOG0933 At5g62410 Structural maintenance of chromosome protein 2 (chromosome condensation complex Condensin, subunit E)	TPX71866.1 hypothetical protein SpCBS45565_g00860 [Spizellomyces sp. 'palustris']	Structural maintenance of chromosomes protein 2-1 OS=Arabidopsis thaliana OX=3702 GN=SMC2-1 PE=2 SV=2

A3815	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	-	-	KOG0544 At5g64350 FKBP-type peptidyl-prolyl cis-trans isomerase	XP_025339882.1 FK506-binding protein 1 [[Candida] haemulonii]	Peptidyl-prolyl cis-trans isomerase FKBP12 OS=Arabidopsis thaliana OX=3702 GN=FKBP12 PE=1 SV=2
A3816	GO:0034220(ion transmembrane transport); GO:1902600(proton transmembrane transport)	GO:0033180(proton-transporting V-type ATPase, V1 domain)	GO:0046961(proton-transporting ATPase activity, rotational mechanism)	K02151 ATPeV1F, ATP6S14; V-type H+-transporting ATPase subunit F	map04145 Phagosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation; map05110 Vibrio cholerae infection;map04150 mTOR signaling pathway;map05120 Epithelial cell signaling in Helicobacter pylori infection;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG3432 CE02404 Vacuolar H+-ATPase V1 sector, subunit F	CCA77949.1 probable VMA7-H+-ATPase V1 domain 14 kDa subunit, vacuolar [Serendipita indica DSM 11827]	V-type proton ATPase subunit F OS=Bos taurus OX=9913 GN=ATP6V1F PE=1 SV=2
A3817	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004965(G protein-coupled GABA receptor activity); GO:0004930(G protein-coupled receptor activity)	-	-	KOG1055 Hs20127671 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	ORZ33105.17 transmembrane sweet-taste receptor of 3 GCPR-domain-containing protein [Catenaria anguillulae PL171]	Gamma-aminobutyric acid type B receptor subunit 2 OS=Mus musculus OX=10090 GN=Gabbr2 PE=1 SV=2
A3818	GO:1990542(mitochondrial transmembrane transport)	-	-	K15119 SLC25A39_40; solute carrier family 25, member 39/40	-	KOG0761 Hs10047122 Mitochondrial carrier protein CGI-69	KIL93159.1 hypothetical protein FAVG1_03136 [Fusarium avenaceum]	Probable mitochondrial glutathione transporter SLC25A40 OS=Xenopus tropicalis OX=8364 GN=slc25a40 PE=2 SV=1
A3819	-	-	-	K10419 DYNLRB, DNCL2; dynein light chain roadblock-type	map05132 Salmonella infection;map04814 Motor proteins	KOG4115 7302786 Dynein-associated protein Roadblock	KAG0152282.1 hypothetical protein CROQUODRAFT_667189 [Cronartium quercuum f. sp. fusiforme G11]	-
A3820	-	-	-	-	-	-	-	-
A3821	-	GO:0016021(integral component of membrane)	GO:0005515(protein binding)	-	-	KOG3511 YIL173w Sortilin and related receptors	OBZ73619.1 Vacuolar protein sorting/targeting protein 10 [Grifola frondosa]	Vacuolar protein sorting/targeting protein 10 OS=Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) OX=441959 GN=vps10 PE=3 SV=1
A3822	-	-	-	-	-	-	-	-
A3823	GO:0006364(rRNA processing)	-	GO:0003676(nucleic acid binding); GO:0008408(3'-5' exonuclease activity)	K18327 REXO4, REX4; RNA exonuclease 4 [EC:3.1.-.-]	-	KOG2249 7294419 3'-5' exonuclease	KZT61135.1 ribonuclease H-like protein [Calocera cornea HHB12733]	RNA exonuclease 4 OS=Xenopus tropicalis OX=8364 GN=rexo4 PE=2 SV=1

A3824	GO:000656(phosphatidylcholine biosynthetic process)	-	GO:0008757(S-adenosylmethionine-dependent methyltransferase activity)	-	-	-	-	Phosphatidyl-N-methylethanolamine N-methyltransferase OS=Arabidopsis thaliana OX=3702 GN=PLMT PE=2 SV=1
A3825	-	-	-	-	-	-	-	-
A3826	GO:0006468(protein phosphorylation)	-	GO:0043169(cation binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG0698 At2g20050 Serine/threonine protein phosphatase	KNE67390.1 hypothetical protein AMAG_11856 [Allomyces macrogynus ATCC 38327]	Protein phosphatase 2C and cyclic nucleotide-binding/kinase domain-containing protein OS=Arabidopsis thaliana OX=3702 GN=At2g20050/At2g20040 PE=2 SV=2
A3827	-	-	GO:0046983(protein dimerization activity)	-	-	-	-	-
A3828	-	-	-	-	-	-	-	-
A3829	-	-	-	-	-	-	KXS14115.1 hypothetical protein M427DRAFT_45211 [Gonapodya prolifera JEL478]	-
A3830	-	-	-	-	-	-	-	-
A3831	-	-	-	-	-	-	-	-
A3832	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At4g28710 Myosin class V heavy chain	KA8444394.1 hypothetical protein EG329_000594 [Helotiales sp. DML_Dod_QoI]	Unconventional myosin-VI OS=Bos taurus OX=9913 GN=MYO6 PE=1 SV=4
A3833	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0003678(DNA helicase activity),GO:0016818(hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides),GO:0003676(nucleic acid binding),GO:0004386(helicase activity),GO:0005524(ATP binding),GO:0003677(DNA binding)	K11273 DDX11, CHL1, CTF1; chromosome transmission fidelity protein 1 [EC:3.6.4.13]	map04110 Cell cycle	KOG1132 Hs14042978 Helicase of the DEAD superfamily	ORZ33420.1 helicase C-terminal domain-containing protein [Catenaria anguillulae PL171]	Fanconi anemia group J protein homolog OS=Mus musculus OX=10090 GN=Brip1 PE=2 SV=1
A3834	-	-	-	-	-	KOG0048 At3g09370 Transcription factor, Myb superfamily	KAF8940947.1 DNA binding transcription coactivator transcription factor [Dissophora ornata]	Transcription factor MYB3R-3 OS=Arabidopsis thaliana OX=3702 GN=MYB3R3 PE=1 SV=1
A3835	-	-	GO:0005515(protein binding)	K09527 DNAJC7; DnaJ homolog subfamily C member 7	-	KOG0550 Hs4507713 Molecular chaperone (DnaJ superfamily)	OBZ87219.1 DnaJ subfamily C member 7 [Choanephora cucurbitarum]	DnaJ homolog subfamily C member 7 homolog OS=Dictyostelium discoideum OX=44689 GN=dnajc7 PE=1 SV=1

A3836	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	CEH12291.1 hypothetical protein CBOM_00290 [Ceraceosorus bombacis]	-
A3837	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3839	-	-	-	-	-	-	XP_018211169.1 uncharacterized protein OGAPODRAFT_93264 [Ogataea polymorpha]	Protein NIF3 homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC126.12 PE=3 SV=1
A3840	-	-	-	-	-	-	-	-
A3841	-	-	-	-	-	-	-	-
A3842	GO:0034508(centromere complex assembly)	GO:0000776(kinetochore)	-	-	-	-	RUS19757.1 Cenp-O kinetochore centromere component-domain-containing protein [Endogone sp. FLAS-F59071]	-
A3843	-	-	-	-	-	-	-	-
A3844	-	-	-	K10427 DCTN5; dynactin 5	map05014 Amyotrophic lateral sclerosis;map05132 Salmonella infection;map04814 Motor proteins;map05022 Pathways of neurodegeneration - multiple diseases;map05016 Huntington disease;map04962 Vasopressin-regulated water reabsorption	-	XP_018262882.1 dynactin 5 [Kwoniella dejecticola CBS 10117]	Gamma carbonic anhydrase 1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=GAMMACA1 PE=1 SV=1
A3845	GO:0006839(mitochondrial transport)	GO:0031966(mitochondrial membrane)	-	K15117 SLC25A34_35, OAC1; solute carrier family 25, member 34/35	-	KOG0753 At3g54110 Mitochondrial fatty acid anion carrier protein/Uncoupling protein	XP_006677260.1 uncharacterized protein BATDEDRAFT_23336 [Batrachochytrium dendrobatidis JAM81]	Mitochondrial uncoupling protein 1 OS=Arabidopsis thaliana OX=3702 GN=PUMP1 PE=1 SV=1

A3846	-	-	GO:0005515(protein binding)	K06062 PCAF, KAT2, GCN5; histone acetyltransferase [EC:2.3.1.48]	map03250 Viral life cycle - HIV-1;map04919 Thyroid hormone signaling pathway;map05203 Viral carcinogenesis; map04330 Notch signaling pathway;map05166 Human T-cell leukemia virus 1 infection	KOG0644[Hs16445438 Uncharacterized conserved protein, contains WD40 repeat and BROMO domains	KAG0023305.1 Bromodomain and WD repeat-containing protein 3 [Entomomortierella chlamydosporae]	Bromodomain and WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=BRWD1 PE=1 SV=4
A3847	-	GO:0016459(myosin complex)	GO:0005515(protein binding),GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160[At4g28710 Myosin class V heavy chain	KAF1798291.1 P-loop containing nucleoside triphosphate hydrolase protein [Mucor lusitanicus]	Myosin-17 OS=Arabidopsis thaliana OX=3702 GN=XI-K PE=1 SV=2
A3848	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K06276 PDK1; 3-phosphoinositide dependent protein kinase-1 [EC:2.7.11.1]	map04360 Axon guidance;map03320 PPAR signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map05223 Non-small cell lung cancer;map04722 Neurotrophin signaling pathway;map04510 Focal adhesion;map04210 Apoptosis;map04071 Sphingolipid signaling pathway;map01524 Platinum drug resistance;map04919 Thyroid hormone signaling	KOG0592[Hs4505695 3-phosphoinositide-dependent protein kinase (PDK1)	G8B93041.1 hypothetical protein RclHR1_00210037 [Rhizophagus clarus]	3-phosphoinositide-dependent protein kinase 1 OS=Mus musculus OX=10090 GN=Pdpk1 PE=1 SV=2
A3849	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity),GO:0016787(hydrolase activity)	-	-	KOG0061[At2g01320 Transporter, ABC superfamily (Breast cancer resistance protein)	OAD08773.1 hypothetical protein MUCCIDRAFT_135137 [Mucor lusitanicus CBS 277.49]	ABC transporter G family member 22 OS=Dictyostelium discoideum OX=44689 GN=abcG22 PE=2 SV=1
A3850	-	-	-	-	-	-	-	-
A3851	-	-	-	K25866 NUDC; nuclear migration protein NudC	-	KOG2265[At5g58740 Nuclear distribution protein NUDC	ORX84292.1 nuclear movement protein nudC [Anaeromyces robustus]	NudC domain-containing protein 2 OS=Homo sapiens OX=9606 GN=NUDCD2 PE=1 SV=1

A3852	-	-	GO:0051287(NAD binding);GO:0004471(malate dehydrogenase (decarboxylating) (NAD+ activity);GO:0004470(malic enzyme activity)	K00027 ME2, sfcA, maeA; malate dehydrogenase (oxaloacetate - decarboxylating) [EC:1.1.1.38]	map01200 Carbon metabolism;map00620 Pyruvate metabolism;map02020 Two-component system	KOG1257 YKL029c NADP+ - dependent malic enzyme	KGQ13333.1 NAD-dependent malic enzyme [Beauveria bassiana D1-5]	NAD-dependent malic enzyme OS=Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / BCRC 13018 / CCUG 14551 / JCM 1027 / KCTC 2358 / NCIMB 9240 / NCTC 8049) OX=380703 GN=maeA PE=3 SV=2
A3853	-	-	GO:0005515(protein binding)	K11293 HIRA, HIR1; protein HIRA/HIR1	-	KOG0973 At3g44530 Histone transcription regulator HIRA, WD repeat superfamily	TPX64104.1 hypothetical protein CcCBS67573_g08493 [Chytridiomycota confervae]	Protein HIRA OS=Oryza sativa subsp. japonica OX=39947 GN=Os09g0567700 PE=2 SV=1
A3854	GO:0005975(carbohydrate metabolic process)	-	GO:0016773(phosphotransferase activity, alcohol group as acceptor);GO:0016301(kinase activity)	-	-	KOG2517 7291929 Ribulose kinase and related carbohydrate kinases	RKP12181.1 xylulokinase, partial [Piptocephalis cylindrospora]	Xylulose kinase OS=Lactiplantibacillus pentosus OX=1589 GN=xylB PE=3 SV=1
A3855	-	-	GO:0106274(NAD+ -protein-arginine ADP-ribosyltransferase activity)	-	-	-	-	-
A3856	GO:0015031(protein transport)	-	-	K19476 IST1; vacuolar protein sorting-associated protein IST1	map04144 Endocytosis	KOG2027 Hs22069058 Spindle pole body protein	TPX46059.1 hypothetical protein SeLEV6574_g03448 [Synchytrium endobioticum]	IST1-like protein OS=Dictyostelium discoideum OX=44689 GN=DDB_G0289029 PE=3 SV=1
A3857	-	-	-	K15283 SLC35E1; solute carrier family 35, member E1	-	KOG1441 At5g33320 Glucose-6-phosphate/p phosphate and phosphoenolpyruvate/phosphate antiporter	RKP20870.1 TPT-domain-containing protein [Rozella allomyces CSF55]	Triose phosphate/phosphate translocator, chloroplastic OS=Flaveria pringlei OX=4226 GN=TPT PE=2 SV=1
A3858	-	-	-	-	-	-	-	-
A3859	GO:0006631(fatty acid metabolic process)	-	GO:0070403(NAD+ binding);GO:0016491(oxidoreductase activity);GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)	K00022 HADH; 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]	map01110 Biosynthesis of secondary metabolites;map00907 Pinene, camphor and geraniol degradation;map01120 Microbial metabolism in diverse environments;map00930 Caprolactam degradation;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00062 Fatty acid elongation;map00310 Lysine degradation;map00380 Tryptophan metabolism;map	KOG2304 CE00852 3-hydroxyacyl-CoA dehydrogenase	KAF9176651.1 hypothetical protein BGZ51_009877 [Haplosporangium sp. Z 767]	Probable 3-hydroxyacyl-CoA dehydrogenase B0272.3 OS=Caenorhabditis elegans OX=6239 GN=B0272.3 PE=3 SV=1
A3860	-	-	-	-	-	-	-	-
A3861	-	-	-	-	-	-	-	-

A3862	GO:0009082(branch ed-chain amino acid biosynthetic process)	-	GO:0000287(magnesium ion binding),GO:0030976(thiamine pyrophosphate binding),GO:0003824(catalytic activity),GO:0003984(acetolactate synthase activity),GO:0050660(flavin adenine dinucleotide binding)	K01652 E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	map00770 Pantothenate and CoA biosynthesis;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00650 Butanoate metabolism;map00660 C5-Branched dibasic acid metabolism;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG4166 YMR108w Thiamine pyrophosphate-requiring enzyme	GBB93573.1 hypothetical protein RcdHRL_00220007 [Rhizophagus clarus]	Acetolactate synthase, mitochondrial OS=Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) OX=214684 GN=ILV2 PE=3 SV=1
A3863	-	-	-	-	-	-	-	-
A3864	-	-	-	-	-	-	-	-
A3865	GO:0051726(regulation of cell cycle)	GO:0071821(FANCM-MHF complex)	GO:0046982(protein heterodimerization activity)	-	-	KOG4164 Hs17482157 Cyclin ik3-1/CABLES	KAF9936487.1 CDK5 and ABL1 enzyme substrate 1 [Mortierella alpina]	CDK5 and ABL1 enzyme substrate 2 OS=Homo sapiens OX=9606 GN=CABLES2 PE=1 SV=3
A3866	-	-	-	-	-	-	KAG1469961.1 hypothetical protein G6F57_011979 [Rhizopus oryzae]	Mitochondrial fission protein ELM1 OS=Arabidopsis thaliana OX=3702 GN=ELM1 PE=1 SV=1
A3867	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	K17970 MDV1, FIS2; mitochondrial division protein 1	-	KOG0288 At5g50230 WD40 repeat protein TipD	XP_013326021.1 hypothetical protein T310_6610 [Rasamsonia emersonii CBS 393.64]	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A3868	GO:0006418(tRNA aminoacylation for protein translation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding)	K01866 YARS, tyrS; tyrosyl-tRNA synthetase [EC:6.1.1.1]	map00970 Aminoacyl-tRNA biosynthesis	KOG2144 At2g33840_1 Tyrosyl-tRNA synthetase, cytoplasmic	XP_013238976.1 uncharacterized protein DI09_15p160 [Mitosporidium daphniae]	Tyrosine--tRNA ligase 1, cytoplasmic OS=Arabidopsis thaliana OX=3702 GN=At2g33840 PE=2 SV=1
A3869	-	-	-	K01267 DNPEP; aspartyl aminopeptidase [EC:3.4.11.21]	-	-	XP_020066112.1 aspartyl aminopeptidase [Suhomyces tanzawaensis NRRL Y-17324]	Lysyl aminopeptidase OS=Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1) OX=186497 GN=PF1861 PE=1 SV=1
A3870	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3871	GO:0000413(protein peptidyl-prolyl isomerization)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	-	-	-	-	-
A3872	-	-	-	-	-	-	-	Ribitol-5-phosphate xylosyltransferase 1 OS=Homo sapiens OX=9606

A3873	-	-	-	-	-	-	PHH74852.1 hypothetical protein CDD80_2789 [Ophiocordyc eps camponoti- rufipedis]	Putative uridine kinase C227.14 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC227.14 PE=3 SV=1
A3874	-	GO:0031011(Ino80 complex), GO:0035267(NuA4 histone acetyltransferase complex), GO:0097255(R2TP complex)	GO:0008094(ATase, acting on DNA),GO:0005524(ATP binding)	K11338 RUVBL2, RVB2, INO80; RuvB-like protein 2 [EC:5.6.2.3]	map03082 ATP-dependent chromatin remodeling	KOG2680 Hs5730023 DNA helicase TIP49, TBP-interacting protein	TPX60611.1 hypothetical protein PhCBS80983_g01710 [Powellomyces hirtus]	RuvB-like 2 OS=Xenopus laevis OX=8355 GN=ruvbl2 PE=2 SV=1
A3875	-	-	-	-	-	-	-	-
A3876	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3877	-	-	GO:0016791(phosphatase activity)	K17619 MDP1; magnesium-dependent phosphatase 1 [EC:3.1.3.48 3.1.3.-]	-	-	ORY32430.1 magnesium-dependent phosphatase P8B7.31 [Rhizoclostium globosum]	Magnesium-dependent phosphatase 1 OS=Homo sapiens OX=9606 GN=MDP1 PE=1 SV=1
A3878	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	-	-
A3879	-	-	-	-	-	-	-	-
A3880	-	-	-	-	-	-	TPX67172.1 hypothetical protein CcCBS67573_g07572 [Chytridiomycetes confervae]	Lipase 1 OS=Psychrobacter immobilis OX=498 GN=lip1 PE=1 SV=2
A3881	-	-	GO:0035673(oligopeptide transmembrane transporter activity)	-	-	-	KZW02937.1 OPT superfamily oligopeptide transporter [Exidia glandulosa HHB12029]	Probable metal-nicotianamine transporter YSL6 OS=Oryza sativa subsp. japonica OX=39947 GN=YSL6 PE=2 SV=1
A3882	-	-	-	-	-	KOG1179 7291518 Very long-chain acyl-CoA synthetase/fatty acid transporter	KAF9929573.1 hypothetical protein FBU30_001468 [Linnemannia zychae]	Long-chain fatty acid transport protein 4 OS=Homo sapiens OX=9606 GN=SLC27A4 PE=1 SV=1
A3883	-	-	GO:0016787(hydrolase activity),GO:0003993(acid phosphatase activity),GO:0046872(metal ion binding)	K22390 ACP7; acid phosphatase type 7	-	KOG1378 At2g16430 Purple acid phosphatase	RSM07223.1 Acid phosphatase [Fusarium sp. AF-4]	Purple acid phosphatase 18 OS=Arabidopsis thaliana OX=3702 GN=PAP18 PE=2 SV=1

A3884	-	-	GO:0016491(oxidoreductase activity)	K06123 AYR1; 1-acylglycerone phosphate reductase [EC:1.1.1.101]	map00564 Glycerophospholipid metabolism;map00565 Ether lipid metabolism;map01100 Metabolic pathways	KOG0725 7290108 Reductases with broad range of substrate specificities	KAG0766884.1 hypothetical protein G6F24_003252 [Rhizopus oryzae]	3-oxoacyl-[acyl-carrier-protein] reductase FabG OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=fabG PE=3 SV=1
A3885	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1205 At3g47360 Predicted dehydrogenase	KAG0766884.1 hypothetical protein G6F24_003252 [Rhizopus oryzae]	3-oxoacyl-[acyl-carrier-protein] reductase FabG OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=fabG PE=3 SV=1
A3886	-	-	-	-	-	-	-	-
A3887	GO:0006629(lipid metabolic process)	-	GO:0035091(phosphatidylinositol binding)	-	-	KOG2088 At2g42450 Predicted lipase/calmodulin-binding heat-shock protein	XP_016610904.1 hypothetical protein SPPG_01945 [Spizellomyces punctatus DAOM BR117]	Diacylglycerol lipase-beta OS=Rattus norvegicus OX=10116 GN=Daglb PE=1 SV=1
A3888	GO:0006412(translation)	GO:0005840(ribosome),GO:0015935(small ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02973 RP-S23e, RPS23; small subunit ribosomal protein S23e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1749 7303214 40S ribosomal protein S23	ORX57588.1 40S ribosomal protein S23 [Hesseltinella vesiculosa]	Small ribosomal subunit protein uS12 OS=Dermacentor variabilis OX=34621 GN=RpS23 PE=2 SV=1
A3889	GO:0006414(translational elongation),GO:0002182(cytoplasmic translational elongation)	GO:0005840(ribosome),GO:0022625(cytosolic large ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02943 RP-LP2, RPLP2; large subunit ribosomal protein LP2	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	-	KAF2682579.1 ribosomal protein 60S [Lentithecium fluviale CBS 122367]	Large ribosomal subunit protein P2A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rpp201 PE=1 SV=1
A3890	-	-	GO:0018580(nitronate monooxygenase activity)	K23948 E1.6.5.9; NADH:quinone reductase (non-electrogenic) [EC:1.6.5.9]	-	-	XP_019024506.1 2-nitropropane dioxigenase [Saitoella complicata NRRL Y-17804]	NADH:quinone reductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA1024 PE=1 SV=1
A3891	-	-	-	-	-	-	-	-
A3892	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3893	-	-	-	-	-	KOG1108 7291021 Predicted heme/steroid binding protein	KIY71763.1 cytochrome b5 [Cylindrobasis dimorpha FP15055 ss-10]	Neuferricin homolog OS=Drosophila pseudoobscura pseudoobscura OX=46245 GN=GA11364 PE=3 SV=1
A3894	GO:0030036(actin cytoskeleton organization)	-	GO:0051015(actin filament binding),GO:0005515(protein binding)	-	-	KOG0518 Hs4503745 Actin-binding cytoskeleton protein, filamin	-	Gelation factor OS=Dictyostelium discoideum OX=44689 GN=abpC PE=1 SV=1
A3895	GO:0006415(translational termination)	-	GO:0003747(translation release factor activity)	K03265 ETF1; ERF1; peptide chain release factor subunit 1	map03015 mRNA surveillance pathway	KOG0688 7296284 Peptide chain release factor 1 (eRF1)	OUM65967.1 hypothetical protein PIROE2DRAFT_67160 [Piromyces sp. E2]	Eukaryotic peptide chain release factor subunit 1 OS=Polyandrocampa misakiensis OX=7723 GN=ERF1 PE=2 SV=1

A3896	-	-	GO:0005515(protein binding)	-	-	-	EPZ35679.1 Quinonprotein alcohol dehydrogenase-like superfamily domain-containing protein [Rozella allomyces CSF55]	Cilia- and flagella-associated protein 57 OS=Mus musculus OX=10090 GN=Cfap57 PE=1 SV=3
A3897	-	-	-	K12860 CDC5L, CDC5, CEF1; pre-mRNA-splicing factor CDC5/CEF1	map03040 Spliceosome	KOG0048 At4g00540 Transcription factor, Myb superfamily	KAG2172771.1 hypothetical protein INT43_000118 [Umbelopsis isabellina]	Transcription factor MYB3R-2 OS=Arabidopsis thaliana OX=3702 GN=MYB3R2 PE=2 SV=1
A3898	-	-	-	-	-	-	-	-
A3899	GO:0009094(L-phenylalanine biosynthetic process), GO:0009072(aromatic amino acid family metabolic process)	-	GO:0004664(prephenate dehydratase activity),GO:0016714(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen),GO:0004497(monooxygenase activity),GO:0005506(iron ion binding)	-	-	KOG3820 CE21050 Aromatic amino acid hydroxylase	KAF7743083.1 hypothetical protein DSO57_004096 [Entomophthora muscae]	Phenylalanine-4-hydroxylase OS=Dictyostelium discoideum OX=44689 GN=pah PE=1 SV=1
A3900	GO:0006457(protein folding)	GO:0016272(prefoldin complex)	GO:0051082(unfolded protein binding)	K09549 PFDN2; prefoldin subunit 2	-	KOG4098 Hs12408675 Molecular chaperone Prefoldin, subunit 2	KAF9974176.1 hypothetical protein BGZ73_002460 [Actinomortierella ambigua]	Prefoldin subunit 2 OS=Mus musculus OX=10090 GN=Pfdn2 PE=1 SV=2
A3901	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4557333 Sulfatase	XP_024663337.1 Arylsulfatase B [Wickerhamia sorbophila]	Arylsulfatase B OS=Rattus norvegicus OX=10116 GN=Arse PE=2 SV=2
A3902	-	-	-	-	-	-	-	-
A3903	GO:0000413(protein peptidyl-prolyl isomerization),GO:0006457(protein folding)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K01802 E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]	-	KOG0865 CE22213 Cyclophilin type peptidyl-prolyl cis-trans isomerase	CDS02793.1 Putative Peptidyl-prolyl cis-trans isomerase [Lichtheimia ramosa]	Peptidyl-prolyl cis-trans isomerase 1 OS=Caenorhabditis elegans OX=6239 GN=cyn-1 PE=2 SV=1

A3904	GO:0005975(carbohydrate metabolic process), GO:1904380(endoplasmic reticulum mannose trimming), GO:1904382(mannose trimming involved in glycoprotein ERAD pathway)	GO:0016020(membrane)	GO:0004571(mannosyl-oligosaccharide 1,2-alpha-mannosidase activity), GO:0005509(calcium ion binding)	K10084 EDEM1; ER degradation enhancer, mannosidase alpha-like 1	map04141 Protein processing in endoplasmic reticulum	KOG2429 At5g43710 Glycosyl hydrolase, family 47	ORY90035.1 glycoside hydrolase [Syncephalaster racemosum]	Alpha-mannosidase I MNS4 OS=Arabidopsis thaliana OX=3702 GN=MNS4 PE=1 SV=1
A3905	-	-	GO:0003725(double-stranded RNA binding)	K26159 PRKRIP1; PRKR-interacting protein 1	-	KOG4055 7302978 Uncharacterized conserved protein	XP_025360082.1 DUF1168-domain-containing protein, partial [Jaminaea rosea]	PRKR-interacting protein 1 homolog OS=Danio rerio OX=7955 GN=prkrip1 PE=2 SV=1
A3906	GO:0030833(regulation of actin filament polymerization), GO:0034314(Arp2/3 complex-mediated actin nucleation)	GO:0005856(cytoskeleton), GO:0005885(Arp2/3 protein complex)	-	K05756 ARPC3; actin related protein 2/3 complex, subunit 3	map04144 Endocytosis; map05135 Yersinia infection; map05132 Salmonella infection; map05130 Pathogenic Escherichia coli infection; map05131 Shigellosis; map04810 Regulation of actin cytoskeleton; map04138 Autophagy - yeast; map05100 Bacterial invasion of epithelial cells; map04666 Fc gamma R-mediated phagocytosis; map04530 Tight junction	KOG3155 At1g60430 Actin-related protein Arp2/3 complex, subunit ARPC3	RKO99395.1 hypothetical protein CXG81DRAFT_14579 [Caulochytrium protostelioides]	Actin-related protein 2/3 complex subunit 3 OS=Arabidopsis thaliana OX=3702 GN=ARPC3 PE=1 SV=1
A3907	-	GO:0016020(membrane)	-	-	-	KOG3083 At3g27280 Prohibitin	XP_038777321.1 Prohibitin-2, subunit of the prohibitin complex (Phb1p-Phb2p) [Brettanomyces nanus]	Prohibitin-4, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=PHB4 PE=1 SV=1
A3908	GO:0006506(GPI anchor biosynthetic process)	GO:0000139(Golgi membrane)	GO:0016757(glycosyltransferase activity)	-	-	-	XP_028492728.1 uncharacterized protein D7B24_000350 [Verticillium nonalfalfae]	-

A3909	GO:0006508(proteolysis),GO:0030163(protein catabolic process)	-	GO:0004176(ATP-dependent peptidase activity),GO:0004252(serine-type endopeptidase activity),GO:0005524(ATP binding),GO:0043565(sequence-specific DNA binding),GO:0016887(ATP hydrolysis activity)	K01338 lon; ATP-dependent Lon protease [EC:3.4.21.53]	map04112 Cell cycle - Caulobacter	KOG2004 At5g47040 Mitochondrial ATP-dependent protease PIM1/LON	TPX66710.1 hypothetical protein SpCBS45565_g04311 [Spizellomyces sp. 'palustris']	Lon protease 2 OS=Myxococcus xanthus OX=34 GN=lon2 PE=1 SV=3
A3910	-	-	-	-	-	-	-	-
A3911	GO:0009082(branch ed-chain amino acid biosynthetic process)	-	GO:0016491(oxidoreductase activity),GO:0004455(ketol-acid reductoisomerase activity)	K00053 ilvC; ketol-acid reductoisomerase [EC:1.1.1.86]	map00770 Pantothenate and CoA biosynthesis;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	-	KAF9180503.1 Bifunctional acetohydroxy acid reductoisomerase [Haplosporangium sp. Z 11]	Ketol-acid reductoisomerase, mitochondrial OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=ilv-2 PE=3 SV=2
A3912	-	-	-	-	-	-	-	-
A3913	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K15505 RAD5; DNA repair protein RAD5 [EC:5.6.2.-]	-	KOG1001 At5g43530 Helicase-like transcription factor HLTf/DNA helicase RAD5, DEAD-box superfamily	XP_021876218.1 SNF2 family N-terminal domain-containing protein [Lobosporangium transversale]	DNA repair protein RAD5B OS=Arabidopsis thaliana OX=3702 GN=RAD5B PE=3 SV=1
A3914	GO:0007154(cell communication),GO:0006816(calcium ion transport),GO:005085(transmembrane transport)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0005432(calcium:sodium antiporter activity)	-	-	KOG1306 Hs10863913 Ca2+/Na+ exchanger NCX1 and related proteins	-	Sodium/calcium exchanger 1 OS=Felis catus OX=9685 GN=SLC8A1 PE=1 SV=1
A3915	GO:0016192(vesicle-mediated transport)	-	-	K19998 SCFD1, SLY1; sec1 family domain-containing protein 1	-	KOG1301 Hs7706371 Vesicle trafficking protein Sly1 (Sec1 family)	ORX84001.1 Sec1-like protein [Basidiobolus meristosporus CBS 931.73]	Sec1 family domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SCFD1 PE=1 SV=4
A3916	-	-	GO:0005515(protein binding)	-	-	KOG0379 At3g07720 Kelch repeat-containing proteins	KAF8499883.1 hypothetical protein F5888DRAFT_117731 [Russula emetica]	RING finger protein B OS=Dictyostelium discoideum OX=44689 GN=rngB PE=2 SV=2

A3917	GO:0006355(regulation of transcription, DNA-templated);GO:0016573(histone acetylation)	GO:0072487(MSL complex)	GO:0004402(histone acetyltransferase activity)	K11304 TIP60, KAT5, ESA1; histone acetyltransferase HTATIP [EC:2.3.1.48]	map03082 ATP-dependent chromatin remodeling;map05017 Spinocerebellar ataxia;map05166 Human T-cell leukemia virus 1 infection	KOG2747 Hs14149875 Histone acetyltransferase (MYST family)	RKP26149.1 acyl-CoA N-acyltransferase [Syncephalis pseudoplumigaleata]	Histone acetyltransferase KAT8 OS=Homo sapiens OX=9606 GN=KAT8 PE=1 SV=2
A3918	GO:0035303(regulation of dephosphorylation)	-	-	-	-	KOG2562 Hs923600 Protein phosphatase 2 regulatory subunit	TPX62819.1 hypothetical protein PhCBS80983_g00213 [Powellomyces hirtus]	Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma OS=Homo sapiens OX=9606 GN=PPP2R3C PE=1 SV=1
A3919	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding);GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K08286 E2.7.11.-.; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0601 CE14884_1 Cyclin-dependent kinase WEE1	KAF9150031.1 hypothetical protein DFQ26_001712, partial [Actinomortierella ambigua]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei brucei OX=5702 GN=CRK2 PE=3 SV=1
A3920	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A3921	-	-	-	-	-	-	-	-
A3922	-	-	GO:0003676(nucleic acid binding);GO:0005524(ATP binding);GO:0003724(RNA helicase activity)	-	-	KOG0328 Z9019 Predicted ATP-dependent RNA helicase FAL1, involved in rRNA maturation, DEAD-box superfamily	XP_003038113.1 uncharacterized protein SCHCODRAFT_63532 [Schizophyllum commune H4-8]	Eukaryotic initiation factor 4A-III OS=Drosophila melanogaster OX=7227 GN=CG7483 PE=1 SV=1
A3923	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A3924	-	-	-	-	-	-	-	-
A3925	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding);GO:0004672(protein kinase activity);GO:0005524(ATP binding)	-	-	KOG0601 CE14884_1 Cyclin-dependent kinase WEE1	KAF9976048.1 hypothetical protein BGZ73_009207 [Actinomortierella ambigua]	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase wee-1.3 OS=Caenorhabditis elegans OX=6239 GN=wee-1.3 PE=1 SV=1
A3926	-	-	-	-	-	-	KAF9410687.1 hypothetical protein BGZ76_005483 [Entomortierella beljakovae]	Putative serine/threonine-protein kinase YrzF OS=Bacillus subtilis (strain 168) OX=224308 GN=yrzF PE=3 SV=2

A3927	GO:0006470 (protein dephosphorylation)	-	GO:0004722 (protein serine/threonine phosphatase activity)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	-	KAF7723192.1 Protein phosphatase 2C 2 [Apophysomycetes ossiformis]	Protein phosphatase 2C homolog 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ptc2 PE=3 SV=1
A3928	GO:0007131 (reciprocal meiotic recombination)	-	-	K20523 SH3YL1; SH3 domain-containing YSC84-like protein 1	-	-	KAF3023027.1 hypothetical protein E8E14_011734 [Neopetalotriopsis sp. 37M]	SH3 domain-containing YSC84-like protein 1 OS=Homo sapiens OX=9606 GN=SH3YL1 PE=1 SV=1
A3929	-	-	-	K01054 MGLL; acylglycerol lipase [EC:3.1.1.23]	map04723 Retrograde endocannabinoid signaling; map04714 Thermogenesis; map00561 Glycerolipid metabolism; map01100 Metabolic pathways; map04923 Regulation of lipolysis in adipocytes	KOG1455[Hs6005786 Lysophospholipase	TGZ82399.1 alpha/beta-hydrolase [Ascodesmis nigricans]	Monoacylglycerol lipase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv0183 PE=1 SV=2
A3930	-	-	-	-	-	-	-	-
A3931	-	-	-	-	-	-	-	-
A3932	GO:0006367 (transcription initiation from RNA polymerase II promoter), GO:0006366 (transcription by RNA polymerase II)	GO:0005674 (transcription factor TFIIF complex)	-	K03139 TFIIF2, GTF2F2, TFG2; transcription initiation factor TFIIF subunit beta [EC:5.6.2.-]	map03022 Basal transcription factors	KOG2905[At3g52270 Transcription initiation factor IIF, small subunit (RAP30)	XP_023469880.1 transcription initiation factor IIF, beta subunit [Rhizopus microsporus ATCC 52813]	General transcription factor IIF subunit 2 OS=Dictyostelium discoideum OX=44689 GN=gtf2f2 PE=3 SV=2
A3933	-	-	-	-	-	-	-	-
A3934	-	-	-	-	-	KOG0802[7301102_2 E3 ubiquitin ligase	EME41179.1 hypothetical protein DOTSEDRAFT_55077 [Dothistroma septosporum NZE10]	E3 ubiquitin-protein ligase RNF8 OS=Bos taurus OX=9913 GN=RNF8 PE=2 SV=1
A3935	-	-	-	-	-	-	KAG0935799.1 hypothetical protein G6F31_015855 [Rhizopus oryzae]	-
A3936	GO:0006412 (translation)	GO:0005840 (ribosome)	GO:0003735 (structural constituent of ribosome)	K02889 RP-L21e, RPL21; large subunit ribosomal protein L21e	map05171 Coronavirus disease - COVID-19; map03010 Ribosome	-	OMH78597.1 60S ribosomal protein L21-A [Zancudomyces culisetiae]	Large ribosomal subunit protein eL21B OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rpl2102 PE=2 SV=2
A3937	-	-	-	-	-	KOG2914[At1g56500_1 Predicted haloacid-halido-hydrolyase and related hydrolases	KAF9138960.1 hypothetical protein BGX30_008531 [Mortierella sp. GBA39]	Hexitol phosphatase B OS=Escherichia coli (strain K12) OX=83333 GN=hxpB PE=1 SV=1

A3938	-	-	GO:0005515(protein binding)	-	-	-	-	-
A3939	-	-	-	K03671 trxA; thioredoxin 1	map05132 Salmonella infection;map05418 Fluid shear stress and atherosclerosis; map04621 NOD-like receptor signaling pathway;map05012 Parkinson disease	KOG0907/CE01745 Thioredoxin	KAF3042945.1 hypothetical protein E8E12_008021 [Didymella heteroderae]	Thioredoxin 1 OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=TRX1 PE=1 SV=1
A3940	GO:0003341(cilium movement),GO:0036158(outer dynein arm assembly)	GO:0005929(cilium)	-	-	-	-	XP_016611048.1 hypothetical protein SPPG_02080 [Spizellomyces punctatus DAOM BR117]	-
A3941	GO:0009058(biosynthetic process),GO:0006520(cellular amino acid metabolic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0003824(catalytic activity),GO:0008483(transaminase activity)	K14455 GOT2; aspartate aminotransferase, mitochondrial [EC:2.6.1.1]	map00950 Isoquinoline alkaloid biosynthesis;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00960 Tropane, piperidine and pyridine alkaloid biosynthesis;map00330 Arginine and proline metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map04975 Fat	KOG1411 At5g19550 Aspartate aminotransferase/Glutamic oxaloacetic transaminase AAT1/GOT2	XP_019001715.1 aspartate aminotransferase, mitochondrial [Kwoniella mangroviensis CBS 8507]	Aspartate aminotransferase, cytoplasmic OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0760600 PE=2 SV=1
A3942	-	-	GO:0004386(helicase activity)	K19783 HCS1; DNA polymerase alpha-associated DNA helicase A [EC:5.6.2.3]	-	-	RYO75746.1 hypothetical protein DL763_011095 [Monosporascus cannonballus]	Uncharacterized ATP-dependent helicase MG140 homolog OS=Mycoplasma pneumoniae (strain ATCC 29342 / M129 / Subtype 1) OX=272634 GN=MPN_153 PE=3 SV=1
A3943	-	-	GO:0005515(protein binding)	-	-	-	CAF9903553.1 hypothetical protein GOMPHAMPRED_000370 [Gomphillus americanus]	-

A3944	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0005524(ATP binding),GO:0019205(nucleobase-containing compound kinase activity)	K00939 adk, AK; adenylate kinase [EC:2.7.4.3]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map00730 Thiamine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3078 At5g47840 Adenylate kinase	KOS23099.1 Adenylate kinase [Escovopsis weberi]	Adenylate kinase, chloroplastic OS=Zea mays OX=4577 GN=ADK1 PE=1 SV=1
A3945	-	-	-	-	-	KOG1208 7290709 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	XP_029753097.1 hypothetical protein PpBr36_03801 [Pyricularia pennisetigena]	Dehydrogenase/reductase SDR family member on chromosome X homolog OS=Mus musculus OX=10090 GN=Dhrsx PE=1 SV=2
A3946	-	-	GO:0004499(N, N-dimethylaniline monooxygenase activity),GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding)	-	-	KOG1399 Hs4503757 Flavin-containing monooxygenase	KAF4604171.1 hypothetical protein EYR38_004593 [Pleurotus pulmonarius]	Monooxygenase ptmN OS=Penicillium simplicissimum OX=69488 GN=ptmN PE=3 SV=1
A3947	-	-	-	-	-	-	-	-
A3948	GO:0006633(fatty acid biosynthetic process)	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups),GO:0016746(acyltransferase activity)	K09458 fabF, OXSM, CEM1, 3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]	map00780 Biotin metabolism;map01240 Biosynthesis of cofactors;map00061 Fatty acid biosynthesis;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG1394 At2g04540 3-oxoacyl-(acyl-carrier-protein) synthase (I and II)	ORY02914.1 3-oxoacyl-synth [Basidiobolus meristosporus CBS 931.73]	3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Rhizobium meliloti (strain 1021) OX=266834 GN=fabF PE=3 SV=2
A3949	-	-	-	-	-	KOG4037 CE06203 Photoreceptor synaptic vesicle protein HRG4/UNC-119	TPX62151.1 hypothetical protein PhCBS80983-g00741 [Powellomyces hirtus]	Protein unc-119 OS=Caenorhabditis elegans OX=6239 GN=unc-119 PE=1 SV=1

A3950	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004707(MAP kinase activity)	K04371 ERK, MAPK1.3; mitogen-activated protein kinase 1/3 [EC:2.7.11.24]	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map04730 Long-term depression;map05135 Yersinia infection;map05132 Salmonella infection;map05133 Pertussis;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04350 TGF-beta signaling pathway;map04810 Regulation	KOG0660[At4g01370 Mitogen-activated protein kinase	XP_031853305.1 uncharacterized protein SAPINGB_P002696 [Saprochaete ingens]	Extracellular signal-regulated kinase 1 OS=Dictyostelium discoideum OX=44689 GN=erkA PE=2 SV=2
A3951	GO:0006414(translational elongation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02942 RP-LP1, RPLP1; large subunit ribosomal protein LP1	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1762[At5g24510 60s acidic ribosomal protein P1	XP_006678329.1 uncharacterized protein BATDEDRAFT_10993 [Batrachochytrium dendrobatidis JAM81]	Large ribosomal subunit protein P1 OS=Chlamydomonas reinhardtii OX=3055 PE=3 SV=1
A3952	-	-	-	K14209 SLC36A, PAT; solute carrier family 36 (proton-coupled amino acid transporter)	map04138 Autophagy - yeast;map04974 Protein digestion and absorption	-	EXF79848.1 transmembrane amino acid transporter [Colletotrichum fioriniae PJ7]	Vacuolar amino acid transporter 3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=avt3 PE=1 SV=1
A3953	GO:0006364(rRNA processing)	GO:0032040(small-subunit processome)	-	K14769 UTP11; U3 small nucleolar RNA-associated protein 11	-	KOG3237[Hs7705809 Uncharacterized conserved protein	ORY94487.1 small-subunit processome [Syncephalaster racemosus]	Probable U3 small nucleolar RNA-associated protein 11 OS=Homo sapiens OX=9606 GN=UTP11 PE=1 SV=2
A3954	-	-	GO:0005509(calcium ion binding)	-	-	KOG0028[At4g37010 Ca2+-binding protein (centrin/caltractin), EF-Hand superfamily protein	TPX63483.1 hypothetical protein SpCBS45565_g06573 [Spizellomyces sp. 'palustris']	Calcium-binding protein CML19 OS=Arabidopsis thaliana OX=3702 GN=CML19 PE=1 SV=1
A3955	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity)	-	-	-	-	-
A3956	GO:0006396(rRNA processing)	GO:0000178(exosome (RNase complex))	-	K03678 RRP45, EXOSC9; exosome complex component RRP45	map03018 RNA degradation	-	RKP09940.1 ribosomal protein S5 domain 2-type protein [Thamnocephalus sphaerosporus]	Exosome complex component RRP45 OS=Bos taurus OX=9913 GN=EXOSC9 PE=2 SV=1

A3957	GO:0008033(tRNA processing),GO:0002943(tRNA dihydrouridine synthesis)	-	GO:0017150(tRNA dihydrouridine synthase activity),GO:0050660(flavin adenine dinucleotide binding)	K05539 dusA; tRNA-dihydrouridine synthase A [EC:1.-.-.-]	-	KOG2335 At5g47970 tRNA-dihydrouridine synthase	KAG1254472.1 hypothetical protein G6F65_017026 [Rhizopus oryzae]	tRNA-dihydrouridine(20/20a) synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) OX=223926 GN=dusA PE=3 SV=1
A3958	-	-	-	K17053 ABP140; tRNAThr (cytosine32-N3)-methyltransferase [EC:2.1.1.268]	-	KOG2361 Hs17445220 Predicted methyltransferase	XP_016608076.1 hypothetical protein SPPG_04381 [Spizellomyces punctatus DAOM BR117]	tRNA N(3)-methylcytidine methyltransferase METTL6 OS=Mus musculus OX=10090 GN=Mettl6 PE=1 SV=2
A3959	-	-	GO:0005524(ATP binding)	K12608 CAF16; CCR4-NOT complex subunit CAF16	map03018 RNA degradation	KOG2355 At5g02270 Predicted ABC-type transport, ATPase component/CCR4 associated factor	XP_019023053.1 uncharacterized protein SAICODRAFT_58980 [Saitoella complicata NRRL Y-17804]	ABC transporter I family member 20 OS=Arabidopsis thaliana OX=3702 GN=ABC120 PE=2 SV=1
A3960	-	-	GO:0005515(protein binding)	-	-	-	XP_016604894.1 hypothetical protein SPPG_07686 [Spizellomyces punctatus DAOM BR117]	Cilia and flagella-associated protein 47 OS=Mus musculus OX=10090 GN=Cfap47 PE=1 SV=2
A3961	-	-	-	-	-	-	TPX56732.1 hypothetical protein PhCBS80983_g04333 [Powellomyces hirtus]	Cilia- and flagella-associated protein 58 OS=Homo sapiens OX=9606 GN=CFAP58 PE=1 SV=1
A3962	-	-	-	K07019 K07019; uncharacterized protein	-	KOG1838 At1g34340 Alpha/beta hydrolase	KLO18587.1 AB-hydrolase YheT [Schizopora paradoxa]	-
A3963	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K06641 CHEK2; serine/threonine-protein kinase CHEK2 [EC:2.7.11.1]	map04218 Cellular senescence;map04115 p53 signaling pathway;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG0192 At4g31170 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	EIF49642.1 ste20 paka protein kinase [Brettanomyces bruxellensis AWRI1499]	Serine/threonine-protein kinase Nek2 OS=Oryza sativa subsp. indica OX=39946 GN=NEK2 PE=3 SV=1
A3964	GO:00055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05643 ABCA3; ATP-binding cassette, subfamily A (ABC1), member 3	map02010 ABC transporters	KOG0059 Hs17865630 Lipid exporter ABCA1 and related proteins, ABC superfamily	OUM63933.1 hypothetical protein PIROE2DRAFT_20607 [Piromyces sp. E2]	Cholesterol transporter ABCA5 OS=Rattus norvegicus OX=10116 GN=Abca5 PE=2 SV=1
A3965	-	-	-	-	-	-	-	-

A3966	-	-	-	K04739 PRKAR; cAMP- dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG1113 729 6360 cAMP- dependent protein kinase types I and II, regulatory subunit	TPX69923.1 hypothetical protein SpCBS45565- g02082 [Spizellomyces sp. 'palustris']	cAMP-dependent protein kinase regulatory subunit OS=Colletotrichum orbiculare (strain 104-T / ATCC 96160 / CBS 514.97 / LARS 414 / MAFF 240422) OX=1213857 GN=PKAR PE=3 SV=1
A3967	-	-	-	K20477 RGP1; RAB6A-GEF complex partner protein 2	-	-	OCL09729.1 Rgp1- domain- containing protein [Glonium stellatum]	-
A3968	-	-	-	-	-	-	-	-
A3969	-	-	-	-	-	-	-	-
A3970	-	-	GO:0016491(oxidoreductase activity),GO:0020037(heme binding)	-	-	KOG0536 730 2484_1 Flavoheмоprotein b5+b5R	PLW13291.1 hypothetical protein PCANC_1777 0 [Puccinia coronata f. sp. avenae]	Uncharacterized protein C1F12.10c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC1F12.10c PE=3 SV=1
A3971	-	-	-	-	-	-	-	-
A3972	-	-	-	K01078 PHO; acid phosphatase [EC:3.1.3.2]	map00730 Thiamine metabolism;map 00740 Riboflavin metabolism;map 01100 Metabolic pathways	KOG3720 Hs4 557010 Lysosomal & prostatic acid phosphatases	RCH78862.1 hypothetical protein CU097_00119 7 [Rhizopus zygosporus]	Lysosomal acid phosphatase OS=Bos taurus OX=9913 GN=ACP2 PE=2 SV=1
A3973	GO:0007165(signal transduction)	-	-	-	-	-	-	-
A3974	-	-	-	-	-	-	-	-
A3975	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07880 RAB4B; Ras- related protein Rab- 4B	-	KOG0098 At4 g17170 GTPase Rab2, small G protein superfamily	ORX71368.1 ras-related protein rab- 2-A [Linderina pennisporea]	Ras-related protein Rab-2-A OS=Zea mays OX=4577 GN=RAB2A PE=2 SV=2
A3976	-	-	-	-	-	-	-	-
A3977	-	-	-	-	-	-	-	-
A3978	-	GO:0005777(peroxisome)	-	K13337 PEX19; peroxin-19	map04146 Peroxisome	KOG3133 At3 g03490 40 kDa farnesylated protein associated with peroxisomes	KAF9999420. 1 Peroxisome chaperone and import receptor [Entomortiera chlamydospora]	Peroxisome biogenesis protein 19-1 OS=Arabidopsis thaliana OX=3702 GN=PEX19-1 PE=1 SV=1
A3979	-	-	GO:0002953(5'-deoxynucleotidase activity)	K07023 YGK1, HDDC2; 5'- deoxynucleot idase [EC:3.1.3.89]	map00230 Purine metabolism;map 00240 Pyrimidine metabolism;map 01232 Nucleotide metabolism;map 01100 Metabolic pathways	KOG3197 729 7141 Predicted hydrolases of HD superfamily	KAJ9384989. 1 HD domain- containing protein [Gymnopus androsaceus JB14]	5'-deoxynucleotidase HDDC2 OS=Danio rerio OX=7955 GN=hddc2 PE=2 SV=1
A3980	-	-	-	-	-	-	-	-
A3981	GO:0006629(lipid metabolic process)	-	-	-	-	KOG4569 CE 19323 Predicted lipase	KAF2099514. 1 alpha/beta- hydrolase [Rhizodiscina lignyota]	Lipase ZK262.3 OS=Caenorhabditis elegans OX=6239 GN=ZK262.3 PE=1 SV=1
A3982	GO:0008608(attachment of spindle microtubules to kinetochore)	GO:0042729(DASH complex),GO:0072686(mitotic spindle)	-	-	-	-	-	-

A3983	-	-	-	-	-	-	-	-
A3984	-	-	-	-	-	-	-	-
A3985	-	-	GO:0003855(3-dehydroquinase dehydratase activity)	-	-	KOG0692 At3g06350 Pentafunctional AROM protein	-	3-dehydroquinase dehydratase OS=Methanosarcina barkeri (strain Fusaro / DSM 804) OX=269797 GN=aroD PE=3 SV=1
A3986	-	-	-	K18158 NCA2; nuclear control of ATPase protein 2	-	-	TPX57764.1 hypothetical protein PhCBS80983_g03581 [Powellomyces hirtus]	Nuclear control of ATPase protein 2 OS=Dictyostelium discoideum OX=44689 GN=nca2 PE=3 SV=1
A3987	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A3988	GO:0006415(translational termination)	-	GO:0003747(translation release factor activity)	K02835 prfA, MTRF1, MRF1; peptide chain release factor 1	-	KOG2726 At2g47020 Mitochondrial polypeptide chain release factor	SAM01253.1 hypothetical protein [Absidia glauca]	Peptide chain release factor 1 OS=Orientia tsutsugamushi (strain Ikeda) OX=334380 GN=prfA PE=3 SV=1
A3989	-	-	-	K20242 EVI5; ecotropic viral integration site 5 protein	-	KOG4436 CE07531 Predicted GTPase activator NB4S/EVI5 (contains TBC domain)/Calmodulin-binding protein Pollux (contains PTB and TBC domains)	XP_025349476.1 RabGAP/TBC [Pseudomonas stroma glucosiphilum]	Rab GTPase-activating protein eat-17 OS=Caenorhabditis elegans OX=6239 GN=eat-17 PE=1 SV=1
A3990	-	GO:0016021(integral component of membrane)	GO:0016757(glycosyltransferase activity)	K05531 MNN10; mannan polymerase II complex MNN10 subunit [EC:2.4.1.-]	map00513 Various types of N-glycan biosynthesis;map01100 Metabolic pathways	KOG4748 YDR245w Subunit of Golgi mannosyltransferase complex	KAF9903603.1 hypothetical protein EC991_003515 [Linnemannia zychae]	Probable alpha-1,6-mannosyltransferase MNN10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN10 PE=1 SV=1
A3991	-	-	GO:0003824(catalytic activity)	-	-	-	-	4-hydroxy-2-oxovalerate aldolase OS=Methyloccella silvestris (strain DSM 15510 / CIP 108128 / LMG 27833 / NCIMB 13906 / BL2) OX=395965 GN=MsiI_1479 PE=3 SV=1
A3992	-	-	-	-	-	-	KZP26963.1 hypothetical protein FIBSPDRAFT_928382 [Fibularhizoctonia sp. CBS 109695]	-
A3993	-	-	-	-	-	-	-	-
A3994	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K24512 VWA8; von Willebrand factor A domain-containing protein 8	-	KOG1808 CE20666 AAA ATPase containing von Willebrand factor type A (vWA) domain	KAG0224829.1 von Willebrand factor A domain-containing protein 8 [Actinomyces rella wolfii]	von Willebrand factor A domain-containing protein 8 OS=Homo sapiens OX=9606 GN=VWA8 PE=1 SV=2
A3995	GO:0042262(DNA protection)	-	GO:0008413(8-oxo-7,8-dihydroguanosine triphosphate pyrophosphatase activity)	-	-	-	EPB83164.1 hypothetical protein HMPREF1544_10100 [Mucor circinelloides 1006PhL]	Oxidized purine nucleoside triphosphate hydrolase OS=Danio rerio OX=7955 GN=nudt1 PE=1 SV=1

A3996	GO:0010960(magnesium ion homeostasis)	-	-	K16302 CNNM; metal transporter CNNM	-	KOG2118 At5g52790 Predicted membrane protein, contains two CBS domains	OBZ91946.1 Protein MAM3 [Choanephora cucurbitarum]	DUF21 domain-containing protein At4g14240 OS=Arabidopsis thaliana OX=3702 GN=CBSDUF1 PE=1 SV=1
A3997	-	-	GO:0051920(peroxidoreductase activity)	-	-	-	XP_024727670.1 uncharacterized protein K444DRAFT_622130 [Hyaloscypha bicolor E]	-
A3998	-	-	GO:0005524(ATP binding);GO:0046872(metal ion binding)	K01968 E6.4.1.4A; 3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4]	map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG0238 Hs13518228 3-Methylcrotonyl-CoA carboxylase, biotin-containing subunit/Propionyl-CoA carboxylase, alpha chain/Acetyl-CoA carboxylase, biotin carboxylase subunit	RKP08848.1 carbamoyl-phosphate synthase L chain, ATP binding domain-containing protein [Thamnocephalus sphaerospora]	Methylcrotonyl-CoA carboxylase subunit alpha, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=mccA PE=3 SV=1
A3999	-	-	GO:0003824(catalytic activity)	K12603 CNOT6, CCR4; CCR4-NOT transcription complex subunit 6 [EC:3.1.13.4]	map03018 RNA degradation	KOG0620 YAL021c Glucose-repressible alcohol dehydrogenase transcriptional effector CCR4 and related proteins	KAG1140614.1 hypothetical protein G6F38_008984 [Rhizopus oryzae]	CCR4-Not complex 3'-5'-exoribonuclease subunit Ccr4 OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=CCR4 PE=3 SV=1
A4000	GO:0016125(sterol metabolic process)	GO:0016021(integral component of membrane)	GO:0047750(cholesterol delta-isomerase activity)	-	-	-	-	-
A4001	-	-	-	-	-	-	-	-
A4002	GO:0007010(cytoskeleton organization)	-	GO:0003779(actin binding)	K17261 CAP1_2, SRV2; adenyl cyclase-associated protein	-	KOG2675 Hs5453595 Adenylate cyclase-associated protein (CAP/Srv2p)	KXS17700.1 hypothetical protein M427DRAFT_68219 [Gonapodya prolifera JEL478]	Adenyl cyclase-associated protein 1 OS=Bos taurus OX=9913 GN=CAP1 PE=2 SV=3
A4003	GO:0000160(phosphorelay signal transduction system)	-	-	-	-	-	EJD41678.1 hypothetical protein AUDEDRAFT_105975 [Auricularia subglabra TFB-10046 SS5]	-
A4004	-	-	-	-	-	-	KAE9979165.1 Non-histone chromosomal protein 6 [Venturia inaequalis]	Non-histone chromosomal protein 6B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NHP6B PE=1 SV=3

A4005	GO:0006457 (protein folding)	-	GO:0005524 (ATP binding); GO:0016887 (ATP hydrolysis activity); GO:0051082 (unfolded protein binding)	K04079 HSP90A, htpG; molecular chaperone HtpG	map05417 Lipid and atherosclerosis; map04141 Protein processing in endoplasmic reticulum; map05132 Salmonella infection; map04217 Necroptosis; map04915 Estrogen signaling pathway; map04914 Progesterone-mediated oocyte maturation; map05418 Fluid shear stress and atherosclerosis; map04657 IL-17 signaling pathway; map04659 Th17 cell differentiation; map05215 Prostate cancer; map0461	KOG0020 At4g24190 Endoplasmic reticulum glucose-regulated protein (GRP94/endoplasmic), HSP90 family	XP_031025003.1 uncharacterized protein SmJEL517_g03109 [Synchytrium microbalum]	Endoplasmic OS=Sus scrofa OX=9823 GN=HSP90B1 PE=2 SV=3
A4006	-	-	GO:0003723 (RNA binding); GO:0019843 (rRNA binding)	K14560 IMP3; U3 small nucleolar ribonucleoprotein protein IMP3	map03008 Ribosome biogenesis in eukaryotes	KOG4655 At5g15750 U3 small nucleolar ribonucleoprotein (snoRNP) component	XP_016612072.1 hypothetical protein SPPG_01479 [Spizellomyces punctatus DAOM BR117]	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMP3 PE=1 SV=1
A4007	-	-	GO:0008289 (lipid binding)	-	-	-	-	-
A4008	-	-	-	-	-	KOG1030 Hs21362014 Predicted Ca2+-dependent phospholipid-binding protein	XP_016644399.1 C2 domain-containing protein [Scedosporium apiospermum]	Multiple C2 and transmembrane domain-containing protein 1 OS=Mus musculus OX=10090 GN=Mctp1 PE=1 SV=1
A4009	-	-	GO:0005506 (iron ion binding); GO:0016705 (oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen); GO:0031418 (L-ascorbic acid binding)	K00472 P4HA; prolyl 4-hydroxylase [EC:1.14.11.2]	map00330 Arginine and proline metabolism; map01100 Metabolic pathways	KOG1591 7301948 Prolyl 4-hydroxylase alpha subunit	RKP22553.1 hypothetical protein SYNPS1DRAFT_8095, partial [Syncephala pseudoplumigaleata]	Probable prolyl 4-hydroxylase 9 OS=Arabidopsis thaliana OX=3702 GN=P4H9 PE=2 SV=1
A4010	-	-	-	-	-	KOG2127 CE19437 Calmodulin-binding protein CRAG, contains DENN domain	XP_016610382.1 hypothetical protein SPPG_02814 [Spizellomyces punctatus DAOM BR117]	DENN domain-containing protein 4C OS=Mus musculus OX=10090 GN=Dennd4c PE=1 SV=1
A4011	GO:0071562 (nucleus-vacuole junction assembly)	-	GO:0005515 (protein binding); GO:0043495 (protein-membrane adaptor activity)	-	-	-	-	-
A4012	-	-	-	-	-	-	-	-

A4013	-	-	-	K20296 ANG2, VPS51; vacuolar protein sorting- associated protein 51	-	KOG2346[Hs8 393009 Uncharacteriz ed conserved protein	CDS07790.1 hypothetical protein LRAMOSAO1 739 [Lichtheimia ramosa]	Vacuolar protein sorting-associated protein 51 homolog OS=Homo sapiens OX=9606 GN=VPS51 PE=1 SV=2
A4014	-	-	-	-	-	-	-	-
A4015	GO:00071 65(signal transducti on)	-	GO:0004114(3',5 '-cyclic- nucleotide phosphodiester ase activity),GO:000 8081(phosphori c diester hydrolase activity)	K18436 PDE7; high affinity cAMP - specific 3',5'- cyclic phosphodiester ase 7 [EC:3.1.4.53]	map00230 Purine metabolism;map 05032 Morphine addition;map01 100 Metabolic pathways	KOG3689[CE 02038 Cyclic nucleotide phosphodiester ase	TPX39348.1 hypothetical protein SeMB42_g06 369 [Synchytrium endobioticu m]	Probable 3',5'-cyclic-AMP phosphodiesterase pde-4 OS=Caenorhabditis elegans OX=6239 GN=pde-4 PE=2 SV=2
A4016	-	-	-	-	-	-	-	-
A4017	-	-	-	-	-	-	-	-
A4018	-	-	-	-	-	-	-	-
A4019	-	-	-	-	-	-	-	-
A4020	-	-	-	-	-	-	-	-
A4021	-	-	-	-	-	-	-	-
A4022	-	-	-	-	-	-	-	-
A4023	GO:00715 62(nucleu s-vacuole junction assembly)	-	GO:0005515(pro tein binding),GO:004 3495(protein- membrane adaptor activity)	-	-	KOG2242[At2 g22020 Scaffold/matr ix specific factor hnRNP- U/SAF-A, contains SPRY domain	RKP27844.1 hypothetical protein SYNPS1DRAFT_26516 [Syncephalis pseudoplumi galeata]	E3 ubiquitin-protein ligase RKP OS=Arabidopsis thaliana OX=3702 GN=RKP PE=2 SV=2
A4024	-	-	-	-	-	-	KXS13197.1 PhyH- domain- containing protein [Gonapodya prolifera JEL478]	Uncharacterized protein MT3735 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=MT3735 PE=3 SV=1
A4025	GO:00068 86(intracel lular protein transport), GO:00161 92(vesicle- mediated transport), GO:00150 31(protein transport), GO:00725 83(clathrin- dependen t endocytosis)	GO:00301 17(membrane coat),GO: 0030122(AP-2 adaptor complex)	GO:0035615(clathrin adaptor activity)	K11824 AP2A; AP-2 complex subunit alpha	map04144 Endocytosis;map 04721 Synaptic vesicle cycle;map05016 Huntington disease;map049 61 Endocrine and other factor-regulated calcium reabsorption	KOG1077[At5 g22770 Vesicle coat complex AP- 2, alpha subunit	ORX99519.1 putative alpha- adaptin C [Basidiobolus meristosporus CBS 931.73]	AP-2 complex subunit alpha-1 OS=Arabidopsis thaliana OX=3702 GN=ALPHA-ADR PE=1 SV=1
A4026	-	-	GO:0005515(pro tein binding),GO:001 6491(oxidoreduc tase activity)	K08008 NOX1, MOX1; NADPH oxidase 1	map05417 Lipid and atherosclerosis; map04933 AGE- RAGE signaling pathway in diabetic complications;map 05418 Fluid shear stress and atherosclerosis; map04380 Osteoclast differentiation;map 05022 Pathways of neurodegeneration - multiple diseases;map052 08 Chemical carcinogenesis - reactive oxygen species;map050 10 Alzheimer disease	KOG0039[At5 g47910 Ferric reductase, NADH/NADP H oxidase and related proteins	XP_01660523 3.1 hypothetical protein SPPG_07581 [Spizellomyces punctatus DAOM BR117]	Superoxide-generating NADPH oxidase heavy chain subunit A OS=Dictyostelium discoideum OX=44689 GN=noxA PE=2 SV=1

A4027	GO:0000724(double-strand break repair via homologous recombination),GO:0006281(DNA repair)	GO:0005657(replication fork),GO:0033063(Rad51B-Rad51C-Rad51D-XRCC2 complex)	-	-	-	KOG2859 Hs4885657 DNA repair protein, member of the recA/RAD51 family	TPX70254.1 hypothetical protein SpCBS45565.g01890 [Spizellomyces sp. 'palustris']	DNA repair protein XRCC2 OS=Mus musculus OX=10090 GN=Xrcc2 PE=1 SV=1
A4028	GO:0042254(ribosome biogenesis)	GO:0005634(nucleus)	-	K14799 TSR1; pre-rRNA-processing protein TSR1	-	KOG1980 At1g42440 Uncharacterized conserved protein	RIA99286.1 hypothetical protein C1645_684977 [Glomus cerebriforme]	Pre-rRNA-processing protein TSR1 homolog OS=Mus musculus OX=10090 GN=Tsr1 PE=1 SV=1
A4029	-	-	-	K16066 ydfG; 3-hydroxy acid dehydrogenase / malonic semialdehyde reductase [EC:1.1.1.381 1.1.1.-]	map00240 Pyrimidine metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	-	TID19489.1 short chain dehydrogenase/ reductase-like protein [Venturia nashicola]	NADP-dependent 3-hydroxy acid dehydrogenase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC521.03 PE=1 SV=1
A4030	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0070588(calcium ion transmembrane transport)	GO:0005886(plasma membrane),GO:0016020(membrane),GO:0005891(voltage-gated calcium channel complex)	GO:0005261(cation channel activity),GO:0005216(ion channel activity),GO:0005245(voltage-gated calcium channel activity)	K21864 CCH1; voltage-dependent calcium channel	-	KOG2301 CE28820 Voltage-gated Ca2+ channels, alpha1 subunits	KAF9913266.1 calcium channel protein [Linnemania zychae]	Voltage-dependent L-type calcium channel subunit alpha-1C OS=Oryctolagus cuniculus OX=9986 GN=CACNA1C PE=1 SV=1
A4031	-	-	-	-	-	-	-	-
A4032	-	-	-	-	-	-	-	-
A4033	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04563 CDC28, CDC2; cyclin-dependent kinase [EC:2.7.11.22]	map04011 MAPK signaling pathway - yeast;map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0594 At3g48750 Protein kinase PCTAIRE and related kinases	XP_01660554.3.1 CMGC/CDK/CDC2 protein kinase [Spizellomyces punctatus DAOM BR117]	Cell division control protein 2 homolog A OS=Antirrhinum majus OX=4151 GN=CDC2A PE=2 SV=2
A4034	-	-	-	-	-	KOG1730 CE25685 Thioredoxin-like protein	KAG2202257.1 hypothetical protein INT46_009983 [Mucor plumbeus]	PITH domain-containing protein 1 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0277951 PE=3 SV=1
A4035	GO:0009058(biosynthetic process)	-	-	K18163 NDUF6; NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 6	map04714 Thermogenesis	KOG4411 Hs2048748 Phytoene/squalene synthetase	CDS05907.1 hypothetical protein LRAMOSA08435 [Lichtheimia ramosa]	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6 OS=Rattus norvegicus OX=10116 GN=Ndufaf6 PE=3 SV=1
A4036	-	-	-	-	-	-	-	-
A4037	-	-	-	-	-	-	-	-
A4038	-	-	-	-	-	-	-	-

A4039	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004965(G protein-coupled GABA receptor activity);GO:0004930(G protein-coupled receptor activity)	-	-	KOG1055[Hs20127671 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	TPX54710.1 hypothetical protein PhCBS80983.g05811 [Powellomyces hirtus]	Gamma-aminobutyric acid type B receptor subunit 2 OS=Mus musculus OX=10090 GN=Gabbr2 PE=1 SV=2
A4040	-	-	-	-	-	-	-	-
A4041	-	-	GO:0003924(GTPase activity);GO:0005525(GTP binding)	K21594 GUF1; translation factor GUF1, mitochondrial [EC:3.6.5.-]	-	KOG0462[Hs11345460 Elongation factor-type GTP-binding protein	ORY04809.1 translation factor GUF1-like protein, mitochondrial [Basidiobolus meristosporus CBS 931.73]	Translation factor GUF1 homolog, mitochondrial OS=Phytophthora infestans (strain T30-4) OX=403677 GN=PITG_12454 PE=3 SV=1
A4042	-	-	-	K23568 EMC7; ER membrane protein complex subunit 7	-	KOG3306[Hs910346 Predicted membrane protein	KAG0310634.1 hypothetical protein BGZ97_012430 [Linnemannia gamsii]	ER membrane protein complex subunit 7 homolog OS=Arabidopsis thaliana OX=3702 GN=At4g32130 PE=2 SV=1
A4043	-	-	GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027[At1g66410 Calmodulin and related proteins (EF-Hand superfamily)]	KAF9978814.1 hypothetical protein BGZ73_000083 [Actinomortierella ambigua]	Calmodulin OS=Macrocystis pyrifera OX=35122 PE=2 SV=3
A4044	-	-	-	-	-	-	-	-
A4045	GO:0006508(proteolysis)	-	GO:0008237(metallopeptidase activity);GO:0008270(zinc ion binding)	K13721 APE2; aminopeptidase 2 [EC:3.4.11.-]	-	KOG1046[7292091 Puromycin-sensitive aminopeptidase and related aminopeptidases	ORY04712.1 aminopeptidase [Basidiobolus meristosporus CBS 931.73]	Aminopeptidase M1-A OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0218200 PE=2 SV=1
A4046	-	-	-	K16369 CHO2; phosphatidylethanolamine N-methyltransferase [EC:2.1.1.17]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	-	XP_016610178.1 hypothetical protein SPPG_02633 [Spizellomyces punctatus DAOM BR117]	Phosphatidylethanolamine N-methyltransferase OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=cho2 PE=3 SV=1

A4047	-	-	GO:0005254(chloride channel activity)	K08994 yneE, BEST; ion channel-forming bestrophin family protein	-	-	XP_01660596.0.1 hypothetical protein SPPG_06910 [Spizellomyces punctatus DAOM BR117]	Voltage-dependent anion channel-forming protein YneE OS=Escherichia coli O157:H7 OX=83334 GN=yneE PE=3 SV=2
A4048	-	-	-	K24121 MPO1; 2-hydroxy fatty acid dioxygenase [EC:1.14.18.12]	-	KOG3292[At1g18720 Predicted membrane protein	PSS03532.1 hypothetical protein BD289DRAFT_478380 [Coniella lustricola]	2-hydroxy-palmitic acid dioxygenase MPO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MPO1 PE=1 SV=2
A4049	-	-	GO:0005524(ATP binding),GO:0016491(oxidoreductase activity)	-	-	KOG3939[CE28704 Selenophosphate synthetase	KAF9121174.1 hypothetical protein BGX30_002737 [Mortierella sp. GBA39]	Selenide, water dikinase OS=Clostridioides difficile (strain 630) OX=272563 GN=selD PE=3 SV=2
A4050	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015075(ion transmembrane transporter activity)	K23503 SFXN5; sideroflexin-5	-	KOG3767[Hs21389351 Sideroflexin	RIA95897.1 Tricarboxylate/iron carrier [Glomus cerebriforme]	Sideroflexin-5 OS=Homo sapiens OX=9606 GN=SFXN5 PE=1 SV=1
A4051	-	-	-	-	-	-	-	-
A4052	-	-	-	-	-	-	-	-
A4053	-	-	-	-	-	-	-	-
A4054	-	-	GO:0005515(protein binding)	K06867 K06867; uncharacterized protein	-	-	TIA73818.1 hypothetical protein E3P91_01302 [Wallemia ichthyophaga]	-
A4055	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0583[7290150 Serine/threonine protein kinase	ORX83832.1 Pkinase-domain-containing protein [Anaeromyces robustus]	Serine/threonine protein kinase OSK1 OS=Oryza sativa subsp. japonica OX=39947 GN=OSK1 PE=1 SV=1
A4056	-	-	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	K09506 DNAJA5; DnaJ homolog subfamily A member 5	-	KOG0717[CE16336 Molecular chaperone (DnaJ superfamily)	ORX90659.1 DnaJ-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	DnaJ homolog subfamily C member 21 OS=Danio rerio OX=7955 GN=dnajc21 PE=2 SV=1
A4057	-	-	-	-	-	-	CEG77101.1 hypothetical protein RMatCC62417_11901 [Rhizopus microsporus]	-
A4058	-	-	GO:0008270(zinc ion binding)	-	-	-	-	-
A4059	-	-	-	K06911 PIR; quercetin 2,3-dioxygenase [EC:1.13.11.24]	-	-	KAG0194711.1 hypothetical protein DFQ28_007857 [Apophysomyces sp. BC1034]	Pirin-like protein CC_3178 OS=Caulobacter vibrioides (strain ATCC 19089 / CB15) OX=190650 GN=CC_3178 PE=3 SV=1

A4060	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0000981(DNA-binding transcription factor activity, RNA polymerase II-specific),GO:0008270(zinc ion binding)	-	-	-	-	-
A4061	GO:0006099(tricarboxylic acid cycle)	-	GO:0051537(iron, 2 sulfur cluster binding),GO:0016491(oxidoreductase activity),GO:0051536(iron-sulfur cluster binding),GO:0009055(electron transfer activity)	K00235 SDHB, SDH2; succinate dehydrogenase (ubiquinone) iron-sulfur subunit [EC:1.3.5.1]	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map04714 Thermogenesis; map00020 Citrate cycle (TCA cycle);map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map052	KOG3049 At5g40650 Succinate dehydrogenase, Fe-S protein subunit	ODV87632.1 hypothetical protein CANARDRAFT_4957 [[Candida] arabinoferrum NRRL YB-2248]	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit OS=Reclinomonas americana OX=48483 GN=SDH2 PE=3 SV=1
A4062	-	-	-	-	-	-	-	cGMP-dependent 3',5'-cGMP phosphodiesterase A OS=Dictyostelium discoideum OX=44689 GN=pdeD PE=1 SV=1
A4063	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4064	-	-	GO:0005515(protein binding)	-	-	KOG0548 At3g04710.2 Molecular chaperone STI1	GEM08972.1 translocation protein SEC72 [Rhodotorula toruloides]	Tetratricopeptide repeat protein 28 OS=Homo sapiens OX=9606 GN=TTC28 PE=1 SV=4
A4065	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At5g43900 Myosin class V heavy chain	TX13452.1 hypothetical protein VHUM_00819 [Vanrija humicola]	Myosin-6 OS=Arabidopsis thaliana OX=3702 GN=XI-2 PE=1 SV=1
A4066	-	-	GO:0035091(phosphatidylinositol binding)	K17922 SNX8, MVP1; sorting nexin-8	-	KOG2273 YMR004w Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	KAF8448967.1 hypothetical protein L210DRAFT_523581 [Boletus edulis BED1]	Sorting nexin MVP1 OS=Cryptococcus neoformans var. neoformans serotype D (strain B-3501A) OX=283643 GN=MVP1 PE=3 SV=1

A4067	GO:0019346(transsulfuration)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	K01758 CTH; cystathionine gamma-lyase [EC:4.4.1.1]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map00450 Selenocompound metabolism;map00270 Cysteine and methionine metabolism	KOG0053 Hs21361334 Cystathionine beta-lyases/cystathionine gamma-synthases	RIB03222.1 Cys/Met metabolism PLP-dependent enzyme-domain-containing protein [Gigaspora rosea]	Cystathionine gamma-synthase OS=Mycobacterium leprae (strain TN) OX=272631 GN=metB PE=3 SV=1
A4068	GO:0006418(tRNA aminoacylation for protein translation),GO:0006428(isoleucyl-tRNA aminoacylation)	-	GO:0004812(aminoacyl-tRNA ligase activity),GO:00010166(nucleotide binding),GO:0005524(ATP binding),GO:0002161(aminoacyl-tRNA editing activity),GO:0000049(tRNA binding),GO:0004822(isoleucine-tRNA ligase activity)	K01870 IARS, ileS; isoleucyl-tRNA synthetase [EC:6.1.1.5]	map00970 Aminoacyl-tRNA biosynthesis	KOG0433 At5g49030 Isoleucyl-tRNA synthetase	OZJ02176.1 hypothetical protein BZG36_04805 [Bifiguratus adelaidae]	Isoleucine--tRNA ligase OS=Synechococcus sp. (strain ATCC 27144 / PCC 6301 / SAUG 1402/1) OX=269084 GN=ileS PE=3 SV=1
A4069	GO:0009102(biotin biosynthetic process)	-	GO:0003824(catalytic activity),GO:0051536(iron-sulfur cluster binding),GO:0004076(biotin synthase activity)	-	-	KOG2900 At2g43360 Biotin synthase	XP_01660570.2.1 biotin synthase [Spizellomyces punctatus DAOM BR117]	Biotin synthase, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=BIO2 PE=1 SV=1
A4070	-	-	-	-	-	KOG1398 At5g51150 Uncharacterized conserved protein	KAG0066095.1 hypothetical protein BGZ89_007624 [Linnemannia elongata]	Transmembrane protein 135 OS=Homo sapiens OX=9606 GN=TMEM135 PE=2 SV=2
A4071	-	-	GO:0016407(acyltransferase activity)	K20793 NAA50, NAT5; N-alpha-acetyltransferase 50 [EC:2.3.1.258 2.3.1.309]	-	KOG3138 Hs13376735 Predicted N-acetyltransferase	KAF9521536.1 acyl-CoA N-acyltransferase [Crepidotus variabilis]	N-alpha-acetyltransferase 50 OS=Danio rerio OX=7955 GN=naa50 PE=1 SV=1
A4072	-	-	-	-	-	-	-	-
A4073	-	-	-	-	-	-	XP_02187581.0.1 hypothetical protein BCR41DRAFT_426538 [Lobosporangium transversale]	-

A4074	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0598 YMR104c Ribosomal protein S6 kinase and related proteins	EPZ33161.1 Protein kinase, catalytic domain-containing protein [Rozella allomycis CSF55]	Serine/threonine-protein kinase YPK2/YKR2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPK2 PE=1 SV=1
A4075	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0606 J294265 Microtubule-associated serine/threonine kinase and related proteins	KNE72867.1 AGC protein kinase [Allomyces macrogynus ATCC 38327]	Protein kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pkgB PE=1 SV=2
A4076	-	-	-	-	-	-	-	-
A4077	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	K08592 SENP1; sentrin-specific protease 1 [EC:3.4.22.68]	-	KOG0778 Hs7657550 Protease, Ulp1 family	KXS19360.1 cysteine proteinase [Gonapodya prolifera JEL478]	Putative ubiquitin-like-specific protease 1B OS=Arabidopsis thaliana OX=3702 GN=ULP1B PE=5 SV=2
A4078	-	-	-	-	-	-	-	-
A4079	-	GO:0035101(FACT complex)	-	K25639 SUPT16H, SPT16; FACT complex subunit SPT16	-	KOG1189 Hs6005757 Global transcriptional regulator, cell division control protein	KAG2174656.1 hypothetical protein INT44_006920 [Umbelopsis vinacea]	FACT complex subunit SPT16 OS=Zea mays OX=4577 GN=SPT16 PE=2 SV=1
A4080	-	-	-	-	-	-	-	-
A4081	-	GO:0008180(COP9 signalosome)	-	K12178 COPS4, CSN4; COP9 signalosome complex subunit 4	-	KOG1497 Hs7705845 COP9 signalosome subunit CSN4	XP_019026539.1 COP9 signalosome complex subunit 4 [Saitoella complicata NRRL Y-17804]	COP9 signalosome complex subunit 4 OS=Danio rerio OX=7955 GN=cops4 PE=2 SV=1
A4082	-	-	-	-	-	KOG2743 At1g15730 Cobalamin synthesis protein	KXS17345.1 cobW-domain-containing protein [Gonapodya prolifera JEL478]	Zinc-regulated GTPase metalloprotein activator 1A OS=Homo sapiens OX=9606 GN=ZNG1A PE=1 SV=1
A4083	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4084	GO:0051260(protein homooligomerization)	-	-	-	-	KOG2716 CE15120 Polymerase delta-interacting protein PDIP1 and related proteins, contain BTB/POZ domain	-	-
A4085	-	-	GO:0016788(hydrolase activity, acting on ester bonds)	K03424 tatD; TatD DNase family protein [EC:3.1.21.-]	-	KOG3020 CE16950 TatD-related DNase	XP_013241371.1 hypothetical protein K437DRAFT_258700 [Tilletiaria anomala UBC951]	3'-5' ssDNA/RNA exonuclease TatD OS=Erwinia tasmaniensis (strain DSM 17950 / CFBP 7177 / CIP 109463 / NCPPB 4357 / Et1/99) OX=465817 GN=tatD PE=3 SV=1
A4086	-	-	GO:0003677(DNA binding)	-	-	-	-	-

A4087	GO:0006418(tRNA aminoacylation for protein translation),GO:0006433(prolyl-tRNA aminoacylation)	GO:0005737(cytoplasmic)	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004827(proline-tRNA ligase activity)	K01881 PARS, proS; prolyl-tRNA synthetase [EC:6.1.1.15]	map00970 Aminoacyl-tRNA biosynthesis	KOG2324 Hs14729163 Prolyl-tRNA synthetase	RIB07460.1 hypothetical protein C2G38_2006774 [Gigaspora rosea]	Probable proline--tRNA ligase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Pars2 PE=2 SV=1
A4088	-	-	-	-	-	-	-	-
A4091	GO:0007018(microtubule-based movement)	GO:0005868(cytoplasmic dynein complex)	-	K10419 DYNLRB, DNCL2; dynein light chain roadblock-type	map05132 Salmonella infection;map04814 Motor proteins	KOG4115 7302786 Dynein-associated protein Roadblock	KAG4084582.1 roadblock-type dynein light chain [Neocallimastix sp. JGI-2020a]	Dynein light chain roadblock-type 2 OS=Bos taurus OX=9913 GN=DYNLRB2 PE=3 SV=1
A4092	-	-	-	-	-	-	RKO89786.1 Iguana/Dzip1-like DAZ-interacting protein N-terminal-domain-containing protein, partial [Blyttiomycetes helicis]	Cilium assembly protein DZIP1L OS=Homo sapiens OX=9606 GN=DZIP1L PE=1 SV=2
A4093	-	-	-	-	-	-	-	-
A4094	-	-	-	-	-	-	-	-
A4095	-	-	-	-	-	-	-	-
A4096	GO:0071805(potassium ion transmembrane transport),GO:1902600(proton transmembrane transport),GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015386(potassium:proton antiporter activity),GO:0015299(solute:proton antiporter activity)	-	-	KOG1650 At2g19600 Predicted K+/H+-antiporter	OON08983.1 hypothetical protein BSLG_01877, partial [Batrachochytrium salamandrivorans]	K(+) efflux antiporter 6 OS=Arabidopsis thaliana OX=3702 GN=KEA6 PE=1 SV=1
A4097	GO:0006488(dolichol-linked oligosaccharide biosynthetic process)	-	-	-	-	KOG3339 Hs21450685 Predicted glycosyltransferase	CDH51007.1 udp-n-acetylglucosamine transferase subunitalg14 homolog [Lichtheimia corymbifera JMRC:FSU:9682]	UDP-N-acetylglucosamine transferase subunit ALG14 homolog OS=Homo sapiens OX=9606 GN=ALG14 PE=1 SV=1
A4098	-	-	-	-	-	-	-	-
A4099	GO:0007186(G protein-coupled receptor signaling pathway)	-	-	-	-	-	-	-
A4100	-	-	-	-	-	-	-	-

A4101	GO:0006807(nitrogen compound metabolic process)	-	GO:0003824(catalytic activity),GO:0046914(transition metal ion binding),GO:0018822(nitrile hydratase activity)	-	-	-	-	Probable nitrile hydratase OS=Monosiga brevicollis OX=81824 GN=37534 PE=3 SV=1
A4102	GO:000103(sulfate assimilation)	-	GO:0004020(adenylsulfate kinase activity),GO:0005524(ATP binding)	K00860 cysC; adenylsulfate kinase [EC:2.7.1.25]	map00230 Purine metabolism;map01120 Microbial metabolism in diverse environments;map00920 Sulfur metabolism;map01100 Metabolic pathways	-	TPX69109.1 adenylsulfate kinase [Spizellomyces sp. 'palustris']	Adenylsulfate kinase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=met14 PE=3 SV=1
A4103	-	-	-	-	-	-	-	-
A4104	GO:0000398(mRNA splicing, via spliceosome)	GO:0005681(spliceosomal complex)	-	K12863 CWC15; protein CWC15	map03040 Spliceosome	KOG3228 At3g13200 Uncharacterized conserved protein	TPX78019.1 hypothetical protein CcCBS67573_g00665 [Chytridiomycetes confervae]	Protein CWC15 homolog A OS=Xenopus laevis OX=8355 GN=cwc15-a PE=2 SV=1
A4105	GO:0000398(mRNA splicing, via spliceosome)	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding),GO:0005515(protein binding),GO:0008270(zinc ion binding),GO:0045131(pre-mRNA branch point binding)	K13095 SF1; splicing factor 1	-	KOG0119 At5g51300 Splicing factor 1/branch point binding protein (RRM superfamily)	PWW75702.1 hypothetical protein C7212DRAFT_357811 [Tuber magnatum]	Splicing factor-like protein 1 OS=Arabidopsis thaliana OX=3702 GN=SF1 PE=1 SV=1
A4106	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4107	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	ORZ03971.1 hypothetical protein BCR43DRAFT_529252 [Syncephalaster racemosus]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A4108	-	-	-	-	-	KOG2641 At5g26734 Predicted seven transmembrane receptor - rhodopsin family	XP_011124868.1 hypothetical protein AOL_s00109g85 [Orbilia oligospora ATCC 24927]	Transmembrane protein 184 homolog DDB_G0279555 OS=Dictyostelium discoideum OX=44689 GN=tmem184C PE=3 SV=1
A4109	-	-	GO:0005515(protein binding)	-	-	KOG3299 CE20291 Uncharacterized conserved protein	TPX69975.1 hypothetical protein SpCBS45565_g02039 [Spizellomyces sp. 'palustris']	Protein IMPACT OS=Xenopus laevis OX=8355 GN=impact PE=2 SV=1

A4110	-	GO:0016020(membrane)	-	-	-	-	KAF9123733.1 hypothetical protein BGX30_001279 [Mortierella sp. GBA39]	Probable transport protein MmpL8 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=mmpL8 PE=3 SV=1
A4111	-	-	-	-	-	-	-	-
A4112	GO:0006813(potassium ion transport), GO:0006811(ion transport), GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005249(voltage-gated potassium channel activity),GO:0005216(ion channel activity)	K10273 FBXL7; F-box and leucine-rich repeat protein 7	-	KOG0498 7291726 K+-channel ERG and related proteins, contain PAS/PAC sensor domain	KNE63751.1 hypothetical protein AMAG_08834 [Allomyces macrogynus ATCC 38327]	Potassium voltage-gated channel unc-103 OS=Caenorhabditis elegans OX=6239 GN=unc-103 PE=1 SV=1
A4113	GO:0009435(NAD biosynthetic process)	-	GO:0016763(pentose transferase activity),GO:0004514(nicotinate-nucleotide diphosphorylase (carboxylating) activity)	K00767 nadC, QPRT; nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19]	map01240 Biosynthesis of cofactors;map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	KOG3008 YFR047c Quinolinate phosphoribosyl transferase	KNE71856.1 nicotinate-nucleotide diphosphorylase (carboxylating) [Allomyces macrogynus ATCC 38327]	Nicotinate-nucleotide pyrophosphorylase [carboxylating] (Fragment) OS=Nematostella vectensis OX=45351 GN=qprt PE=3 SV=1
A4114	-	-	-	K03676 grxC, GLRX, GLRX2; glutaredoxin 3	-	-	KAG0750833.1 hypothetical protein G6F24_014896 [Rhizopus oryzae]	Glutaredoxin OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=grx PE=3 SV=1
A4115	-	-	-	-	-	-	-	-
A4116	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1199 7293420 Short-chain alcohol dehydrogenase/3-hydroxyacyl-CoA dehydrogenase	KAG2177264.1 hypothetical protein INT43_007921 [Umbelopsis isabellina]	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Bos taurus OX=9913 GN=HSD17B10 PE=1 SV=3
A4117	GO:0019674(NAD metabolic process)	-	GO:0003951(NAD+ kinase activity)	K00858 ppnK NADK; NAD+ kinase [EC:2.7.1.23]	map01240 Biosynthesis of cofactors;map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	KOG2178 7303295 Predicted sugar kinase	KNE72189.1 hypothetical protein AMAG_16675 [Allomyces macrogynus ATCC 38327]	NAD kinase OS=Mus musculus OX=10090 GN=Nadk PE=1 SV=2
A4118	-	-	-	-	-	-	-	-
A4119	-	GO:0005634(nucleus)	GO:0018024(histone-lysine N-methyltransferase activity),GO:0005515(protein binding)	K23700 SET2; [histone H3]-lysine36 N-trimethyltransferase [EC:2.1.1.359]	map00310 Lysine degradation;map01100 Metabolic pathways	KOG4442 At1g76710 Clathrin coat binding protein/Huntingtin interacting protein HIP1, involved in regulation of endocytosis	KAF6063978.1 SET domain family protein [Candida albicans]	Histone-lysine N-methyltransferase, H3 lysine-36 specific OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SET2 PE=3 SV=1
A4120	-	-	-	-	-	-	KAF9939549.1 hypothetical protein BGZ67_009315 [Mortierella alpina]	Transmembrane protein DDB_G0269096 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0269096 PE=4 SV=1

A4121	-	-	GO:0035091(phosphatidylinositol binding)	K17919 SNX4; sorting nexin-4	map04144 Endocytosis	KOG2273 YJL036w Membrane coat complex Retromer, subunit VPS5/SNX1, Sorting nexins, and related PX domain-containing proteins	RPB10127.1 hypothetical protein P167DRAFT_537826 [Morchella conica CCBAS932]	Sorting nexin-4 OS=Eremothecium gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=SNX4 PE=3 SV=1
A4122	-	GO:0071203(WASH complex)	-	-	-	KOG1924 Hs4885183 RhoA GTPase effector DIA/Diaphanous	RKP20512.1 FH2-domain-containing protein, partial [Rozella allomyces CSF55]	Formin-H OS=Dictyostelium discoideum OX=44689 GN=forH PE=1 SV=1
A4123	-	-	-	-	-	KOG0048 At5g67300 Transcription factor, Myb superfamily	XP_013245387.1 hypothetical protein K437DRAFT_210979, partial [Tilletiaria anomala UBC 951]	Transcription factor MYB44 OS=Arabidopsis thaliana OX=3702 GN=MYB44 PE=1 SV=1
A4124	-	-	-	-	-	KOG0048 At5g02320 Transcription factor, Myb superfamily	KXN66846.1 ternary protein-Dna Complex1, partial [Conidiobolus coronatus NRRL 28638]	Transcription factor MYB3R-2 OS=Oryza sativa subsp. japonica OX=39947 GN=MYB3R-2 PE=2 SV=1
A4125	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4126	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity),GO:0005515(protein binding)	-	-	-	CEH12291.1 hypothetical protein CBOM_00290 [Ceraceosorus bombacis]	E3 ubiquitin-protein ligase SspH1 OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=sspH1 PE=1 SV=1
A4127	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1542 At2g21430 Cysteine proteinase Cathepsin F	KFH62689.1 hypothetical protein MVEG_12081 [Podila verticillata NRRL 6337]	Probable cysteine protease RD19B OS=Arabidopsis thaliana OX=3702 GN=RD19B PE=2 SV=2
A4128	-	-	-	-	-	-	-	-
A4129	-	-	-	-	-	-	-	-
A4130	-	-	GO:0005515(protein binding)	-	-	-	OUM62104.1 hypothetical protein PIROE2DRAFT_62105 [Piromyces sp. E2]	Sperm flagellar protein 1 OS=Xenopus laevis OX=8355 GN=spef1 PE=2 SV=1

A4131	GO:0006164(purine nucleotide biosynthetic process)	-	GO:0000166(nucleotide binding),GO:0004019(adenylosuccinate synthase activity),GO:0005525(GTP binding)	K01939 purA,ADSS; adenylosuccinate synthase [EC:6.3.4.4]	map00230 Purine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG1355 7300663 Adenylosuccinate synthase	KAG0371318.1 phosphoribosylaminoimidazole carboxylase ade2 [Gamsiella multidivariata]	Adenylosuccinate synthetase OS=Paramecium tetraurelia OX=5888 GN=GSPATT00004603001 PE=3 SV=1
A4132	GO:0000387(spliceosomal snRNP assembly),GO:0045292(mRNA cis splicing, via spliceosome)	-	GO:0003723(RNA binding),GO:0005515(protein binding),GO:0046872(metal ion binding),GO:0003676(nucleic acid binding),GO:0017070(U6 snRNA binding),GO:0036002(pre-mRNA binding)	-	-	-	XP_016609115.1 hypothetical protein SPPG_04167 [Spizellomyces punctatus DAOM BR117]	Pre-mRNA-splicing factor CWC2 OS=Pyricularia oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) OX=242507 GN=CWC2 PE=3 SV=2
A4133	-	-	-	-	-	-	-	-
A4134	GO:0016192(vesicle-mediated transport),GO:0006886(intracellular protein transport)	GO:0005794(Golgi apparatus),GO:0016020(membrane)	GO:0005484(SNAP receptor activity)	-	-	-	-	-
A4135	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4136	-	-	GO:0005515(protein binding)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0697 CE05722 Protein phosphatase 1B (formerly 2C)	XP_023471595.1 PP2C-domain-containing protein [Rhizopus microsporus ATCC 52813]	Protein phosphatase ppm-1.A OS=Caenorhabditis elegans OX=6239 GN=ppm-1.A PE=1 SV=1
A4137	-	-	-	-	-	-	-	-
A4138	GO:0006508(proteolysis)	-	GO:0004176(ATP-dependent peptidase activity),GO:0004252(serine-type endopeptidase activity)	K01358 clpP, CLPP; ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]	map04212 Longevity regulating pathway - worm;map04112 Cell cycle - Caulobacter	KOG0840 At5g23140 ATP-dependent Clp protease, proteolytic subunit	ORX66628.1 ATP-dependent Clp protease proteolytic subunit [Linderina pennisporea]	ATP-dependent Clp protease proteolytic subunit OS=Azospirillum brasilense OX=192 GN=clpP PE=3 SV=1

A4139	-	-	GO:0008237(metallopeptidase activity),GO:0061578(Lys63-specific deubiquitinase activity),GO:0005515(protein binding),GO:0008233(peptidase activity)	K03030 PSMD14, RPN11, POH1; 26S proteasome regulatory subunit N11	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG1555 Hs5031981.26S proteasome regulatory complex, subunit RPN11	ORZ37431.1 JAB1/Mov34/MPN/PAD-1 ubiquitin protease-domain-containing protein [Catenaria anguillulae PL171]	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens OX=9606 GN=PSMD14 PE=1 SV=1
A4140	-	-	-	-	-	-	KNE54146.1 hypothetical protein AMAG_00144 [Allomyces macrogynus ATCC 38327]	Cilia- and flagella-associated protein 58 OS=Homo sapiens OX=9606 GN=CFAP58 PE=1 SV=1
A4141	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02930 RP-L4e, RPL4; large subunit ribosomal protein L4e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1475 At3g09630 Ribosomal protein RPL1/RPL2/RPL4L4	ORX89502.1 hypothetical protein K493DRAFT_305719 [Basidiobolus meristosporus CBS 931.73]	Large ribosomal subunit protein uL4z OS=Arabidopsis thaliana OX=3702 GN=RPL4A PE=1 SV=1
A4142	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	KOG1697 At3g49080 Mitochondrial/chloroplast ribosomal protein S9	XP_003030423.1 uncharacterized protein SCHCODRAFT_57796 [Schizophyllum commune H4-8]	Small ribosomal subunit protein uS9 OS=Caulobacter vibrioides (strain ATCC 19089 / CB15) OX=190650 GN=rpsl PE=3 SV=1
A4143	GO:0006468(protein phosphorylation),GO:0001522(pseudouridine synthesis),GO:0009451(RNA modification)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0003723(RNA binding),GO:0009982(pseudouridine synthase activity)	K18670 YAK1; dual specificity protein kinase YAK1 [EC:2.7.12.1]	-	KOG0667 Hs18765756 Dual-specificity tyrosine-phosphorylation regulated kinase	ORY50999.1 kinase-like protein [Rhizoclostium globosum]	Dual specificity tyrosine-phosphorylation-regulated kinase 1B OS=Homo sapiens OX=9606 GN=DYRK1B PE=1 SV=1
A4144	-	-	-	K11982 RNF115_126; E3 ubiquitin-protein ligase RNF115/126 [EC:2.3.2.27]	-	KOG0800 At3g19950 FOG: Predicted E3 ubiquitin ligase	EPZ35251.1 hypothetical protein O9G_000647 [Rozella allomyces CSF55]	E3 ubiquitin-protein ligase RING1-like OS=Arabidopsis thaliana OX=3702 GN=At3g19950 PE=1 SV=1
A4145	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07943 ARL2; ADP-ribosylation factor-like protein 2	-	KOG0073 Hs4502229 GTP-binding ADP-ribosylation factor-like protein ARL2	KAG1445846.1 hypothetical protein G6F56_00976 [Rhizopus delemar]	ADP-ribosylation factor-like protein 2 OS=Homo sapiens OX=9606 GN=ARL2 PE=1 SV=4

A4146	-	-	-	-	-	-	XP_01660798.0.1 hypothetical protein SPPG_05313 [Spizellomyces punctatus DAOM BR117]	-
A4147	GO:0006260(DNA replication)	GO:0000808(origin recognition complex), GO:0005634(nucleus)	GO:0003677(DNA binding)	K02606 ORC4; origin recognition complex subunit 4	map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG2228 Hs20535209 Origin recognition complex, subunit 4	ORX90963.1 origin recognition complex, subunit 4 [Basidiobolus meristosporus CBS 931.73]	Origin recognition complex subunit 4 OS=Bos taurus OX=9913 GN=ORC4 PE=2 SV=1
A4148	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1200 CE04339 Mitochondrial/plastidial beta-ketoacyl-ACP reductase	RKP09908.1 hypothetical protein THASP1DRAFT_28306 [Thamnocephalus sphaerosporus]	3-oxoacyl-[acyl-carrier-protein] reductase OS=Mus musculus OX=10090 GN=Cbr4 PE=1 SV=2
A4149	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4150	-	-	GO:0005515(protein binding)	-	-	KOG1093 Hs20542273_2 Predicted protein kinase (contains TBC and RHOD domains)	XP_016612201.1 hypothetical protein SPPG_01596 [Spizellomyces punctatus DAOM BR117]	TBC1 domain family member 31 OS=Oryzias latipes OX=8090 GN=tbc1d31 PE=3 SV=2
A4151	-	-	-	-	-	-	-	-
A4152	-	-	GO:0020037(heme binding)	-	-	-	XP_019010397.1 hypothetical protein I206_04866 [Kwoniella pini CBS 10737]	-
A4153	-	-	GO:0020037(heme binding)	-	-	-	GIJ92646.1 hypothetical protein Asppvi_001924 [Aspergillus pseudoviridinus]	-
A4154	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	KIM83425.1 hypothetical protein PILCRDRAFT_69679 [Piloderma croceum F 1598]	-
A4155	-	-	GO:0004842(ubiquitin-protein transferase activity)	K10592 HUWE1, MULE, ARF-BP1, TOM1; E3 ubiquitin-protein ligase HUWE1 [EC:2.3.2.26]	map04120 Ubiquitin mediated proteolysis	-	ORX71339.1 HECT-domain-containing protein [Linderina pennisporea]	E3 ubiquitin-protein ligase TOM1-like OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=B11B22.010 PE=3 SV=4

A4156	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K12854 SNRNP200, BRR2: pre-mRNA-splicing helicase BRR2 [EC:3.6.4.13]	map03040 Spliceosome	KOG0951[Hs2042312 RNA helicase BRR2, DEAD-box superfamily	XP_016612203.1 hypothetical protein SPPG_01598 [Spizellomyces punctatus DAOM BR117]	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens OX=9606 GN=SNRNP200 PE=1 SV=2
A4157	GO:0050848(regulation of calcium-mediated signaling)	-	GO:0035381(ATP-gated ion channel activity)	-	-	-	RKP11124.1 hypothetical protein THASP1DRAFT_27103 [Thamnocephalus sphaerospora]	P2X receptor D OS=Dictyostelium discoideum OX=44689 GN=p2xD PE=3 SV=1
A4158	-	-	-	-	-	-	-	-
A4159	-	-	GO:0046872(metal ion binding),GO:0035091(phosphatidylinositol binding)	-	-	KOG2308[YOR022c Phosphatidic acid-preferring phospholipase A1, contains DDHD domain	XP_018710571.1 DDHD-domain-containing protein [Metschnikowia bicuspidata var. bicuspidata NRRL YB-4993]	Probable phospholipase YOR022C, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YOR022C PE=1 SV=1
A4160	GO:0009089(lysine biosynthetic process via diaminopimelate)	-	GO:0008836(diaminopimelate decarboxylase activity),GO:0003824(catalytic activity)	-	-	KOG0622[At3g14390 Ornithine decarboxylase	KAG0320815.1 hypothetical protein BGZ97_012779 [Linnemannia gamsii]	Protein TabA OS=Pseudomonas amygdali pv. tabaci OX=322 GN=tabA PE=3 SV=1
A4161	-	GO:0005747(mitochondrial respiratory chain complex I)	-	K03950 NDUFA6; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 6	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG3426[Hs4505359 NADH:ubiquinone oxidoreductase, NDUFA6/B14 subunit	XP_031025471.1 uncharacterized protein SmJEL517_g02576 [Synchytrium microbalum]	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Bos taurus OX=9913 GN=NDUFA6 PE=1 SV=2
A4162	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0004386(helicase activity)	-	-	KOG0922[At1g26370 DEAH-box RNA helicase	KAF9919107.1 putative ATP-dependent RNA helicase dhr2 [Lobosporangium transversale]	Pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH10 OS=Arabidopsis thaliana OX=3702 GN=RID1 PE=1 SV=1
A4163	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08286 E2.7.11.-.; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0589[At1g54510 Serine/threonine protein kinase	OJT05228.1 MAP kinase kinase kinase mkh1 [Trametes pubescens]	Serine/threonine-protein kinase Nek1 OS=Arabidopsis thaliana OX=3702 GN=NEK1 PE=2 SV=2
A4164	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4165	-	-	-	-	-	-	-	-
A4166	-	-	-	-	-	-	-	-
A4167	-	-	-	-	-	-	-	-

A4168	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	KOG2208 7302610 Vigilin	TGO62083.1 hypothetical protein BCON_0022g00210 [Botryotinia convoluta]	Far upstream element-binding protein 1 OS=Mus musculus OX=10090 GN=Fubp1 PE=1 SV=1
A4169	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4170	-	-	-	-	-	-	ORY44401.1 Biopterin transport-related protein BT1 [Rhizoclostium globosum]	Probable folate-biopterin transporter 2 OS=Arabidopsis thaliana OX=3702 GN=At5g25050 PE=2 SV=1
A4171	-	-	GO:0008237(metallopeptidase activity)	K06974 amzA, AMZ2, AMZ1; archaeemetzincin [EC:3.4.-.-]	-	-	OJJ30275.1 hypothetical protein ASPWEDRAFT_121155 [Aspergillus wentii DTO 134E9]	Archaeemetzincin-2 OS=Pongo abelii OX=9601 GN=AMZ2 PE=2 SV=1
A4172	-	-	GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027 Hs4885109 Calmodulin and related proteins (EF-Hand superfamily)	KAF9074772.1 calmodulin [Rhodocollybia butyracea]	Calmodulin OS=Triticum aestivum OX=4565 PE=1 SV=3
A4173	-	-	-	-	-	-	-	-
A4174	GO:0006468(protein phosphorylation),GO:0007010(cytoskeleton organization)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding),GO:0003779(actin binding)	K20523 SH3YL1; SH3 domain-containing YSC84-like protein 1	-	KOG1843 YH R016c Uncharacterized conserved protein	KAG1146867.1 hypothetical protein G6F38_004635 [Rhizopus oryzae]	LAS seventeen-binding protein 3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=LSB3 PE=3 SV=2
A4175	-	-	GO:0005515(protein binding)	-	-	KOG1079 Hs M4758324 Transcriptional repressor EZH1	KJA17890.1 hypothetical protein HYP5UDRAFT_45906 [Hypholoma sublateritium FD-334 SS-4]	Histone-lysine N-methyltransferase, H3 lysine-4 specific OS=Yarrowia lipolytica (strain CLUB 122 / E 150) OX=284591 GN=SET1 PE=3 SV=1

A4176	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K17535 TNNI3K; serine/threonine-protein kinase TNNI3K [EC:2.7.11.1]	-	KOG0192 At3g06640 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9161184.1 hypothetical protein DFG26_004789 [Actinomortierella ambigua]	Probable serine/threonine-protein kinase drkA OS=Dictyostelium discoideum OX=44689 GN=drkA PE=3 SV=1
A4177	GO:0006412(translation)	GO:0015934(large ribosomal subunit)	GO:0003723(RNA binding),GO:0003735(structural constituent of ribosome)	K02865 RP-L10Ae, RPL10A; large subunit ribosomal protein L10Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1570 At5g22440 60S ribosomal protein L10A	ORZ16880.1 60S ribosomal protein L1-B [Absidia repens]	Large ribosomal subunit protein uL1z OS=Arabidopsis thaliana OX=3702 GN=RPL10AA PE=1 SV=1
A4178	-	-	GO:0004518(nuclease activity)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518 YOR033c 5'-3' exonuclease	KAF8515840.1 PIN domain-like protein [Hysterangium stoloniferum]	Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EXO1 PE=1 SV=2
A4179	-	-	-	K18083 MTMR6_7_8; myotubularin-related protein 6/7/8 [EC:3.1.3.64 3.1.3.95]	map04070 Phosphatidylinositol signaling system;map04138 Autophagy - yeast;map00562 inositol phosphate metabolism;map01100 Metabolic pathways	KOG4471 Hs7705564 Phosphatidylinositol 3-phosphate 3-phosphatase myotubularin MTM1	KAF5138562.1 Phosphoinositide 3-phosphatase [Metarhizium anisopliae]	Myotubularin-related protein 2 OS=Danio rerio OX=7955 GN=mtmr2 PE=2 SV=2
A4180	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	-	-
A4181	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9161199.1 hypothetical protein DFG26_004784 [Actinomortierella ambigua]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei brucei OX=5702 GN=CRK2 PE=3 SV=1
A4182	-	-	-	-	-	KOG0017 At1g33817 FOG: Transposon-encoded proteins with TYA, reverse transcriptase, integrase domains in various combinations	RKK07627.1 hypothetical protein BFI65_g17832 [Fusarium oxysporum f. sp. cepae]	Retrovirus-related Pol polyprotein from transposon RE2 OS=Arabidopsis thaliana OX=3702 GN=RE2 PE=4 SV=1
A4183	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=1 SV=3
A4184	-	-	-	K10997 TIMELESS, TOF1, SWI1; replication fork protection complex subunit TIMELESS/Tof1/Swi1	-	KOG1974 At5g52910 DNA topoisomerase I-interacting protein	TPX58885.1 hypothetical protein PhCBS80983_g02824 [Powellomyces hirtus]	Protein timeless homolog OS=Mus musculus OX=10090 GN=Timeless PE=1 SV=3

A4185	-	-	-	-	-	-	-	-
A4186	GO:0055085(transmembrane transport),GO:0007186(G protein-coupled receptor signaling pathway)	GO:0043190(ATP-binding cassette (ABC) transporter complex),GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity),GO:0004930(G protein-coupled receptor activity)	K21804 METTL21A; protein N-lysine methyltransferase METTL21A [EC:2.1.1.-]	-	KOG2793 Hs21687066 Putative N2.N2-dimethylguanosine tRNA methyltransferase	KNE66342.1 hypothetical protein AMAG_19570 [Allomyces macrogynus ATCC 38327]	Protein N-lysine methyltransferase METTL21A OS=Homo sapiens OX=9606 GN=METTL21A PE=1 SV=2
A4187	GO:0007186(G protein-coupled receptor signaling pathway),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane),GO:0043190(ATP-binding cassette (ABC) transporter complex)	GO:0004930(G protein-coupled receptor activity),GO:0022857(transmembrane transporter activity),GO:0004965(G protein-coupled GABA receptor activity)	-	-	-	ORZ29355.1 hypothetical protein BCR44DRAFT_1451456 [Catenaria anguillulae PL171]	Metabotropic glutamate receptor-like protein J OS=Dictyostelium discoideum OX=44689 GN=grlJ PE=2 SV=1
A4188	GO:0007186(G protein-coupled receptor signaling pathway),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane),GO:0043190(ATP-binding cassette (ABC) transporter complex)	GO:0004965(G protein-coupled GABA receptor activity),GO:0004930(G protein-coupled receptor activity),GO:0022857(transmembrane transporter activity)	-	-	-	KNE66342.1 hypothetical protein AMAG_19570 [Allomyces macrogynus ATCC 38327]	Metabotropic glutamate receptor-like protein J OS=Dictyostelium discoideum OX=44689 GN=grlJ PE=2 SV=1
A4189	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K07359 CAMKK2; calcium/calmodulin-dependent protein kinase 2 [EC:2.7.11.17]	map04140 Autophagy - animal;map04211 Longevity regulating pathway;map05034 Alcoholism;map04936 Alcoholic liver disease;map04152 AMPK signaling pathway;map04920 Adipocytokine signaling pathway;map04921 Oxytocin signaling pathway	KOG0585 At5g60550 Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	EPB85061.1 CAMK/CAMKL/BRSK protein kinase [Mucor circinelloides 1006PhL]	Serine/threonine-protein kinase GRIK2 OS=Arabidopsis thaliana OX=3702 GN=GRIK2 PE=1 SV=1
A4190	-	-	GO:0016491(oxidoreductase activity),GO:0008270(zinc ion binding)	K00344 qor, CRYZ; NADPH:quinone reductase [EC:1.6.5.5]	-	KOG1197 At5g61510 Predicted quinone oxidoreductase	XP_007915863.1 putative quinone oxidoreductase protein [Phaeoacremonium minimum UCRPA7]	Quinone oxidoreductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=qor PE=3 SV=2

A4191	GO:0006886 (intracellular protein transport); GO:0016192 (vesicle-mediated transport)	GO:0030131 (clathrin adaptor complex)	-	K11826 AP2M1; AP-2 complex subunit mu-1	map04144 Endocytosis; map04721 Synaptic vesicle cycle; map05016 Huntington disease; map04961 Endocrine and other factor-regulated calcium reabsorption	KOG0938 Hs14917109 Adaptor complexes medium subunit family	CAE6442130.1 unnamed protein product, partial [Rhizoctonia solani]	AP-2 complex subunit mu OS=Dictyostelium discoideum OX=44689 GN=apm2 PE=2 SV=2
A4192	-	-	-	-	-	-	-	-
A4193	GO:0006325 (chromatin organization); GO:0016573 (histone acetylation); GO:0031509 (subtelomeric heterochromatin assembly)	GO:0005634 (nucleus)	GO:0004402 (histone acetyltransferase activity); GO:0016407 (acetyltransferase activity)	-	-	KOG2696 CE03495 Histone acetyltransferase type b catalytic subunit	XP_025343420.1 hypothetical protein CXQ85_005049 [[Candida] haemulonii]	Histone acetyltransferase type B catalytic subunit OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=hat1 PE=3 SV=2
A4194	GO:0006508 (proteolysis)	-	GO:0004198 (calcium-dependent cysteine-type endopeptidase activity)	-	-	KOG0045 At1g55350 Cytosolic Ca2+-dependent cysteine protease (calpain), large subunit (EF-Hand protein superfamily)	KAG0332695.1 hypothetical protein BG000_009805 [Podila horticola]	Calpain-type cysteine protease ADL1 OS=Oryza sativa subsp. japonica OX=39947 GN=ADL1 PE=1 SV=1
A4195	-	-	-	K16639 LACTB2; endoribonuclease LACTB2 [EC:3.1.27.-]	-	KOG0813 Hs7705793 Glyoxylase	KAG2184975.1 hypothetical protein INT43_000888 [Umbelopsis isabellina]	Endoribonuclease LACTB2 OS=Bos taurus OX=9913 GN=LACTB2 PE=2 SV=1
A4196	GO:0007165 (signal transduction)	-	-	K20643 RGD1; Rho GTPase-activating protein RGD1	-	KOG1453 7290597 Chimaerin and related Rho GTPase activating proteins	XP_033592588.1 uncharacterized protein BDY17DRAFT_320853 [Neohortaea acidophila]	Rho GTPase-activating protein 24 OS=Mus musculus OX=10090 GN=Arhgap24 PE=1 SV=2
A4197	-	-	-	-	-	-	XP_006680166.1 uncharacterized protein BATDEDRAFT_89767 [Batrachochytrium dendrobatidis JAM81]	-
A4198	-	-	GO:0005515 (protein binding)	-	-	KOG1128 CE01407 Uncharacterized conserved protein, contains TPR repeats	KNE55978.1 hypothetical protein AMAG_01824 [Allomyces macrogynus ATCC 38327]	-

A4199	GO:0006367(transcription initiation from RNA polymerase II promoter)	GO:0000124(SAGA complex), GO:0005669(transcription factor TFIID complex), GO:0046695(SLIK (SAGA-like) complex)	GO:0046982(protein heterodimerization activity), GO:0016251(RNA polymerase II general transcription initiation factor activity)	K03131 TAF6; transcription initiation factor TFIID subunit 6	map03022 Basal transcription factors	-	XP_016609435.1 hypothetical protein SPPG_09096 [Spizellomyces punctatus DAOM BR117]	Transcription initiation factor TFIID subunit 6 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=taf6 PE=1 SV=1
A4200	GO:0045039(protein insertion into mitochondrial inner membrane)	GO:0042719(mitochondrial intermembrane space protein transporter complex)	-	K17778 TIM10; mitochondrial import inner membrane translocase subunit TIM10	-	KOG3480[Hs6912708 Mitochondrial import inner membrane translocase, subunits TIM10/TIM12	KAF8213296.1 Tim10/DDP family zinc finger-domain-containing protein, partial [Mycena galopus ATCC 62051]	Mitochondrial import inner membrane translocase subunit Tim10 OS=Bos taurus OX=9913 GN=TIMM10 PE=3 SV=1
A4201	-	GO:0016021(integral component of membrane)	-	-	-	KOG3140[At1g03260 Predicted membrane protein	ORY51488.1 hypothetical protein BCR33DRAFT_712530 [Rhizoclostium globosum]	TVP38/TMEM64 family membrane protein slr0305 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=slr0305 PE=3 SV=1
A4202	-	-	GO:0019239(deaminase activity)	K19572 CECR1, ADA2; adenosine deaminase CECR1 [EC:3.5.4.4]	map00230 Purine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG1097[7293948 Adenosine deaminase/adenosine deaminase	TFY61302.1 hypothetical protein EVJ58_g4596 [Fomitopsis rosea]	Adenosine deaminase 2 OS=Dictyostelium discoideum OX=44689 GN=ADA2 PE=2 SV=1
A4203	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity), GO:0005524(ATP binding), GO:0005515(protein binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0192[At2g35050_2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9161199.1 hypothetical protein DFQ26_004784 [Actinomortierella ambigua]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei OX=5702 GN=CRK2 PE=3 SV=1
A4204	-	-	-	-	-	-	-	-
A4205	-	-	-	-	-	-	XP_031023134.1 uncharacterized protein SmJEL517_g04986 [Synchytrium microbalum]	Uncharacterized protein FLJ43738 OS=Homo sapiens OX=9606 PE=2 SV=1
A4206	GO:0006508(proteolysis)	-	GO:0005515(protein binding), GO:0004222(metalloendopeptidase activity), GO:0004252(serine-type endopeptidase activity)	K22686 NMA111; pro-apoptotic serine protease NMA111 [EC:3.4.21.-]	-	KOG1320[At5g27660 Serine protease	ORY37077.1 trypsin-like serine protease [Rhizoclostium globosum]	Putative protease Do-like 14 OS=Arabidopsis thaliana OX=3702 GN=DEGP14 PE=3 SV=2

A4207	-	-	GO:0016504(peptidase activator activity);GO:0070577(lysine-acetylated histone binding);GO:0070628(proteasome binding)	K06699 PSME4; proteasome activator subunit 4	map03050 Proteasome	KOG1851 At3g13330 Uncharacterized conserved protein	KAG2173838.1 hypothetical protein INT43_005258 [Umbelopsis isabellina]	Proteasome activator subunit 4 OS=Arabidopsis thaliana OX=3702 GN=PA200 PE=2 SV=2
A4208	-	-	-	-	-	-	-	-
A4209	-	-	GO:0016491(oxidoreductase activity)	K00231 PPOX, hemY; protoporphyrinogen/coproprophyrinogen III oxidase [EC:1.3.3.4 1.3.3.15]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG1276 Hs4506001 Protoporphyrinogen oxidase	TPX75518.1 protoporphyrinogen oxidase [Chytridiomycetes confervae]	Protoporphyrinogen oxidase OS=Macaca fascicularis OX=9541 GN=PPOX PE=2 SV=1
A4210	-	-	GO:0005515(protein binding)	K06694 PSMD10; 26S proteasome non-ATPase regulatory subunit 10	-	KOG0513 Hs20561564 Ca2+-independent phospholipase A2	OBZ88340.1 Histone-lysine N-methyltransferase EHMT2 [Choanephora cucurbitarum]	85/88 kDa calcium-independent phospholipase A2 OS=Homo sapiens OX=9606 GN=PLA2G6 PE=1 SV=2
A4211	-	-	-	-	-	-	-	-
A4212	-	-	GO:0004089(carbonate dehydratase activity);GO:0008270(zinc ion binding)	-	-	KOG0382 Hs4557395 Carbonic anhydrase	RPA98376.1 carbonic anhydrase [Choiromyces venosus 120613-1]	Carbonic anhydrase 2 OS=Oryctolagus cuniculus OX=9986 GN=CA2 PE=1 SV=3
A4213	-	-	GO:0004089(carbonate dehydratase activity);GO:0008270(zinc ion binding)	-	-	KOG0382 7299299 Carbonic anhydrase	KDN60608.1 putative carbonic anhydrase [Colletotrichum sublineola]	Carbonic anhydrase OS=Danio rerio OX=7955 GN=cahz PE=1 SV=2
A4214	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	-	KN motif and ankyrin repeat domain-containing protein 3 OS=Mus musculus OX=10090 GN=Kank3 PE=1 SV=1
A4215	GO:0015986(ATP synthesis coupled proton transport);GO:0046034(ATP metabolic process);GO:1902600(proton transmembrane transport)	GO:0045261(proton transport);GO:0046034(ATP synthase complex, catalytic core F(1))	GO:0005524(ATP binding);GO:0046933(proton-transporting ATP synthase activity, rotational mechanism)	K02133 ATPeF1B, ATP5B, ATP2; F-type H+-transporting ATPase subunit beta [EC:7.1.2.2]	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map04714 Thermogenesis;map00190 Oxidative phosphorylation;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease;map01100 Metabolic pathways	KOG1350 Hs4502295 F0F1-type ATP synthase, beta subunit	XP_453538.1 uncharacterized protein KLLA0_D10703g [Kluyveromyces lactis]	ATP synthase subunit beta, mitochondrial OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=ATP2 PE=3 SV=2
A4216	-	-	-	-	-	-	-	-
A4217	-	-	-	-	-	-	-	-

A4218	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015205(nucleobase transmembrane transporter activity),GO:0022857(transmembrane transporter activity)	K06901 pbuG, azgA, ghxP, ghxQ, adeQ; adenine/guanine/hypoxanthine permease	-	-	KAG1275723.1 hypothetical protein G6F65_009715 [Rhizopus oryzae]	Putative permease MJ0326 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ0326 PE=3 SV=1
A4219	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin---tyrosine ligase [EC:6.3.2.25]	-	KOG2156[Hs7661970 Tubulin-tyrosine ligase-related protein	ORY52254.1 TTL-domain-containing protein [Neocallimastix californiae]	Tubulin monoglutamylase TTL4 OS=Homo sapiens OX=9606 GN=TTL4 PE=1 SV=2
A4220	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4221	GO:0006433(prolyl-tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation)	GO:0005737(cytoplasm)	GO:0004827(proline-tRNA ligase activity),GO:0005524(ATP binding),GO:000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity)	-	-	KOG4163[At3g62120 Prolyl-tRNA synthetase	KAG5366900.1 putative proline--tRNA ligase [Yarrowia sp. B02]	Proline--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana OX=3702 GN=At3g62120 PE=1 SV=1
A4222	-	GO:0016021(integral component of membrane)	-	-	-	-	RKP14897.1 Na+/H+ antiporter family-domain-containing protein [Piptocephalis cylindrospora]	Uncharacterized protein HI_1586 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_1586 PE=4 SV=1
A4223	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A4224	GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	-	ORY30930.1 cation efflux protein [Rhizoclostium globosum]	Zinc transporter ZitB OS=Yersinia pestis OX=632 GN=zitB PE=3 SV=1
A4225	-	-	GO:0008270(zinc ion binding)	K06874 K06874; zinc finger protein	-	KOG2703[7291018 C4-type Zn-finger protein	XP_033571884.1 zf-ZPR1-domain-containing protein [Mytilinidion resinicola]	Zinc finger protein ZPR1 OS=Drosophila melanogaster OX=7227 GN=Zpr1 PE=2 SV=1
A4226	-	-	-	-	-	-	-	-
A4227	GO:0006396(RNA processing),GO:0031124(mRNA 3'-end processing)	GO:0005634(nucleus)	GO:0005515(protein binding)	K14408 CSTF3, RNA14; cleavage stimulation factor subunit 3	map03015 mRNA surveillance pathway	KOG1914[728899 mRNA cleavage and polyadenylation factor I complex, subunit RNA14	RIB09976.1 hypothetical protein C2G38_2021196 [Gigaspora rosea]	Cleavage stimulation factor subunit 3 OS=Mus musculus OX=10090 GN=Cstf3 PE=1 SV=1

A4228	-	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	KOG0939 At1g70320 E3 ubiquitin-protein ligase/Putative upstream regulatory element binding protein	XP_001730143.1 hypothetical protein MGL_2525 [Malassezia globosa CBS 7966]	E3 ubiquitin-protein ligase UPL2 OS=Arabidopsis thaliana OX=3702 GN=UPL2 PE=1 SV=3
A4229	-	-	GO:0005085(guanylyl-nucleotide exchange factor activity)	-	-	KOG2432 At1g73930 Uncharacterized conserved protein	KAG1047337.1 hypothetical protein G6F43_010207 [Rhizopus deleamar]	Protein DENND6A OS=Homo sapiens OX=9606 GN=DENND6A PE=1 SV=1
A4230	GO:0045454(cell redox homeostasis)	-	GO:0016491(oxidoreductase activity),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG1336 Hs21389617 Monodehydroascorbate/ferredoxin reductase	OCK78639.1 FAD-dependent pyridine nucleotide-disulfide oxidoreductase [Lepidoptera] a palustris CBS 459.81]	NAD(P)H coenzyme A polysulfide/persulfide reductase OS=Pyrococcus horikoshii (strain ATCC 700860 / DSM 12428 / JCM 9974 / NBRC 100139 / OT-3) OX=70601 GN=PH0572 PE=1 SV=1
A4231	GO:0055085(transmembrane transport)	GO:001620(membrane)	GO:0015267(channel activity)	K03441 GLP-F, aquaglyceroporin related protein, other eukaryote	-	KOG0224 Hs10280624 Aquaporin (major intrinsic protein family)	RKO92673.1 glycerol uptake facilitator protein [Blyttiomycetes helicus]	Propanediol uptake facilitator PduF OS=Citrobacter freundii OX=546 GN=pduF PE=3 SV=1
A4232	GO:0008299(isoprenoid biosynthetic process)	GO:0005737(cytoplasm)	GO:0004496(mevalonate kinase activity),GO:0005524(ATP binding)	K00869 MVK, mvaK1; mevalonate kinase [EC:2.7.1.36]	map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis;map01100 Metabolic pathways	KOG1511 7303424 Mevalonate kinase MVK/ERG12	KAF9573838.1 Mevalonate kinase [Mortierella alpina]	Mevalonate kinase OS=Pyrococcus horikoshii (strain ATCC 700860 / DSM 12428 / JCM 9974 / NBRC 100139 / OT-3) OX=70601 GN=mvk PE=3 SV=1
A4233	-	-	GO:0005096(GTPase activator activity)	-	-	KOG0703 At3g17660 Predicted GTPase-activating protein	XP_003037702.1 uncharacterized protein SCHCODRAFT_34626, partial [Schizophyllum commune H4-8]	Probable ADP-ribosylation factor GTPase-activating protein AGD15 OS=Arabidopsis thaliana OX=3702 GN=AGD15 PE=2 SV=1
A4234	-	-	-	-	-	-	-	-
A4235	-	GO:0030991(intracellular transport particle A)	-	-	-	-	-	-
A4236	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG0192 At2g17700 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	XP_007308914.1 kinase-like protein [Stereum hirsutum FP-91666 SS1]	Serine/threonine-protein kinase STY8 OS=Arabidopsis thaliana OX=3702 GN=STY8 PE=1 SV=2

A4237	-	-	-	K10592 HUWE1, MULE, ARF- BP1, TOM1; E3 ubiquitin- protein ligase HUWE1 [EC:2.3.2.26]	map04120 Ubiquitin mediated proteolysis	-	XP_00786461. 0.1 hypothetical protein GLOTRDRAFT _137834 [Gloeophyllu m trabeum ATCC 11539]	-
A4238	-	-	-	-	-	KOG0939 At1 g70320 E3 ubiquitin- protein ligase/Putativ e upstream regulatory element binding protein	KAF0392672. 1 E3 ubiquitin- protein ligase HUWE1 [Gigaspora margarita]	E3 ubiquitin-protein ligase UPL2 OS=Arabidopsis thaliana OX=3702 GN=UPL2 PE=1 SV=3
A4239	-	-	-	-	-	-	-	-
A4240	-	-	GO:0005515(pro tein binding)	-	-	KOG0531 729 2542 Protein phosphatase 1, regulatory subunit, and related proteins	-	-
A4241	-	-	GO:0005515(pro tein binding)	K11723 BRD7; bromodomain- containing protein 7	map03082 ATP- dependent chromatin remodeling;map 05225 Hepatocellular carcinoma	-	XP_03102260 7.1 uncharacteriz ed protein SmJEL517_g0 5503 [Synchytrium microbalum]	-
A4242	-	-	-	-	-	-	-	-
A4243	-	-	GO:0005515(pro tein binding)	-	-	-	TPX70562.1 hypothetical protein SpCBS45565. g01631 [Spizellomyces sp. 'palustris']	Cilia- and flagella-associated protein 43 OS=Xenopus laevis OX=8355 GN=cfap43 PE=2 SV=1
A4244	-	-	-	-	-	-	-	-
A4245	-	-	-	-	-	-	-	-
A4246	GO:00071 65(signal transducti on),GO:00 07186(G protein- coupled receptor signaling pathway)	-	GO:0003924(GT Pase activity),GO:001 9001(guanyl nucleotide- binding),GO:003 1683(G-protein beta/gamma- subunit complex binding)	K19860 GPA1; guanine nucleotide- binding protein alpha-1 subunit	map04011 MAPK signaling pathway - yeast	KOG0082 Hs2 0542545 G- protein alpha subunit (small G protein superfamily)	OEJ83912.1 Guanine nucleotide- binding protein alpha-1 subunit [Hanseniaspo ra osmophila]	Guanine nucleotide-binding protein G(t) subunit alpha-3 OS=Homo sapiens OX=9606 GN=GNAT3 PE=2 SV=2
A4247	GO:00065 08(proteo lysis)	GO:00160 20(memb rane)	GO:0004176(AT P-dependent peptidase activity),GO:000 4222(metalloen dopeptidase activity),GO:000 5524(ATP binding),GO:001 6887(ATP hydrolysis activity)	K08955 YME1; ATP- dependent metalloprote ase [EC:3.4.24.-]	map04139 Mitophagy - yeast	KOG0734 At2 g26140 AAA+ -type ATPase containing the peptidase M41 domain	ORE17222.1 ATP - dependent metallopepti dase Hfl [Rhizopus microsporus]	ATP-dependent zinc metalloprotease FTSH 5, mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=FTSH5 PE=3 SV=1

A4248	-	GO:0005758(mitochondrial intermembrane space)	-	K17780 TIM8; mitochondrial import inner membrane translocase subunit TIM8	-	KOG3489 At5g50810 Mitochondrial import inner membrane translocase, subunit TIM8	GEM08314.1 mitochondria l import inner membrane translocase subunit TIM8 [Rhodotorula toruloides]	Mitochondrial import inner membrane translocase subunit TIM8 OS=Arabidopsis thaliana OX=3702 GN=TIM8 PE=1 SV=1
A4249	-	-	-	-	-	-	-	-
A4250	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding),GO:0000287(magnesium ion binding)	K03979 obgE, cgtA, MTG2; GTPase [EC:3.6.5.-]	-	KOG1489 Hs22049574 Predicted GTP-binding protein (ODN superfamily)	CEP07467.1 hypothetical protein [Parasitella parasitica]	GTPase Obg OS=Thermodesulfovibrio yellowstonii (strain ATCC 51303 / DSM 11347 / YP87) OX=289376 GN=obg PE=3 SV=1
A4251	-	-	-	-	-	-	-	-
A4252	GO:0006281(DNA repair),GO:0006310(DNA recombination)	-	-	K10873 RAD52; DNA repair and recombination protein RAD52	map03440 Homologous recombination	KOG4141 Hs20143952 DNA repair and recombination protein RAD52/RAD22	XP_025361539.1 rad52-like protein, partial [Jaminaea rosea]	DNA repair protein RAD52 homolog OS=Gallus gallus OX=9031 GN=RAD52 PE=2 SV=1
A4253	-	-	-	-	-	-	-	-
A4254	-	-	-	-	-	-	-	-
A4255	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0504 Hs13386462 FOG: Ankyrin repeat	OUM62929.1 hypothetical protein PIROE2DRAFT_61592 [Piromyces sp. E2]	Ankyrin repeat domain-containing protein 61 OS=Homo sapiens OX=9606 GN=ANKRD61 PE=4 SV=2
A4256	GO:0046294(formaldehyde catabolic process)	-	GO:0018738(S-formylglutathione hydrolase activity)	K01070 frmB, ESD, fghA; S-formylglutathione hydrolase [EC:3.1.2.12]	map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00680 Methane metabolism;map01100 Metabolic pathways	KOG3101 Hs20547663 Esterase D	ORX90743.1 s-formylglutathione hydrolase [Basidiobolus meristosporus CBS 931.73]	S-formylglutathione hydrolase OS=Homo sapiens OX=9606 GN=ESD PE=1 SV=2
A4257	GO:0016192(vesicle-mediated transport),GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport),GO:0042147(retrograde transport, endosome to Golgi)	-	-	K26683 GOLT1, GOT1; vesicle transport protein GOT1	-	KOG1743 Hs7705636 Ferric reductase-like proteins	KAG0032699.1 Golgi Transport [Podila clonocystis]	Vesicle transport protein GOT1B OS=Bos taurus OX=9913 GN=GOLT1B PE=2 SV=1
A4258	-	-	GO:0004518(nuclease activity)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518 YOR033c 5'-3' exonuclease	KAF8515840.1 PIN domain-like protein [Hysterangium stoloniferum]	Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EXO1 PE=1 SV=2

A4259	GO:0009691(cytokinin biosynthetic process)	-	GO:0016787(hydrolase activity)	-	-	-	TPX64729.1 hypothetical protein SpCBS45565_g05659 [Spizellomyces sp. 'palustris']	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG OS=Oryza sativa subsp. japonica OX=39947 GN=LOG PE=1 SV=1
A4260	-	-	-	-	-	-	ESK95668.1 2og-fe oxygenase [Moniliophthora roreri MCA 2997]	2-oxoglutarate-dependent dioxygenase 33 OS=Oryza sativa subsp. japonica OX=39947 GN=2ODD33 PE=1 SV=1
A4261	-	-	GO:0003824(catalytic activity)	-	-	KOG3957 7300628 Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	XP_018692932.1 hypothetical protein AYL99_06863 [Fonsecaea erecta]	Cinnamoyl-CoA:phenyllactate CoA-transferase OS=Clostridium sporogenes OX=1509 GN=fldA PE=1 SV=1
A4262	GO:0044237(cellular metabolic process)	-	GO:0051537(2 iron, 2 sulfur cluster binding),GO:0005506(iron ion binding)	-	-	-	KAF1841290.1 ISP domain-containing protein [Cucurbitaria berberidis CBS 394.84]	Carnitine monooxygenase oxygenase subunit OS=Acinetobacter calcoaceticus (strain PHEA-2) OX=871585 GN=yeaW PE=1 SV=1
A4263	-	-	GO:0005515(protein binding),GO:0016491(oxidoreductase activity)	K00309 dmgl:dimethylglycine oxidase [EC:1.5.3.10]	map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG2844 Hs7019365 Dimethylglycine dehydrogenase precursor	XP_014540188.1 Dimethylglycine Oxidase, partial [Metarhizium brunneum ARSEF 3297]	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=DMGDH PE=1 SV=2
A4264	-	-	GO:0016491(oxidoreductase activity),GO:0005515(protein binding)	K00309 dmgl:dimethylglycine oxidase [EC:1.5.3.10]	map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG2844 Hs21361378 Dimethylglycine dehydrogenase precursor	XP_013257277.1 hypothetical protein A1O9_09129 [Exophiala aquamarina CBS 119918]	Sarcosine dehydrogenase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Sardh PE=1 SV=2
A4265	-	-	-	-	-	-	-	-
A4266	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A4267	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A4268	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-

A4269	GO:0046488(phosphatidylinositol metabolic process)	-	GO:0016307(phosphatidylinositol phosphate kinase activity),GO:0005524(ATP binding),GO:0000285(1-phosphatidylinositol-3-phosphate 5-kinase activity)	K00921 PIKFYVE, FAB1; 1-phosphatidylinositol-3-phosphate 5-kinase [EC:2.7.1.150]	map04145 Phagosome;map04810 Regulation of actin cytoskeleton;map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0230 At1g71010 Phosphatidylinositol-4-phosphate 5-kinase and related FYVE finger-containing proteins	EPZ33824.1 Phosphatidylinositol-4-phosphate 5-kinase domain-containing protein [Rozella allomycis CSF55]	Putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1C OS=Arabidopsis thaliana OX=3702 GN=FAB1C PE=2 SV=1
A4270	-	-	-	-	-	-	-	-
A4271	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A4272	-	-	GO:0005085(guanylyl-nucleotide exchange factor activity),GO:0005515(protein binding)	-	-	KOG3519 Hs4507501 Invasion-inducing protein TIAM1/CDC24 and related RhoGEF GTPases	ORX44374.1 Dbl homology domain-containing protein [Piromyces finnis]	Myosin-M heavy chain OS=Dictyostelium discoideum OX=44689 GN=myoM PE=1 SV=1
A4273	-	-	-	K09425 K09425; Myb-like DNA-binding protein FlbD	-	KOG0048 Hs13641706_1 Transcription factor, Myb superfamily	XP_003074017.1 Myb-like transcription factor [Encephalitozoon intestinalis ATCC 50506]	Transcriptional activator Myb OS=Mus musculus OX=10090 GN=Myb PE=1 SV=2
A4274	GO:0055085(transmembrane transport)	-	-	-	-	KOG0758 7295910 Mitochondrial carnitine-acylcarnitine carrier protein	KAF0534794.1 mitochondria l carrier [Gigaspora margarita]	Solute carrier family 25 member 45 OS=Mus musculus OX=10090 GN=Slc25a45 PE=1 SV=1
A4275	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	KOG0144 At1g03457 RNA-binding protein CUGBP1/BRUNO (RRM superfamily)	KAF8137880.1 hypothetical protein K438DRAFT_733578 [Mycenagalopus ATCC 62051]	RNA-binding protein BRN2 OS=Arabidopsis thaliana OX=3702 GN=BRN2 PE=1 SV=1
A4276	-	-	GO:0016491(oxidoreductase activity)	K00384 trxB, TRR; thioredoxin reductase (NADPH) [EC:1.8.1.9]	map00450 Selenocompound metabolism	KOG0404 At2g41680_1 Thioredoxin reductase	KAF9121586.1 hypothetical protein BGX30_002481, partial [Mortierella sp. GBA39]	Thioredoxin reductase OS=Rickettsia conorii (strain ATCC VR-613 / Malish 7) OX=272944 GN=trxB PE=3 SV=1
A4277	-	-	-	-	-	-	-	-
A4278	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A4279	-	-	-	-	-	-	-	-
A4280	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE00800 FOG: Reverse transcriptase	OMJ12941.1 Transposon TX1 protein [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1

A4281	-	-	-	-	-	KOG4521 Hs2065253 Nuclear pore complex, Nup160 component	RKP08682.1 nucleoporin Nup120/160-domain-containing protein [Thamnocephalis sphaerospora]	Nuclear pore complex protein Nup160 OS=Mus musculus OX=10090 GN=Nup160 PE=1 SV=2
A4282	-	-	-	-	-	-	-	-
A4283	-	-	-	-	-	-	-	-
A4284	-	-	-	-	-	-	-	-
A4285	-	-	-	-	-	-	-	-
A4286	-	-	-	-	-	-	-	-
A4287	GO:0046854(phosphatidylinositol phosphate biosynthetic process), GO:0048015(phosphatidylinositol-mediated signaling)	-	GO:0016301(kinase activity)	K19801 PI4KB; phosphatidylinositol 4-kinase B [EC:2.7.1.67]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0903 Hs4505809 Phosphatidylinositol 4-kinase, involved in intracellular trafficking and secretion	KAF8466658.1 kinase-like domain-containing protein [Kalahariturber pfeilii]	Phosphatidylinositol 4-kinase beta OS=Sorex araneus OX=42254 GN=PI4KB PE=3 SV=1
A4288	-	-	-	-	-	-	-	-
A4289	-	-	-	K09531 DNAJC11; DnaJ homolog subfamily C member 11	-	-	RKP39806.1 hypothetical protein BJ085DRAFT_17432 [Dimargaris cristalligena]	-
A4290	-	-	-	K09531 DNAJC11; DnaJ homolog subfamily C member 11	-	KOG0718 Hs8922629 Molecular chaperone (DnaJ superfamily)	KAG0657840.1 hypothetical protein C6P46_006202 [Rhodotorula mucilaginosa]	DnaJ homolog subfamily C member 11 OS=Homo sapiens OX=9606 GN=DNAJC11 PE=1 SV=2
A4291	-	-	GO:0005515(protein binding)	-	-	KOG4177 CE26238_1 Ankyrin	-	-
A4292	GO:0006486(protein glycosylation)	GO:0016020(membrane)	GO:0004576(oligosaccharyl transferase activity)	K07151 STT3; dolichyl-diphosphooligosaccharide--protein glycosyltransferase [EC:2.4.99.18]	map04141 Protein processing in endoplasmic reticulum;map00513 Various types of N-glycan biosynthesis;map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG2292 CE01395 Oligosaccharyltransferase, STT3 subunit	RKP05630.1 Oligosaccharyl transferase STT3 subunit-domain-containing protein [Thamnocephalis sphaerospora]	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit stt-3 OS=Caenorhabditis elegans OX=6239 GN=stt-3 PE=1 SV=1
A4293	-	-	-	-	-	-	XP_007690854.1 hypothetical protein COCMIDRAFT_102964 [Bipolaris oryzae ATCC 44560]	-
A4294	-	-	-	K14997 SLC38A11; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 11	-	KOG1305 7303957 Amino acid transporter protein	XP_016612134.1 hypothetical protein SPPG_01537 [Spizellomyces punctatus DAOM BR117]	Putative sodium-coupled neutral amino acid transporter 11 OS=Danio rerio OX=7955 GN=slc38a11 PE=2 SV=2

A4296	GO:0035025(positive regulation of Rho protein signal transduction)	-	GO:0003779(actin binding)	-	-	KOG3376 Hs21040251 Uncharacterized conserved protein	KXS19922.1 C6orf115 protein [Gonapodya prolifera JEL478]	Actin-binding Rho-activating protein OS=Mus musculus OX=10090 GN=Abra PE=1 SV=1
A4297	GO:0006508(proteolysis)	-	GO:0004222(metalloendopeptidase activity),GO:0046872(metal ion binding)	K17732 PMPCB, MAS1; mitochondria l-processing peptidase subunit beta [EC:3.4.24.64]	-	KOG0960 At3g02090 Mitochondrial processing peptidase, beta subunit, and related enzymes (insulinase superfamily)	XP_00291071.1.1 mitochondrial-processing peptidase subunit beta [Coprinopsis cinerea okayama7#130]	Probable mitochondrial-processing peptidase subunit beta, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MPPbeta PE=1 SV=2
A4298	-	-	-	-	-	-	TFK54317.1 NAD(P)-binding protein [Heliocybe sulcata]	Uncharacterized oxidoreductase C736.13 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC736.13 PE=3 SV=1
A4299	GO:0000184(nuclear-transcribed mRNA catabolic process, nonsense-mediated decay)	GO:0005737(cytoplasm)	GO:0003723(RNA binding),GO:0003724(RNA helicase activity),GO:0005524(ATP binding),GO:0008270(zinc ion binding),GO:0003677(DNA binding),GO:0016787(hydrolase activity),GO:0004386(helicase activity)	K14326 UPF1, RENT1; regulator of nonsense transcripts 1 [EC:3.6.4.13 5.6.2.3]	map03013 Nucleocytoplasmic transport;map03015 mRNA surveillance pathway	KOG1802 At5g47010 RNA helicase nonsense mRNA reducing factor (pNORF1)	KAF0514312.1 P-loop containing nucleoside triphosphate hydrolase protein [Gigaspora margarita]	Regulator of nonsense transcripts 1 homolog OS=Arabidopsis thaliana OX=3702 GN=UPF1 PE=1 SV=2
A4300	-	-	-	-	-	-	-	-
A4301	GO:0006886(intracellular protein transport)	-	GO:0005515(protein binding)	K15296 NAPA, SNAP, SEC17; alpha-soluble NSF attachment protein	map04138 Autophagy - yeast;map04721 Synaptic vesicle cycle	KOG1586 Hs4505329 Protein required for fusion of vesicles in vesicular transport, alpha-SNAP	KAF9346994.1 hypothetical protein BGX26_001479 [Mortierella sp. AD094]	Alpha-soluble NSF attachment protein OS=Vitis vinifera OX=29760 PE=2 SV=1
A4302	-	-	-	K24781 BPH1; beige protein homolog 1	-	KOG1786 Hs4505465.2 Lysosomal trafficking regulator LYST and related BEACH and WD40 repeat proteins	ONH68201.1 Beige protein 1 [Cyberlindnera fabianii]	BEACH domain-containing protein lvsF OS=Dictyostelium discoideum OX=44689 GN=lvsF PE=4 SV=1
A4303	-	-	-	K21249 UVRAG; UV radiation resistance-associated gene protein	map04140 Autophagy - animal	-	XP_031866478.1 Uncharacterized protein BP5553_08424 [Venustampulla echinocandica]	-
A4304	-	-	GO:0005515(protein binding)	-	-	KOG2827 Hs18548124 Uncharacterized conserved protein	-	Splicing regulator SDE2 OS=Danio rerio OX=7955 GN=sde2 PE=2 SV=2
A4305	-	-	-	-	-	-	-	-

A4306	-	-	-	K11493 RCC1; regulator of chromosome condensation	-	KOG1426 Hs4 758520 FOG: RCC1 domain	KAF9957055. 1 hypothetical protein BGZ72_00219 8 [Mortierella alpina]	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens OX=9606 GN=HERC2 PE=1 SV=2
A4307	GO:00086 10(lipid biosynthe tic process)	-	GO:0005506(iron ion binding);GO:001 6491(oxidoredu ctase activity)	K00227 SC5DL, ERG3; Delta7-sterol 5-desaturase [EC:1.14.19.2 0]	map01110 Biosynthesis of secondary metabolites;map 00100 Steroid biosynthesis;ma p01100 Metabolic pathways	KOG0872 Hs2 0558831 Sterol C5 desaturase	RIB16404.1 putative sterol delta 5,6- desaturase [Gigaspora rosea]	Lathosterol oxidase OS=Homo sapiens OX=9606 GN=SC5D PE=1 SV=2
A4308	-	-	-	-	-	-	-	-
A4309	-	GO:00481 88(Set1C/ COMPAS S complex)	GO:0005515(pro tein binding)	K14961 RBBP5, SWD1, CPS50; COMPASS component SWD1	map04934 Cushing syndrome	KOG1273 At3 g21060 WD40 repeat protein	KAF8968648. 1 hypothetical protein BGZ46_01083 4, partial [Entomortiere lla lignicola]	Protein RBL OS=Arabidopsis thaliana OX=3702 GN=RBL PE=1 SV=1
A4310	-	-	-	-	-	-	-	-
A4311	GO:00060 98(pentos e- phosphat e shunt);GO :0005975(carbohydr ate metabolic process)	-	GO:0004750(rib ulose- phosphate 3- epimerase activity);GO:001 6857(racemase and epimerase activity, acting on carbohydrates and derivatives)	K01783 rpe, RPE; ribulose- phosphate 3- epimerase [EC:5.1.3.1]	map00040 Pentose and glucuronate interconversions; map01110 Biosynthesis of secondary metabolites;map 01200 Carbon metabolism;map 01120 Microbial metabolism in diverse environments;m ap01230 Biosynthesis of amino acids;map00710 Carbon fixation in photosynthetic organisms;map0 0030 Pentose phosphate pathway;map01 100 Metabolic pathways	KOG3111 CE 27934 D- ribulose-5- phosphate 3- epimerase	XP_03401497 2.1 uncharacteriz ed protein DIURU_00025 6 [Ditiutina rugosa]	Ribulose-phosphate 3-epimerase OS=Homo sapiens OX=9606 GN=RPE PE=1 SV=1
A4312	GO:00066 29(lipid metabolic process)	-	GO:0016627(oxi doreductase activity, acting on the CH-CH group of donors)	-	-	KOG4650 At1 g18180 Predicted steroid reductase	KNE68799.1 hypothetical protein AMAG_13440 [Allomyces macrogynus ATCC 38327]	Uncharacterized protein C594.04c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC594.04c PE=3 SV=2
A4313	-	-	GO:0005509(cal cium ion binding)	-	-	KOG0498 Hs4 885407 K+- channel ERG and related proteins, contain PAS/PAC sensor domain	XP_03102671 6.1 uncharacteriz ed protein SmJEL517_g0 1330 [Synchronium microbalum]	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1 OS=Oryctolagus cuniculus OX=9986 GN=HCN1 PE=2 SV=2
A4314	-	-	GO:0005524(AT P binding)	-	-	KOG0927 YD R061w Predicted transporter (ABC superfamily)	POY71432.1 hypothetical protein BMF94_5745 [Rhodotorula taiwanensis]	ABC transporter ATP-binding protein ModF OS=Escherichia coli (strain K12) OX=83333 GN=modF PE=2 SV=2

A4315	-	-	GO:0016491(oxidoreductase activity)	K00326 CYB5R; cytochrome-b5 reductase [EC:1.6.2.2]	map00520 Amino sugar and nucleotide sugar metabolism	KOG0534 Hs6552328 NADH-cytochrome b-5 reductase	ORY07232.1 NAD(P)H-nitrate reductase [Basidiobolus meristosporus CBS 931.73]	NADH-cytochrome b5 reductase 2 OS=Xenopus tropicalis OX=8364 GN=cyb5r2 PE=2 SV=1
A4316	-	-	-	-	-	-	-	-
A4317	-	-	-	-	-	-	-	-
A4318	-	-	-	-	-	-	KAF4562965.1 hypothetical protein EYR36_003398 [Pleurotus pulmonarius]	-
A4319	-	-	-	-	-	-	-	-
A4320	-	-	-	-	-	-	-	-
A4321	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0612 Hs4505831 Rho-associated, coiled-coil containing protein kinase	PVU97072.1 hypothetical protein BB561_000784 [Smittium simullii]	Ribosomal protein S6 kinase 2 alpha OS=Xenopus laevis OX=8355 GN=rps6ka PE=1 SV=1
A4322	-	-	-	-	-	-	-	-
A4323	GO:0006629(lipid metabolic process)	-	GO:0016491(oxidoreductase activity),GO:0020037(heme binding)	K13076 SLD; sphingolipid 8-(E)-desaturase [EC:1.14.19.18]	-	KOG4232 Hs1181775 Delta 6-fatty acid desaturase/delta-8 sphingolipid desaturase	RHZ46577.1 hypothetical protein Glove_613g9 [Diversispora epigaea]	Acyl-lipid (8-3)-desaturase OS=Rebecca salina OX=561169 GN=D5Des PE=1 SV=1
A4324	-	-	-	-	-	KOG2385 CE02716 Uncharacterized conserved protein	ORX84152.1 DUF726-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Uncharacterized membrane protein F35D11.3 OS=Caenorhabditis elegans OX=6239 GN=F35D11.3 PE=3 SV=2
A4325	-	-	GO:0003756(protein disulfide isomerase activity)	K09584 PDIA6, TXNDC7; protein disulfide-isomerase A6 [EC:5.3.4.1]	map04141 Protein processing in endoplasmic reticulum	KOG0191 CE03880 Thioredoxin/protein disulfide isomerase	PBP27918.1 protein disulfide-isomerase tigma precursor [Diplocarpon rosae]	Protein disulfide-isomerase A6 homolog OS=Caenorhabditis elegans OX=6239 GN=pdi-6 PE=3 SV=1
A4326	GO:0006413(translational initiation)	-	GO:0003723(RNA binding),GO:0003743(translation initiation factor activity)	K03259 EIF4E; translation initiation factor 4E	map04211 Longevity regulating pathway;map01521 EGFR tyrosine kinase inhibitor resistance;map04910 Insulin signaling pathway;map04151 PI3K-Akt signaling pathway;map04150 mTOR signaling pathway;map04066 HIF-1 signaling pathway	KOG1669 Hs4757702 Predicted mRNA cap-binding protein related to eIF-4E	CDH52559.1 eukaryotic translation initiation factor 4e type2 isoform3 [Lichtheimia corymbifera JMRC.FSU:9682]	Eukaryotic translation initiation factor 4E type 2 OS=Mus musculus OX=10090 GN=EIF4e2 PE=1 SV=1

A4327	-	-	-	K01102 PDP; pyruvate dehydrogenase phosphatase [EC:3.1.3.43]	-	KOG0700 At4g38520 Protein phosphatase 2C/pyruvate dehydrogenase (lipoamide) phosphatase	XP_031026834.1 uncharacterized protein SmJEL517_g01289 [Synchytrium microbalum]	Probable protein phosphatase 2C 64 OS=Arabidopsis thaliana OX=3702 GN=PP2C64 PE=1 SV=1
A4328	-	-	-	-	-	-	KZM27624.1 hypothetical protein ST47_g1341 [Ascochyta rabiei]	-
A4329	-	-	-	-	-	-	-	-
A4330	-	-	-	-	-	-	-	-
A4331	GO:0006260(DNA replication),GO:0032508(DNA duplex unwinding)	-	GO:0003677(DNA binding),GO:0005524(ATP binding)	K02542 MCM6; DNA replication licensing factor MCM6 [EC:5.6.2.3]	map03030 DNA replication;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0480 Hs19923727 DNA replication licensing factor, MCM6 component	XP_016611361.1 hypothetical protein SPPG_02368 [Spizellomyces punctatus DAOM BR117]	DNA helicase MCM8 OS=Rattus norvegicus OX=10116 GN=Mcm8 PE=3 SV=1
A4332	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 At2g21540 Phosphatidylinositol transfer protein SEC14 and related proteins	PPQ65350.1 hypothetical protein CVT26_000065 [Gymnopilus dilepis]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH3 OS=Arabidopsis thaliana OX=3702 GN=SFH3 PE=2 SV=1
A4333	-	-	-	-	-	-	-	-
A4334	-	-	-	K24104 GPN; GPN-loop GTPase	-	KOG1533 Hs8922366 Predicted GTPase	KAF0389242.1 GPN-loop GTPase [Gigaspora margarita]	GPN-loop GTPase 2 OS=Sus scrofa OX=9823 GN=GPN2 PE=2 SV=1
A4335	-	-	-	-	-	-	-	-
A4336	GO:0006099(tricarboxylic acid cycle)	GO:0016020(membrane),GO:0045281(succinate dehydrogenase complex)	GO:0000104(succinate dehydrogenase activity),GO:0009055(electron transfer activity),GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors)	K00236 SDHC, SDH3; succinate dehydrogenase (ubiquinone) cytochrome b560 subunit	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map04714 Thermogenesis;map00020 Citrate cycle (TCA cycle);map00190 Oxidative phosphorylation;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map052	KOG0449 Hs4506863 Succinate dehydrogenase, cytochrome b subunit	XP_028483806.1 succinate dehydrogenase cytochrome b560 subunit [Byssoschlamys spectabilis]	Succinate dehydrogenase cytochrome b560 subunit OS=Paracoccus denitrificans OX=266 GN=sdhC PE=3 SV=1
A4337	GO:0035025(positive regulation of Rho protein signal transduction)	-	GO:0003779(activin binding)	-	-	-	-	Actin-binding Rho-activating protein OS=Mus musculus OX=10090 GN=Abra PE=1 SV=1
A4338	-	-	-	-	-	-	-	-

A4339	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0030131(clathrin adaptor complex)	-	K12393 AP1M; AP-1 complex subunit mu	map04142 Lysosome;map05170 Human immunodeficiency virus 1 infection	KOG0937 At4g24550 Adaptor complexes medium subunit family	XP_025175475.1 Adaptor complexes medium subunit family protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	AP-4 complex subunit mu OS=Arabidopsis thaliana OX=3702 GN=AP4M PE=2 SV=1
A4340	GO:0022900(electron transport chain),GO:0006099(tricarboxylic acid cycle)	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding),GO:0016491(oxidoreductase activity)	-	K00234 SDHA, SDH1; succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1]	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map04714 Thermogenesis;map00020 Citrate cycle (TCA cycle);map00190 Oxidative phosphorylation;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map052	KOG2403 At5g66760 Succinate dehydrogenase, flavoprotein subunit	KXS12740.1 succinate dehydrogenase [Gonapodya prolifera JEL478]	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=SDH1 PE=1 SV=1
A4341	-	-	-	-	-	-	-	-
A4342	-	-	-	-	-	-	-	-
A4343	GO:0032259(methylation)	GO:0003676(nucleic acid binding),GO:0008168(methyltransferase activity)	-	-	-	-	ORY49486.1 S-adenosyl-L-methionine-dependent methyltransferase [Rhizoclosmatium globosum]	Release factor glutamine methyltransferase OS=Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIMB 8255 / S1) OX=269796 GN=prmc PE=3 SV=1
A4344	-	-	-	-	-	KOG3599 Hs7706639 Ca2+-modulated nonselective cation channel polycystin	-	Polycystin-2 OS=Danio rerio OX=7955 GN=pkd2 PE=1 SV=1
A4345	-	-	-	-	-	KOG0048 At5g11510 Transcription factor, Myb superfamily	KXN66846.1 ternary protein-Dna Complex1, partial [Conidiobolus coronatus NRRL 28638]	Transcription factor MYB3R-4 OS=Arabidopsis thaliana OX=3702 GN=MYB3R4 PE=1 SV=1
A4346	-	-	-	-	-	-	-	-
A4347	-	-	-	K17278 PGRMC1_2; membrane-associated progesterone receptor component	map04080 Neuroactive ligand-receptor interaction	KOG1110 At2g24940 Putative steroid membrane receptor Hpr6.6/25-Dx	KAF9955506.1 hypothetical protein BGZ72_003672 [Mortierella alpina]	Probable steroid-binding protein 3 OS=Arabidopsis thaliana OX=3702 GN=MP3 PE=1 SV=1
A4348	-	-	GO:0004364(glutathione transferase activity)	K07393 ECM4, yqjG; glutathionyl-hydroquinone reductase [EC:1.8.5.7]	-	KOG2903 At5g45020 Predicted glutathione S-transferase	KAG1138587.1 hypothetical protein G6F38_010447 [Rhizopus oryzae]	Glutathionyl-hydroquinone reductase YqjG OS=Escherichia coli (strain K12) OX=83333 GN=yqjG PE=1 SV=1

A4349	-	-	-	-	-	KOG3329[Hs7705529 RAN guanine nucleotide release factor	TPX59938.1 hypothetical protein PhCBS80983.g02128 [Powellomyces hirtus]	Ran guanine nucleotide release factor OS=Danio rerio OX=7955 GN=rangrf PE=2 SV=1
A4350	-	-	GO:0016872(intramolecular lyase activity)	-	-	-	-	-
A4351	GO:0006508(proteolysis)	-	GO:0005509(calcium ion binding),GO:0008236(serine-type peptidase activity)	-	-	KOG2281[At5g24260 Dipeptidyl aminopeptidases/acylaminoacyl-peptidases	KAG1467508.1 hypothetical protein G6F57_012982 [Rhizopus oryzae]	Dipeptidyl aminopeptidase 4 OS=Pseudoxanthomonas mexicana OX=128785 GN=dap4 PE=1 SV=1
A4352	-	-	-	-	-	-	-	-
A4353	-	-	GO:0003824(catalytic activity)	-	-	-	ORX66868.1 ClpP/crotonase, partial [Linderina pennisporea]	Enoyl-CoA delta isomerase 1, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=ECI1 PE=1 SV=1
A4354	-	-	-	-	-	-	-	-
A4355	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1543[At4g35350 Cysteine proteinase Cathepsin L	KFH62689.1 hypothetical protein MVEG_12081 [Podila verticillata NRRL 6337]	KDEL-tailed cysteine endopeptidase CEP2 OS=Arabidopsis thaliana OX=3702 GN=CEP2 PE=1 SV=1
A4356	-	-	-	-	-	-	-	-
A4357	-	-	-	-	-	-	-	-
A4358	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003714(transcription corepressor activity)	K11644 SIN3A; paired amphipathic helix protein Sin3a	map04350 TGF-beta signaling pathway;map04919 Thyroid hormone signaling pathway;map04139 Mitophagy yeast;map05202 Transcriptional misregulation in cancer;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG4204[Hs2056376 Histone deacetylase complex, SIN3 component	XP_018227360.1 hypothetical protein T552_00476 [Pneumocystis carinii B80]	Paired amphipathic helix protein Sin3b OS=Mus musculus OX=10090 GN=Sin3b PE=1 SV=2
A4359	-	-	-	-	-	-	-	-
A4360	GO:0035025(positive regulation of Rho protein signal transduction)	-	GO:0003779(actin binding)	-	-	KOG3376[CE15975 Uncharacterized conserved protein	-	Actin-binding Rho-activating protein OS=Rattus norvegicus OX=10116 GN=Abra PE=1 SV=2
A4361	-	-	-	K10355 ACTF; actin, other eukaryote	map04814 Motor proteins	KOG0676[CE12358 Actin and related proteins	RK099664.1 hypothetical protein CXG81DRAFT_27595 [Caulochytrium protostelioides]	Actin OS=Achlya bisexualis OX=4766 PE=3 SV=1
A4362	-	-	-	-	-	KOG0954[CE26165 PHD finger protein	-	-

A4363	-	-	GO:0005515(protein binding)	K22696 EEF2KMT; protein-lysine N-methyltransferase EEF2KMT [EC:2.1.1.-]	-	KOG2497 7293566 Predicted methyltransferase	XP_01621201.5.1 hypothetical protein PV09_06631 [Verruconis gallopava]	Methyltransferase-like protein 22 OS=Mus musculus OX=10090 GN=Mettl22 PE=2 SV=1
A4364	GO:0000398(mRNA splicing, via spliceosome),GO:0006396(RNA processing)	-	GO:0005515(protein binding)	K12867 SYF1, XAB2; pre-mRNA-splicing factor SYF1	map03040 Spliceosome	KOG2047 7303287 mRNA splicing factor	RUS18302.1 pre-mRNA splicing factor syf-1, partial [Endogone sp. FLAS-F59071]	Pre-mRNA-splicing factor syf1 homolog OS=Drosophila melanogaster OX=7227 GN=fand PE=1 SV=1
A4365	-	-	-	-	-	-	ORZ39445.1 hypothetical protein BCR44DRAFT_110117, partial [Catenaria anguillulae PL171]	-
A4366	-	-	-	-	-	-	-	-
A4367	-	GO:0005852(eukaryotic translation initiation factor 3 complex)	-	K03254 EIF3A; translation initiation factor 3 subunit A	-	KOG2072 At4g11420 Translation initiation factor 3, subunit a (eIF-3a)	KAF9373344.1 eukaryotic translation initiation factor 3 subunit A [Podila verticillata]	Eukaryotic translation initiation factor 3 subunit A OS=Arabidopsis thaliana OX=3702 GN=TIF3A1 PE=1 SV=1
A4368	-	-	-	-	-	-	-	-
A4369	-	-	-	-	-	-	-	Protein TOM THREE HOMOLOG 1 OS=Arabidopsis thaliana OX=3702
A4370	GO:0006364(rRNA processing)	GO:0005634(nucleus),GO:0005732(snoRNA-containing ribonucleoprotein complex),GO:0034457(Mpp10 complex)	-	K14559 MPP10; U3 small nucleolar RNA-associated protein MPP10	map03008 Ribosome biogenesis in eukaryotes	KOG2600 YJR002w U3 small nucleolar ribonucleoprotein complex, subunit Mpp10p	RIA92789.1 U3 small nucleolar ribonucleoprotein complex, subunit Mpp10 [Glomus cerebriforme]	U3 small nucleolar RNA-associated protein MPP10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MPP10 PE=1 SV=1
A4371	-	-	-	-	-	-	-	-
A4372	-	-	GO:0005515(protein binding),GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07897 RAB7A; Ras-related protein Rab-7A	map04144 Endocytosis;map04145 Phagosome;map04140 Autophagy - animal;map05132 Salmonella infection;map04138 Autophagy - yeast;map04137 Mitophagy - animal;map05146 Amoebiasis;map05152 Tuberculosis	KOG4423 Hs1641237 GTP-binding protein-like, RAS superfamily	KAG2188100.1 hypothetical protein INT44_000851 [Umbelopsis vinacea]	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A4373	-	-	-	-	-	-	-	-
A4374	-	-	GO:0016746(acyltransferase activity)	K00624 E2.3.1.7; carnitine O-acetyltransferase [EC:2.3.1.7]	map04146 Peroxisome	KOG3717 Hs21618334 Carnitine O-acetyltransferase CRAT	KNE59800.1 hypothetical protein AMAG_05259 [Allomyces macrogynus ATCC 38327]	Carnitine O-acetyltransferase OS=Columba livia OX=8932 GN=CRAT PE=1 SV=1

A4375	GO:0006468(protein phosphorylation),GO:0007093(mitotic cell cycle checkpoint signaling),GO:0051304(chromosome separation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004712(protein serine/threonine/tyrosine kinase activity)	K08866 TTK, MPS1; serine/threonine-protein kinase TTK/MPS1 [EC:2.7.12.1]	map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0596 At1g77720 Dual specificity; serine/threonine and tyrosine kinase	XP_019023379.1 Pkinase-domain-containing protein [Saitoella complicata NRRL Y-17804]	Probable serine/threonine-protein kinase mps1 OS=Dictyostelium discoideum OX=44689 GN=mps1 PE=3 SV=1
A4376	GO:0015937(coenzyme A biosynthetic process)	-	GO:0004594(pantothenate kinase activity),GO:0005524(ATP binding)	K09680 PANK1_2_3, CAB1, coaW; type II pantothenate kinase [EC:2.7.1.33]	map00770 Pantothenate and CoA biosynthesis;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG2201 7296298 Pantothenate kinase PanK and related proteins	ORX86478.1 pantothenate kinase 1 [Basidiobolus meristosporus CBS 931.73]	Pantothenate kinase 3 OS=Mus musculus OX=10090 GN=Pank3 PE=1 SV=1
A4377	-	-	GO:0003723(RNA binding)	K17943 PUM; pumilio RNA-binding family	map05017 Spinocerebellar ataxia	KOG2049 At1g22240 Translational repressor MPT5/PUF4 and related RNA-binding proteins (Puf superfamily)	KNZ71768.1 Pumilio like protein [Termitomyces sp. J132]	Putative pumilio homolog 8, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=APUM8 PE=3 SV=2
A4378	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4503899 Sulfatase	KAG5355441.1 putative sulfatase PB10D8.02c [Yarrowia sp. C11]	N-acetylgalactosamine-6-sulfatase OS=Mus musculus OX=10090 GN=Galns PE=1 SV=2
A4379	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4380	-	-	-	-	-	-	-	-
A4381	GO:0008033(tRNA processing)	-	-	-	-	-	XP_036498239.1 tRNA dimethylallyltransferase [Colletotrichum siamense]	tRNA dimethylallyltransferase OS=Mus musculus OX=10090 GN=Trit1 PE=1 SV=2
A4382	-	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups),GO:0016746(acyltransferase activity)	K00626 ACAT, atoB; acetyl-CoA C-acyltransferase [EC:2.3.1.9]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00900 Terpenoid backbone biosynthesis;map01120 Microbial metabolism in diverse environments;map00720 Carbon fixation pathways in prokaryotes;map04975 Fat digestion and absorption;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00620 Pyruvate metabolism;map	KOG1392 Hs4504327 Acetyl-CoA acetyltransferase	KAG1715825.1 hypothetical protein ID866_1343 [Astraeus odoratus]	Trifunctional enzyme subunit beta, mitochondrial OS=Macaca fascicularis OX=9541 GN=HADHB PE=2 SV=1

A4383	GO:0006298(mismatch repair),GO:0016579(protein deubiquitination)	-	GO:0005524(ATP binding),GO:0030983(mismatched DNA binding),GO:0004843(thiol-dependent deubiquitinase),GO:0008270(zinc ion binding)	K08737 MSH6; DNA mismatch repair protein MSH6	map01524 Platinum drug resistance;map05210 Colorectal cancer;map05200 Pathways in cancer;map03430 Mismatch repair	KOG0217 Hs4504191 Mismatch repair ATPase MSH6 (MutS family)	RKP38593.1 muts domain V-domain-containing protein [Dimargaris cristalligena]	DNA mismatch repair protein Msh6 OS=Mus musculus OX=10090 GN=Msh6 PE=1 SV=3
A4384	-	-	GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG0023 At4g37990 Alcohol dehydrogenase, class V	KAF9139747.1 hypothetical protein BGX30_007546 [Mortierella sp. GBA39]	NADP-dependent alcohol dehydrogenase C 1 OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=adhC1 PE=1 SV=1
A4385	-	-	-	-	-	-	-	-
A4386	-	-	GO:0005515(protein binding)	K14555 UTP13, TBL3; U3 small nucleolar RNA-associated protein 13	map03008 Ribosome biogenesis in eukaryotes	KOG4155 At1g24130 FOG:WD40 repeat	RUP45740.1 hypothetical protein BC936DRAFT_147797 [Jimgerdennia flammicorona]	CCR4-associated factor 4 homolog OS=Candida glabrata (strain ATCC 2001 / BCRC 20586 / JCM 3761 / NBRC 0622 / NRRL Y-65 / CBS 138) OX=284593 GN=CAF4 PE=3 SV=1
A4387	-	-	-	-	-	-	KAG1083363.1 hypothetical protein G6F42_022236 [Rhizopus oryzae]	-
A4388	GO:0006414(translational elongation)	-	GO:0005525(GTP binding),GO:0003924(GTPase activity),GO:0003746(translation elongation factor activity)	K02355 fusa, GFM, EFG; elongation factor G	-	KOG0465 At1g45332 Mitochondrial elongation factor	KAG0261003.1 Elongation factor G, mitochondrial [Actinomyces rella ambigua]	Elongation factor G-1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MEFG1 PE=1 SV=1
A4389	GO:0006066(protein import into nucleus)	-	-	-	-	KOG4674 Hs4507659 Uncharacterized conserved coiled-coil protein	KZV92725.1 hypothetical protein EXIGLDRAFT_836242 [Exidia glandulosa HHB12029]	Nucleoprotein TPR (Fragment) OS=Xenopus laevis OX=8355 GN=tpR PE=1 SV=1
A4390	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A4391	-	-	-	-	-	-	KAF8273130.1 NADP+-dependent D-mannitol dehydrogenase [Lactarius quietus]	2-deoxy-scyllo-inosamine dehydrogenase OS=Streptomyces ribosidificus OX=80859 GN=rbmC PE=3 SV=1
A4392	GO:0006508(proteolysis)	-	GO:0004181(metalloprotease activity),GO:0008270(zinc ion binding)	K08783 ECM14; extracellular matrix protein 14 [EC:3.4.17.-]	-	KOG4059 Hs13129018 Uncharacterized conserved protein	EPZ32777.1 Peptidase M14, carboxypeptidase A domain-containing protein [Rozella allomycis CSF55]	Gamma-glutamylcyclotransferase OS=Bos taurus OX=9913 GN=GGCT PE=2 SV=1
A4393	-	-	-	-	-	-	-	-

A4394	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K24887 GTPBP1; GTP-binding protein 1	-	KOG1143 7296654 Predicted translation elongation factor	TPX58892.1 hypothetical protein PhCBS80983.g02842 [Powellomyces hirtus]	GTP-binding protein 2 OS=Homo sapiens OX=9606 GN=GTPBP2 PE=1 SV=1
A4395	GO:0006366(transcription by RNA polymerase II)	GO:0005669(transcription factor TFIIID complex)	GO:0005515(protein binding),GO:0001091(RNA polymerase II general transcription initiation factor binding),GO:0004402(histone acetyltransferase activity),GO:0017025(TBP-class protein binding)	K23358 TAF1; transcription initiation factor TFIIID subunit 1, fungi type [EC:2.3.1.48]	map03022 Basal transcription factors	KOG0008 At1g32750 Transcription initiation factor TFIIID, subunit TAF1	GBC03956.1 hypothetical protein RchHR1_05410012 [Rhizophagus clarus]	Transcription initiation factor TFIIID subunit 1 OS=Oryza sativa subsp. japonica OX=39947 GN=TAF1 PE=2 SV=1
A4396	-	-	-	-	-	-	OON06951.1 hypothetical protein BSLG_03496 [Batrachochytrium salamandrivorans]	Protein TPX2 OS=Arabidopsis thaliana OX=3702 GN=TPX2 PE=1 SV=1
A4397	-	-	-	K15280 SLC35C2; solute carrier family 35, member C2	-	KOG1443 Hs21314776 Predicted integral membrane protein	XP_023466855.1 TPT-domain-containing protein [Rhizopus microsporus ATCC 52813]	Solute carrier family 35 member C2 OS=Mus musculus OX=10090 GN=Slc35c2 PE=1 SV=1
A4398	GO:0009086(methionine biosynthetic process), GO:0044237(cellular metabolic process), GO:0042558(pteridine-containing compound metabolic process)	-	GO:0008705(methionine synthase activity),GO:0031419(cobalamin binding),GO:0046872(metal ion binding),GO:0008270(zinc ion binding)	-	-	-	ORX69735.1 methionine synthase-like protein [Linderina pennisporea]	Methionine synthase OS=Bos taurus OX=9913 GN=MTR PE=2 SV=1
A4399	GO:0006508(proteolysis)	-	GO:0004190(aspartic-type endopeptidase activity)	K01381 PEP4; saccharopepsin [EC:3.4.23.25]	map04138 Autophagy - yeast	KOG1339 YPL154c Aspartyl protease	OCF78120.1 saccharopepsin [Kwoniella mangroviensis CBS 8886]	Aspartic protease 3 OS=Toxoplasma gondii OX=5811 GN=ASP3 PE=1 SV=1
A4400	-	-	GO:0005515(protein binding)	K09523 DnaJC3; DnaJ homolog subfamily C member 3	map04141 Protein processing in endoplasmic reticulum;map05164 Influenza A	KOG0624 Hs5453980 dsRNA-activated protein kinase inhibitor P58, contains TPR and DnaJ domains	CAF9903781.1 hypothetical protein ALECFALPRE.D_002975 [Alectoria fallacina]	DnaJ homolog subfamily C member 3 OS=Mus musculus OX=10090 GN=Dnajc3 PE=1 SV=1
A4401	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-

A4402	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity),GO:0004965(G protein-coupled GABA receptor activity)	-	-	KOG1055[Hs20127671 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	KNE54717.1 hypothetical protein AMAG_17696 [Allomyces macrogynus ATCC 38327]	Metabotropic glutamate receptor-like protein E OS=Dictyostelium discoideum OX=44689 GN=grIE PE=2 SV=2
A4403	-	-	GO:0016874(ligase activity)	K01969 E6.4.1.4B; 3-methylcrotonyl-CoA carboxylase beta subunit [EC:6.4.1.4]	map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG0540[Hs11545863 3-Methylcrotonyl-CoA carboxylase, non-biotin containing subunit/Acetyl-CoA carboxylase carboxyl transferase, subunit beta	GBC09920.1 hypothetical protein RclHR1_09200005 [Rhizophagus clarus]	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Rattus norvegicus OX=10116 GN=Mccc2 PE=2 SV=1
A4404	GO:0005975(carbohydrate metabolic process)	-	-	-	-	-	XP_035370581.1 Glutaminase [Lasiodiplodia theobromae]	Glutaminase A OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) OX=510516 GN=gtaA PE=1 SV=2
A4405	-	-	-	-	-	KOG0143[At3g49620 Iron/ascorbate family oxidoreductases	CEL62727.1 hypothetical protein RSOLAG1IB_05084 [Rhizoctonia solani AG-1 IB]	Probable 2-oxoglutarate-dependent dioxygenase At3g50210 OS=Arabidopsis thaliana OX=3702 GN=At3g50210 PE=2 SV=1
A4406	GO:0006072(glycerol-3-phosphate metabolic process), GO:0005975(carbohydrate metabolic process), GO:0046168(glycerol-3-phosphate catabolic process)	GO:0009331(glycerol-3-phosphate dehydrogenase complex)	GO:0016491(oxidoreductase activity),GO:0004367(glycerol-3-phosphate dehydrogenase [NAD+] activity),GO:0042803(protein homodimerization activity),GO:0051287(NAD binding),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)	K00006 GPD1; glycerol-3-phosphate dehydrogenase (NAD+) [EC:1.1.1.8]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map04011 MAPK signaling pathway - yeast	KOG2711[Hs11440382 Glycerol-3-phosphate dehydrogenase/dihydroxyacetone 3-phosphate reductase	KAG2172263.1 hypothetical protein INT43_004804 [Umbelopsis isabellina]	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Takifugu rubripes OX=31033 GN=gpd1 PE=3 SV=1
A4407	-	-	GO:0005515(protein binding)	-	-	-	XP_016612759.1 glutathione S-transferase [Spizellomyces punctatus DAOM BR117]	-

A4408	GO:0006413(translational initiation)	-	GO:0003723(RNA binding);GO:0003743(translation initiation factor activity)	K03259 EIF4E; translation initiation factor 4E	map04211 Longevity regulating pathway;map01521 EGFR tyrosine kinase inhibitor resistance;map04910 Insulin signaling pathway;map04151 PI3K-Akt signaling pathway;map04150 mTOR signaling pathway;map04066 HIF-1 signaling pathway	KOG1670 7295331 Translation initiation factor 4F, cap-binding subunit (eIF-4E) and related cap-binding proteins	RKP37453.1 translation initiation factor eIF 4e-like domain-containing protein [Dimargaris cristalligena]	Eukaryotic translation initiation factor 4E1 OS=Drosophila melanogaster OX=7227 GN=eIF4E1 PE=1 SV=1
A4409	-	-	GO:0005515(protein binding)	-	-	KOG3785 Hs13376400 Uncharacterized conserved protein	XP_016607349.1 tetratricopeptide repeat protein 26 [Spizellomyces punctatus DAOM BR117]	Intraflagellar transport protein 56 OS=Danio rerio OX=7955 GN=ift56 PE=2 SV=2
A4410	-	-	-	-	-	-	PBK73803.1 hypothetical protein ARMSODRAFT_952875 [Armillaria solidipes]	-
A4411	-	-	GO:0005515(protein binding);GO:0005509(calcium ion binding)	-	-	KOG0306 CE27127 WD40-repeat-containing subunit of the 18S rRNA processing complex	ORZ37998.1 WD40-repeat-containing domain protein [Catenaria anguillulae PL171]	Eukaryotic translation initiation factor 3 subunit I OS=Aedes aegypti OX=7159 GN=AAEL013144 PE=3 SV=1
A4412	-	-	GO:0003824(catalytic activity)	K05607 AUH; methylglutacyl-CoA hydratase [EC:4.2.1.18]	map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG1679 7303420 Enoyl-CoA hydratase	KWU41475.1 ClpP/crotonase [Rhodotorula sp. JG-1b]	Putative enoyl-CoA hydratase/isomerase YngF OS=Bacillus subtilis (strain 168) OX=224308 GN=yngF PE=3 SV=1
A4413	GO:0030833(regulation of actin filament polymerization);GO:0034314(Arp2/3 complex-mediated actin nucleation)	GO:0005885(Arp2/3 protein complex);GO:0015629(actin cytoskeleton)	GO:0005515(protein binding)	K05757 ARPC1A_B; actin related protein 2/3 complex, subunit 1A/1B	map04144 Endocytosis;map05135 Yersinia infection;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04810 Regulation of actin cytoskeleton;map04138 Autophagy - yeast;map05100 Bacterial invasion of epithelial cells;map04666 Fc gamma R-mediated phagocytosis;map04530 Tight junction	KOG1523 At2g31300 Actin-related protein Arp2/3 complex, subunit ARPC1/p41-ARC	KAG0218392.1 hypothetical protein BGX33_007534 [Mortierella sp. NVP41]	Actin-related protein 2/3 complex subunit 1B OS=Arabidopsis thaliana OX=3702 GN=ARPC1B PE=2 SV=1
A4414	-	-	-	-	-	-	-	-
A4415	-	-	-	-	-	-	-	-

A4416	GO:0007165(signal transduction),GO:0001600(phosphorelay signal transduction system),GO:0016310(phosphorylation)	-	GO:0000155(phosphorelay sensor kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups)	K11231 SLN1; osmolarity two-component system, sensor histidine kinase SLN1 [EC:2.7.13.3]	map04139 Mitophagy - yeast;map04011 MAPK signaling pathway - yeast;map02020 Two-component system	KOG0519[At1g27320 Sensory transduction histidine kinase	XP_01660776.1.1 PAS domain S-box protein, variant [Spizellomyces punctatus DAOM BR117]	Hybrid signal transduction histidine kinase K OS=Dictyostelium discoideum OX=44689 GN=dhkk PE=1 SV=1
A4417	-	-	-	K07152 SCO1; protein SCO1	-	KOG2792[7296911 Putative cytochrome C oxidase assembly protein	ORY00494.1 mitochondrial metallochaperone Sco1 [Basidiobolus meristosporus CBS 931.73]	Protein SCO1 homolog, mitochondrial OS=Bos taurus OX=9913 GN=SCO1 PE=2 SV=1
A4418	GO:0006811(ion transport),GO:0034220(ion transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005230(extracellular ligand-gated ion channel activity),GO:0004888(transmembrane signaling receptor activity),GO:0005216(ion channel activity)	-	-	-	-	Cys-loop ligand-gated ion channel OS=Dickeya chrysanthemi OX=556 PE=1 SV=1
A4419	-	-	-	K17822 DCUN1D1.2; DCN1-like protein 1/2	-	KOG3077[At3g12760 Uncharacterized conserved protein	RUS16940.1 Cullin binding-domain-containing protein [Jimgerdeman nia flammicorona]	DCN1-like protein 2 OS=Mus musculus OX=10090 GN=Dcn1d2 PE=1 SV=3
A4420	GO:0016192(vesicle-mediated transport)	GO:0016020(membrane)	-	K08490 STX5; syntaxin 5	map04130 SNARE interactions in vesicular transport	KOG0812[7298290 SNARE protein SED5/Syntaxin 5	THH06351.1 hypothetical protein EW145_g4150 [Phellinidium pouzarii]	Syntaxin-5 OS=Drosophila melanogaster OX=7227 GN=Syx5 PE=2 SV=2
A4421	-	-	-	-	-	-	-	-
A4422	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A4423	-	-	-	-	-	-	-	-
A4424	-	-	-	-	-	-	KAF9888583.1 hypothetical protein FE257_008515 [Aspergillus nanangensis]	-
A4425	-	-	-	-	-	-	XP_01326670.5.1 hypothetical protein Z518_11307 [Rhinocladia mackenziei CBS 650.93]	-
A4426	-	-	GO:0050661(NADP binding),GO:0016491(oxidoreductase activity),GO:0051287(NAD binding)	-	-	KOG0409[7302557 Predicted dehydrogenase	KAG5353736.1 hypothetical protein C0989_003162 [Termitomyces sp. Mn162]	2-(hydroxymethyl)glutarate dehydrogenase OS=Eubacterium barkeri OX=1528 GN=Hgd PE=1 SV=1

A4427	GO:0007015(actin filament organization),GO:0034314(Arp2/3 complex-mediated actin nucleation)	GO:0005885(Arp2/3 protein complex)	GO:0005524(ATP binding)	K18584 ACTR3, ARP3; actin-related protein 3	map04144 Endocytosis;map05135 Yersinia infection;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04810 Regulation of actin cytoskeleton;map04138 Autophagy - yeast;map05100 Bacterial invasion of epithelial cells;map04666 Fc gamma R-mediated phagocytosis;map04530 Tight junction	KOG0678 7295163 Actin-related protein Arp2/3 complex, subunit Arp3	RKP26578.1 actin family [Syncephalis pseudoplumigaleata]	Actin-related protein 3 OS=Acanthamoeba castellanii OX=5755 GN=ARP3 PE=2 SV=1
A4428	GO:0006629(lipid metabolic process)	-	-	-	-	-	-	-
A4429	-	-	GO:0005515(protein binding)	-	-	KOG0546 Hs4826932 HSP90 co-chaperone CPR7/Cyclophilin	KAG0233421.1 hypothetical protein BGW41_001479 [Actinomortierella wolfii]	70 kDa peptidyl-prolyl isomerase OS=Triticum aestivum OX=4565 GN=FKBP70 PE=1 SV=1
A4430	-	-	-	-	-	-	EPS95100.1 hypothetical protein FOMPIDRAFT_110567 [Fomitopsis pinicola FP-58527 SS1]	-
A4431	GO:0006662(nucleotide transport)	GO:0016021(integral component of membrane)	GO:0005471(ATP:ADP antiporter activity)	K03301 TC.AAA; ATP:ADP antiporter, AAA family	-	-	OAG29309.1 ATP:ADP antiporter, AAA family [Nematocida displodere]	ADP,ATP carrier protein 1 OS=Chlamydia trachomatis (strain D/UW-3/Cx) OX=272561 GN=tlcA PE=3 SV=1
A4432	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG2615 At5g13750 Permease of the major facilitator superfamily	KAF2097575.1 MFS general substrate transporter [Rhizodiscina lignyota]	Protein ZINC INDUCED FACILITATOR-LIKE 1 OS=Arabidopsis thaliana OX=3702 GN=ZIFL1 PE=2 SV=1
A4433	-	-	-	-	-	-	-	-
A4434	GO:0009225(nucleotide-sugar metabolic process)	-	GO:0008460(dTDP-glucose 4,6-dehydratase activity)	-	-	KOG0747 At1g53500 Putative NAD+-dependent epimerases	KXS21925.1 dTDP-D-glucose 4,6-dehydratase [Gonapodya prolifera JEL478]	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM2 OS=Arabidopsis thaliana OX=3702 GN=RHM2 PE=1 SV=1
A4435	GO:0046856(phosphatidylinositol dephosphorylation)	-	GO:0016791(phosphatase activity)	-	-	KOG0565 Hs9845291 Inositol polyphosphate 5-phosphatase and related proteins	ORX91022.1 DNase I-like protein [Basilidiobolus meristosporus CBS 931.73]	Phosphatidylinositol polyphosphate 5-phosphatase type IV OS=Rattus norvegicus OX=10116 GN=Inpp5e PE=1 SV=3

A4436	-	-	GO:0003824(catalytic activity)	K00797 speE, SRM, SPE3; spermidine synthase [EC:2.5.1.16]	map00330 Arginine and proline metabolism;map00480 Glutathione metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG1562[Hs4507209 Spermidine synthase	ORY35169.1 hypothetical protein BCR33DRAFT_722516 [Rhizoclostium globosum]	Protein rliB OS=Dictyostelium discoideum OX=44689 GN=rliB PE=3 SV=2
A4437	-	-	-	-	-	-	-	-
A4438	-	-	-	-	-	-	-	-
A4440	GO:0006886(intracellular protein transport)	-	-	K18466 VPS26A, B; vacuolar protein sorting-associated protein 26A/B	map04144 Endocytosis	KOG3063[7290217 Membrane coat complex Retromer, subunit VPS26	EJU01248.1 vacuolar protein sorting-associated protein 26 [Dacryopinax primogenitus]	Vacuolar protein sorting-associated protein 26 OS=Dictyostelium discoideum OX=44689 GN=vps26 PE=2 SV=1
A4441	-	-	-	K15728 LPIN; phosphatidate phosphatase LPIN [EC:3.1.3.4]	map01110 Biosynthesis of secondary metabolites;map04936 Alcoholic liver disease;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism;map04150 mTOR signaling pathway;map01100 Metabolic pathways	KOG2116[YM165c Protein involved in plasmid maintenance/nuclear protein involved in lipid metabolism	RKP14608.1 Lipin/Ned1/Smp2-domain-containing protein, partial [Piptocephalis cylindrospora]	Phosphatidic acid phosphohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAH1 PE=1 SV=1
A4442	GO:0006414(translational elongation)	GO:0005853(eukaryotic translation elongation factor 1 complex)	GO:0003746(translation elongation factor activity)	-	-	KOG1668[YA1003w Elongation factor 1 beta/delta chain	KAG5362075.1 Elongation factor 1-beta [Yarrowia sp. C11]	Elongation factor 1-beta OS=Candida albicans (strain WO-1) OX=294748 GN=EFB1 PE=3 SV=1
A4443	-	-	-	-	-	-	-	-
A4444	GO:0036211(protein modification process)	-	-	-	-	KOG2157[7297165 Predicted tubulin-tyrosine ligase	OMJ26434.1 putative tubulin-tyrosine ligase [Smittium culicis]	Protein polyglycylase TTLL10 OS=Macaca fascicularis OX=9541 GN=TTLL10 PE=2 SV=1
A4445	GO:0006996(organelle organization)	-	GO:0005515(protein binding)	K03255 TIF31, CLU1; protein TIF31	-	KOG1839[CE00213 Uncharacterized protein CLU1/cluA/TIF31 involved in mitochondria morphology/distribution, also found associated with eIF-3	GAN11300.1 conserved hypothetical protein [Mucor ambiguus]	Clustered mitochondria protein homolog OS=Aedes aegypti OX=7159 GN=AAEL000794 PE=3 SV=1
A4446	-	-	-	-	-	-	-	Putative 6-carboxy-5,6,7,8-tetrahydropterin synthase OS=Methanothermobacter thermoautotrophicus (strain ATCC 29096 /
A4447	-	-	-	-	-	-	-	-

A4448	-	-	-	-	-	-	-	-
A4449	-	-	GO:0016407(acyltransferase activity)	-	-	-	XP_018156554.1 hypothetical protein CH63R_09557 [Colletotrichum higginsianum IMI 349063]	-
A4450	-	-	-	-	-	-	-	-
A4451	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration;map04024 cAMP signaling pathway;map04020 Calcium signaling pathway;map05414 Dilated cardiomyopathy;map04140 Autophagy - animal;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map01522 Endocrine resistance;map04919 Thyroid hormone signaling pathway;map04918 Thyroid hormone synthesis;map04	KOG0616[CE15473 cAMP-dependent protein kinase catalytic subunit (PKA)]	RKP25471.1 kinase-like domain-containing protein [Syncephalis pseudoplumigaleata]	cAMP-dependent protein kinase catalytic subunit PRKX OS=Homo sapiens OX=9606 GN=PRKX PE=1 SV=1
A4452	-	-	-	-	-	-	-	-
A4453	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0030126(COPI vesicle coat),GO:0005737(cyttoplasm),GO:0030117(membrane coat)	GO:0005198(structural molecule activity)	K17301 COPB1, SEC26; coatomer subunit beta	-	KOG1058[At4g31480 Vesicle coat complex COPI, beta subunit]	TPX70594.1 hypothetical protein SpCBS45565_g01657 [Spizellomyces sp. 'palustris']	Coatomer subunit beta-1 OS=Arabidopsis thaliana OX=3702 GN=At4g31480 PE=3 SV=2
A4454	-	-	-	-	-	-	-	-
A4455	GO:0006396(RNA processing)	-	GO:0051731(polynucleotide 5'-hydroxyl-kinase activity)	K06947 GRC3, NOL9; polynucleotide 5'-hydroxyl-kinase GRC3/NOL9 [EC:2.7.1.-]	-	KOG2750[YLL035w Uncharacterized conserved protein similar to ATP/GTP-binding protein]	CEJ91896.1 hypothetical protein VHEMI07580 [Torrubiella hemipterigena]	Polynucleotide 5'-hydroxyl-kinase GRC3 OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=GRC3 PE=3 SV=2
A4456	GO:0006400(tRNA modification),GO:0035600(tRNA methylation)	-	GO:0016740(transferase activity),GO:0051539(4 iron, 4 sulfur cluster binding),GO:0035596(methylthio transferase activity),GO:0003824(catalytic activity),GO:0051536(iron-sulfur cluster binding),GO:0035598(N6-threonylcarbamoyladenosine methylthiotransferase activity)	-	-	KOG4355[At1g72090 Predicted Fe-S oxidoreductase]	XP_006674883.1 uncharacterized protein BATDEDRAFT_1672, partial [Batrachochytrium dendrobatidis JAM81]	Threonylcarbamoyladenosine tRNA methylthiotransferase OS=Drosophila melanogaster OX=7227 GN=CG6550 PE=2 SV=1

A4457	GO:0006683(galactosylceramide catabolic process)	-	GO:0004336(galactosylceramidase activity)	K01201 GBA, srf; glucosylceramidase [EC:3.2.1.45]	map04142 Lysosome;map00511 Other glycan degradation;map00600 Sphingolipid metabolism;map01100 Metabolic pathways	-	CDO77140.1 Glycoside Hydrolase Family 30 protein [Trametes cinnabarina]	Galactocerebrosidase OS=Xenopus tropicalis OX=8364 GN=galc PE=2 SV=1
A4458	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0163 Hs4826846 Myosin class VI heavy chain	RKP37203.1 myosin-2 [Dimargaris cristalligena]	Unconventional myosin-VI OS=Bos taurus OX=9913 GN=MYO6 PE=1 SV=4
A4459	-	-	GO:0005515(protein binding)	-	-	-	KAF9940715.1 hypothetical protein BGZ65_006280 [Modicella reniformis]	CCR4-associated factor 4 homolog OS=Candida glabrata (strain ATCC 2001 / BCRC 20586 / JCM 3761 / NBRC 0622 / NRRL Y-65 / CBS 138) OX=284593 GN=CAF4 PE=3 SV=1
A4460	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG2533 At3g47420 Permease of the major facilitator superfamily	-	Putative glycerol-3-phosphate transporter 1 OS=Arabidopsis thaliana OX=3702 GN=At3g47420 PE=2 SV=1
A4461	-	-	-	-	-	-	-	-
A4462	-	-	-	K23469 CLB2; G2/mitotic-specific cyclin 2	map04011 MAPK signaling pathway - yeast;map04111 Cell cycle - yeast	KOG0653 At4g35620 Cyclin B and related kinase-activating proteins	ORX90880.1 A/B/D/E cyclin [Basidiobolus meristosporus CBS 931.73]	Cyclin-B2-1 OS=Oryza sativa subsp. japonica OX=39947 GN=CYCB2-1 PE=1 SV=2
A4463	-	-	-	-	-	-	-	-
A4464	GO:0019538(protein metabolic process), GO:0006508(proteolysis)	GO:0005737(cytoplasm)	GO:0030145(manganese ion binding),GO:0070006(metalloaminopeptidase activity)	K09611 NPEPL1; probable aminopeptidase NPEPL1 [EC:3.4.11.-]	-	KOG2597 7299691 Predicted aminopeptidase of the M17 family	KNE67562.1 hypothetical protein AMAG_12014 [Allomyces macrogynus ATCC 38327]	Probable aminopeptidase NPEPL1 OS=Homo sapiens OX=9606 GN=NPEPL1 PE=1 SV=3
A4465	-	-	-	-	-	KOG1208 CE27908 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	CCG83805.1 protein of unknown function [Taphrina deformans PYCC 5710]	Dehydrogenase/reductase SDR family member on chromosome X homolog OS=Mus musculus OX=10090 GN=Dhrsx PE=1 SV=2
A4466	-	-	-	-	-	KOG2743 At1g80480 Cobalamin synthesis protein	XP_002173337.2 cobW [Schizosaccharomyces japonicus yFS275]	Zinc-regulated GTPase metalloprotein activator 1 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0274527 PE=3 SV=1
A4467	-	-	GO:0008270(zinc ion binding),GO:0005515(protein binding)	K10661 MARCH6, DOA10; E3 ubiquitin-protein ligase MARCH6 [EC:2.3.2.27]	map04141 Protein processing in endoplasmic reticulum	-	-	-

A4468	-	-	GO:0005509(calcium ion binding)	-	-	KOG0032 7299682 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KNE55050.1 hypothetical protein AMAG_00987 [Allomyces macrogynus ATCC 38327]	Crustacean calcium-binding protein 23 OS=Faxonius limosus OX=28379 PE=1 SV=1
A4469	GO:0006412(translation),GO:0006418(tRNA aminoacylation for protein translation),GO:0006425(glutamyl-tRNA aminoacylation),GO:0043039(tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004819(glutamine-tRNA ligase activity)	K01886 QARS, glnS; glutamyl-tRNA synthetase [EC:6.1.1.18]	map00970 Aminoacyl-tRNA biosynthesis;map01100 Metabolic pathways	KOG1148 At1g25350 Glutamyl-tRNA synthetase	XP_031024584.1 uncharacterized protein SmJEL517_g03539 [Synchytrium microbalum]	Probable glutamine--tRNA ligase OS=Dictyostelium discoideum OX=44689 GN=glnS PE=2 SV=2
A4470	-	-	-	-	-	-	-	-
A4471	-	-	-	-	-	-	-	-
A4472	-	-	GO:0005515(protein binding)	-	-	KOG4626 At3g11540 O-linked N-acetylglucosamine transferase OGT	-	Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SPINDLY OS=Petunia hybrida OX=4102 GN=SPY PE=2 SV=1
A4473	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015075(ion transmembrane transporter activity)	K23503 SFXN5; sideroflexin-5	-	KOG3767 YOR271c Sideroflexin	KAG2178979.1 hypothetical protein INT43_001828 [Umbelopsis isabellina]	Sideroflexin OS=Dictyostelium discoideum OX=44689 GN=sfxn PE=3 SV=1
A4474	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0008569(minus-end-directed microtubule motor activity)	-	-	KOG3595 Hs17864092 Dyneins, heavy chain	TPX78372.1 hypothetical protein CcCBS67573_g00338 [Chytridiomycetes confervae]	Dynein axonemal heavy chain 7 OS=Homo sapiens OX=9606 GN=DNAH7 PE=1 SV=2
A4475	-	-	-	-	-	-	-	-
A4476	-	-	-	-	-	-	RK094199.1 hypothetical protein BDK51DRAFT_25629 [Blyttiomycetes helicus]	-
A4477	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4478	-	-	GO:0016791(phosphatase activity)	K21797 SAC1, SACM1L; phosphatidylinositol 4-phosphatase [EC:3.1.3.-]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG1889 Hs7662338 Putative phosphoinositide phosphatase	ORY93211.1 Sac1 homology domain-containing protein [Syncephalaster racemosum]	Phosphatidylinositol-3-phosphatase SAC1 OS=Xenopus laevis OX=8355 GN=sacm1l PE=2 SV=1

A4479	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K01551 arsA, ASNA1, GET3; arsenite/tail-anchored protein-transporting ATPase [EC:7.3.2.7 7.3.-.-]	-	KOG2825 7304195 Putative arsenite-translocating ATPase	PIA16677.1 anion-transporting ATPase [Coemansia reversa NRRL 1564]	ATPase GET3A OS=Arabidopsis thaliana OX=3702 GN=GET3A PE=1 SV=1
A4480	GO:0046854(phosphatidylinositol phosphate biosynthetic process), GO:0048015(phosphatidylinositol-mediated signaling)	-	GO:0016301(kinase activity)	K19801 PI4KB; phosphatidylinositol 4-kinase B [EC:2.7.1.67]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0903 At5g09350 Phosphatidylinositol 4-kinase, involved in intracellular trafficking and secretion	XP_01821289.9.1 uncharacterized protein OGAPODRAFT_15090 [Ogataea polymorpha]	Phosphatidylinositol 4-kinase OS=Dictyostelium discoideum OX=44689 GN=pikD PE=3 SV=3
A4481	-	-	-	K14997 SLC38A11; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 11	-	KOG1305 7303957 Amino acid transporter protein	XP_01661213.4.1 hypothetical protein SPPG_01537 [Spizellomyces punctatus DAOM BR117]	Putative sodium-coupled neutral amino acid transporter 11 OS=Rattus norvegicus OX=10116 GN=Slc38a11 PE=2 SV=1
A4482	GO:0006396(RNA processing)	-	GO:0008173(RNA methyltransferase activity),GO:0030697(S-adenosylmethionine-dependent tRNA (m5U54) methyltransferase activity)	K15331 TRMT2B, TRM2; tRNA (uracil-5-)-methyltransferase [EC:2.1.1.35]	-	KOG2187 At3g21300 tRNA uracil-5-methyltransferase and related tRNA-modifying enzymes	KGQ11042.1 tRNA (uracil(5)-C(5))-methyltransferase [Beauveria bassiana D1-5]	tRNA/tmRNA (uracil-C(5))-methyltransferase OS=Teredinibacter turnerae (strain ATCC 39867 / T7901) OX=377629 GN=trmA PE=3 SV=1
A4483	-	-	GO:0016422(mRNA (2'-O-methyladenosine-N6-)-methyltransferase activity),GO:009122(RNA polymerase II C-terminal domain binding)	-	-	-	TPX75241.1 hypothetical protein CcBS67573.g03506 [Chytridiomycetes confervae]	mRNA (2'-O-methyladenosine-N(6)-)-methyltransferase OS=Danio rerio OX=7955 GN=pcif1 PE=1 SV=1
A4484	GO:0043666(regulation of phosphoprotein phosphatase activity)	-	GO:0019903(protein phosphatase binding)	K15458 SAP185_190; SIT4-associating protein SAP185/190	-	KOG2073 Hs7662252 SAP family cell cycle dependent phosphatase-associated protein	KAF2452429.1 SIT4 phosphatase-associated protein-domain-containing protein [Lineolata rhizophorae]	Serine/threonine-protein phosphatase 6 regulatory subunit 2 OS=Homo sapiens OX=9606 GN=PPP6R2 PE=1 SV=2
A4485	-	-	-	-	-	-	-	-
A4486	-	-	-	K10273 FBXL7; F-box and leucine-rich repeat protein 7	-	KOG0500 Hs4502917 Cyclic nucleotide-gated cation channel CNGA1-3 and related proteins	KNE61876.1 hypothetical protein AMAG_07148 [Allomyces macrogynus ATCC 38327]	Cyclic nucleotide-gated cation channel alpha-3 OS=Homo sapiens OX=9606 GN=CNGA3 PE=1 SV=2
A4487	-	-	-	-	-	-	-	-

A4488	GO:0006164(purine nucleotide biosynthetic process)	-	GO:0003824(catalytic activity),GO:0003938(IMP dehydrogenase activity)	-	-	KOG2550 YLR432w IMP dehydrogenase/GMP reductase	XP_031856702.1 uncharacterized protein SAPINGB_P006097 [Saprochaete ingens]	Inosine-5'-monophosphate dehydrogenase OS=Dictyostelium discoideum OX=44689 GN=impdh PE=1 SV=1
A4489	GO:0006886(intracellular protein transport)	GO:0017119(Golgi transport complex)	-	K20294 COG7; conserved oligomeric Golgi complex subunit 7	-	KOG4182 At5g51430 Uncharacterized conserved protein	RIA92149.1 oligomeric Golgi complex subunit 7, partial [Glomus cerebriforme]	Conserved oligomeric Golgi complex subunit 7 OS=Arabidopsis thaliana OX=3702 GN=COG7 PE=1 SV=1
A4490	-	-	-	-	-	-	TPX61858.1 hypothetical protein PhCBS80983.g00885 [Powellomyces hirtus]	Cilia- and flagella-associated protein 91 OS=Mus musculus OX=10090 GN=Cfap91 PE=1 SV=3
A4491	-	-	-	-	-	-	-	-
A4492	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	-	-	KOG0032 At5g23580 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KAF9998236.1 hypothetical protein BGZ79_008088 [Entomortierella chlamydospora]	Probable myosin light chain kinase DDB_G0282429 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0282429 PE=3 SV=1
A4493	GO:0006165(nucleoside diphosphate phosphorylation),GO:0006183(GTP biosynthetic process),GO:0006228(UTP biosynthetic process),GO:0006241(CTP biosynthetic process)	-	GO:0004550(nucleoside diphosphate kinase activity)	K00940 ndk, NME; nucleoside-diphosphate kinase [EC:2.7.4.6]	map00983 Drug metabolism - other enzymes;map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map04016 MAPK signaling pathway - plant;map01100 Metabolic pathways	KOG0888 At4g09320 Nucleoside diphosphate kinase	ORY79790.1 nucleoside diphosphate kinase [Leucosporidium creatinivorum]	Nucleoside diphosphate kinase B OS=Flaveria bidentis OX=4224 PE=2 SV=1
A4494	-	-	-	-	-	-	-	-
A4495	-	-	-	K01205 NAGLU; alpha-N-acetylglucosaminidase [EC:3.2.1.50]	map04142 Lysosome;map00531 Glycosaminoglycan degradation;map01100 Metabolic pathways	KOG2233 At5g13690 Alpha-N-acetylglucosaminidase	THH26499.1 hypothetical protein EUX98.g7689 [Antridiella citrinella]	Alpha-N-acetylglucosaminidase OS=Arabidopsis thaliana OX=3702 GN=NAGLU PE=2 SV=1
A4496	-	-	-	-	-	-	-	-
A4497	-	-	-	-	-	-	-	-
A4498	-	-	-	-	-	-	-	-
A4499	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	-	-	K20179 VPS11, PEP5; vacuolar protein sorting-associated protein 11	map04140 Autophagy - animal;map05132 Salmonella infection;map04138 Autophagy - yeast	KOG2114 Hs17978477 Vacuolar assembly/sorting protein PEP5/VPS11	XP_016607160.1 hypothetical protein SPPG_05379 [Spizellomyces punctatus DAOM BR117]	Vacuolar protein sorting-associated protein 11 homolog OS=Homo sapiens OX=9606 GN=VPS11 PE=1 SV=1
A4500	-	-	-	-	-	-	-	-

A4501	-	-	GO:0005515(protein binding),GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	-	-	KOG0384 Hs2047300 Chromodomain-helicase DNA-binding protein	KAG0243186.1 hypothetical protein BGX31_01114.1, partial [Mortierella sp. GBA43]	Chromodomain-helicase-DNA-binding protein 7 OS=Gallus gallus OX=9031 GN=CHD7 PE=2 SV=1
A4502	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY44048.1 TPR-like protein [Rhizoclostium globosum]	-
A4503	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K09489 HSPA4; heat shock 70kDa protein 4	map05417 Lipid and atherosclerosis; map04612 Antigen processing and presentation;map04530 Tight junction	KOG0103 YPL106c Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily	ORZ32808.1 heat shock protein 70 family [Catenaria anguillulae PL171]	Heat shock protein homolog SSE1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MSI3 PE=1 SV=2
A4504	-	-	-	-	-	-	-	-
A4505	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2157 Hs7661564 Predicted tubulin-tyrosine ligase	ORY41798.1 TTL-domain-containing protein [Neocallimastix californiae]	Protein polyglycolase TTL10 OS=Rattus norvegicus OX=10116 GN=Ttl10 PE=2 SV=2
A4506	GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K18342 OTUD6; OTU domain-containing protein 6 [EC:3.4.19.12]	-	KOG2605 Hs22054569 OTU (ovarian tumor)-like cysteine protease	GJH84558.1 hypothetical protein NliqN6_0960 [Naganishia liquefaciens]	OVARIAN TUMOR DOMAIN-containing deubiquitinating enzyme 6 OS=Arabidopsis thaliana OX=3702 GN=OTU6 PE=1 SV=2
A4507	-	-	GO:0016409(palmitoyltransferase activity)	K18932 ZDHHC; palmitoyltransferase [EC:2.3.1.225]	-	KOG1313 Hs14150106 DHHC-type Zn-finger proteins	XP_031026163.1 phenylalanine--tRNA ligase [Synchytrium microbalum]	Palmitoyltransferase ZDHHC16B OS=Danio rerio OX=7955 GN=zdhhc16b PE=3 SV=1
A4508	-	-	-	-	-	-	-	-
A4509	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	-	-
A4510	-	-	GO:0005515(protein binding)	-	-	-	PVG03971.1 hypothetical protein CPB86DRAFT_694417 [Serendipita vermifera 'subsp. besicii']	NCK-interacting protein with SH3 domain OS=Mus musculus OX=10090 GN=Nckipsd PE=1 SV=2

A4511	GO:0032968(positive regulation of transcription elongation from RNA polymerase II promoter),GO:0000077(DNA damage checkpoint signaling)	GO:0030896(checkpoint clamp complex)	-	K11292 SUPT6H, SPT6; transcription elongation factor SPT6	-	KOG1856 7290693 Transcription elongation factor SPT6	XP_003345971.1 uncharacterized protein SMAC_06525 [Sordaria macrospora k-hell]	Transcription elongation factor spt-6 OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=spt-6 PE=3 SV=1
A4512	-	GO:0016021(integral component of membrane)	-	-	-	KOG4561 At1g31300 Uncharacterized conserved protein, contains TBC domain	KNE64810.1 hypothetical protein AMAG_10148 [Allomyces macrogynus ATCC 38327]	TLC domain-containing protein 4-B OS=Danio rerio OX=7955 GN=tlcd4b PE=2 SV=1
A4513	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	-	-	-	-	-
A4514	GO:0007005(mitochondrion organization)	GO:0005739(mitochondrion)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K13525 VCP, CDC48; transitional endoplasmic reticulum ATPase	map05014 Amyotrophic lateral sclerosis;map04141 Protein processing in endoplasmic reticulum;map05134 Legionellosis;map05022 Pathways of neurodegeneration - multiple diseases	KOG0742 CE03405 AAA+ -type ATPase	EPS32861.1 hypothetical protein PDE_07822 [Penicillium oxalicum 114-2]	ATPase family AAA domain-containing protein 3 OS=Caenorhabditis elegans OX=6239 GN=atad-3 PE=1 SV=2
A4515	-	-	-	-	-	-	-	-
A4516	-	-	-	-	-	-	XP_027484374.1 uncharacterized protein MRET_2181 [Malassezia restricta]	-
A4517	GO:0009966(regulation of signal transduction)	-	-	K17606 IGBP1, TAP42; immunoglobulin-binding protein 1	map04140 Autophagy - animal;map04138 Autophagy - yeast;map04136 Autophagy - other	-	GES78101.1 TAP42-like protein [Rhizophagus clarus]	PP2A regulatory subunit TAP46 OS=Oryza sativa subsp. japonica OX=39947 GN=TAP46 PE=2 SV=1
A4518	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K12831 SF3B4, SAP49; splicing factor 3B subunit 4	map03040 Spliceosome	KOG0131 At2g18510 Splicing factor 3b, subunit 4	XP_016276572.1 splicing factor 3B subunit 4 [Rhodotorula toruloides NP11]	Splicing factor 3B subunit 4 OS=Homo sapiens OX=9606 GN=SF3B4 PE=1 SV=1

A4519	GO:0006750(glutathione biosynthetic process)	-	GO:0004357(glutamate-cysteine ligase activity),GO:0003824(catalytic activity)	K11204 GCLC; glutamate--cysteine ligase catalytic subunit [EC:6.3.2.2]	map04216 Ferroptosis;map04212 Longevity regulating pathway - worm;map01240 Biosynthesis of cofactors;map00480 Glutathione metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG3754[Hs4557625 Gamma-glutamylcysteine synthetase	ORY03394.1 GCS-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens OX=9606 GN=GCLC PE=1 SV=2
A4520	-	-	-	-	-	-	-	-
A4521	GO:0055085(transmembrane transport)	-	-	-	-	KOG0770[YM R166c Predicted mitochondrial carrier protein	KXS18084.1 mitochondria l carrier [Gonapodya prolifera JEL478]	Mitochondrial substrate carrier family protein E OS=Dictyostelium discoideum OX=44689 GN=mcfE PE=3 SV=1
A4522	-	-	-	-	-	-	-	-
A4523	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K06655 PHO85; negative regulator of the PHO system [EC:2.7.11.22]	map04138 Autophagy - yeast;map04111 Cell cycle - yeast	KOG0192[At3g22750 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF7683473.1 putative cell division protein kinase [Thelephania contejeani]	Serine/threonine-protein kinase PrkC OS=Bacillus subtilis (strain 168) OX=224308 GN=prkC PE=1 SV=1
A4524	-	-	-	-	-	-	RGB36972.1 hypothetical protein C1646_695975 [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	-
A4525	-	-	GO:0003824(catalytic activity)	K00953 FLAD1; FAD synthetase [EC:2.7.7.2]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00740 Riboflavin metabolism;map01100 Metabolic pathways	-	OLN86644.1 putative FAD synthase [Colletotrichum chlorophyti]	FAD synthase OS=Danio rerio OX=7955 GN=flad1 PE=2 SV=1
A4526	-	-	GO:0004518(nuclease activity)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	-	KAF9269671.1 PIN domain-like protein [Marasmius fiardii PR-910]	-

A4527	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K24512 VWA8; von Willebrand factor A domain-containing protein 8	-	KOG1808 CE20667 AAA ATPase containing von Willebrand factor type A (vWA) domain	KAF9969381.1 von Willebrand factor A domain-containing protein 8, partial [Actinomortierella ambigua]	von Willebrand factor A domain-containing protein 8 OS=Danio rerio OX=7955 GN=si:dkey-18l1.1 PE=3 SV=1
A4528	-	-	-	-	-	-	-	-
A4529	GO:0046314(phosphocreatine biosynthetic process)	-	GO:0016301(kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups),GO:0004111(creatine kinase activity),GO:0003824(catalytic activity)	-	-	KOG3581 Hs21536286 Creatine kinases	KAF9118610.1 hypothetical protein BGX30_004456 [Mortierella sp. GBA39]	Arginine kinase Oct f 2 OS=Amphioctopus fangsiao OX=515817 PE=1 SV=1
A4530	-	-	-	-	-	KOG0048 At3g09370 Transcription factor, Myb superfamily	ORE15519.1 hypothetical protein BCV71DRAFT_159810, partial [Rhizopus microsporus]	Transcription factor MYB3R-3 OS=Arabidopsis thaliana OX=3702 GN=MYB3R3 PE=1 SV=1
A4531	-	-	-	-	-	-	-	-
A4532	-	-	-	-	-	-	-	-
A4533	GO:0006431(methionyl-tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation)	-	GO:0004825(methionine-tRNA ligase activity),GO:0000049(tRNA binding),GO:0000166(nucleotide binding),GO:0005524(ATP binding),GO:0004812(aminoacyl-tRNA ligase activity)	K01874 MARS, metG; methionyl-tRNA synthetase [EC:6.1.1.10]	map00970 Aminoacyl-tRNA biosynthesis;map01100 Metabolic pathways;map00450 Selenocompound metabolism	KOG0436 At3g55400 Methionyl-tRNA synthetase	KAF9116186.1 hypothetical protein BGX30_006017 [Mortierella sp. GBA39]	Methionine--tRNA ligase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=metG PE=3 SV=1
A4534	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0051082(unfolded protein binding)	K03544 clpX, CLPX; ATP-dependent Clp protease ATP-binding subunit ClpX	map04112 Cell cycle - Caulobacter	KOG0745 At5g53350 Putative ATP-dependent Clp-type protease (AAA+ ATPase superfamily)	KAG1716911.1 hypothetical protein ID866_324 [Astraeus odoratus]	ATP-dependent Clp protease ATP-binding subunit ClpX OS=Acinetobacter baumannii (strain AB307-0294) OX=557600 GN=clpX PE=3 SV=1
A4535	-	-	GO:0005515(protein binding),GO:0003676(nucleic acid binding)	K22991 WDR45, WIP1, WIP3; WD repeat-containing protein 45	map04140 Autophagy - animal	KOG2111 At2g40810 Uncharacterized conserved protein, contains WD40 repeats	KAF9995989.1 WD repeat domain phosphoinositide-interacting protein 3 [Entomortierella chlamydospora]	Autophagy-related protein 18c OS=Arabidopsis thaliana OX=3702 GN=ATG18C PE=2 SV=1
A4536	GO:0006508(proteolysis)	-	GO:0008237(metallopeptidase activity),GO:0008270(zinc ion binding)	-	-	KOG1047 Hs4505029 Bifunctional leukotriene A4 hydrolase/aminopeptidase LTA4H	RKP36275.1 peptidase family M1-domain-containing protein [Dimargaris cristalligena]	Leukotriene A-4 hydrolase OS=Bos taurus OX=9913 GN=LTA4H PE=2 SV=3

A4537	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity)	-	-	-	OIR58834.1 uncharacterized protein A8A55_0389 [Amphiblyss sp. WSBS2006]	-
A4538	GO:0016043(cellular component organization),GO:0030036(activation of cytoskeleton organization)	GO:0071203(WASH complex)	GO:0003779(activation binding),GO:0031267(small GTPase binding)	-	-	KOG1922[Hs2060175 Rho GTPase effector BNI1 and related formins	CDR35942.1 RHTO0S01e1066g1_1 [Rhodotorula toruloides]	Disheveled-associated activator of morphogenesis 2 OS=Gallus gallus OX=9031 GN=DAAM2 PE=1 SV=2
A4539	-	-	-	-	-	KOG2933[At3g01450 Uncharacterized conserved protein	-	-
A4540	-	-	GO:0016491(oxidoreductase activity)	K00109 L2HGDH; 2-hydroxyglutarate dehydrogenase [EC:1.1.99.2]	map00650 Butanoate metabolism;map01100 Metabolic pathways	KOG2665[Hs13376331 Predicted FAD-dependent oxidoreductase	TPX75834.1 hypothetical protein CcCBS67573_g02906 [Chytridiomycota confervae]	Glycerol 3-phosphate dehydrogenase OS=Caloramator mitchellensis OX=908809 GN=IhgO_1 PE=1 SV=1
A4541	GO:0007034(vacuolar transport)	-	-	K12191 CHMP2A; charged multivesicular body protein 2A	map04144 Endocytosis;map04217 Necroptosis	KOG3230[CE21987 Vacuolar assembly/sorting protein DID4	RUP44117.1 Snf7-domain-containing protein, partial [Jimgerdmania flammicorona]	Charged multivesicular body protein 2b OS=Danio rerio OX=7955 GN=chmp2b PE=2 SV=1
A4542	-	-	-	-	-	-	-	-
A4543	-	-	-	-	-	-	RKO87137.1 hypothetical protein BDK51DRAFT_26657, partial [Blyttiomycetes helicus]	Translin-associated factor X-interacting protein 1 OS=Mus musculus OX=10090 GN=Tsnaxip1 PE=1 SV=2
A4544	-	-	GO:0016746(acyltransferase activity)	K09699 DBT, bkdB; 2-oxoisovalerate dehydrogenase E2 component (dihydrolipoyl transacylase) [EC:2.3.1.168]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map00640 Propanoate metabolism;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0558[CE01115 Dihydrolipoamide transacylase (alpha-keto acid dehydrogenase E2 subunit)	KAG0290332.1 hypothetical protein BGZ98_003501 [Dissophora globulifera]	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Caenorhabditis elegans OX=6239 GN=dbt-1 PE=2 SV=1

A4545	-	-	GO:0005515(protein binding)	K10415 DYNC11, DNCI; dynein cytoplasmic 1 intermediate chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG1587 Hs18552731 Cytoplasmic dynein intermediate chain	KAF9159511.1 hypothetical protein DFO26_006464 [Actinomortierella ambigua]	Dynein, cytoplasmic 1, intermediate chain 2a OS=Danio rerio OX=7955 GN=dync1i2a PE=3 SV=2
A4546	GO:0000413(protein peptidyl-prolyl isomerization),GO:0006457(protein folding)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K12737 SDCCAG10; peptidyl-prolyl cis-trans isomerase SDCCAG10 [EC:5.2.1.8]	-	KOG0885 CE19042 Peptidyl-prolyl cis-trans isomerase	KAG0269606.1 Peptidyl-prolyl isomerase cwc27, partial [Linnemannia exigua]	Spliceosome-associated protein CWC27 homolog OS=Danio rerio OX=7955 GN=cwc27 PE=2 SV=1
A4547	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	-	-	-
A4548	-	-	-	-	-	-	KXS11889.1 methylmalonyl-CoA epimerase [Gonapodya prolifera JEL478]	-
A4549	-	-	-	-	-	-	-	-
A4550	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4551	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	K16794 PAFAH1B1, LIS1; platelet-activating factor acetylhydrolase IB subunit alpha	map00565 Ether lipid metabolism;map01100 Metabolic pathways	KOG0308 Hs18874090 Conserved WD40 repeat-containing protein	TPX70972.1 hypothetical protein CcCBS67573_g06381 [Chytridiomycota confervae]	Nuclear distribution protein nudF OS=Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / IAM 13836 / NRRL 3357 / JCM 12722 / SRRCL167) OX=332952 GN=nudF PE=3 SV=2
A4552	-	-	-	-	-	-	-	Gametogenetin-binding protein 2 OS=Homo sapiens OX=9606
A4553	GO:0006508(proteolysis)	-	GO:0004181(metalloprotease activity),GO:0008270(zinc ion binding)	-	-	KOG3641 Hs7662452.3 Zinc carboxypeptidase	ORY85891.1 Zn-dependent exopeptidase [Neocallimastix californiae]	Cytosolic carboxypeptidase 1 OS=Xenopus laevis OX=8355 GN=agtpbp1 PE=2 SV=1
A4554	GO:0007165(signal transduction)	-	GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity),GO:0008081(phosphoric diester hydrolase activity)	K01120 cpdP; 3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]	map00230 Purine metabolism;map01100 Metabolic pathways	KOG3689 CE02038 Cyclic nucleotide phosphodiesterase	KXS11892.1 HD-domain/PDEase-like protein [Gonapodya prolifera JEL478]	Probable 3',5'-cyclic-AMP phosphodiesterase pde-4 OS=Caenorhabditis elegans OX=6239 GN=pde-4 PE=2 SV=2
A4555	-	-	GO:0003691(double-stranded telomeric DNA binding)	-	-	-	PWN51642.1 hypothetical protein IE53DRAFT_303215, partial [Violaceomyces palustris]	Single myb histone 5 OS=Zea mays OX=4577 GN=SMH5 PE=2 SV=1

A4556	GO:0006914 (autophagy)	-	-	K19730 ATG101; autophagy-related protein 101	map05014 Amyotrophic lateral sclerosis; map04140 Autophagy - animal; map04211 Longevity regulating pathway; map04136 Autophagy - other; map05022 Pathways of neurodegeneration - multiple diseases; map05010 Alzheimer disease; map05017 Spinocerebellar ataxia; map05016 Huntington disease	KOG4493 At5g66930 Uncharacterized conserved protein	CEJ89277.1 Putative DUF1649 domain protein [Torrubiella hemipterigena]	Autophagy-related protein 101 OS=Arabidopsis thaliana OX=3702 GN=ATG101 PE=1 SV=1
A4557	GO:0070588 (calcium ion transmembrane transport)	GO:0016020 (membrane)	GO:0005262 (calcium channel activity)	-	-	-	-	-
A4558	-	-	GO:0005509 (calcium ion binding)	-	-	-	-	-
A4559	-	-	-	K00326 CYB5R; cytochrome-b5 reductase [EC:1.6.2.2]	map00520 Amino sugar and nucleotide sugar metabolism	KOG0537 Hs13385594 Cytochrome b5	KAF9266278.1 cytochrome b5 [Marasmius fiardii PR-910]	Acyl-lipid (8-3)-desaturase B OS=Dictyostelium discoideum OX=44689 GN=fadB PE=1 SV=1
A4560	GO:0007059 (chromosome segregation), GO:0051301 (cell division)	-	GO:0008017 (microtubule binding)	-	-	-	-	-
A4561	-	GO:0005743 (mitochondrial inner membrane), GO:0005751 (mitochondrial respiratory chain complex IV)	-	-	-	-	-	-
A4562	-	-	-	-	-	-	-	-
A4563	-	-	GO:0005515 (protein binding)	K20523 SH3YL1; SH3 domain-containing YSC84-like protein 1	-	-	SAM01247.1 hypothetical protein [Absidia glauca]	LAS seventeen-binding protein 3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=LSB3 PE=3 SV=2
A4564	GO:0006468 (protein phosphorylation)	-	GO:0004672 (protein kinase activity), GO:0005524 (ATP binding)	K03114 SWE1; mitosis inhibitor protein kinase SWE1 [EC:2.7.11.1]	map04011 MAPK signaling pathway - yeast; map04113 Meiosis - yeast; map04111 Cell cycle - yeast	KOG0601 Hs4507917 Cyclin-dependent kinase WEE1	XP_001732508.1 hypothetical protein MGL_0283 [Malassezia globosa CBS 7966]	Wee1-like protein kinase OS=Oryza sativa subsp. japonica OX=39947 GN=WEE1 PE=3 SV=1
A4565	-	-	GO:0005509 (calcium ion binding)	K16466 CETN3, CDC31; centrin-3	-	KOG0027 At2g41100 Calmodulin and related proteins (EF-Hand superfamily)	XP_007416888.1 uncharacterized protein MELLADRAFT_40080 [Melampsora larici-populina 98AG31]	Calmodulin-like protein 12 OS=Arabidopsis thaliana OX=3702 GN=CML12 PE=1 SV=3

A4566	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K14787 MRD1, RBM19; multiple RNA-binding domain-containing protein 1	-	KOG0110 Hs7662250 RNA-binding protein (RRM superfamily)	KAF7722066.1 Multiple RNA-binding domain-containing protein 1 [Apophysomyces ossiformis]	Probable RNA-binding protein 19 OS=Homo sapiens OX=9606 GN=RBM19 PE=1 SV=3
A4567	-	-	GO:0005515(protein binding)	K15361 WDR48, UAF1; WD repeat-containing protein 48	map03460 Fanconi anemia pathway	KOG0284 Hs13129110 Polyadenylation factor I complex, subunit PFS2	PCH34582.1 hypothetical protein WOLCODRAFT_27311 [Wolffiporia cocos MD-104 SS10]	Methylosome protein WDR77 OS=Xenopus laevis OX=8355 GN=wdr77 PE=1 SV=1
A4568	GO:0006694(steroid biosynthetic process)	-	GO:0003854(3-beta-hydroxy-delta5-steroid dehydrogenase activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)	K07748 NSDHL, ERG26; sterol-4alpha-carboxylate 3-dehydrogenase (decarboxylating) [EC:1.1.1.170]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG1430 At1g47290 C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	XP_016612121.1 hypothetical protein SPPG_01524 [Spizellomyces punctatus DAOM BR117]	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Rattus norvegicus OX=10116 GN=Nsdhl PE=2 SV=1
A4569	GO:0015031(protein transport), GO:0036211(protein modification process)	-	-	K12183 TSG101, STP22, VPS23; ESCRT-I complex subunit TSG101	map04144 Endocytosis;map03250 Viral life cycle - HIV-1	KOG2391 At5g13860 Vacuolar sorting protein/ubiquitin receptor VPS23	KAG0030475.1 hypothetical protein BGZ82_007412 [Podila clonocystis]	Protein ELC-like OS=Arabidopsis thaliana OX=3702 GN=ELCL PE=1 SV=1
A4570	-	-	-	-	-	-	-	-
A4571	-	-	-	-	-	-	XP_034011214.1 uncharacterized protein DIURU_003995 [Ditina rugosa]	-
A4572	-	-	-	-	-	-	-	-
A4573	GO:0006637(acyl-CoA metabolic process)	-	GO:0047617(acyl-CoA hydrolase activity)	-	-	KOG3016 Hs4885565 Acyl-CoA thioesterase	KAF9284127.1 Acyl-CoA thioesterase 8 [Mortierella alpina]	Acyl-coenzyme A thioesterase 8 OS=Mus musculus OX=10090 GN=Acot8 PE=1 SV=1
A4574	-	-	GO:0005515(protein binding)	-	-	-	PKC17569.1 hypothetical protein RhiirA5_405751 [Rhizophagus irregularis]	-
A4575	-	-	-	-	-	-	-	-

A4576	-	-	-	K15015 SLC32A, VGAT; solute carrier family 32 (vesicular inhibitory amino acid transporter)	map04727 GABAergic synapse;map04721 Synaptic vesicle cycle;map04723 Retrograde endocannabinoid signaling;map05033 Nicotine addiction;map05032 Morphine addiction	KOG1303 At3g54830 Amino acid transporters	KAG0169415.1 hypothetical protein DFQ29_009692 [Apophysom yces sp. BC1021]	Amino acid transporter AVT1B OS=Arabidopsis thaliana OX=3702 GN=AVT1B PE=3 SV=2
A4577	-	-	GO:0009882(blue light photoreceptor activity),GO:0071949(FAD binding)	-	-	-	CCG84725.1 protein of unknown function [Taphrina deformans PYCC 5710]	-
A4578	GO:0006414(translational elongation)	GO:0005853(eukaryotic translation elongation factor 1 complex)	GO:0003746(translation elongation factor activity)	K03232 EEF1B; elongation factor 1-beta	-	KOG1668 CE00548 Elongation factor 1 beta/delta chain	KAG5362075.1 Elongation factor 1-beta [Yarrowia sp. C11]	Elongation factor 1-beta OS=Artemia salina OX=85549 PE=1 SV=3
A4579	-	-	-	-	-	-	-	-
A4580	GO:0006813(potassium ion transport),GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005249(voltage-gated potassium channel activity),GO:0005216(ion channel activity)	-	-	KOG0500 Hs4502917 Cyclic nucleotide-gated cation channel CNGA1-3 and related proteins	KNE71946.1 hypothetical protein AMAG_16369 [Allomyces macrogynus ATCC 38327]	Cyclic nucleotide-gated cation channel alpha-3 OS=Homo sapiens OX=9606 GN=CNGA3 PE=1 SV=2
A4581	GO:0006811(ion transport)	GO:0016021(integral component of membrane)	GO:0005216(ion channel activity),GO:0005515(protein binding)	-	-	KOG3676 Hs22062916 Ca2+-permeable cation channel OSM-9 and related channels (OTRPC family)	ORY31546.1 ankyrin [Rhizoclostium globosum]	Transient receptor potential cation channel subfamily V member 3 OS=Homo sapiens OX=9606 GN=TRPV3 PE=1 SV=2
A4582	GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	-	-	-	KAF9118221.1 hypothetical protein BGX30_004727 [Mortierella sp. GBA39]	-
A4583	-	-	-	-	-	-	-	-
A4584	GO:0030261(chromosome condensation)	-	-	-	-	KOG2359 At3g16730 Uncharacterized conserved protein	KXS20866.1 hypothetical protein M427DRAFT_151597 [Gonapodya prolifera JEL478]	Condensin-2 complex subunit H2 OS=Xenopus tropicalis OX=8364 GN=ncaph2 PE=2 SV=1
A4585	-	-	GO:0000287(magnesium ion binding),GO:0008897(holo-[acyl-carrier-protein] synthase activity)	K06133 LYS5, acpT; 4'-phosphopantetheinyl transferase [EC:2.7.8.-]	map00770 Pantothenate and CoA biosynthesis;map01100 Metabolic pathways	KOG0945 Hs20357568 Alpha-amino acid semialdehyde dehydrogenase-phosphopantetheinyl transferase	ORX85622.1 4'-phosphopantetheinyl transferase [Basidiobolus meristosporus CBS 931.73]	Phosphopantetheinyl transferase OS=Thraustochytrium sp. (strain ATCC 26185 / S-3) OX=672127 GN=PPTase PE=1 SV=1

A4586	GO:0006568(tryptophan metabolic process)	-	GO:0004834(tryptophan synthase activity)	K01694 TRP; tryptophan synthase [EC:4.2.1.20]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map01100 Metabolic pathways	KOG4175(YG L026c_1 Tryptophan synthase alpha chain	XP_006680001.1 uncharacterized protein BATDEDRAFT_35440 [Batrachochytrium dendrobatidis JAM81]	Tryptophan synthase OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=trp-3 PE=1 SV=1
A4587	GO:0009082(branch ed-chain amino acid biosynthetic process)	-	GO:1990610(acetolactate synthase regulator activity)	K01653 E2.2.1.6S, ilvH, ilvN; acetolactate synthase I/III small subunit [EC:2.2.1.6]	map00770 Pantothenate and CoA biosynthesis;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00650 Butanoate metabolism;map00660 C5-Branched dibasic acid metabolism;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	-	OUM57536.1 hypothetical protein PIROE2DRAFT_55204 [Piromyces sp. E2]	Probable acetolactate synthase small subunit OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC14C8.04 PE=1 SV=2
A4588	GO:0006164(purine nucleotide biosynthetic process)	-	GO:0003937(IMP cyclohydrolase activity);GO:0004643(phosphoribosylaminoimidazolecarboxamide formyltransferase activity);GO:0003824(catalytic activity)	K00602 purH; phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase [EC:2.1.2.3 3.5.4.10]	map00230 Purine metabolism;map00670 One carbon pool by folate;map01110 Biosynthesis of secondary metabolites;map01523 Antifolate resistance;map01100 Metabolic pathways	KOG2555(J730 1227 AICAR transformylase/IMP cyclohydrolase/methylglyoxal synthase	XP_016608871.1 phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Spizellomyces punctatus DAOM BR117]	Bifunctional purine biosynthesis protein ATIC OS=Gallus gallus OX=9031 GN=ATIC PE=1 SV=1
A4589	-	-	-	-	-	-	-	-
A4590	-	-	-	-	-	-	-	-
A4591	-	-	-	-	-	-	TPX63075.1 hypothetical protein SpCBS45565_g06902 [Spizellomyces sp. 'palustris']	Tiny macrocysts protein C OS=Dictyostelium discoideum OX=44689 GN=tmcC PE=2 SV=1
A4592	-	-	GO:0043169(cation binding)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0697(Hs4505995 Protein phosphatase 1B (formerly 2C)	ORY96350.1 phosphatase 2C-domain-containing protein [Syncephalaster racemosum]	Probable protein phosphatase 1N OS=Mus musculus OX=10090 GN=Ppm1n PE=2 SV=1

A4593	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4757782 Sulfatase	XP_019018673.1 hypothetical protein PICMEDRAFT_15488 [Pichia membranifaciens NRRL Y-2026]	N-acetylglactosamine-6-O-sulfatase OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / JCM 5827 / CCUG 10774 / NCTC 10582 / VPI-5482 / E50) OX=226186 GN=BT_3333 PE=1 SV=1
A4594	GO:0009067(aspartate family amino acid biosynthetic process), GO:0006520(cellular amino acid metabolic process)	-	GO:0004072(aspartate kinase activity),GO:0004412(homoserine dehydrogenase activity),GO:0016491(oxidoreductase activity)	-	-	KOG0455 At5g21060 Homoserine dehydrogenase	KUL85960.1 hypothetical protein ZTR_06477 [Talaromyces verruculosus]	Homoserine dehydrogenase OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=AN2882 PE=1 SV=1
A4595	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02984 RP-S3Ae, RPS3A; small subunit ribosomal protein S3Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1628 At4g34670 40S ribosomal protein S3A	GBC06733.1 hypothetical protein RclHR1_07000003 [Rhizophagus clarus]	Small ribosomal subunit protein eS1 OS=Nicotiana tabacum OX=4097 GN=cyc07 PE=1 SV=1
A4596	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0198 At1g54960 MEKK and related serine/threonine protein kinases	XP_008035984.1 kinase [Trametes versicolor FP-101664 SS1]	Mitogen-activated protein kinase kinase kinase 2 OS=Arabidopsis thaliana OX=3702 GN=ANP2 PE=2 SV=1
A4597	GO:0005975(carbohydrate metabolic process)	-	GO:0042132(fructose 1,6-bisphosphate 1-phosphatase activity),GO:0016791(phosphatase activity),GO:0042578(phosphoric ester hydrolase activity)	K03841 FBP, fbp; fructose-1,6-bisphosphatase I [EC:3.1.3.11]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map04910 Insulin signaling pathway;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00051 Fructose and mannose metabolism;map00680 Methane metabolism;map00710 Carbon fixation in photosynthetic organisms;map04152 AMPK signaling pathway;map00030 Pentose	KOG1458 At1g43670 Fructose-1,6-bisphosphatase	RIA89847.1 fructose-1,6-bisphosphatase class 1/Sedoheptulose-1,7-bisphosphatase [Glomus cerebriforme]	Fructose-1,6-bisphosphatase class 1 OS=Chlorobium phaeobacteroides (strain BS1) OX=331678 GN=fbp PE=3 SV=1
A4598	GO:0022904(respiratory electron transport chain)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0009055(electron transfer activity)	-	-	-	ORY50533.1 hypothetical protein BCR33DRAFT_846987 [Rhizoclostium globosum]	Probable superoxide oxidase CybB OS=Yersinia pestis OX=632 GN=cybB PE=3 SV=1
A4599	-	-	-	-	-	-	EWC46891.1 hypothetical protein DRE_03903 [Drechslerella stenobrocha 248]	-

A4600	GO:0042073(intracellular transport)	-	-	-	-	-	TPX64202.1 hypothetical protein SpCBS45565_g06063 [Spizellomyces sp. 'palustris']	Intraflagellar transport protein 46 homolog OS=Danio rerio OX=7955 GN=ift46 PE=2 SV=2
A4601	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors).GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG0137 Hs21361497 Very-long-chain acyl-CoA dehydrogenase	RKL20528.1 hypothetical protein BFJ72_g15033, partial [Fusarium proliferatum]	3-methylmercaptopropionyl-CoA dehydrogenase OS=Roseovarius nubinhibens (strain ATCC BAA-591 / DSM 15170 / ISM) OX=89187 GN=dmdC PE=1 SV=1
A4602	-	-	-	-	-	-	KNE66443.1 PAS domain S-box protein [Allomyces macrogynus ATCC 38327]	Tiny macrocysts protein B OS=Dictyostelium discoideum OX=44689 GN=tmcB PE=2 SV=1
A4603	-	-	-	K17987 NBR1; next to BRCA1 gene 1 protein	map04140 Autophagy - animal;map04137 Mitophagy - animal	KOG4351 Hs13236514_1 Uncharacterized conserved protein	KAF8272869.1 hypothetical protein EI94DRAFT_1716927 [Lactarius quietus]	Next to BRCA1 gene 1 protein OS=Pongo abelii OX=9601 GN=NBR1 PE=2 SV=1
A4604	-	-	-	-	-	-	-	-
A4605	-	-	-	-	-	-	-	-
A4606	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4607	-	GO:0016021(integral component of membrane)	GO:0008146(sulfotransferase activity)	-	-	-	-	-
A4608	-	GO:0016459(myosin complex)	GO:0003774(motor activity).GO:0005524(ATP binding).GO:0005515(protein binding)	K26404 CIAO3; cytosolic iron-sulfur assembly component 3	-	KOG2439 Hs11968051 Nuclear architecture related protein	XP_018293964.1 hypothetical protein PHYBLDRAFT_15794 [Phycomyces blakesleeanus NRRL 1555(-)]	Cytosolic iron-sulfur assembly component 3 OS=Rattus norvegicus OX=10116 GN=Ciao3 PE=2 SV=1
A4609	-	-	GO:0005515(protein binding)	K15082 RAD7; DNA repair protein RAD7	-	-	NP_587702.1 DNA repair protein [Schizosaccharomyces pombe]	DNA repair protein rhp7 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rhp7 PE=3 SV=1
A4610	-	-	-	-	-	-	-	-
A4611	-	-	-	-	-	-	-	-
A4612	-	-	-	-	-	-	-	-
A4613	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4614	-	-	-	-	-	-	-	-
A4615	-	-	GO:0005515(protein binding)	-	-	KOG1947 At3g07550 Leucine rich repeat proteins, some proteins contain F-box	KAF9357915.1 hypothetical protein BGX26_002853 [Mortierella sp. AD094]	-

A4616	-	-	GO:0016491(oxidoreductase activity),GO:0004029(aldehyde dehydrogenase (NAD+) activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	-	-	KOG2451 At5g62530 Aldehyde dehydrogenase	CAF9926524.1 hypothetical protein HETSPECPRD_006356 [Heterodermis speciosa]	Delta-1-pyrroline-5-carboxylate dehydrogenase 12A1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=ALDH12A1 PE=1 SV=1
A4617	-	-	-	-	-	-	XP_01815132.1.1 Membrane protein [Colletotrichum higginsianum IMI 349063]	-
A4618	-	-	GO:0008137(NADH dehydrogenase (ubiquinone) activity),GO:0048038(quinone binding),GO:0051539(4 iron, 4 sulfur cluster binding),GO:0051536(iron-sulfur cluster binding)	K03940 NDUF57; NADH dehydrogenase (ubiquinone) Fe-S protein 7 [EC:7.1.1.2]	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG1687 Hs14149625 NADH-ubiquinone oxidoreductase, NUF57/PSST/20 kDa subunit	XP_01324642.2.1 NADH-quinone oxidoreductase [Tilletiaria anomala UBC 951]	NADH-ubiquinone oxidoreductase 20 kDa subunit OS=Reclinomonas americana OX=48483 GN=NAD10 PE=3 SV=1
A4619	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0029 7293681 Amine oxidase	KAF8245914.1 hypothetical protein K440DRAFT_586403 [Wilcoxina mikolae CBS 423.85]	Lysine-specific histone demethylase 1A OS=Homo sapiens OX=9606 GN=KDM1A PE=1 SV=2
A4620	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4621	-	-	GO:0000334(3-hydroxyanthranilate 3,4-dioxygenase activity),GO:0005506(iron ion binding)	K00452 HAAO; 3-hydroxyanthranilate 3,4-dioxygenase [EC:1.13.11.6]	map01240 Biosynthesis of cofactors;map00380 Tryptophan metabolism;map01100 Metabolic pathways	KOG3995 Hs6912406 3-hydroxyanthranilate dioxygenase HAAO	KAF9288214.1 3-hydroxyanthranilic acid dioxygenase [Mortierella alpina]	3-hydroxyanthranilate 3,4-dioxygenase OS=Bos taurus OX=9913 GN=HAAO PE=1 SV=1
A4622	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1235 At1g79600 Predicted unusual protein kinase	KAG0165063.1 hypothetical protein DFQ30_009018 [Apophysomycetes sp. BC1015]	Probable protein kinase UbiB OS=Ralstonia nicotianae (strain GMI1000) OX=267608 GN=ubiB PE=3 SV=1

A4623	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1235 At1g79600 Predicted unusual protein kinase	KAG0165063.1 hypothetical protein DFQ30_009018 [Apophysomyces sp. BC1015]	Probable protein kinase UbiB OS=Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) OX=243365 GN=ubiB PE=3 SV=1
A4624	-	-	-	-	-	-	-	-
A4625	-	-	-	-	-	-	-	-
A4626	-	-	GO:0005509(calcium ion binding)	-	-	KOG0027 At5g17470 Calmodulin and related proteins (EF-Hand superfamily)	RUS19205.1 the N-terminal domain of Centrin 2 [Endogone sp. FLAS-F59071]	Probable calcium-binding protein CML32 OS=Arabidopsis thaliana OX=3702 GN=CML32 PE=2 SV=1
A4627	-	-	-	K17508 PTC7, PPTC7; protein phosphatase PTC7 [EC:3.1.3.16]	-	KOG1379 At4g16580 Serine/threonine protein phosphatase	ORZ38074.1 phosphatase 2C-like domain-containing protein [Catenaria anguillulae PL171]	Probable protein phosphatase 2C 71 OS=Oryza sativa subsp. japonica OX=39947 GN=Os10g0370000 PE=2 SV=1
A4628	GO:0006388(tRNA splicing, via endonucleolytic cleavage and ligation)	-	GO:0003972(RNA ligase (ATP) activity)	-	-	-	-	-
A4629	GO:0006508(proteolysis)	-	GO:0004181(metalloprotease activity),GO:0008270(zinc ion binding)	K08637 CPA4; carboxypeptidase A4 [EC:3.4.17.-]	-	KOG2650 7295242 Zinc carboxypeptidase	KAF9018994.1 hypothetical protein BGZ52_003805 [Haplosporangium bisporale]	Carboxypeptidase O OS=Homo sapiens OX=9606 GN=CPO PE=1 SV=1
A4630	-	-	-	-	-	-	-	-
A4631	-	-	-	K15523 FN3KRP; protein-ribulosamine 3-kinase [EC:2.7.1.172]	-	KOG3021 At3g61080 Predicted kinase	XP_007877925.1 hypothetical protein PFL1_02221 [Anthracocystis flocculosa PF-1]	Protein-ribulosamine 3-kinase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=At3g61080 PE=1 SV=2
A4632	-	-	-	-	-	-	-	-
A4633	GO:0006413(translational initiation)	-	GO:0003743(translation initiation factor activity)	K03238 EIF2S2; translation initiation factor 2 subunit 2	-	KOG2768 At5g20920 Translation initiation factor 2, beta subunit (eIF-2beta)	TPX60115.1 hypothetical protein PhCBS80983_g01978 [Powellomyces hirtus]	Eukaryotic translation initiation factor 2 subunit beta OS=Triticum aestivum OX=4565 PE=1 SV=1
A4634	-	-	GO:0005525(GTP binding)	K16186 RRAGC_D; Ras-related GTP-binding protein C/D	map04140 Autophagy - animal;map05131 Shigellosis;map04150 mTOR signaling pathway	KOG3887 Hs11995472 Predicted small GTPase involved in nuclear protein import	XP_016608858.1 hypothetical protein SPPG_03925 [Spizellomyces punctatus DAOM BR117]	Ras-related GTP-binding protein C OS=Mus musculus OX=10090 GN=RRagc PE=1 SV=1
A4635	-	-	-	K14997 SLC38A11; solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 11	-	KOG3832 CE05193 Predicted amino acid transporter	-	Transmembrane protein 104 homolog OS=Caenorhabditis elegans OX=6239 GN=C03A3.2 PE=1 SV=2
A4636	-	-	-	-	-	-	-	-

A4637	GO:003420(ion transmembrane transport),GO:0006811(ion transport)	GO:0016021(integral component of membrane)	GO:0004888(transmembrane signaling receptor activity),GO:0005216(ion channel activity),GO:0005230(extracellular ligand-gated ion channel activity)	-	-	-	-	-
A4638	-	-	GO:0005515(protein binding),GO:0004842(ubiquitin-protein transferase activity)	-	-	KOG0940[HsM14719404 Ubiquitin protein ligase RSP5/NEDD4	KTB39831.1 hypothetical protein WG66_7532 [Moniliophthora roreri]	Probable E3 ubiquitin-protein ligase hula OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) OX=341663 GN=hula PE=3 SV=1
A4639	-	-	GO:0016407(acetyltransferase activity),GO:0008080(N-acetyltransferase activity)	K25762 NAT9; tubulin N-terminal N-acetyltransferase [EC:2.3.1.308]	-	KOG4135[Hs7661604 Predicted phosphoglucoamine acetyltransferase	GBB92804.1 hypothetical protein RclHR1_02060007 [Rhizophagus clarus]	GCN5-related N-acetyltransferase 9 OS=Arabidopsis thaliana OX=3702 GN=GNAT9 PE=1 SV=1
A4640	-	-	-	-	-	-	RIB23694.1 hypothetical protein C2G38_1959034 [Gigaspora rosea]	Uncharacterized protein C594.04c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC594.04c PE=3 SV=2
A4641	-	-	-	-	-	-	RIB23694.1 hypothetical protein C2G38_1959034 [Gigaspora rosea]	-
A4642	-	-	-	-	-	-	-	-
A4643	GO:0055085(transmembrane transport)	-	-	K15100 SLC25A1, CTP; solute carrier family 25 (mitochondrial citrate transporter), member 1	-	KOG0756[Hs21389315 Mitochondrial tricarboxylate/dicarboxylate carrier proteins	GBB94447.1 hypothetical protein RclHR1_02360005 [Rhizophagus clarus]	Tricarboxylate transport protein, mitochondrial OS=Rattus norvegicus OX=10116 GN=Slc25a1 PE=1 SV=1
A4644	-	-	-	-	-	-	-	-
A4645	GO:0098789(pre-mRNA cleavage required for polyadenylation)	-	GO:0003723(RNA binding),GO:0046872(metal ion binding),GO:0003676(nucleic acid binding)	-	-	KOG1040[At1g30460.1 Polyadenylation factor I complex, subunit, Yth1 (CPSF subunit)	QIE48484.1 hypothetical protein [Lenzites gibbosa]	30-kDa cleavage and polyadenylation specificity factor 30 OS=Arabidopsis thaliana OX=3702 GN=CPSF30 PE=1 SV=1
A4646	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239[At5g65930.2 Kinesin (KAR3 subfamily)	KAG0263431.1 kinesin-like nuclear fusion protein [Actinomotie rella ambigua]	Kinesin-like protein KIN-14I OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14I PE=2 SV=1
A4647	-	-	-	-	-	-	-	-

A4648	-	-	-	K13174 THOC5; THO complex subunit 5	map03013 Nucleocytoplas mic transport	KOG2216 At5 g42920 Conserved coiled/coiled coil protein	XP_01661224 1.1 hypothetical protein SPPG_01635 [Spizellomyces punctatus DAOM BR117]	THO complex subunit 5 homolog OS=Danio rerio OX=7955 GN=thoc5 PE=2 SV=1
A4649	-	-	GO:0016491(oxi doreductase activity),GO:001 6620(oxidoredu ctase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	-	-	KOG2454 At3 g66658 Betaine aldehyde dehydrogena se	RKO93033.1 Aldehyde/hist idinol dehydrogena se [Blyttomyces helicus]	Aldehyde dehydrogenase 22A1 OS=Arabidopsis thaliana OX=3702 GN=ALDH22A1 PE=2 SV=2
A4650	GO:00071 86(G protein- coupled receptor signaling pathway)	GO:00160 21(integra l compone nt of membran e)	GO:0004930(G protein-coupled receptor activity)	-	-	KOG3656 Hs1 3435405 FOG: 7 transmembra ne receptor	-	Histamine H2 receptor OS=Gorilla gorilla gorilla OX=9595 GN=HRH2 PE=3 SV=1
A4651	-	-	-	-	-	-	-	-
A4652	-	-	-	-	-	-	-	-
A4653	GO:00072 64(small GTPase mediated signal transducti on)	-	GO:0003924(GT Pase activity),GO:000 5525(GTP binding)	K04392 RAC1; Ras- related C3 botulinum toxin substrate 1	map04360 Axon guidance;map04 361 Axon regeneration;ma p05014 Amyotrophic lateral sclerosis;map040 24 cAMP signaling pathway;map05 415 Diabetic cardiomyopathy; map05417 Lipid and atherosclerosis; map05416 Viral myocarditis;map 04145 Phagosome;map 05135 Yersinia infection;map05 132 Salmonella infection;map05 130 Pathogenic Escherichia coli infection;map05 131 Shigellosis;map0 4810 Regulation	KOG0393 Hs9 845511 Ras- related small GTPase, Rho type	GJH87111.1 hypothetical protein NliqN6_3513 [Naganishia liquefaciens]	Ras-related C3 botulinum toxin substrate 1 OS=Bos taurus OX=9913 GN=RAC1 PE=1 SV=1
A4654	-	-	-	-	-	-	-	-
A4655	-	-	-	-	-	-	ORY06624.1 Aldo/keto reductase [Basidiobolus meristosporus CBS 931.73]	-
A4656	-	-	GO:0008374(O- acyltransferase activity),GO:001 6746(acyltransfe rase activity)	-	-	KOG4666 729 1068_2 Predicted phosphate acyltransferas e, contains PlsC domain	KNE86455.1 hypothetical protein PSTG_20184, partial [Puccinia striiformis f. sp. tritici PST- 78]	Lysophosphatidylcholine acyltransferase OS=Drosophila melanogaster OX=7227 GN=LPCAT PE=2 SV=1
A4657	-	-	GO:0005515(pro tein binding)	-	-	KOG2003 Hs5 729800 TPR repeat- containing protein	ORY40383.1 TPR-like protein [Rhizoclosma tium globosum]	Intraflagellar transport protein 88 homolog OS=Mus musculus OX=10090 GN=Ift88 PE=1 SV=2
A4658	-	-	GO:0005515(pro tein binding)	-	-	-	-	-

A4659	GO:0006886 (intracellular protein transport) GO:0007033 (vacuole organization)	GO:0005737 (cytoplasm)	-	K20180 VPS16; vacuolar protein sorting-associated protein 16	map04140 Autophagy - animal; map05132 Salmonella infection; map04138 Autophagy - yeast	KOG2280 Hs17978483 Vacuolar assembly/sorting protein VPS16	RPB25843.1 vacuolar protein sorting-associated protein 16 [Terfezia boudieri ATCC MYA-4762]	Vacuolar protein sorting-associated protein 16 homolog OS=Bos taurus OX=9913 GN=VPS16 PE=2 SV=1
A4660	GO:0000184 (nuclear-transcribed mRNA catabolic process, nonsense-mediated decay), GO:0000290 (deadenylation-dependent decapping of nuclear-transcribed mRNA)	-	GO:0003723 (RNA binding), GO:0016787 (hydrolase activity), GO:0030145 (manganese ion binding), GO:0050072 (m7G(5')pppN diphosphatase activity)	K12613 DCP2; mRNA-decapping enzyme subunit 2 [EC:3.6.1.62]	map03018 RNA degradation	-	K1194386.1 hypothetical protein PLICRDRAFT_99875 [Plicaturopsis crispa FD-325 SS-3]	mRNA decapping complex subunit 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=dcp2 PE=1 SV=1
A4661	GO:0006629 (lipid metabolic process)	-	GO:0016491 (oxidoreductase activity)	-	-	KOG4232 Hs13375616 Delta 6-fatty acid desaturase/delta-8 sphingolipid desaturase	KAF9921944.1 sphingolipid delta-4 desaturase [Linnemannia zychae]	Acyl-lipid (7-3)-desaturase OS=Thraustochytrium sp. OX=145168 GN=Fad4 PE=1 SV=1
A4662	GO:0006468 (protein phosphorylation)	-	GO:0005524 (ATP binding), GO:0004672 (protein kinase activity)	K12761 SNF1; carbon catabolite-derepressing protein kinase [EC:2.7.11.1]	map04138 Autophagy - yeast; map04113 Meiosis - yeast	KOG0586 Hs8923922 Serine/threonine protein kinase	XP_006680638.1 uncharacterized protein BATDEDRAFT_13136, partial [Batrachochytrium dendrobatidis JAM81]	Serine/threonine-protein kinase MARK1 OS=Rattus norvegicus OX=10116 GN=Mark1 PE=1 SV=1
A4663	-	-	GO:0005515 (protein binding)	-	-	KOG0504 Hs18254462 FOG: Ankyrin repeat	KAF4948057.1 hypothetical protein FGADL_9922 [Fusarium gaditjirri]	Ankyrin repeat and SOCS box protein 16 OS=Homo sapiens OX=9606 GN=ASB16 PE=1 SV=2
A4664	GO:0006335 (DNA replication-dependent nucleosome assembly)	-	GO:0005515 (protein binding)	K10751 CHAF1B; chromatin assembly factor 1 subunit B	-	KOG1009 Hs4885105 Chromatin assembly complex 1 subunit B/CAC2 (contains WD40 repeats)	PWW73050.1 WD40 repeat-like protein [Tuber magnatum]	Chromatin assembly factor 1 subunit B OS=Mus musculus OX=10090 GN=Chaf1b PE=1 SV=1
A4665	-	-	GO:0005515 (protein binding)	K14963 WDR5, SWD3, CPS30; COMPASS component SWD3	map03083 Polycomb repressive complex; map04934 Cushing syndrome	KOG0266 CE06574 WD40 repeat-containing protein	KAF7790245.1 hypothetical protein EIP86_001197 [Pleurotus ostreatoroseus]	WD repeat-containing protein wdr-5.3 OS=Caenorhabditis elegans OX=6239 GN=wdr-5.3 PE=3 SV=1
A4666	-	-	GO:0005515 (protein binding)	-	-	KOG0266 CE11748 WD40 repeat-containing protein	EXX79030.1 Cop1p [Rhizophagus irregularis DAOM 197198w]	WD repeat-containing protein wdr-5.2 OS=Caenorhabditis elegans OX=6239 GN=wdr-5.2 PE=4 SV=1

A4667	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K06641 CHEK2; serine/threonine-protein kinase CHEK2 [EC:2.7.11.1]	map04218 Cellular senescence;map04115 p53 signaling pathway;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG0597 At1g50230 Serine-threonine protein kinase FUSED	KAF9153351.1 hypothetical protein DFQ26_000595, partial [Actinomortierella ambigua]	Mitogen-activated protein kinase kinase kinase 6 OS=Homo sapiens OX=9606 GN=MAP3K6 PE=1 SV=3
A4668	-	-	-	-	-	KOG1551 At3g12150 Uncharacterized conserved protein	-	-
A4669	-	-	-	-	-	KOG4621 At5g05930 Uncharacterized conserved protein	KAG0321360.1 guanylyl cyclase domain-containing protein 1 [Podila horticola]	Guanylyl cyclase 1 OS=Arabidopsis thaliana OX=3702 GN=GC1 PE=1 SV=1
A4670	-	GO:0000178(exosome (RNase complex))	GO:0003723(RNA binding)	K03681 RRP40, EXOSC3; exosome complex component RRP40	map03018 RNA degradation	-	ORX90869.1 hypothetical protein K493DRAFT_317681 [Basidiobolus meristosporus CBS 931.73]	Putative exosome complex component rrp40 OS=Dictyostelium discoideum OX=44689 GN=exosc3 PE=3 SV=1
A4671	-	-	-	K01078 PHO; acid phosphatase [EC:3.1.3.2]	map00730 Thiamine metabolism;map00740 Riboflavin metabolism;map01100 Metabolic pathways	KOG3720 HsM7705955 Lysosomal & prostatic acid phosphatases	KAG1565034.1 hypothetical protein G6F50_010453 [Rhizopus delemar]	Lysophosphatidic acid phosphatase type 6 OS=Pongo abelii OX=9601 GN=ACP6 PE=2 SV=1
A4672	-	-	-	-	-	-	KAF7721905.1 hypothetical protein EC973_003944 [Apophysomyces ossiformis]	Uncharacterized protein C6G9.01c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC6G9.01c PE=4 SV=2
A4673	-	-	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	-	-	-	-	-
A4674	GO:0006260(DNA replication),GO:0006281(DNA repair)	GO:0005663(DNA replication factor C complex)	GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0003689(DNA clamp loader activity)	K10754 RFC1; replication factor C subunit 1	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03430 Mismatch repair	KOG1968 Hs15011931 Replication factor C, subunit RFC1 (large subunit)	XP_016606495.1 hypothetical protein SPPG_09353 [Spizellomyces punctatus DAOM BR117]	Replication factor C subunit 1 OS=Homo sapiens OX=9606 GN=RFC1 PE=1 SV=4

A4675	-	-	GO:0008017(microtubule binding)	-	-	KOG3809[Hs20070262 Microtubule-binding protein MIP-T3	XP_006679588.1 uncharacterized protein BATDEDRAFT_35344 [Batrachochytrium dendrobatidis JAM81]	TRAF3-interacting protein 1 OS=Mus musculus OX=10090 GN=Traf3ip1 PE=1 SV=2
A4676	-	-	-	-	-	-	-	-
A4677	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003723(RNA binding),GO:0003735(structural constituent of ribosome)	K02988 RP-S5, MRPS5, rpsE; small subunit ribosomal protein S5	map03010 Ribosome	KOG2646[Hs13994259 Ribosomal protein S5	ORY51981.1 ribosomal protein S5 domain 2-like protein [Rhizoclostium globosum]	Small ribosomal subunit protein uS5 OS=Vibrio campbellii (strain ATCC BAA-1116) OX=2902295 GN=rpsE PE=3 SV=1
A4678	-	-	-	-	-	-	-	-
A4679	-	-	GO:0005525(GTP binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K19788 OLA1; obg-like ATPase 1	-	KOG1491[CE14708 Predicted GTP-binding protein (ODN superfamily)	KNE65005.1 GTP-binding protein YchF [Allomyces macrogynus ATCC 38327]	Obg-like ATPase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=YCHF1 PE=1 SV=1
A4680	GO:0008654(phospholipid biosynthetic process)	GO:0016020(membrane)	GO:0005515(protein binding),GO:0016780(phosphotransferase activity, for other substituted phosphate groups)	-	-	KOG1408[Hs2057360 WD40 repeat protein	GBB90231.1 hypothetical protein RclHR1_01710031 [Rhizophagus clarus]	WD repeat-containing protein 62 OS=Sus scrofa OX=9823 GN=WDR62 PE=3 SV=1
A4681	-	-	-	-	-	-	-	-
A4682	-	-	-	-	-	-	-	-
A4683	-	-	-	-	-	-	-	-
A4684	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K08711 PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065[At2g29940 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	ORX91233.1 hypothetical protein K493DRAFT_330676 [Basidiobolus meristosporus CBS 931.73]	ABC transporter G family member 36 OS=Oryza sativa subsp. japonica OX=39947 GN=ABCG36 PE=2 SV=1
A4685	-	-	GO:0005509(calcium ion binding),GO:0005515(protein binding)	K16466 CETN3, CDC31; centrin-3	-	KOG0032[7299682 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	XP_016609864.1 hypothetical protein SPPG_03615 [Spizellomyces punctatus DAOM BR117]	Crustacean calcium-binding protein 23 OS=Faxonius limosus OX=28379 PE=1 SV=1
A4686	-	-	GO:0005515(protein binding)	K26797 GORASP, GRASP65_55; golgi reassembly-stacking protein	map04140 Autophagy - animal	KOG3834[CE25278 Golgi reassembly-stacking protein GRASP65, contains PDZ domain	KAF9410689.1 Golgi reassembly-stacking protein 2 [Podila epigama]	Golgi reassembly-stacking protein 2 OS=Mus musculus OX=10090 GN=Gorasp2 PE=1 SV=3
A4687	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4689	-	-	-	-	-	-	PVU87440.1 hypothetical protein BB561_006329, partial [Smittium simulii]	-
A4690	-	-	GO:0005515(protein binding)	-	-	-	-	-

A4691	GO:0006508(proteolysis)	-	GO:0004185(serine-type carboxypeptidase activity)	K13289 CTSA, CPY; cathepsin A (carboxypeptidase C) [EC:3.4.16.5]	map04142 Lysosome;map04614 Renin-angiotensin system	KOG1282 Hs4505989 Serine carboxypeptidases (lysosomal cathepsin A)	XP_002555727.1 KLTH0G15950p [Lachancea thermotolerans CBS 6340]	Lysosomal protective protein OS=Mus musculus OX=10090 GN=Ctsa PE=1 SV=1
A4692	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	-	-
A4693	GO:0006629(lipid metabolic process)	-	GO:0008374(O-acyltransferase activity)	K00679 E2.3.1.158; phospholipid:diacylglycerol acyltransferase [EC:2.3.1.158]	map00561 Glycerolipid metabolism;map01100 Metabolic pathways	KOG2369 At1g04010 Lecithin:cholesterol acyltransferase (LCAT)/Acyl-ceramide synthase	KXS21833.1 hypothetical protein M427DRAFT_151099 [Gonapodya prolifera JEL478]	Phospholipid--sterol O-acyltransferase OS=Arabidopsis thaliana OX=3702 GN=PSAT PE=2 SV=2
A4694	-	-	-	-	-	-	KXS21750.1 hypothetical protein M427DRAFT_107149 [Gonapodya prolifera JEL478]	Dynein-1-alpha heavy chain, flagellar inner arm I1 complex OS=Chlamydomonas reinhardtii OX=3055 GN=DHC1 PE=1 SV=1
A4695	-	-	-	-	-	-	-	-
A4696	GO:0006355(regulation of transcription, DNA-templated),GO:0007165(signal transduction)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A4698	-	-	GO:0005515(protein binding)	K13124 MORF1; mitogen-activated protein kinase organizer 1	-	KOG0316 CE27149 Conserved WD40 repeat-containing protein	XP_037158714.1 uncharacterized protein HO173_012537 [Letharia columbiana]	WD repeat domain-containing protein 83 OS=Rattus norvegicus OX=10116 GN=Wdr83 PE=1 SV=1
A4699	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11251 H2A; histone H2A	map04217 Necroptosis;map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map03082 ATP-dependent chromatin remodeling	KOG1756 CE04501A Histone 2A	RUO96772.1 histone-fold-containing protein [Jimgerdennia flammicorona]	Histone H2A-III OS=Volvox carteri OX=3067 PE=3 SV=1

A4700	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11252 H2B; histone H2B	map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG1744 YBL002w Histone H2B	ORE18420.1 histone H2b, partial [Rhizopus microsporus]	Histone H2B OS=Olisthodiscus luteus OX=83000 PE=1 SV=2
A4701	-	-	GO:0005515(protein binding)	-	-	-	KAF3942002.1 hypothetical protein ABW19_dt02_03625 [Dactylella cylindrospora]	-
A4702	-	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups),GO:0016746(acyltransferase activity)	-	-	KOG1390 Hs14755394 Acetyl-CoA acetyltransferase	KAG0190236.1 hypothetical protein DFQ28_002370 [Apophysomyces sp. BC1034]	Acetyl-CoA acetyltransferase OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) OX=572477 GN=phaA PE=3 SV=2
A4703	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07901 RAB8A, MEL; Ras-related protein Rab-8A	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map04140 Autophagy - animal;map04972 Pancreatic secretion;map04530 Tight junction;map05022 Pathways of neurodegeneration - multiple diseases;map04152 AMPK signaling pathway	KOG0078 At5g03520 GTP-binding protein SEC4, small G protein superfamily, and related Ras family GTP-binding proteins	KAG0230693.1 GTP-binding protein [Actinomotirella wolffii]	Ras-related protein RAB1BV OS=Beta vulgaris OX=161934 GN=RAB1BV PE=2 SV=1
A4704	-	-	-	-	-	-	-	-
A4705	GO:0006139(nucleobase-containing compound metabolic process), GO:0006207('de novo' pyrimidine nucleobase biosynthetic process), GO:0006221(pyrimidine nucleotide biosynthetic process)	-	GO:0005524(ATP binding),GO:0019205(nucleobase-containing compound kinase activity),GO:0004127(cytidylate kinase activity),GO:0009041(uridylate kinase activity)	K13800 CMPK1, UMPK; UMP-CMP kinase [EC:2.7.4.14]	map00983 Drug metabolism - other enzymes;map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3079 Hs7706497 Uridylate kinase/adenylylate kinase	XP_016605769.1 UMP-CMP kinase, partial [Spizellomyces punctatus DAOM BR117]	UMP-CMP kinase OS=Bos taurus OX=9913 GN=CMPK1 PE=2 SV=2

A4706	GO:0006508(proteolysis)	-	GO:0070006(metalloaminopeptidase activity)	K01265 map; methionyl aminopeptidase [EC:3.4.11.18]	-	KOG2738 At1g13270 Putative methionine aminopeptidase	KAG2231778.1 hypothetical protein INT48_004057 [Thamnidium elegans]	Methionine aminopeptidase 1B, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=MAP1B PE=2 SV=2
A4707	GO:0006281(DNA repair)	-	GO:0003684(damaged DNA binding)	K03509 POLH; DNA polymerase eta [EC:2.7.7.7]	map01524 Platinum drug resistance;map03460 Fanconi anemia pathway	KOG2095 At5g44740 DNA polymerase iota/DNA damage inducible protein	XP_016604783.1 hypothetical protein SPPG_07951 [Spizellomyces punctatus DAOM BR117]	DNA polymerase eta OS=Arabidopsis thaliana OX=3702 GN=POLH PE=1 SV=1
A4708	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At1g08720 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	RIA90537.1 kinase-like domain-containing protein [Glomus cerebiforme]	Proto-oncogene serine/threonine-protein kinase mos OS=Sus scrofa OX=9823 GN=MOS PE=2 SV=1
A4709	-	-	-	K18802 DUG3; glutamine amidotransferase	-	KOG1268 YNL191w Glucosamine 6-phosphate synthetases, contain amidotransferase and phosphosugar isomerase domains	KAG2185743.1 hypothetical protein INT43_002178 [Umbelopsis isabellina]	Probable glutamine amidotransferase DUG3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DUG3 PE=1 SV=1
A4710	-	-	GO:0018580(nitrate monooxygenase activity)	-	-	-	ORY45234.1 2-nitropropane dioxygenase [Rhizoclostium globosum]	(3aS,4S,5R,7aS)-5-hydroxy-7a-methyl-1-oxo-octahydro-1H-indene-4-carboxyl-CoA dehydrogenase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=ipdC PE=3 SV=1
A4711	-	-	GO:0018580(nitrate monooxygenase activity)	-	-	-	ORY45234.1 2-nitropropane dioxygenase [Rhizoclostium globosum]	(3aS,4S,5R,7aS)-5-hydroxy-7a-methyl-1-oxo-octahydro-1H-indene-4-carboxyl-CoA dehydrogenase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=ipdC PE=3 SV=1
A4712	-	-	-	-	-	KOG1014 At3g50560 17 beta-hydroxysteroid dehydrogenase type 3, HSD17B3	RKP28209.1 short-chain dehydrogenase/reductase SDR [Syncephalis pseudoplumigaleata]	3-oxoacyl-[acyl-carrier-protein] reductase OS=Mus musculus OX=10090 GN=Cbr4 PE=1 SV=2
A4713	GO:0006886(intracellular protein transport)	GO:0005741(mitochondrial outer membrane)	-	-	-	-	-	-

A4714	-	-	GO:0003860(3-hydroxyisobutyryl-CoA hydrolase activity)	K05605 HIBCH; 3-hydroxyisobutyryl-CoA hydrolase [EC:3.1.2.4]	map00410 beta-Alanine metabolism;map01200 Carbon metabolism;map00640 Propanoate metabolism;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG1684 CE00689 Enoyl-CoA hydratase	KAG0302655.1 hypothetical protein BGZ98_007329 [Dissophora globulifera]	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Danio rerio OX=7955 GN=hibch PE=2 SV=1
A4715	-	-	-	-	-	-	-	-
A4716	-	-	-	-	-	-	-	-
A4717	GO:0006526(arginine biosynthetic process)	GO:0005737(cytoplasm)	GO:0004042(acyl-CoA: L-glutamate N-acyltransferase activity);GO:0016407(acyltransferase activity)	-	-	KOG2436 At2g22910 Acetylglutamate kinase/acylglutamate synthase	KAG0162389.1 hypothetical protein DFQ30_002134 [Apophysomyces sp. BC1015]	Amino-acid acetyltransferase OS=Pseudomonas fluorescens (strain SBW25) OX=216595 GN=argA PE=3 SV=1
A4718	GO:0006396(RNA processing);GO:0000398(mRNA splicing, via spliceosome)	-	GO:0005515(protein binding)	K12869 CRN, CRNKL1, CLF1, SYF3; crooked neck	map03040 Spliceosome	KOG1915 Hs11072091 Cell cycle control protein (crooked neck)	KZL81816.1 pre-mrna-splicing factor clf1 [Colletotrichum incanum]	Crooked neck-like protein 1 OS=Homo sapiens OX=9606 GN=CRNKL1 PE=1 SV=4
A4719	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0140359(ABC-type transporter activity);GO:0005524(ATP binding)	-	-	KOG0059 At5g61730 Lipid exporter ABCA1 and related proteins, ABC superfamily	KAF9585397.1 ATP-binding cassette sub-A member 1 [Lunasporea selenospora]	ABC transporter A family member 9 OS=Arabidopsis thaliana OX=3702 GN=ABCA9 PE=1 SV=1
A4720	-	-	GO:0005515(protein binding)	-	-	KOG3689 Hs19923440 Cyclic nucleotide phosphodiesterase	XP_016611506.1 hypothetical protein SPPG_00950 [Spizellomyces punctatus DAOM BR117]	Dual 3',5'-cyclic-AMP and -GMP phosphodiesterase 11A OS=Homo sapiens OX=9606 GN=PDE11A PE=1 SV=2
A4721	-	-	-	-	-	-	-	Outer dynein arm protein 1 OS=Chlamydomonas reinhardtii OX=3055
A4722	-	-	-	-	-	-	-	Pleckstrin homology domain-containing family D member 1 OS=Homo sapiens OX=9606 GN=PLEKHD1 PE=2 SV=3
A4723	-	-	GO:0005515(protein binding)	-	-	KOG0505 Hs2064802 Myosin phosphatase, regulatory subunit	CDS12731.1 hypothetical protein LRAMOSA04915 [Lichtheimia ramosa]	-
A4724	-	-	-	-	-	-	-	-
A4725	-	-	-	-	-	-	-	-
A4726	GO:0007034(vacuolar transport)	-	-	K12197 CHMP1, VPS46, DID2; charged multivesicular body protein 1	map04144 Endocytosis;map04217 Necroptosis	KOG3232 At1g73030 Vacuolar assembly/sorting protein DID2	KAG4102644.1 hypothetical protein H8356DRAFT_1324569 [Neocallimastix sp. JGI-2020a]	Charged multivesicular body protein 1 OS=Dictyostelium discoideum OX=44689 GN=chmp1 PE=3 SV=1
A4727	-	-	-	-	-	-	-	-
A4728	-	-	-	-	-	-	-	-

A4729	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0051082(unfolded protein binding)	K09496 CCT4; T-complex protein 1 subunit delta	-	KOG0358 Hs5453605 Chaperonin complex component, TCP-1 delta subunit (CCT4)	ORZ15740.1 T-complex protein 1 subunit delta [Absidia repens]	T-complex protein 1 subunit delta OS=Dictyostelium discoideum OX=44689 GN=cct4 PE=3 SV=1
A4730	GO:0030317(flagellated sperm motility),GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0036128(CatSper complex),GO:0016020(membrane)	GO:0005227(calcium activated cation channel activity),GO:0005216(ion channel activity)	-	-	KOG2301 Hs4502523 Voltage-gated Ca2+ channels, alpha1 subunits	ORX78529.1 hypothetical protein BCR32DRAFT_46369 [Anaeromyces robustus]	Cation channel sperm-associated protein 4 OS=Homo sapiens OX=9606 GN=CATSPER4 PE=1 SV=1
A4731	-	-	-	-	-	-	-	-
A4732	-	-	GO:0005515(protein binding)	K12472 EPS15; epidermal growth factor receptor substrate 15	map04144 Endocytosis	KOG0998 Hs4503593 Synaptic vesicle protein EHS-1 and related EH domain proteins	XP_018284915.1 hypothetical protein PHYBLDRAFT_128422, partial [Phycomyces blakesleeanus NRRL 1555(-)]	Intersectin-1 OS=Rattus norvegicus OX=10116 GN=Itsn1 PE=1 SV=2
A4733	-	-	-	-	-	-	-	-
A4734	-	-	GO:0005509(calcium ion binding)	-	-	KOG0027 Hs18559881 Calmodulin and related proteins (EF-Hand superfamily)	KNE56253.1 hypothetical protein AMAG_02087 [Allomyces macrogynus ATCC 38327]	EF-hand calcium-binding domain-containing protein 9 OS=Mus musculus OX=10090 GN=Efcab9 PE=1 SV=2
A4735	-	-	-	-	-	-	-	-
A4736	GO:0006633(fatty acid biosynthetic process)	GO:0009317(acetyl-CoA carboxylase complex)	GO:0003989(acetyl-CoA carboxylase activity),GO:0016874(ligase activity)	K01969 E6.4.1.4B: 3-methylcrotonyl-CoA carboxylase beta subunit [EC:6.4.1.4]	map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways	KOG0540 Hs22043827 3-Methylcrotonyl-CoA carboxylase, non-biotin containing subunit/Acetyl-CoA carboxylase carboxyl transferase, subunit beta	TPX63765.1 acetyl-CoA carboxylase [Chytridiomycetes confervae]	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Sus scrofa OX=9823 GN=PCCB PE=1 SV=1
A4737	-	-	GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups)	K11778 DHDDS, RER2, SRT1; ditrans,polycis-polyprenyl diphosphate synthase [EC:2.5.1.87]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis	KOG1602 Hs13376337 Cis-prenyltransferase	RKP05668.1 dehydrodolichyl diphosphate synthase [Thamnocephalis sphaerospora]	Dehydrodolichyl diphosphate synthase complex subunit DHDDS OS=Homo sapiens OX=9606 GN=DHDDS PE=1 SV=3
A4738	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A4739	-	-	-	-	-	-	-	-
A4740	-	-	-	-	-	-	-	-
A4741	GO:0006396(RNA processing)	-	GO:0003723(RNA binding),GO:0008173(RNA methyltransferase activity)	-	-	KOG0838 At4g15520 RNA Methylase, SpoU family	OAA33515.1 tRNA/rRNA methyltransferase, SpoU [Moelleriella libera RCEF 2490]	tRNA (guanosine(18)-2'-O)-methyltransferase OS=Thermus thermophilus (strain ATCC BAA-163 / DSM 7039 / HB27) OX=262724 GN=trmH PE=1 SV=1

A4742	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 CE25046 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	XP_006682367.1 uncharacterized protein BATDEDRAFT_20919 [Batrachochytrium dendrobatidis JAM81]	Calcium/calmodulin-dependent protein kinase type 1 OS=Caenorhabditis briggsae OX=6238 GN=cmk-1 PE=3 SV=4
A4743	GO:1902600(proton transmembrane transport)	GO:0016020(membrane)	GO:0004427(inorganic diphosphatase activity),GO:0009678(pyrophosphate hydrolysis-driven proton transmembrane transporter activity)	-	-	-	KAG1209907.1 hypothetical protein G6F35_010653 [Rhizopus oryzae]	Pyrophosphate-energized vacuolar membrane proton pump OS=Vigna radiata var. radiata OX=3916 PE=1 SV=4
A4744	GO:0009058(biosynthetic process)	-	GO:0016844(striktosidine synthase activity)	-	-	KOG1520 Hs14772303 Predicted alkaloid synthase/Surface mucin Hemomucin	-	Adipocyte plasma membrane-associated protein OS=Rattus norvegicus OX=10116 GN=Apmmap PE=2 SV=2
A4745	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	-	-
A4746	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0065 At2g29940 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	ORX82845.1 hypothetical protein K493DRAFT_388413 [Basidiobolus meristosporus CBS 931.73]	ABC transporter G family member 31 OS=Arabidopsis thaliana OX=3702 GN=ABCG31 PE=1 SV=1
A4747	GO:0006096(glycolytic process)	-	GO:0004618(phosphoglycerate kinase activity)	K00927 PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00710 Carbon fixation in photosynthetic organisms;map01100 Metabolic pathways;map04066 HIF-1 signaling pathway	KOG1367 CE13100 3-phosphoglycerate kinase	KNE71217.1 phosphoglycerate kinase [Allomyces macrogynus ATCC 38327]	Probable phosphoglycerate kinase OS=Caenorhabditis elegans OX=6239 GN=pgk-1 PE=3 SV=1
A4748	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0065 At2g29940 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	ORX82845.1 hypothetical protein K493DRAFT_388413 [Basidiobolus meristosporus CBS 931.73]	ABC transporter G family member 36 OS=Oryza sativa subsp. japonica OX=39947 GN=ABCG36 PE=2 SV=1

A4749	-	GO:0016020(membrane)	GO:0140359(ABC-type transporter activity),GO:0005524(ATP binding)	K08711 PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065 At3g16340 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	ORX82845.1 hypothetical protein K493DRAFT_388413 [Basidiobolus meristosporus CBS 931.73]	ABC transporter G family member 29 OS=Arabidopsis thaliana OX=3702 GN=ABCG29 PE=2 SV=2
A4750	-	-	GO:0005524(ATP binding)	K08711 PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065 At2g29940 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	OBT84674.1 hypothetical protein VE02_07846 [Pseudogymnoascus sp. 03VT05]	ABC transporter G family member 32 OS=Oryza sativa subsp. japonica OX=39947 GN=ABCG32 PE=2 SV=1
A4751	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K08711 PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065 At2g29940 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	ORX82845.1 hypothetical protein K493DRAFT_388413 [Basidiobolus meristosporus CBS 931.73]	Pleiotropic drug resistance protein 1 OS=Nicotiana tabacum OX=4097 GN=PDR1 PE=2 SV=1
A4752	-	-	-	-	-	-	-	-
A4753	GO:0006213(pyrimidine nucleoside metabolic process), GO:0006206(pyrimidine nucleobase metabolic process)	-	GO:0016763(pentose transferase activity),GO:0016757(glycosyltransferase activity),GO:0004645(1,4-alpha-D-glucan phosphorylase activity)	-	-	-	KAF9123525.1 hypothetical protein BGX30_001420 [Mortierella sp. GBA39]	Pyrimidine-nucleoside phosphorylase OS=Staphylococcus aureus (strain Mu50 / ATCC 700699) OX=158878 GN=pdp PE=3 SV=2
A4754	-	GO:0016020(membrane)	GO:0140359(ABC-type transporter activity),GO:0005524(ATP binding)	K08711 PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065 At2g29940 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	ORX92222.1 hypothetical protein K493DRAFT_316721 [Basidiobolus meristosporus CBS 931.73]	Pleiotropic drug resistance protein 1 OS=Nicotiana tabacum OX=4097 GN=PDR1 PE=2 SV=1
A4755	-	GO:0016020(membrane)	GO:0140359(ABC-type transporter activity),GO:0005524(ATP binding)	K08711 PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065 At2g29940 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	RKP35305.1 P-loop containing nucleoside triphosphate hydrolase protein [Dimargaris cristalligena]	ABC transporter G family member 31 OS=Arabidopsis thaliana OX=3702 GN=ABCG31 PE=1 SV=1
A4756	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K08711 PDR, CDR1; ATP-binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065 At1g59870 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	RKP35305.1 P-loop containing nucleoside triphosphate hydrolase protein [Dimargaris cristalligena]	ABC transporter G family member 36 OS=Arabidopsis thaliana OX=3702 GN=ABCG36 PE=1 SV=1

A4757	-	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0065 At1g15210 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	KAG0348059.1 hypothetical protein BG004_006193 [Podila humilis]	ABC transporter G family member 44 OS=Oryza sativa subsp. japonica OX=39947 GN=ABCG44 PE=2 SV=2
A4758	-	-	GO:0008410(CoA-transferase activity)	K01027 OXCT; 3-oxoacid CoA-transferase [EC:2.8.3.5]	map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map01100 Metabolic pathways	-	KZN89949.1 Succinyl-CoA:3-ketoacid coenzyme A transferase [Penicillium chrysogenum]	Caffeate CoA-transferase OS=Acetobacterium woodii OX=33952 GN=carA PE=1 SV=1
A4759	-	-	-	-	-	-	-	-
A4760	-	-	-	-	-	KOG4028 Hs13385568 Uncharacterized conserved protein	ORX78245.1 B9-domain-containing protein [Anaeromyces robustus]	B9 domain-containing protein 2 OS=Bos taurus OX=9913 GN=B9D2 PE=2 SV=1
A4761	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4762	GO:0007165(signal transduction)	-	GO:0005085(guanylyl-nucleotide exchange factor activity)	-	-	KOG3519 Hs19882229_1 Invasion-inducing protein TIAM1/CDC24 and related RhoGEF GTPases	GBC03133.1 hypothetical protein RclHR1_00050041 [Rhizophagus clarus]	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein OS=Mus musculus OX=10090 GN=Prex1 PE=1 SV=2
A4763	-	-	-	-	-	-	-	-
A4764	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0000981(DNA-binding transcription factor activity, RNA polymerase II-specific),GO:0008270(zinc ion binding)	-	-	-	RIB13458.1 hypothetical protein C2G38_2040954 [Gigaspora rosea]	Transcription factor asR4 OS=Sarocladium schorii OX=2203296 GN=asR4 PE=1 SV=1
A4765	-	-	-	-	-	-	-	-
A4766	GO:0006614(SRP-dependent cotranslational protein targeting to membrane)	GO:0048500(signal recognition particle)	GO:0008312(7S RNA binding)	-	-	-	-	-
A4767	-	-	-	-	-	-	-	-
A4768	GO:0006402(mRNA catabolic process)	-	GO:0003723(RNA binding),GO:0004654(polyribonucleotide nucleotidyltransferase activity),GO:0003676(nucleic acid binding)	-	-	KOG1067 At5g14580 Predicted RNA-binding polyribonucleotide nucleotidyltransferase	KAG0291721.1 hypothetical protein BGZ96_004882 [Linnemannia gamsii]	Polyribonucleotide nucleotidyltransferase OS=Methylobacterium infernorum (isolate V4) OX=481448 GN=pnp PE=3 SV=2

A4769	-	-	GO:0008410(CoA-transferase activity)	K01027 OXCT; 3-oxoacid CoA-transferase [EC:2.8.3.5]	map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map01100 Metabolic pathways	-	OQD97328.1 hypothetical protein PENSOL_c012G05268 [Penicillium solitum]	Caffeate CoA-transferase OS=Acetobacterium woodii OX=33952 GN=carA PE=1 SV=1
A4770	GO:0006470(protein dephosphorylation)	-	GO:0043169(cation binding),GO:0004722(protein serine/threonine phosphatase activity)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 At2g20050 Serine/threonine protein phosphatase	TPX58761.1 hypothetical protein SpCBS45565_g07922 [Spizellomyces sp. 'palustris']	Probable protein phosphatase 2C 65 OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0646100 PE=2 SV=1
A4771	-	-	GO:0005515(protein binding)	K20520 DBNL, ABP1; drebrin-like protein	-	KOG4226 CE29644 Adaptor protein NCK/Dock, contains SH2 and SH3 domains	KAG0184050.1 hypothetical protein DFQ28_000220 [Apophysomyces sp. BC1034]	UPF0246 protein Sde_3824 OS=Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024) OX=203122 GN=Sde_3824 PE=3 SV=1
A4772	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K15562 BUR1, SGV1; serine/threonine-protein kinase BUR1 [EC:2.7.11.22 2.7.11.23]	-	KOG0600 At5g10270 Cdc2-related protein kinase	KAG4093944.1 kinase-like domain-containing protein [Neocallimastix sp. JGI-2020a]	Cyclin-dependent kinase C-1 OS=Oryza sativa subsp. japonica OX=39947 GN=CDKC-1 PE=2 SV=1
A4773	-	-	-	-	-	-	ORX45763.1 hypothetical protein BCR36DRAFT_357866 [Piromyces finnis]	-
A4774	GO:0006413(translational initiation)	-	GO:0003743(translation initiation factor activity)	-	-	-	KAG0323188.1 hypothetical protein BGZ97_012347 [Linnemannia gamsii]	Translation initiation factor IF-3 OS=Aquifex aeolicus (strain VF5) OX=224324 GN=infC PE=3 SV=1
A4775	-	-	GO:0005515(protein binding)	-	-	KOG1947 At1g55590 Leucine rich repeat proteins, some proteins contain F-box	ONH69344.1 Antagonist of mitotic exit network protein 1 [Cyberlindnera fabianii]	F-box protein At-B OS=Arabidopsis thaliana OX=3702 GN=ATB PE=2 SV=1
A4776	-	-	-	-	-	-	-	-
A4777	-	-	GO:0005525(GTP binding),GO:0005515(protein binding)	K11684 BDF1; bromodomain-containing factor 1	-	KOG2485 Hs2050818 Conserved ATP/GTP binding protein	KAF9117424.1 hypothetical protein BGX30_005497, partial [Mortierella sp. GBA39]	Ribosome biogenesis GTPase A OS=Geobacillus sp. (strain WCH70) OX=471223 GN=rbgA PE=3 SV=1

A4778	GO:0006457(protein folding)	GO:0005783(endoplasmic reticulum)	GO:0005509(calcium ion binding);GO:0051082(unfolded protein binding);GO:0005515(protein binding)	K08054 CANX; calnexin	map04145 Phagosome;map04141 Protein processing in endoplasmic reticulum;map04918 Thyroid hormone synthesis;map04612 Antigen processing and presentation;map05166 Human T-cell leukemia virus 1 infection	KOG0675[At5g07340 Calnexin	RKO91687.1 Calreticulin/calnexin [Blyttomyces helicus]	Calnexin (Fragment) OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=CNE1 PE=1 SV=1
A4779	-	-	-	-	-	-	-	-
A4780	-	-	-	-	-	-	-	-
A4781	GO:0009113(purine nucleobase biosynthetic process)	-	GO:0004637(phosphoribosylamine-glycine ligase activity);GO:0005524(ATP binding);GO:00046872(metal ion binding)	K11788 ADE5; phosphoribosylamine--glycine ligase / phosphoribosylformylglycin amidine cyclo-ligase [EC:6.3.4.13 6.3.3.1]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01100 Metabolic pathways	-	KAE8448661.1 hypothetical protein EG329_009086 [Helotiales sp. DML_Dod_Qo]	Bifunctional purine biosynthetic protein ADE1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ade1 PE=1 SV=1
A4782	-	-	-	-	-	-	RKP09277.1 hypothetical protein THASP1DRAFT_28926 [Thamnocephalis sphaerospora]	-
A4783	-	-	-	-	-	-	RKP08991.1 hypothetical protein THASP1DRAFT_29219 [Thamnocephalis sphaerospora]	-
A4784	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0619[7300644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A4785	-	-	GO:0004842(ubiquitin-protein transferase activity);GO:0005515(protein binding)	K11493 RCC1; regulator of chromosome condensation	-	KOG1426[At5g63860 FOG: RCC1 domain	OIR57735.1 regulator of chromosome condensation 1 [Amphiblysis sp. WSBS2006]	Ultraviolet-B receptor UVR8 OS=Arabidopsis thaliana OX=3702 GN=UVR8 PE=1 SV=1
A4786	GO:0018216(peptidyl-arginine methylation)	-	GO:0016274(protein-arginine N-methyltransferase activity)	K11434 PRMT1; type I protein arginine methyltransferase [EC:2.1.1.319]	map04068 FoxO signaling pathway;map04922 Glucagon signaling pathway	KOG1501[7291527 Arginine N-methyltransferase	KAF8313081.1 protein arginine N-methyltransferase [Clavulina sp. PMI_390]	Protein arginine N-methyltransferase 7 OS=Drosophila ananassae OX=7217 GN=Art7 PE=3 SV=1
A4787	-	-	-	-	-	-	-	-
A4788	-	-	-	-	-	-	-	-

A4789	-	-	GO:0003950(NAD+ ADP-ribosyltransferase activity)	K15258 PARP6.8; poly [ADP-ribose] polymerase 6/8 [EC:2.4.2.30]	-	-	KZO91180.1 hypothetical protein CALVIDRAFT_602424 [Calocera viscosa TUFC12733]	Protein mono-ADP-ribosyltransferase PARP6 OS=Pongo abelii OX=9601 GN=PARP6 PE=2 SV=1
A4790	-	-	-	-	-	-	-	-
A4791	-	-	-	-	-	-	-	-
A4792	-	-	-	-	-	-	-	-
A4793	-	-	-	K13993 HSP20; HSP20 family protein	map04141 Protein processing in endoplasmic reticulum	KOG0710 At4g10250 Molecular chaperone (small heat- shock protein Hsp26/Hsp42)	KAG2220520.1 hypothetical protein INT45_000931 [Mucor circinatus]	22.0 kDa heat shock protein OS=Arabidopsis thaliana OX=3702 GN=HSP22.0 PE=2 SV=1
A4794	-	-	GO:0005515(protein binding)	-	-	-	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A4795	-	-	-	K15711 SMARCA3, HLTF; SWI/SNF- related matrix- associated actin- dependent regulator of chromatin subfamily A3 [EC:5.6.2.2.3.2.27]	-	KOG0298 Hs2054523 DEAD box- containing helicase-like transcription factor/DNA repair protein	ORX99471.1 hypothetical protein K493DRAFT_279635 [Basidiobolus meristosporus CBS 931.73]	E3 ubiquitin-protein ligase SHPRH OS=Mus musculus OX=10090 GN=Shprh PE=1 SV=1
A4796	GO:0007165(signal transduction)	-	GO:0005515(protein binding);GO:0005096(GTPase activator activity)	K18470 ARHGAP1, CDC42GAP; Rho GTPase- activating protein 1	-	KOG4270 At4g03100 GTPase- activator protein	KAG4098367.1 RhoGAP- domain- containing protein [Neocallimastix sp. JGI-2020a]	Rho GTPase-activating protein gacA OS=Dictyostelium discoideum OX=44689 GN=gacA PE=3 SV=1
A4797	-	-	GO:0005515(protein binding)	-	-	KOG0504 Hs2062923 FOG: Ankyrin repeat	ORY38922.1 ankyrin [Rhizoclostium globosum]	Rabankyrin-5 OS=Homo sapiens OX=9606 GN=ANKFY1 PE=1 SV=2
A4798	-	-	-	-	-	-	-	-
A4799	-	GO:0016021(integral component of membrane)	-	K24195 XPR1, PHO1; xenotropic and polytropic retrovirus receptor 1	-	KOG1162 Hs19923272 Predicted small molecule transporter	KAF9365822.1 hypothetical protein BGX34_008153 [Mortierella sp. NVP85]	Solute carrier family 53 member 1 OS=Mus spretus OX=10096 GN=Xpr1 PE=2 SV=1
A4800	GO:0015031(protein transport)	GO:0016021(integral component of membrane)	GO:0005515(protein binding)	-	-	-	-	-
A4801	-	-	-	-	-	-	-	-
A4802	-	GO:0016021(integral component of membrane)	GO:0008146(sulfotransferase activity)	-	-	-	-	-

A4803	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K10875 RAD54L, RAD54; DNA repair and recombination protein RAD54 and RAD54-like protein [EC:5.6.2.-]	map03440 Homologous recombination	KOG0390 At3g19210 DNA repair protein, SNF2 family	RPA79564.1 DNA repair and recombination protein RAD54 [Ascobolus immersus RN42]	DNA repair and recombination protein RAD54 OS=Oryza sativa subsp. japonica OX=39947 GN=RAD54 PE=1 SV=1
A4804	-	-	-	-	-	-	TPX63176.1 hypothetical protein SpCBS45565.g06817 [Spizellomyces sp. 'palustris']	Hydrolase phiM OS=Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) OX=441959 GN=tstM PE=1 SV=1
A4805	-	-	-	-	-	-	-	-
A4806	-	-	GO:0005515(protein binding)	-	-	-	XP_016610328.1 hypothetical protein SPPG_02764 [Spizellomyces punctatus DAOM BR117]	Tetratricopeptide repeat protein 21B OS=Homo sapiens OX=9606 GN=TTC21B PE=1 SV=2
A4807	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0008569(minus-end-directed microtubule motor activity)	-	-	KOG3595 Hs13876382 Dyneins, heavy chain	OON10512.1 hypothetical protein BSLG_00682 [Batrachochytrium salamandrivorans]	Dynein beta chain, flagellar outer arm OS=Chlamydomonas reinhardtii OX=3055 GN=ODA4 PE=3 SV=1
A4808	GO:0042450(arginine biosynthetic process via ornithine)	-	GO:0004056(argininosuccinate lyase activity),GO:0003824(catalytic activity)	K01755 argH, ASL; argininosuccinate lyase [EC:4.3.2.1]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map00220 Arginine biosynthesis;map01100 Metabolic pathways	-	ORE23366.1 argininosuccinate lyase [Rhizopus microsporus]	Argininosuccinate lyase OS=Chlamydomonas reinhardtii OX=3055 GN=ARG7 PE=2 SV=2
A4809	GO:1902600(proton transmembrane transport)	GO:0016471(vacuolar proton-transporting V-type ATPase complex)	GO:0046961(proton-transporting ATPase activity, rotational mechanism)	-	-	-	-	-
A4810	-	-	GO:0008641(ubiquitin-like modifier activating enzyme activity)	K10684 UBL1A, SAE1; ubiquitin-like 1-activating enzyme E1 A [EC:6.2.1.45]	map04120 Ubiquitin mediated proteolysis	KOG2014 Hs4885585 SMT3/SUMO-activating complex, AOS1/RAD31 component	EPS98454.1 hypothetical protein FOMPIDRAFT_161995 [Fomitopsis pinicola FP-58527 SS1]	SUMO-activating enzyme subunit 1 OS=Xenopus laevis OX=8355 GN=sae1 PE=2 SV=1

A4811	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At2g31900 Myosin class V heavy chain	XP_002174179.2 myosin-52 [Schizosaccharomyces japonicus yFS275]	Protein OPAQUE1 OS=Zea mays OX=4577 GN=O1 PE=1 SV=1
A4812	GO:1902600(proton transmembrane transport)	GO:0033179(proton-transporting V-type ATPase, V0 domain), GO:0033177(proton-transporting two-sector ATPase complex, proton-transporting domain)	GO:0046961(proton-transporting ATPase activity, rotational mechanism),GO:0015078(proton transmembrane transporter activity)	K02155 ATPeV0C, ATP6L; V-type H+-transporting ATPase 16kDa proteolipid subunit	map04145 Phagosome;map04142 Lysosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation; map05110 Vibrio cholerae infection;map05120 Epithelial cell signaling in Helicobacter pylori infection;map05152 Tuberculosis;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG0232 CE06290A Vacuolar H+-ATPase V0 sector, subunits c/c'	KAF7749248.1 H(+)-transporting V0 sector ATPase subunit c [Entomophthora muscae]	V-type proton ATPase 16 kDa proteolipid subunit c 2 OS=Caenorhabditis briggsae OX=6238 GN=vha-2 PE=3 SV=1
A4813	-	GO:0016021(integral component of membrane)	GO:0008146(sulfotransferase activity)	-	-	-	-	-
A4814	GO:1902600(proton transmembrane transport) GO:0046034(ATP metabolic process)	GO:0033180(proton-transporting V-type ATPase, V1 domain)	GO:0046961(proton-transporting ATPase activity, rotational mechanism),GO:0005524(ATP binding)	K02145 ATPeV1A, ATP6A; V-type H+-transporting ATPase subunit A [EC:7.1.2.2]	map04145 Phagosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation; map05110 Vibrio cholerae infection;map04150 mTOR signaling pathway;map05120 Epithelial cell signaling in Helicobacter pylori infection;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG1352 CE22210 Vacuolar H+-ATPase V1 sector, subunit A	KAG2172783.1 hypothetical protein INT43_000130 [Umbelopsis isabellina]	V-type proton ATPase catalytic subunit A OS=Dictyostelium discoideum OX=44689 GN=vatA PE=1 SV=2
A4815	-	-	-	-	-	-	-	-
A4816	-	-	GO:0005509(calcium ion binding)	K16466 CETN3, CDC31; centrin-3	-	KOG0028 Hs4757976 Ca2+-binding protein (centrin/caltractin), EF-Hand superfamily protein	VEU23869.1 DEKNAAC104880 [Brettanomyces naardenensis]	Centrin-3 OS=Homo sapiens OX=9606 GN=CETN3 PE=1 SV=2
A4817	GO:0008033(tRNA processing)	-	GO:0003824(catalytic activity),GO:0051536(iron-sulfur cluster binding),GO:0010181(FMN binding),GO:0051539(4 iron, 4 sulfur cluster binding)	K15449 TYW1; tRNA wybutosine-synthesizing protein 1 [EC:4.1.3.44]	-	KOG1160 At1g75200 Fe-S oxidoreductase	EPZ36965.1 Flavodoxin/nitric oxide synthase domain-containing protein [Rozella allomycis CSF55]	S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase OS=Arabidopsis thaliana OX=3702 GN=TYW1 PE=2 SV=1

A4818	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	KOG2309 At2g18020 60s ribosomal protein L2/L8	CEP13374.1 hypothetical protein [Parasitella parasitica]	Large ribosomal subunit protein uL2z OS=Arabidopsis thaliana OX=3702 GN=RPL8A PE=1 SV=2
A4819	GO:0033014(tetrapyrrole biosynthetic process)	-	GO:0004655(porphobilinogen synthase activity),GO:0046872(metal ion binding)	-	-	KOG2794 Hs4557297 Delta-aminolevulinic acid dehydratase	SHO76542.1 Aminolevulinic acid dehydratase [Malassezia sympodialis ATCC 42132]	Delta-aminolevulinic acid dehydratase OS=Candida glabrata (strain ATCC 2001 / BCRC 20586 / JCM 3761 / NBRC 0622 / NRRL Y-65 / CBS 138) OX=284593 GN=HEM2 PE=1 SV=1
A4820	-	-	GO:0005515(protein binding),GO:0003677(DNA binding)	-	-	KOG0520 At3g16940 Uncharacterized conserved protein, contains IPT/TIG domain	-	Calmodulin-binding transcription activator 2 OS=Arabidopsis thaliana OX=3702 GN=CAMTA2 PE=1 SV=1
A4821	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K11229 BCK1; mitogen-activated protein kinase kinase kinase [EC:2.7.11.25]	map04139 Mitophagy - yeast;map04011 MAPK signaling pathway - yeast	KOG0198 At1g09000 MEKK and related serine/threonine protein kinases	KAF5095880.1 hypothetical protein DOZ00.002967 [Geotrichum candidum]	Mitogen-activated protein kinase kinase kinase 2 OS=Arabidopsis thaliana OX=3702 GN=ANP2 PE=2 SV=1
A4822	GO:0072488(ammonium transmembrane transport)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 CE06770 Ammonia permease	KAF9137593.1 hypothetical protein BGX30_010076 [Mortierella sp. GBA39]	Ammonium transporter 2 OS=Dictyostelium discoideum OX=44689 GN=amtB PE=1 SV=1
A4823	GO:0008612(peptidyl-lysine modification to peptidyl-hypusine)	-	GO:0019135(deoxyhypusine monooxygenase activity)	-	-	KOG0567 7302088 HEAT repeat-containing protein	RKP15341.1 PBS lyase HEAT-like repeat family protein [Piptocephalis cylindrospora]	Deoxyhypusine hydroxylase OS=Danio rerio OX=7955 GN=dohh PE=2 SV=1
A4824	-	-	GO:0008270(zinc ion binding)	-	-	KOG2502 Hs21536436 Tub family proteins	XP_031022326.1 uncharacterized protein SmJEL517_g05775 [Synchytrium microbalum]	Tubby-related protein 3 OS=Homo sapiens OX=9606 GN=TULP3 PE=1 SV=2
A4825	-	-	-	-	-	KOG4169 Hs4504479 15-hydroxyprostaglandin dehydrogenase and related dehydrogenases	TPX57660.1 hypothetical protein PhCBS80983_g03705 [Powellomyces hirtus]	15-hydroxyprostaglandin dehydrogenase [NAD(+)] OS=Bos taurus OX=9913 GN=HPGD PE=2 SV=1
A4826	GO:0042819(vitamin B6 biosynthetic process), GO:0042823(pyridoxal phosphate biosynthetic process)	-	-	K06215 pdxS, pdx1; pyridoxal 5'-phosphate synthase pdxS subunit [EC:4.3.3.6]	map01240 Biosynthesis of cofactors;map00750 Vitamin B6 metabolism;map01100 Metabolic pathways	KOG1606 At5g01410 Stationary phase-induced protein, SOR/SNZ family	KAG2219665.1 hypothetical protein INT45_011849 [Mucor circinatus]	Pyridoxal 5'-phosphate synthase subunit PdxS OS=Chloroflexus aurantiacus (strain ATCC 29366 / DSM 635 / J-10-fl) OX=324602 GN=pdxS PE=3 SV=1

A4827	-	-	GO:0005509(cal cium ion binding)	-	-	KOG0027 Hs4 885109 Calmodulin and related proteins (EF- Hand superfamily)	CCA71197.1 probable Calmodulin [Serendipita indica DSM 11827]	Calmodulin OS=Triticum aestivum OX=4565 PE=1 SV=3
A4828	GO:00717 04(organi c substance metabolic process)	-	GO:0004553(hy drolase activity, hydrolyzing O- glycosyl compounds)	-	-	-	XP_03102753 4.1 uncharacteriz ed protein SmJEL517_g0 0430 [Synchytrium microbalum]	Glucosylceramidase OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) OX=246409 GN=ERC1 PE=1 SV=1
A4829	-	-	GO:0005515(pro tein binding),GO:000 5509(calcium ion binding)	-	-	-	-	-
A4831	GO:00091 90(cyclic nucleotid e biosynthe tic process), GO:00355 56(intrace llular signal transducti on)	-	-	-	-	-	-	-
A4832	-	GO:00446 66(MLL3/ 4 complex), GO:00481 88(Set1C/ COMPAS S complex)	-	-	-	KOG4109 Hs1 4211889 Histone H3 (Lys4) methyltransfe rase complex, subunit CPS25/DPY- 30	KAF9348847. 1 hypothetical protein BGX34_00220 8 [Mortierella sp. NVP85]	Protein dpy-30 homolog OS=Bos taurus OX=9913 GN=DPY30 PE=3 SV=1
A4833	GO:00068 07(nitroge n compoun d metabolic process)	-	GO:0004356(glu tamate- ammonia ligase activity),GO:000 3824(catalytic activity)	-	-	KOG0683 At3 g53180 Glutamine synthetase	TPX71889.1 glutamine synthetase [Spizellomyces sp. 'palustris']	Type-1 glutamine synthetase 1 OS=Dictyostelium discoideum OX=44689 GN=glnA1 PE=3 SV=1
A4834	GO:00071 86(G protein - coupled receptor signaling pathway), GO:00192 36(respon se to pheromo ne)	-	-	-	-	KOG4290 Hs2 0545671 Predicted membrane protein	-	Integral membrane protein GPR180 OS=Homo sapiens OX=9606 GN=GPR180 PE=2 SV=1
A4835	-	-	-	-	-	-	-	-
A4836	-	-	-	-	-	-	-	-
A4837	-	-	-	K13711 PI4K2; phosphatidyl inositol 4- kinase type 2 [EC:2.7.1.67]	map04070 Phosphatidylin ositol signaling system;map0056 2 Inositol phosphate metabolism;map 01100 Metabolic pathways	KOG2381 At2 g46500.2 Phosphatidyl inositol 4- kinase	ORY52830.1 phosphatidyl inositol 3 and 4-kinase- domain- containing protein [Leucosporidi um creatinivorum]	Phosphatidylinositol 4-kinase gamma 4 OS=Oryza sativa subsp. japonica OX=39947 GN=PI4KG4 PE=1 SV=1
A4838	-	-	-	-	-	-	XP_00786692 2.1 NAD P- binding protein [Gloeophyllum trabeum ATCC 11539]	Uncharacterized oxidoreductase C736.13 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC736.13 PE=3 SV=1

A4839	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02867 RP-L11, MRPL11, rplK; large subunit ribosomal protein L11	map03010 Ribosome	KOG3257 At4g35490 Mitochondria/chloroplast ribosomal protein L11	PVU95248.1 hypothetical protein BB559_002810 [Furculomyces boomerangs]	Large ribosomal subunit protein uL11m OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=mrp19 PE=3 SV=1
A4840	-	-	-	-	-	-	-	-
A4841	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	K00472 P4HA; prolyl 4-hydroxylase [EC:1.14.11.2]	map00330 Arginine and proline metabolism;map01100 Metabolic pathways	KOG1591 7301953 Prolyl 4-hydroxylase alpha subunit	RKP24551.1 hypothetical protein SYNPS1DRAFT_23375 [Syncephalis pseudoplumigaleata]	Prolyl 4-hydroxylase subunit alpha-3 OS=Homo sapiens OX=9606 GN=P4HA3 PE=1 SV=1
A4842	-	GO:0016021(integral component of membrane)	-	K03321 TC.SULP; sulfate permease, SulP family	-	-	XP_021870931.1 sulfate transporter family-domain-containing protein [Kockovaella imperatae]	Uncharacterized protein C24H6.11c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC24H6.11c PE=4 SV=1
A4843	GO:0051726(regulation of cell cycle),GO:0006355(regulation of transcription, DNA-templated)	GO:0005667(transcription regulator complex)	-	K04683 TFDP1; transcription factor Dp-1	map04350 TGF-beta signaling pathway;map03083 Polycomb repressive complex;map04110 Cell cycle	KOG2829 Hs5454112 E2F-like protein	EPZ37077.1 Transcription factor E2F/dimerization partner (TDP) domain-containing protein [Rozella allomyces CSF55]	Transcription factor Dp-2 OS=Homo sapiens OX=9606 GN=TFDP2 PE=1 SV=2
A4844	GO:0015031(protein transport),GO:0016192(vesicle-mediated transport),GO:0072583(clathrin-dependent endocytosis)	GO:0030122(AP-2 adaptor complex)	GO:0035615(clathrin adaptor activity)	K11827 AP2S1; AP-2 complex subunit sigma-1	map04144 Endocytosis;map04721 Synaptic vesicle cycle;map05016 Huntington disease;map04961 Endocrine and other factor-regulated calcium reabsorption	KOG0935 At1g47830 Clathrin adaptor complex, small subunit	KAG0146597.1 hypothetical protein CROQUODRAFT_722801 [Cronartium quercuum f. sp. fusiforme G11]	AP-2 complex subunit sigma OS=Arabidopsis thaliana OX=3702 GN=AP17 PE=2 SV=1
A4845	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0031201(SNARE complex),GO:0016020(membrane)	GO:0005484(SNAP receptor activity)	K08489 STX16; syntaxin 16	map04130 SNARE interactions in vesicular transport	KOG0809 At5g26980 SNARE protein TLG2/Syntaxin 16	ORX71987.1 t-SNARE protein [Linderina pennisporea]	Syntaxin-42 OS=Arabidopsis thaliana OX=3702 GN=SYP42 PE=1 SV=1

A4846	GO:0019441(tryptophan catabolic process to kynurenine)	-	GO:0020037(heme binding);GO:0046872(metal ion binding)	K00463 IDO, INDO; indoleamine 2,3-dioxygenase [EC:1.13.11.5.2]	map01240 Biosynthesis of cofactors;map05143 African trypanosomiasis; map00380 Tryptophan metabolism;map01100 Metabolic pathways	-	KAG0936168.1 hypothetical protein G6F30_008949 [Rhizopus oryzae]	Indoleamine 2,3-dioxygenase 1 OS=Rattus norvegicus OX=10116 GN=Ido1 PE=2 SV=1
A4847	GO:0055085(transmembrane transport)	-	-	-	-	KOG0753 At1g14140 Mitochondrial fatty acid anion carrier protein/Uncoupling protein	PKK69733.1 mitochondrial carrier [Rhizophagus irregularis]	Mitochondrial uncoupling protein 3 OS=Arabidopsis thaliana OX=3702 GN=PUMP3 PE=2 SV=1
A4848	-	-	GO:0005515(protein binding)	-	-	-	RKO93747.1 hypothetical protein BDK51DRAFT_29285 [Blyttomyces helicus]	-
A4849	-	-	GO:0005515(protein binding)	-	-	KOG1034 Hs14523052 Transcriptional repressor EED/ESC/FIE, required for transcriptional silencing, WD repeat superfamily	PIA16874.1 WD40 repeat-like protein [Coemansia reversa NRRL 1564]	Polycomb protein eed-A OS=Xenopus laevis OX=8355 GN=eed-a PE=1 SV=1
A4850	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	Solute carrier family 49 member 4 homolog OS=Xenopus laevis OX=8355 GN=slc49a4 PE=2 SV=1
A4851	-	-	-	K12306 MSFD7, SLC49A4; MFS transporter, FLVCR family, MFS-domain-containing protein 7	-	KOG2563 Hs14249552 Permease of the major facilitator superfamily	KXN71697.1 hypothetical protein CONCODRAFT_69637 [Conidiobolus coronatus NRRL 28638]	Solute carrier family 49 member 4 OS=Rattus norvegicus OX=10116 GN=Slc49a4 PE=2 SV=1
A4852	-	-	-	-	-	-	-	-
A4853	-	-	GO:0004488(methylenetetrahydrofolate dehydrogenase (NADP+) activity)	K00288 MTHFD; methylenetetrahydrofolate dehydrogenase (NADP+) / methylenetetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase [EC:1.5.1.5.3.5.4.9.6.3.4.3]	map00670 One carbon pool by folate;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	-	KAG2182117.1 hypothetical protein INT43_007044 [Umbelopsis isabellina]	Bifunctional protein FOLD 2 OS=Mesorhizobium japonicum (strain LMG 29417 / CECT 9101 / MAFF 303099) OX=266835 GN=fold2 PE=3 SV=1

A4854	-	-	GO:0005515(protein binding)	K24736 WDR1, AIP1; WD repeat-containing protein 1 (actin-interacting protein 1)	-	KOG0318 729 4479 WD40 repeat stress protein/actin interacting protein	XP_016610460.1 hypothetical protein SPPG_02887 [Spizellomyces punctatus DAOM BR117]	66 kDa stress protein OS=Physarum polycephalum OX=5791 PE=2 SV=1
A4855	-	-	GO:0016787(hydrolase activity)	K06269 PPP1C; serine/threonine-protein phosphatase PP1 catalytic subunit [EC:3.1.3.16]	map04390 Hippo signaling pathway;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05415 Diabetic cardiomyopathy; map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04218 Cellular senescence;map04910 Insulin signaling pathway;map04728 Dopaminergic synapse;map04720 Long-term potentiation;map05031 Amphetamine addiction;map04	KOG0374 YER133w Serine/threonine specific protein phosphatase PP1, catalytic subunit	EHY65229.1 serine/threonine-protein phosphatase PP1-gamma catalytic subunit [Nematocida sp. 1 ERTm2]	Serine/threonine-protein phosphatase PP1-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLC7 PE=1 SV=1
A4856	-	-	GO:0005515(protein binding);GO:0004386(helicase activity);GO:0003677(DNA binding);GO:0005524(ATP binding)	K19783 HCS1; DNA polymerase alpha-associated DNA helicase A [EC:5.6.2.3]	-	KOG1803 Hs4504623 DNA helicase	XP_016606826.1 hypothetical protein SPPG_05763 [Spizellomyces punctatus DAOM BR117]	DNA-binding protein SMUBP-2 OS=Rattus norvegicus OX=10116 GN=Ighmbp2 PE=1 SV=1
A4857	-	-	-	-	-	KOG1176 At3g16170 Acyl-CoA synthetase	XP_016608955.1 hypothetical protein SPPG_04016 [Spizellomyces punctatus DAOM BR117]	Malonate--CoA ligase ACSF3, mitochondrial OS=Mus musculus OX=10090 GN=Acsf3 PE=1 SV=2
A4858	-	-	GO:0016746(acyltransferase activity)	K00624 E2.3.1.7; carnitine O-acetyltransferase [EC:2.3.1.7]	map04146 Peroxisome	KOG3718 Hs10863953 Carnitine O-acyltransferase CROT	KNE64307.1 hypothetical protein AMAG_09336 [Allomyces macrogynus ATCC 38327]	Peroxisomal carnitine O-octanoyltransferase OS=Homo sapiens OX=9606 GN=CROT PE=1 SV=2
A4859	GO:0055085(transmembrane transport)	-	-	K15100 SLC25A1, CTP; solute carrier family 25 (mitochondrial citrate transporter), member 1	-	KOG0756 CE00474 Mitochondrial tricarboxylate/dicarboxylate carrier proteins	KAG0226057.1 hypothetical protein BGW41_004406 [Actinomyces rella wolfii]	Tricarboxylate transport protein B, mitochondrial OS=Danio rerio OX=7955 GN=slc25a1b PE=3 SV=2
A4860	-	-	-	-	-	-	-	-
A4861	-	-	GO:0016209(antioxidant activity);GO:0016491(oxidoreductase activity)	-	-	-	XP_017995306.1 hypothetical protein AB675_9975 [Phialophora attinorum]	-

A4862	-	-	-	-	-	-	-	-
A4863	GO:0006006(glucose metabolic process)	-	GO:0016614(oxidoreductase activity, acting on CH-OH group of donors),GO:0050661(NADP binding),GO:0004345(glucose-6-phosphate dehydrogenase activity)	K00036 G6PD, zwf; glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49 1.1.1.363]	map05415 Diabetic cardiomyopathy; map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00480 Glutathione metabolism;map00030 Pentose phosphate pathway;map05230 Central carbon metabolism in cancer;map01110 Metabolic pathways	KOG0563 Hs4758498.1 Glucose-6-phosphate 1-dehydrogenase	KAG1526568.1 hypothetical protein G6F52_002318 [Rhizopus delemar]	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens OX=9606 GN=H6PD PE=1 SV=2
A4864	-	-	GO:0005515(protein binding)	K14555 UTP13, TBL3; U3 small nucleolar RNA-associated protein 13	map03008 Ribosome biogenesis in eukaryotes	KOG0272 7301796 U4/U6 small nuclear ribonucleoprotein Prp4 (contains WD40 repeats)	RKO89148.1 WD40-repeat-containing domain protein, partial [Blyttiomycetes helicus]	Dynein assembly factor with WD repeat domains 1 OS=Chlamydomonas reinhardtii OX=3055 GN=DAW1 PE=1 SV=1
A4865	GO:0001932(regulation of protein phosphorylation)	GO:0005952(cAMP-dependent protein kinase complex)	GO:0008603(cAMP-dependent protein kinase regulator activity)	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG1113 Hs4506063 cAMP-dependent protein kinase types I and II, regulatory subunit	KAA8907878.1 hypothetical protein TRICL_004885 [Trichomonas cucumeris]	cAMP-dependent protein kinase regulatory subunit OS=Aplysia californica OX=6500 PE=2 SV=2
A4866	-	-	GO:0005515(protein binding)	-	-	KOG1987 At3g43700 Speckle-type POZ protein SPOP and related proteins with TRAF, MATH and BTB/POZ domains	KAF8492373.1 hypothetical protein F5888DRAFT_1858822 [Russula emetica]	BTB/POZ and MATH domain-containing protein 6 OS=Arabidopsis thaliana OX=3702 GN=BPM6 PE=1 SV=1
A4867	-	-	-	-	-	-	-	-
A4868	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04563 CDC28, CDC2; cyclin-dependent kinase [EC:2.7.11.22]	map04011 MAPK signaling pathway - yeast;map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0594 Hs16936528 Protein kinase PCTAIRE and related kinases	XP_006675915.1 uncharacterized protein BATDEDRAFT_85661 [Batrachochytrium dendrobatidis JAM81]	Cyclin-dependent kinase 20 OS=Danio rerio OX=7955 GN=cdk20 PE=2 SV=1
A4869	GO:0006281(DNA repair)	-	GO:0004518(nuclease activity)	K10772 APEX2; AP endonuclease 2 [EC:3.1.11.2]	-	KOG1294 Hs18375501 Apurinic/aprimidinic endonuclease and related enzymes	KKY28969.1 putative dna lyase [Diplodia seriata]	DNA-(apurinic or apyrimidinic site) endonuclease OS=Mus musculus OX=10090 GN=Apex1 PE=1 SV=2

A4870	GO:000672(glycerol-3-phosphate metabolic process)	GO:000931(glycerol-3-phosphate dehydrogenase complex)	GO:0004368(glycerol-3-phosphate dehydrogenase (quinone) activity),GO:0016491(oxidoreductase activity),GO:0005509(calcium ion binding)	K00111 glpA, glpD; glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism	KOG0042[Hs4504085 Glycerol-3-phosphate dehydrogenase	XP_007330857.1 hypothetical protein AGABI1DRAFT_75708 [Agaricus bisporus var. burnettii JB137-S8]	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Bos taurus OX=9913 GN=GPD2 PE=2 SV=1
A4871	-	-	-	-	-	-	-	-
A4872	-	-	-	K12386 CTNS; cystinosis	map04142 Lysosome	KOG3145[Hs4826682 Cystine transporter Cystinosis	KAG0024167.1 hypothetical protein BGZ80_005473 [Entomortierella chlamydospora]	Cystinosis OS=Homo sapiens OX=9606 GN=CTNS PE=1 SV=2
A4873	-	-	-	-	-	-	-	Leucine zipper transcription factor-like protein 1 OS=Bos taurus
A4874	-	-	-	-	-	-	-	-
A4875	GO:0036211(protein modification process)	-	GO:0004077(biotin-[acetyl-CoA-carboxylase] ligase activity)	K01942 HLCS; biotin--protein ligase [EC:6.3.4.9 6.3.4.10 6.3.4.11 6.3.4.15]	map00780 Biotin metabolism;map01100 Metabolic pathways	KOG1536[At2g25710 Biotin holocarboxylase synthetase/biotin-protein ligase	CZR61034.1 related to BPL1-biotin holocarboxylase synthetase [Phialocephala subalpina]	Biotin--protein ligase 2 OS=Arabidopsis thaliana OX=3702 GN=HCS2 PE=2 SV=1
A4876	-	-	-	K23802 LENG8, THP3; SAC3 family protein LENG8/THP3	-	KOG1861[At2g39340 Leucine permease transcriptional regulator	ORY49459.1 hypothetical protein BCR33DRAFT_657076 [Rhizoclostium globosum]	SAC3 family protein A OS=Arabidopsis thaliana OX=3702 GN=SAC3A PE=1 SV=1
A4877	GO:0044237(cellular metabolic process)	-	-	K03239 EIF2B1; translation initiation factor eIF-2B subunit alpha	map05168 Herpes simplex virus 1 infection	KOG1466[Hs4503503 Translation initiation factor 2B, alpha subunit (eIF-2B)alpha/GCN3)	EPZ36205.1 Initiation factor 2B-related domain-containing protein [Rozella allomyces CSF55]	Translation initiation factor eIF2B subunit alpha OS=Dictyostelium discoideum OX=44689 GN=eif2b1 PE=3 SV=1
A4878	-	-	GO:0008168(methyltransferase activity)	-	-	KOG2084[At3g21820 Predicted histone tail methylase containing SET domain	KNE58493.1 hypothetical protein AMAG_04063 [Allomyces macrogynus ATCC 38327]	Histone-lysine N-methyltransferase ATXR2 OS=Arabidopsis thaliana OX=3702 GN=ATXR2 PE=1 SV=1
A4879	-	-	-	-	-	-	-	-
A4880	-	-	GO:0009916(alternative oxidase activity)	-	-	-	RKP10927.1 alternative oxidase-domain-containing protein [Thamnocephalis sphaerospora]	Ubiquinol oxidase, mitochondrial OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) OX=684364 GN=AOX PE=3 SV=1
A4881	-	-	-	-	-	KOG2130[At1g78280 Phosphatidylserine-specific receptor PtdSerR, contains JmjC domain	TPX63146.1 hypothetical protein SpCBS45565_g06828 [Spizellomyces sp. 'palustris']	Lysine-specific demethylase JM21 OS=Arabidopsis thaliana OX=3702 GN=JM21 PE=2 SV=3

A4882	-	-	GO:0005509(cal- cium ion binding)	K06268 PPP3R, CNB; serine/threon- ine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05 014 Amyotrophic lateral sclerosis;map040 22 cGMP-PKG signaling pathway;map04 020 Calcium signaling pathway;map05 417 Lipid and atherosclerosis; map04218 Cellular senescence;map 05170 Human immunodeficien- cy virus 1 infection;map04 650 Natural killer cell mediated cytotoxicity;map 04658 Th1 and Th2 cell differentiation;m ap04659 Th17 cell	KOG0034 CE 23771 Ca2+/calmod- ulin- dependent protein phosphatase (calcineurin subunit B), EF-Hand superfamily protein	XP_01660949 4.1 calcineurin subunit B, variant 2 [Spizellomyces punctatus DAOM BR117]	-
A4883	-	-	GO:0003755(pe- ptidyl-prolyl cis-trans isomerase activity)	K09568 FKBP1; FK506- binding protein 1 [EC:5.2.1.8]	-	KOG0544 CE 21417 FKBP- type peptidyl- prolyl cis- trans isomerase	KAF5356094. 1 hypothetical protein D9756_00438 6 [Leucoagaricus leucothites]	FK506-binding protein 1 OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=FPR1 PE=3 SV=1
A4884	-	-	GO:0005515(pro- tein binding)	-	-	-	-	-
A4885	-	-	-	K22544 SAMHD1; deoxynucleos- ide triphosphate triphosphohy- drolase SAMHD1 [EC:3.1.5.-]	map03250 Viral life cycle - HIV- 1;map05170 Human immunodeficien- cy virus 1 infection;map04 623 Cytosolic DNA-sensing pathway	KOG2681 Hs1 4770705 Metal- dependent phosphohydr- olase	RKP13824.1 HD phosphohydr- olase domain- containing protein [Piptocephali- s cylindrospora]	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens OX=9606 GN=SAMHD1 PE=1 SV=2
A4886	-	GO:00361 28(CatSpe- r complex)	-	-	-	-	RKP17495.1 hypothetical protein ROZALSC1DR AFT_24147, partial [Rozella allomycis CSF55]	Cation channel sperm-associated auxiliary subunit epsilon OS=Homo sapiens OX=9606 GN=CATSPERE PE=2 SV=1
A4887	-	-	-	-	-	-	-	-
A4888	GO:00060 96(glycoly- tic process)	-	GO:0004618(ph- osphoglycerate kinase activity)	K00927 PGK, pgk; phosphoglyc- erate kinase [EC:2.7.2.3]	map01110 Biosynthesis of secondary metabolites;map 01200 Carbon metabolism;map 00010 Glycolysis / Gluconeogenesi- s;map01120 Microbial metabolism in diverse environments;m ap01230 Biosynthesis of amino acids;map00710 Carbon fixation in photosynthetic organisms;map0 1100 Metabolic pathways;map04 066 HIF-1 signaling pathway	KOG1367 Hs4 505763 3- phosphoglyc- erate kinase	KAG2231695. 1 hypothetical protein INT48_00043 5 [Thamnidium elegans]	Phosphoglycerate kinase OS=Hypocrea rufa OX=5547 GN=pgk1 PE=3 SV=2

A4889	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity)	-	-	KOG3033 At4g02860 Predicted PhzC/PhzF-type epimerase	OON08445.1 hypothetical protein BSLG_02278 [Batrachochytrium salamandrivorans]	Uncharacterized isomerase BH0283 OS=Halalkalibacterium halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) OX=272558 GN=BH0283 PE=3 SV=1
A4890	GO:0009058(biosynthetic process)	-	GO:0016407(acyltransferase activity),GO:0003824(catalytic activity)	-	-	KOG3033 At1g03210 Predicted PhzC/PhzF-type epimerase	XP_016613027.1 phenazine biosynthesis protein PhzF family protein [Spizellomyces punctatus DAOM BR117]	Uncharacterized isomerase BH0283 OS=Halalkalibacterium halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) OX=272558 GN=BH0283 PE=3 SV=1
A4891	-	-	-	-	-	-	-	-
A4892	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 Hs7110715 Phosphatidylinositol transfer protein SEC14 and related proteins	KAF7790786.1 hypothetical protein EIP86_001743 [Pleurotus ostreatoroseus]	SEC14-like protein 2 OS=Bos taurus OX=9913 GN=SEC14L2 PE=1 SV=2
A4893	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08832 SRPK3, STK23; serine/threonine-protein kinase SRPK3 [EC:2.7.11.1]	-	KOG1290 Hs4507221 Serine/threonine protein kinase	OAJ43075.1 hypothetical protein BDEG_26460 [Batrachochytrium dendrobatidis JEL423]	SRSF protein kinase 2 OS=Homo sapiens OX=9606 GN=SRPK2 PE=1 SV=3
A4894	-	-	-	-	-	-	-	-
A4895	-	-	GO:0005509(calcium ion binding)	-	-	KOG0032 7299682 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KAG0305901.1 hypothetical protein BGZ99_001943, partial [Dissophora globulifera]	Crustacean calcium-binding protein 23 OS=Faxonius limosus OX=28379 PE=1 SV=1
A4896	-	-	-	K01440 PNC1; nicotinamide [EC:3.5.1.19]	map04213 Longevity regulating pathway - multiple species;map01240 Biosynthesis of cofactors;map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	-	KAG1218806.1 hypothetical protein G6F35_008028 [Rhizopus oryzae]	Nicotinamidase OS=Escherichia coli (strain K12) OX=83333 GN=pncA PE=1 SV=1
A4897	GO:0006289(nucleotide-excision repair),GO:0006355(regulation of transcription, DNA-templated)	GO:0000439(transcription factor TFIIF core complex)	-	K03143 TFIIF3, TFIIF2H3, TFIIF4; transcription initiation factor TFIIF subunit 3	map03420 Nucleotide excision repair;map03022 Basal transcription factors;map05203 Viral carcinogenesis	-	KAG0145160.1 hypothetical protein CROQUUDRAFT_64141 [Cronartium quercuum f. sp. fusiforme G11]	General transcription and DNA repair factor IIF subunit ttf4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ttf4 PE=1 SV=1

A4898	-	-	GO:0005515(protein binding)	K08770 UBC; ubiquitin C	map03320 PPAR signaling pathway;map04140 Autophagy - animal;map05131 Shigellosis;map04137 Mitophagy - animal;map04120 Ubiquitin mediated proteolysis;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease;map05167 Kaposi sarcoma-associated herpesvirus infection	KOG0001[Hs16163829 Ubiquitin and ubiquitin-like proteins	TPX76768.1 hypothetical protein CcCBS67573_g01994 [Chytridiomycetes confervae]	Polyubiquitin-C OS=Sus scrofa OX=9823 GN=UBC PE=2 SV=1
A4899	-	-	GO:0003824(catalytic activity);GO:0030976(thiamine pyrophosphate binding);GO:0000287(magnesium ion binding)	-	-	KOG1185[Hs6912418 Thiamine pyrophosphate-requiring enzyme	KXS22039.1 2-hydroxyacyl-CoA lyase 1-like protein [Gonapodya prolifera JEL478]	2-hydroxyacyl-CoA lyase 1 OS=Homo sapiens OX=9606 GN=HACL1 PE=1 SV=2
A4900	-	-	GO:0008168(methyltransferase activity)	K22857 EEF1AKMT4; EEF1A lysine methyltransferase 4 [EC:2.1.1.-]	-	KOG2352[At3g60910 Predicted spermine/spermidine synthase	RIA99282.1 S-adenosyl-L-methionine-dependent methyltransferase [Glomus cerebriforme]	EEF1A lysine methyltransferase 4 OS=Homo sapiens OX=9606 GN=EEF1AKMT4 PE=1 SV=1
A4901	-	-	GO:0005524(ATP binding);GO:0046872(metal ion binding);GO:0000829(inositol heptakisphosphate kinase activity)	-	-	KOG1057[At3g01310 Arp2/3 complex-interacting protein VIP1/Asp1, involved in regulation of actin cytoskeleton	KAG2182624.1 hypothetical protein INT44_005603, partial [Umbelopsis vinacea]	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase VIP1 OS=Arabidopsis thaliana OX=3702 GN=VIP1 PE=1 SV=1
A4902	-	-	GO:0016409(palmitoyltransferase activity)	-	-	-	-	-
A4903	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4904	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02910 RP-L31e, RPL31; large subunit ribosomal protein L31e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0893[At5g56710 60S ribosomal protein L31	KAG2418008.1 60S ribosomal protein L31 [Aspergillus terreus]	Large ribosomal subunit protein eL31 OS=Cyanophora paradoxa OX=2762 GN=RPL31 PE=3 SV=1
A4905	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02929 RP-L44e, RPL44; large subunit ribosomal protein L44e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3464[YH R141c 60S ribosomal protein L44	KAF8418423.1 zinc-binding ribosomal protein, partial [Tirmania nivea]	Large ribosomal subunit protein eL42 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / BCRC 21394 / JCM 1990 / NBRC 0083 / IGC 2968) OX=284592 GN=RPL44 PE=3 SV=3
A4906	-	-	-	-	-	-	-	-

A4907	GO:0009062(fatty acid catabolic process)	-	GO:0008670(2,4-dienoyl-CoA reductase (NADPH) activity)	K13237 DECR2, SPS19; 2,4-dienoyl-CoA reductase [(3E)-enoyl-CoA-producing], peroxisomal [EC:1.3.1.124]	map04146 Peroxisome	KOG0725 YNL202w Reductases with broad range of substrate specificities	ORY06937.1 NAD(P)-binding protein [Basidiobolus meristosporus CBS 931.73]	Peroxisomal 2,4-dienoyl-CoA reductase [(3E)-enoyl-CoA-producing] OS=Arabidopsis thaliana OX=3702 GN=At3g12800 PE=2 SV=1
A4908	GO:0016558(protein import into peroxisome matrix)	GO:0005779(integral component of peroxisomal membrane)	GO:0008022(protein C-terminus binding),GO:0008270(zinc ion binding)	K13345 PEX12, PAF3; peroxin-12	map04146 Peroxisome	KOG0826 Hs4505721 Predicted E3 ubiquitin ligase involved in peroxisome organization	XP_016611266.1 hypothetical protein SPPG_02281 [Spizellomyces punctatus DAOM BR117]	Putative peroxisome assembly protein 12 OS=Dictyostelium discoideum OX=44689 GN=pex12 PE=3 SV=1
A4909	GO:0016567(protein ubiquitination),GO:000956(nuclear-transcribed mRNA catabolic process)	-	GO:0004842(ubiquitin-protein transferase activity)	K12620 LSM1; U6 snRNA-associated Sm-like protein LSM1	map03018 RNA degradation	KOG1782 CE05848 Small Nuclear ribonucleoprotein splicing factor	XP_016612533.1 hypothetical protein SPPG_00222 [Spizellomyces punctatus DAOM BR117]	U6 snRNA-associated Sm-like protein LSM1 OS=Bos taurus OX=9913 GN=LSM1 PE=2 SV=1
A4910	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	CEH12291.1 hypothetical protein CBOM_00290 [Ceraceosorus bombacis]	E3 ubiquitin-protein ligase SlrP OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=slrP PE=1 SV=1
A4911	-	-	GO:0005515(protein binding)	-	-	-	ORY76958.1 ankyrin repeat-containing domain protein [Protomyces lactucaedebilis]	E3 ubiquitin-protein ligase XBAT33 OS=Arabidopsis thaliana OX=3702 GN=XBAT33 PE=2 SV=1
A4912	GO:0006813(potassium ion transport),GO:0000462(maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)),GO:0055085(transmembrane transport),GO:0006396(RNA processing)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity),GO:0030515(snoRNA binding),GO:0005515(protein binding)	K14557 UTP6; U3 small nucleolar RNA-associated protein 6	map03008 Ribosome biogenesis in eukaryotes	KOG2396 At4g28200 HAT (Half-A-TPR) repeat-containing protein	TPX53440.1 hypothetical protein PhCBS80983.g06289 [Powellomyces hirtus]	Probable sodium/sulfate cotransporter 3 OS=Chlamydomonas reinhardtii OX=3055 GN=SLT3 PE=2 SV=1
A4913	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0051082(unfolded protein binding)	K09499 CCT7; T-complex protein 1 subunit eta	-	KOG0361 At3g11830 Chaperonin complex component, TCP-1 eta subunit (CCT7)	TPX60603.1 hypothetical protein PhCBS80983.g01730 [Powellomyces hirtus]	T-complex protein 1 subunit eta OS=Arabidopsis thaliana OX=3702 GN=CCT7 PE=1 SV=1

A4914	GO:0006813(potassium ion transport) GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	-	TPX53440.1 hypothetical protein PhCBS80983.g06289 [Powellomyces hirtus]	Probable sodium/sulfate cotransporter 3 OS=Chlamydomonas reinhardtii OX=3055 GN=SLT3 PE=2 SV=1
A4915	-	-	-	-	-	-	-	-
A4916	GO:0006364(rRNA processing)	GO:0005634(nucleus)	-	-	-	KOG2318 At3g01160 Uncharacterized conserved protein	ORX66990.1 hypothetical protein K493DRAFT_309382 [Basidiobolus meristosporus CBS 931.73]	Pre-rRNA-processing protein esf1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=esf1 PE=1 SV=1
A4917	-	-	-	-	-	-	RPB01466.1 hypothetical protein L873DRAFT_59034 [Choiromyces venosus 120613-1]	-
A4918	-	-	-	-	-	-	RPB01466.1 hypothetical protein L873DRAFT_59034 [Choiromyces venosus 120613-1]	-
A4919	-	-	-	-	-	-	ORY44048.1 TPR-like protein [Rhizoclostium globosum]	-
A4920	-	-	-	-	-	-	-	-
A4921	-	-	-	-	-	-	-	-
A4922	GO:0006468(protein phosphorylation)	-	GO:0035091(phosphatidylinositol binding),GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K19800 SCH9; serine/threonine protein kinase SCH9 [EC:2.7.11.1]	map04213 Longevity regulating pathway - multiple species;map04138 Autophagy - yeast	KOG0598 Hs20127541 Ribosomal protein S6 kinase and related proteins	PKC56514.1 Pkinase-domain-containing protein [Rhizophagus irregularis]	Serine/threonine-protein kinase Sgk2 OS=Homo sapiens OX=9606 GN=SGK2 PE=1 SV=2
A4923	GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding)	-	-	-	RUP44963.1 hypothetical protein BC936DRAFT_148790 [Jimgerdennia flammicorona]	Alpha-protein kinase 1 OS=Dictyostelium discoideum OX=44689 GN=ak1 PE=3 SV=1
A4924	-	-	-	-	-	-	KXS18079.1 hypothetical protein M427DRAFT_67912 [Gonapodya prolifera JEL478]	-

A4925	GO:0030488(tRNA methylation)	-	GO:0009019(tRNA (guanine-N1)-methyltransferase activity)	K15429 TRM5; TRMT5; tRNA (guanine37-N1)-methyltransferase [EC:2.1.1.228]	-	KOG2078 Hs14752839 tRNA modification enzyme	KAF7729879.1 tRNA (guanine(37)-N1)-methyltransferase [Apophysomyces ossiformis]	tRNA (guanine(37)-N1)-methyltransferase OS=Phytophthora infestans (strain T30-4) OX=403677 GN=PI TG_12867 PE=3 SV=1
A4926	-	-	-	-	-	-	-	-
A4927	-	-	GO:0005515(protein binding)	-	-	KOG1947 At2g25490 Leucine rich repeat proteins, some proteins contain F-box	ODV92916.1 hypothetical protein CADCADRAFT_30926 [Tortispora caseinolytica NRRL Y-17796]	Ein3-binding F-box protein 1 OS=Arabidopsis thaliana OX=3702 GN=EBF1 PE=1 SV=1
A4928	GO:0035556(intracellular signal transduction)	-	-	-	-	-	-	-
A4929	GO:0006120(mitochondrial electron transport, NADH to ubiquinone)	-	-	K03952 NDUFA8; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 8	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG3458 At5g18800 NADH:ubiquinone oxidoreductase, NDUFA8/PGIV/19 kDa subunit	KAF7725693.1 hypothetical protein DSO57_021155 [Entomophthora muscae]	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B OS=Arabidopsis thaliana OX=3702 GN=At5g18800 PE=1 SV=1
A4930	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	-	-	-	KAG1056454.1 hypothetical protein G6F43_001648 [Rhizopus delemar]	DEAD-box ATP-dependent RNA helicase 28 OS=Oryza sativa subsp. japonica OX=39947 GN=Os12g0481100 PE=2 SV=2
A4931	GO:0006801(superoxide metabolic process)	-	GO:0046872(metal ion binding)	K04565 SOD1; superoxide dismutase, Cu-Zn family [EC:1.15.1.1]	map05014 Amyotrophic lateral sclerosis;map04146 Peroxisome;map04213 Longevity regulating pathway - multiple species;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05012 Parkinson disease;map05016 Huntington disease	KOG0441 Hs4507149 Cu2+/Zn2+ superoxide dismutase SOD1	KAG0166241.1 Superoxide dismutase [Cu-Zn] [Apophysomyces sp. BC1015]	Superoxide dismutase [Cu-Zn] OS=Solidago canadensis var. scabra OX=59294 GN=SODCC PE=2 SV=3

A4932	-	-	GO:0005515(protein binding)	K14298 RAE1, GLE2; mRNA export factor	map05014 Amyotrophic lateral sclerosis;map03013 Nucleocytoplasmic transport;map05164 Influenza A	-	-	Zinc finger CCCH domain-containing protein 17 OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0677700 PE=2 SV=2
A4933	-	-	-	-	-	-	-	-
A4934	-	-	-	-	-	-	-	-
A4935	-	GO:0016021(integral component of membrane)	GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups),GO:0004659(prenyltransferase activity)	K06125 COQ2; 4-hydroxybenzoate polyprenyltransferase [EC:2.5.1.39]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00130 Ubiquinone and other terpenoid-quinone biosynthesis;map01100 Metabolic pathways	KOG1381 7299020 Para-hydroxybenzoate-polyprenyltransferase	ORY04853.14-hydroxybenzoate polyprenyltransferase [Basidiobolus meristosporus CBS 931.73]	4-hydroxybenzoate polyprenyltransferase, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=PPT1 PE=2 SV=1
A4936	GO:0016226(iron-sulfur cluster assembly)	GO:0005737(cytoplasm)	GO:0051536(iron-sulfur cluster binding)	K22746 CIAPIN1, DRE2; anamorsin	-	KOG4020 CE01413 Protein DRE2, required for cell viability	ORY04235.1 DUF689-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Anamorsin homolog OS=Culex quinquefasciatus OX=7176 GN=CPIJ009364 PE=3 SV=1
A4937	-	-	-	-	-	-	-	-
A4938	-	GO:0016021(integral component of membrane)	-	-	-	KOG1623 AT5g13170 Multitransmembrane protein	TPX39259.1 hypothetical protein SeLEV6574.g07350 [Synchytrium endobioticum]	Bidirectional sugar transporter SWEET16 OS=Arabidopsis thaliana OX=3702 GN=SWEET16 PE=1 SV=1
A4939	-	-	-	K09022 ridA, tdcF, RIDA; 2-iminobutanolate/2-iminopropanoate deaminase [EC:3.5.99.10]	-	-	KAF9137398.1 hypothetical protein BGX30_010280 [Mortierella sp. GBA39]	Protein TCP17 OS=Trypanosoma cruzi OX=5693 GN=TCP17 PE=1 SV=1
A4940	GO:0018344(protein geranylgeranylation)	-	GO:0003824(catalytic activity),GO:0008318(protein prenyltransferase activity),GO:0004663(Rab geranylgeranyltransferase activity)	K05956 RABGGTB; geranylgeranyl transferase type-2 subunit beta [EC:2.5.1.60]	-	KOG0366 7295883 Protein geranylgeranyltransferase type II, beta subunit	RPA87333.1 type-2 protein geranylgeranyltransferase subunit beta [Ascobolus immersus RN42]	Geranylgeranyl transferase type-2 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BET2 PE=1 SV=3
A4941	-	GO:0072546(EMC complex)	-	K23569 EMC8_9; ER membrane protein complex subunit 8/9	-	-	XP_025357516.1 UPF0172-domain-containing protein [Meira miltomrushi]	ER membrane protein complex subunit 8/9 homolog OS=Dictyostelium discoideum OX=44689 GN=DDb_G0268048 PE=3 SV=1

A4942	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07889 RAB5C; Ras-related protein Rab-5C	map04144 Endocytosis;map04145 Phagosome;map05132 Salmonella infection;map05146 Amoebiasis;map04014 Ras signaling pathway;map05152 Tuberculosis;map04962 Vasopressin-regulated water reabsorption	KOG0092 CE09711 GTPase Rab5/YPT51 and related small G protein superfamily GTPases	ORX92736.1 ras protein [Basidiobolus meristosporus CBS 931.73]	Ras-related protein Rab-5A OS=Dictyostelium discoideum OX=44689 GN=rab5A PE=3 SV=1
A4943	-	-	GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	-	-	KOG0118 Hs2059019 FOG; RRM domain	RHZ53333.1 hypothetical protein Glove_443g54 [Diversispora epigaea]	Serine/arginine-rich SC35-like splicing factor SCL28 OS=Arabidopsis thaliana OX=3702 GN=SCL28 PE=1 SV=1
A4944	-	-	GO:0005515(protein binding)	K22696 EEF2KMT; protein-lysine N-methyltransferase EEF2KMT [EC:2.1.1.-]	-	KOG2793 At1g73320 Putative N2,N2-dimethylguanosine tRNA methyltransferase	VDC06214.1 unnamed protein product [Peniophora sp. CBMAI 1063]	Protein N-lysine methyltransferase METTL21A OS=Danio rerio OX=7955 GN=mettl21a PE=2 SV=1
A4945	GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	GO:0016020(membrane)	-	K22943 YIPF6; protein YIPF6	-	KOG2946 7295714 Uncharacterized conserved protein	KAF9098637.1 hypothetical protein BGX23_005703 [Mortierella sp. AD031]	Protein YIPF6 homolog OS=Dictyostelium discoideum OX=44689 GN=yipf6 PE=3 SV=2
A4946	-	-	-	-	-	-	-	-
A4947	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	KOG2208 CE23530 Vigilin	KAF9926224.1 hypothetical protein FBU30_004151 [Linnemannia zychae]	-
A4948	-	-	-	K09518 DNAJB12; DnaJ homolog subfamily B member 12	map04141 Protein processing in endoplasmic reticulum	KOG0714 At5g49060 Molecular chaperone (DnaJ superfamily)	CDI52143.1 related to HUJ1-Co-chaperone for Hsp40p [Melanopsichium pennsylvanicum 4]	Chaperone protein dnaJ 49 OS=Arabidopsis thaliana OX=3702 GN=ATJ49 PE=2 SV=2
A4949	-	-	-	K00761 upp, UPRT; uracil phosphoribosyltransferase [EC:2.4.2.9]	map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	-	TPX60438.1 uracil phosphoribosyltransferase [Chytridiomycetes confervae]	Uracil phosphoribosyltransferase OS=Roseiflexus castenholzii (strain DSM 13941 / HLO8) OX=383372 GN=upp PE=3 SV=1
A4950	-	-	-	-	-	KOG2861 At5g13610 Uncharacterized conserved protein	ELQ74466.1 hypothetical protein THOM_2613, partial [Trachipleistophora hominis]	Protein RETARDED ROOT GROWTH-LIKE OS=Arabidopsis thaliana OX=3702 GN=RRL PE=2 SV=1

A4951	-	-	-	K11493 RCC1; regulator of chromosome condensation	-	KOG1426 At5 g63860 FOG: RCC1 domain	PIA14479.1 nucleotide exchange factor for Gsp1p, localizes to the nucleus [Coemansia reversa NRRL 1564]	Ultraviolet-B receptor UVR8 OS=Arabidopsis thaliana OX=3702 GN=UVR8 PE=1 SV=1
A4952	GO:00064 12(transla tion)	GO:00058 40(riboso me)	GO:0003735(str uctural constituent of ribosome)	K02974 RP- S24e, RPS24; small subunit ribosomal protein S24e	map05171 Coronavirus disease - COVID- 19;map03010 Ribosome	KOG3424 At3 g04920 40S ribosomal protein S24	VEU20033.1 DEKNAAC10 0796 [Brettanomyces naardenensis]	Small ribosomal subunit protein eS24z OS=Arabidopsis thaliana OX=3702 GN=RPS24A PE=2 SV=1
A4953	GO:00001 60(phosp horelay signal transducti on system)	-	-	-	-	KOG0614 729 6166 cGMP- dependent protein kinase	TPX60262.1 hypothetical protein SpCBS45565. g07547 [Spizellomyces sp. 'palustris']	cGMP-dependent protein kinase, isozyme 1 OS=Drosophila melanogaster OX=7227 GN=Pkg21D PE=1 SV=2
A4954	-	-	-	-	-	-	-	-
A4955	-	-	GO:0005524(AT P binding).GO:001 6887(ATP hydrolysis activity)	K11269 CTF18, CHL12; chromosome transmission fidelity protein 18	-	KOG1969 Hs1 4777079 DNA replication checkpoint protein CHL12/CTF18	KAG0222039. 1 hypothetical protein BGX31_00939 8 [Mortierella sp. GBA43]	Chromosome transmission fidelity protein 18 homolog OS=Drosophila melanogaster OX=7227 GN=cutlet PE=2 SV=2
A4956	GO:00060 96(glycoly tic process)	-	GO:0004619(ph osphoglycerate mutase activity).GO:001 6868(intramolec ular transferase activity, phosphotransfer ases).GO:00038 24(catalytic activity)	K01834 PGAM, gpmA; 2,3- bisphosphogly cerate-depen dent phosphoglyc erate mutase [EC:5.4.2.11]	map01110 Biosynthesis of secondary metabolites;map 01200 Carbon metabolism;map 00010 Glycolysis / Gluconeogenesi s;map01120 Microbial metabolism in diverse environments;m ap01230 Biosynthesis of amino acids;map00680 Methane metabolism;map 00260 Glycine, serine and threonine metabolism;map 05230 Central carbon metabolism in cancer;map0110 0 Metabolic pathways;map04	KOG0235 At1 g22170 Phosphoglyc erate mutase	XP_00217323 0.1 monomeric 2,3- bisphosphogl ycerate (BPG)- dependent phosphoglyc erate mutase [Schizosacch aromyces japonicus yFS275]	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 1 OS=Arabidopsis thaliana OX=3702 GN=gpmA1 PE=2 SV=1
A4957	GO:00067 77(Mo- molybdop terin cofactor biosynthe tic process)	GO:00190 08(molyb dopterin synthase complex)	GO:0003824(cat alytic activity).GO:005 1536(iron-sulfur cluster binding).GO:005 1539(4 iron, 4 sulfur cluster binding).GO:004 6872(metal ion binding)	K03639 moaA, CNX2; GTP 3',8- cyclase [EC:4.1.99.22]	map01240 Biosynthesis of cofactors;map04 122 Sulfur relay system;map0110 0 Metabolic pathways;map00 790 Folate biosynthesis	KOG2876 Hs2 0555317 Molybdenum cofactor biosynthesis pathway protein	SPO34904.1 related to molybdenum cofactor biosynthesis protein 1 B [Anthracocyst is flocculosa]	Molybdenum cofactor biosynthesis protein 1 OS=Mus musculus OX=10090 GN=Mocs1 PE=1 SV=2
A4958	-	-	-	-	-	-	-	-
A4959	-	-	-	-	-	-	-	-
A4960	-	-	-	-	-	-	-	-

A4961	GO:0006508(proteolysis)	-	GO:0004190(serine-type endopeptidase activity)	-	-	KOG1339 At5g43100 Aspartyl protease	KDQ20078.1 hypothetical protein BOTBODRAFT_101585 [Botryobasidium botryosum FD-172 SS1]	Plasmeprin V OS=Plasmodium vivax (strain Salvador I) OX=126793 GN=PMV PE=1 SV=1
A4962	GO:0006334(nucleosome assembly)	GO:0000786(nucleosome)	GO:0003677(DNA binding)	K15223 UAF30, SPP27; upstream activation factor subunit UAF30	-	KOG1946 At4g22360 RNA polymerase I transcription factor UAF	PIA12795.1 SWIB-domain-containing protein [Coemansia reversa NRRL 1564]	Upstream activation factor subunit UAF30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UAF30 PE=1 SV=1
A4963	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4964	-	-	-	-	-	-	-	-
A4965	-	-	-	K07019 K07019; uncharacterized protein	-	-	KAF2711055.1 AB-hydrolase YheT [Pleiomassaria siparia CBS 279.74]	Monoacylglycerol lipase ABHD2 OS=Danio rerio OX=7955 GN=abhd2b PE=2 SV=1
A4966	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin-tyrosine ligase [EC:6.3.2.25]	-	KOG2157 Hs1068135 Predicted tubulin-tyrosine ligase	TPX59531.1 hypothetical protein PhCBS80983_g02429 [Powellomyces hirtus]	Probable tubulin polyglutamylase TTL9 OS=Bos taurus OX=9913 GN=TLL9 PE=2 SV=1
A4967	-	-	-	-	-	-	-	-
A4968	GO:0044255(cellular lipid metabolic process)	-	GO:0008374(O-acyltransferase activity),GO:0016746(acyltransferase activity)	-	-	KOG3730 Hs7657134 Acyl-CoA: dihydroxyacetone-phosphate acyltransferase DHAPAT	RSL96320.1 hypothetical protein CEP52_011547 [Fusarium sp. AF-4]	Glycerol-3-phosphate acyltransferase OS=Pseudomonas fluorescens (strain SBW25) OX=216595 GN=plsB PE=3 SV=1
A4969	-	-	-	-	-	-	-	-
A4970	GO:0046856(phosphatidylinositol dephosphorylation)	-	GO:0005515(protein binding),GO:0003824(catalytic activity),GO:0016791(phosphatase activity)	K20279 SYNJ; synaptojanin [EC:3.1.3.36]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0565 Hs22068673 Inositol polyphosphate 5-phosphatase and related proteins	XP_016292053.1 hypothetical protein PSEUBRA_SC AF22g00034 [Kalmanozyma brasiliensis GHG001]	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A OS=Mus musculus OX=10090 GN=Inpp5j PE=1 SV=2
A4971	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K19001 HELLS, DDM1; ATP-dependent DNA helicase	-	KOG0385 Hs21914927 Chromatin remodeling complex WSTF-ISWI, small subunit	ORZ00495.1 SNF2 family N-terminal domain-containing protein [Syncephalastrium racemosum]	Lymphoid-specific helicase OS=Homo sapiens OX=9606 GN=HELLS PE=1 SV=1
A4972	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity)	-	-	-	-	-
A4973	-	-	-	-	-	-	-	-
A4974	GO:0006366(transcription by RNA polymerase II)	-	-	K20826 RPAP1; RNA polymerase II-associated protein 1	-	KOG1894 YDR527w Uncharacterized conserved protein	CEP10933.1 hypothetical protein [Parasitella parasitica]	RNA polymerase II-associated protein 1 OS=Mus musculus OX=10090 GN=Rpap1 PE=1 SV=2

A4975	-	-	GO:0003824(catalytic activity)	K01796 E5.1.99.4, AMACR, mcr; alpha-methylacyl-CoA racemase [EC:5.1.99.4]	map04146 Peroxisome;map00120 Primary bile acid biosynthesis;map01100 Metabolic pathways	KOG3957 Hs14725900 Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	KAF9168308.1 hypothetical protein DQ26_009527 [Actinomortierella ambigua]	Alpha-methylacyl-CoA racemase OS=Mus musculus OX=10090 GN=Amacr PE=1 SV=4
A4976	GO:0006355(regulation of transcription, DNA-templated);GO:0016573(histone acetylation)	-	GO:0004402(histone acetyltransferase activity)	K11304 TIP60, KAT5, ESA1; histone acetyltransferase HTATIP [EC:2.3.1.48]	map03082 ATP-dependent chromatin remodeling;map05017 Spinocerebellar ataxia;map05166 Human T-cell leukemia virus 1 infection	KOG2747 At5g64610 Histone acetyltransferase (MYST family)	RMV09233.1 hypothetical protein D0866_14650 [Hortaea werneckii]	Histone acetyltransferase esa1 OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=esa1 PE=3 SV=1
A4977	-	-	-	K05841 E2.4.1.173; sterol 3beta-glucosyltransferase [EC:2.4.1.173]	-	-	PRQ74812.1 sterol 3-beta-glucosyltransferase [Rhodotorula toruloides]	Pleckstrin homology domain-containing protein 1 OS=Arabidopsis thaliana OX=3702 GN=PH1 PE=2 SV=2
A4978	-	-	GO:0005515(protein binding)	-	-	-	-	-
A4979	-	-	GO:0051087(chaperone binding)	-	-	-	-	-
A4980	-	-	-	-	-	-	TPX33150.1 hypothetical protein SeMB42_g07516 [Synchronytrium endobioticum]	Outer dynein arm protein 1 OS=Chlamydomonas reinhardtii OX=3055 GN=ODA1 PE=1 SV=1
A4981	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity);GO:0030170(pyridoxal phosphate binding)	-	-	KOG0257 At1g77670 Kynurenine aminotransferase, glutamine transaminase K	KXN69321.1 class I and II aminotransferase [Conidiobolus coronatus NRRL 28638]	Capreomycin synthase OS=Streptomyces vinaceus OX=1960 GN=vioD PE=1 SV=1
A4982	-	-	-	-	-	-	-	-
A4983	-	-	GO:0019789(SUMO transferase activity)	K10577 UBE2I, UBC9; ubiquitin-conjugating enzyme E2 I	map04120 Ubiquitin mediated proteolysis;map03013 Nucleocytoplasmic transport;map05206 MicroRNAs in cancer;map04064 NF-kappa B signaling pathway	-	XP_025431160.1 ubiquitin-conjugating enzyme E2-18 kDa [Aspergillus saccharolyticus JOP 1030-1]	SUMO-conjugating enzyme ubc9 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=hus5 PE=1 SV=1
A4984	-	-	-	-	-	KOG2382 At3g52570 Predicted alpha/beta hydrolase	KWU42475.1 alpha/beta-hydrolase [Rhodotorula sp. JG-1b]	Probable alcohol acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMO32 PE=1 SV=1

A4985	GO:0043328(protein transport to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway)	-	GO:0035091(phosphatidylinositol binding);GO:0043130(ubiquitin binding)	K12182 HGS, HRS, VPS27; hepatocyte growth factor-regulated tyrosine kinase substrate	map04144 Endocytosis;map04145 Phagosome;map03250 Viral life cycle - HIV-1	KOG1087 At3g08790 Cytosolic sorting protein GGA2/TOM1	XP_025600348.1 ubiquitin binding protein [Tilletiopsis washingtonensis]	Target of Myb protein 1 OS=Dictyostelium discoideum OX=44689 GN=tom1 PE=1 SV=1
A4986	-	-	-	K14794 RRP12; ribosomal RNA-processing protein 12	-	KOG1248 Hs15987121 Uncharacterized conserved protein	KND94518.1 Ribosomal RNA-processing protein 12 [Tolypocladium ophioglossoides CBS 100239]	RRP12-like protein OS=Mus musculus OX=10090 GN=Rrp12 PE=1 SV=1
A4987	-	-	GO:0005515(protein binding)	K09527 DNAJC7; DnaJ homolog subfamily C member 7	-	KOG0550 Hs4507713 Molecular chaperone (DnaJ) superfamily)	AYO43438.1 chaperone protein DnaJ [Malassezia restricta CBS 7877]	DnaJ homolog subfamily C member 7 OS=Homo sapiens OX=9606 GN=DNAJC7 PE=1 SV=2
A4988	GO:0009394(2'-deoxyribonucleotide metabolic process)	-	GO:0008829(dCTP deaminase activity)	-	-	-	ELR03039.1 hypothetical protein GMDG_08871 [Pseudogymnoascus destructans 20631-21]	dCTP deaminase, dUMP-forming OS=Methanospaera stadtmanae (strain ATCC 43021 / DSM 3091 / JCM 11832 / MCB-3) OX=339860 GN=dcd PE=3 SV=1
A4989	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0005524(ATP binding);GO:0019205(nucleobase-containing compound kinase activity)	K13800 CMPK1, UMPK; UMP-CMP kinase [EC:2.7.4.14]	map00983 Drug metabolism - other enzymes;map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3079 CE02218 Uridylate kinase/adenylate kinase	XP_006682405.1 uncharacterized protein BATDEDRAFT_28095 [Batrachochytrium dendrobatidis JAM81]	Adenylate kinase isoenzyme 1 OS=Mus musculus OX=10090 GN=Ak1 PE=1 SV=1
A4990	-	-	-	-	-	-	-	-
A4991	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding);GO:0005509(calcium ion binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At5g12180 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	GBC05564.1 hypothetical protein RclHR1_00630011 [Rhizophagus clarus]	Calcium-dependent protein kinase 17 OS=Arabidopsis thaliana OX=3702 GN=CPK17 PE=2 SV=1

A4992	GO:0045039(protein insertion into mitochondrial inner membrane)	GO:0042721(TIM22 mitochondrial import inner membrane insertion complex)	-	K17790 TIM22; mitochondria l import inner membrane translocase subunit TIM22	-	KOG3225 YD L217c Mitochondria l import inner membrane translocase, subunit TIM22	RPB03587.1 Tim17 - domain-containing protein [Choiromyces venosus 120613-1]	Mitochondrial import inner membrane translocase subunit TIM22 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=TIM22 PE=1 SV=1
A4993	-	-	-	K14765 NGDN, LCP5; U3 small nucleolar ribonucleoprotein protein LCP5	-	KOG3117 729 7016 Protein involved in rRNA processing	EPZ33023.1 Sas10 domain-containing protein [Rozella allomycis CSF55]	Neuroguidin OS=Danio rerio OX=7955 GN=ngdn PE=2 SV=1
A4994	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1199 729 3420 Short-chain alcohol dehydrogenase/3-hydroxyacyl-CoA dehydrogenase	KAG1255224.1 hypothetical protein G6F65_016726 [Rhizopus oryzae]	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Drosophila melanogaster OX=7227 GN=scu PE=1 SV=1
A4995	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08286 E2.7.11.-.; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0610 YN R047w Putative serine/threonine protein kinase	KAG0787087.1 hypothetical protein G6F22_007427 [Rhizopus oryzae]	Flippase kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPK1 PE=1 SV=1
A4996	GO:0006470(protein dephosphorylation), GO:0016311(dephosphorylation)	-	GO:0008138(protein tyrosine/serine/threonine phosphatase activity)	K14165 K14165; atypical dual specificity phosphatase [EC:3.1.3.16 3.1.3.48]	-	KOG1718 Hs5 902002 Dual specificity phosphatase	OCH84355.1 DSPC-domain-containing protein, partial [Obba rivulosa]	Dual specificity protein phosphatase 14 OS=Mus musculus OX=10090 GN=Dusp14 PE=2 SV=2
A4997	-	-	-	-	-	KOG0712 Hs4 504511 Molecular chaperone (DnaJ superfamily)	KAF7564458.1 DnaJ, DnaJ-class molecular chaperone with C-terminal Zn finger domain protein [Pyrenophora tritici-repentis]	DnaJ homolog subfamily A member 4 OS=Homo sapiens OX=9606 GN=DNAJA4 PE=1 SV=1
A4998	-	-	-	-	-	-	-	-
A4999	-	-	GO:0000287(magnesium ion binding),GO:00030976(thiamine pyrophosphate binding),GO:0003824(catalytic activity)	-	-	KOG1185 Hs2 1361361 Thiamine pyrophosphate-requiring enzyme	KXS14708.1 Thiamin diphosphate-binding protein [Gonapodya prolifera JEL478]	2-hydroxyacyl-CoA lyase 2 OS=Danio rerio OX=7955 GN=ilvbl PE=2 SV=1
A5000	GO:0060271(cilium assembly)	GO:0036064(ciliary basal body)	-	-	-	-	TPX43110.1 hypothetical protein CcCBS67573_g10469 [Chytridiomycetes confervae]	LisH domain-containing protein ARMC9 OS=Xenopus tropicalis OX=8364 GN=armc9 PE=2 SV=1
A5001	-	GO:0016020(membrane)	GO:0005227(calcium activated cation channel activity)	K21989 TMEM63, CSC1; calcium permeable stress-gated cation channel	-	KOG1134 At3 g21620 Uncharacterized conserved protein	RUS31164.1 hypothetical protein BC938DRAFT_478342 [Jimgerdmania flammicorona]	CSC1-like protein At4g15430 OS=Arabidopsis thaliana OX=3702 GN=At4g15430 PE=2 SV=1

A5002	-	-	-	-	-	KOG1672 Hs18104959 ATP binding protein	EPZ35342.1 Thioredoxin-like fold domain-containing protein [Rozella allomyces CSF55]	Thioredoxin domain-containing protein 9 OS=Homo sapiens OX=9606 GN=TXNDC9 PE=1 SV=2
A5003	GO:0016485(protein processing)	GO:0016021(integral component of membrane)	GO:0004190(serine-type endopeptidase activity)	-	-	KOG2736 Hs4506163 Presenilin	EPB83259.1 hypothetical protein HMPREF1544_10003 [Mucor circinelloides 1006PhL]	Presenilin-1 OS=Microcebus murinus OX=30608 GN=PSEN1 PE=2 SV=1
A5004	-	-	-	-	-	-	-	-
A5005	-	-	-	-	-	KOG3661 Hs7019335 Uncharacterized conserved protein	-	Myelin regulatory factor OS=Xenopus laevis OX=8355 GN=myrf PE=2 SV=1
A5006	-	-	-	K17981 MTFP1, MTP18; mitochondria fission process protein 1	-	KOG3945 7293405 Uncharacterized conserved protein	OAJ44965.1 hypothetical protein BDEG_28140 [Batrachochytrium dendrobatidis JEL423]	Mitochondrial fission process protein 1 OS=Caenorhabditis elegans OX=6239 GN=mtp-18 PE=3 SV=2
A5007	-	-	-	-	-	-	-	-
A5008	-	-	GO:0005509(calcium ion binding)	K16466 CETN3, CDC31; centrin-3	-	KOG0028 7289491 Ca2+-binding protein (centrin/caltractin), EF-Hand superfamily protein	XP_031024820.1 uncharacterized protein SmJEL517_g03191 [Synchytrium microbalum]	Caltractin OS=Scherffelia dubia OX=3190 PE=1 SV=1
A5009	-	GO:0005789(endoplasmic reticulum membrane)	-	-	-	KOG0439 At2g45140 VAMP-associated protein involved in inositol metabolism	ORZ21203.1 PapD-like protein [Absidia repens]	Vesicle-associated protein 1-2 OS=Arabidopsis thaliana OX=3702 GN=PVA12 PE=1 SV=1
A5010	-	-	-	-	-	-	-	-
A5011	GO:0045292(mRNA cis splicing, via spliceosome)	GO:0005846(nuclear cap binding complex)	GO:0003676(nucleic acid binding),GO:0003723(RNA binding),GO:0000339(RNA cap binding)	-	-	-	XP_019024836.1 RNA-binding domain-containing protein, partial [Saitoella complicata NRRL Y-17804]	Nuclear cap-binding protein subunit 2 OS=Aedes aegypti OX=7159 GN=Cbp20 PE=3 SV=1
A5012	-	GO:0005737(cytoplasm),GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0003743(translation initiation factor activity)	K15029 EIF3L; translation initiation factor 3 subunit L	-	KOG3677 Hs7705433 RNA polymerase II-associated factor - PAF67	ORX89652.1 hypothetical protein K493DRAFT_288996 [Basidiobolus meristosporus CBS 931.73]	Eukaryotic translation initiation factor 3 subunit L OS=Xenopus tropicalis OX=8364 GN=eif3l PE=2 SV=1
A5013	-	-	GO:0005507(copper ion binding),GO:0016491(oxidoreductase activity)	K08100 E1.3.3.5; bilirubin oxidase [EC:1.3.3.5]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism	-	TPX74821.1 hypothetical protein CcBS67573_g03909 [Chytridiomycetes confervae]	Multicopper oxidase CueO OS=Escherichia coli O157:H7 OX=83334 GN=cueO PE=3 SV=1

A5014	-	-	GO:0005515(protein binding)	-	-	KOG2080 7292095 Uncharacterized conserved protein, contains DENN and RUN domains	-	DENN domain-containing protein 2A OS=Mus musculus OX=10090 GN=Dennd2a PE=1 SV=1
A5015	-	-	-	-	-	-	-	-
A5016	-	-	-	-	-	-	KAG0054511.1 GATS protein-like 3 [Gryganskiella cystojenkini]	Cytosolic arginine sensor for mTORC1 subunit 1 OS=Rattus norvegicus OX=10116 GN=Castor1 PE=2 SV=1
A5017	-	GO:0032040(small-subunit processome)	-	K14566 UTP24, FCF1; U3 small nucleolar RNA-associated protein 24	map03008 Ribosome biogenesis in eukaryotes	KOG3165 Hs7705730 Predicted nucleic-acid-binding protein, contains PIN domain	ORX69110.1 Fcf1 - domain-containing protein [Linderina pennisporea]	rRNA-processing protein FCF1 homolog OS=Bos taurus OX=9913 GN=FCF1 PE=2 SV=1
A5018	-	-	-	-	-	KOG4293 At3g61750 Predicted membrane protein, contains DoH and Cytochrome b-561/ferric reductase transmembrane domains	KAF1352995.1 CBD9-like protein, partial [Lizonia empirigonia]	Cytochrome b561 and DOMON domain-containing protein At3g61750 OS=Arabidopsis thaliana OX=3702 GN=At3g61750 PE=3 SV=1
A5019	-	-	-	-	-	-	-	-
A5020	-	-	-	-	-	-	-	-
A5021	-	-	GO:0005227(calcium activated cation channel activity),GO:0003676(nucleic acid binding)	-	-	-	-	-
A5022	-	-	GO:0005227(calcium activated cation channel activity)	-	-	-	-	-
A5023	GO:0006631(fatty acid metabolic process)	-	GO:0016491(oxidoreductase activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0003824(catalytic activity),GO:0070403(NAD+ binding)	K00022 HADH; 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]	map01110 Biosynthesis of secondary metabolites;map00907 Pinene, camphor and geraniol degradation;map01120 Microbial metabolism in diverse environments;map00930 Caprolactam degradation;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00062 Fatty acid elongation;map00310 Lysine degradation;map00380 Tryptophan metabolism;map	KOG1683 Hs4503497 Hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase	KXS17231.1 3-hydroxyacyl-CoA dehydrogenase [Gonapodya prolifera JEL478]	Peroxisomal bifunctional enzyme OS=Mus musculus OX=10090 GN=Ehhadh PE=1 SV=4

A5024	GO:0006457(protein folding)	GO:0016272(prefoldin complex)	GO:0051082(unfolded protein binding)	K04798 prfB, PFDN6; prefoldin beta subunit	-	KOG3478 Hs7657162 Prefoldin subunit 6, KE2 family	EKD03917.1 hypothetical protein A1Q2_01930 [Trichosporon asahii var. asahii CBS 8904]	Prefoldin subunit 6 OS=Mus musculus OX=10090 GN=Pfdn6 PE=1 SV=1
A5025	-	-	GO:0000287(magnesium ion binding),GO:0030976(thiamine pyrophosphate binding),GO:0016491(oxidoreductase activity),GO:0003824(catalytic activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	K00135 gabD; succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]	map01120 Microbial metabolism in diverse environments;map00760 Nicotinate and nicotinamide metabolism;map00250 Alanine, aspartate and glutamate metabolism;map00650 Butanoate metabolism;map00310 Lysine degradation;map00350 Tyrosine metabolism;map01100 Metabolic pathways	KOG2451 At1g79440 Aldehyde dehydrogenase	KAG1259014.1 hypothetical protein G6F65_015413 [Rhizopus oryzae]	3-sulfolactaldehyde dehydrogenase OS=Priestia aryabhatai OX=412384 GN=sftD PE=1 SV=1
A5026	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K12765 IME2; meiosis induction protein kinase IME2/SME1 [EC:2.7.11.1]	map04113 Meiosis - yeast	KOG0661 Hs7662388 MAPK related serine/threonine protein kinase	XP_006677720.1 uncharacterized protein BATDEDRAFT_10426, partial [Batrachochytrium dendrobatidis JAM81]	Serine/threonine-protein kinase ICK OS=Mus musculus OX=10090 GN=Cilk1 PE=1 SV=2
A5027	-	-	-	-	-	-	-	Outer dynein arm protein 1 OS=Chlamydomonas reinhardtii OX=3055
A5028	-	GO:0016020(membrane)	-	-	-	-	KAG0185191.1 hypothetical protein DFQ28_009820 [Apophysomycetes sp. BC1034]	Uncharacterized protein YhiD OS=Escherichia coli O157:H7 OX=83334 GN=yhiD PE=3 SV=1
A5029	GO:0044319(sodium-dependent phosphate transport)	GO:0016020(membrane)	GO:0005436(sodium:phosphate symporter activity)	-	-	-	-	Sodium-dependent phosphate transport protein 2B OS=Mus musculus OX=10090 GN=Slc34a2 PE=1 SV=1
A5030	GO:0006419(alanyl-tRNA aminoacylation),GO:0043039(tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0000166(nucleotide binding),GO:0003676(nucleic acid binding),GO:0004813(alanine-tRNA ligase activity),GO:0005524(ATP binding),GO:0004812(aminoacyl-tRNA ligase activity)	K01872 AARS, alaS; alanyl-tRNA synthetase [EC:6.1.1.7]	map00970 Aminoacyl-tRNA biosynthesis	KOG0188 At1g50200 Alanyl-tRNA synthetase	KAF9088198.1 hypothetical protein BGX23_007564 [Mortierella sp. AD031]	Alanine--tRNA ligase OS=Moorella thermoacetica (strain ATCC 39073 / JCM 9320) OX=264732 GN=alaS PE=3 SV=1
A5031	-	-	-	-	-	-	-	-

A5032	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K09578 PIN1; peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 [EC:5.2.1.8]	map03250 Viral life cycle - HIV-1;map04622 RIG-I-like receptor signaling pathway	KOG3259 Hs5453898 Peptidyl-prolyl cis-trans isomerase	KAG1261183.1 hypothetical protein G6F65_014924 [Rhizopus oryzae]	Peptidyl-prolyl cis-trans isomerase C OS=Escherichia coli O157:H7 OX=83334 GN=ppiC PE=3 SV=2
A5033	GO:0006418(tRNA aminoacylation for protein translation),GO:0006429(leucyl-tRNA aminoacylation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004823(leucine-tRNA ligase activity),GO:0002161(aminoacyl-tRNA editing activity)	K01869 LARS, leuS; leucyl-tRNA synthetase [EC:6.1.1.4]	map00970 Aminoacyl-tRNA biosynthesis	-	SAM02498.1 hypothetical protein [Absidia glauca]	Leucine--tRNA ligase OS=Thermosynechococcus vestitus (strain NIES-2133 / IAM M-273 / BP-1) OX=197221 GN=leuS PE=3 SV=1
A5034	-	-	-	-	-	-	-	-
A5035	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0030130(clathrin coat of trans-Golgi network vesicle),GO:0030132(clathrin coat of coated pit)	GO:0005198(structural molecule activity)	-	-	-	-	-
A5036	GO:0006303(double-strand break repair via nonhomologous end joining)	-	GO:0003677(DNA binding)	K10885 XRCC5, KU80, G22P2; ATP-dependent DNA helicase 2 subunit 2	map03450 Non-homologous end-joining	KOG2326 At1g48050 DNA-binding subunit of a DNA-dependent protein kinase (Ku80 autoantigen)	RKP19882.1 SPOC domain-like protein [Rozella allomyces CSF55]	X-ray repair cross-complementing protein 5 OS=Dictyostelium discoideum OX=44689 GN=ku80 PE=3 SV=1
A5037	GO:0009190(cyclic nucleotide biosynthetic process),GO:0035556(intracellular signal transduction)	-	GO:0005515(protein binding)	-	-	KOG3689 7298454 Cyclic nucleotide phosphodiesterase	ORY49320.1 hypothetical protein BCR33DRAFT_579690 [Rhizoclostium globosum]	Adenylate cyclase 1 OS=Stigmatella aurantiaca OX=41 GN=cyaA PE=1 SV=3
A5038	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5039	GO:0000413(protein peptidyl-prolyl isomerization),GO:0006457(protein folding)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K12734 PPIL3; peptidyl-prolyl cis-trans isomerase-like 3 [EC:5.2.1.8]	-	KOG0884 Hs19557636 Similar to cyclophilin-type peptidyl-prolyl cis-trans isomerase	KNE72896.1 peptidyl-prolyl cis-trans isomerase-like 3 [Allomyces macrogynus ATCC 38327]	Peptidyl-prolyl cis-trans isomerase-like 3 OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=CYP10 PE=3 SV=2
A5040	-	-	-	-	-	-	-	-
A5041	-	-	-	K01046 lip, TGL2; triacylglycerol lipase [EC:3.1.1.3]	map00561 Glycerolipid metabolism;map01100 Metabolic pathways	-	PBP21411.1 triacylglycerol lipase [Diplocarpon rosae]	Triacylglycerol lipase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TGL2 PE=1 SV=1
A5042	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	KOG0400 Hs4506685 40S ribosomal protein S13	ORX40388.1 40S ribosomal protein S13 [Piromyces finnis]	Small ribosomal subunit protein uS15 OS=Glycine max OX=3847 GN=RPS13 PE=2 SV=1

A5043	GO:0046514(ceramide catabolic process)	-	GO:0017040(N-acylsphingosine amidohydrolase activity)	K12349 ASAH2; neutral ceramidase [EC:3.5.1.23]	map04071 Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG2232 Hs9845267 Ceramidases	ORX82000.1 Neutral/alkaline nonlysosomal ceramidase [Basidiobolus meristosporus CBS 931.73]	Neutral ceramidase B OS=Dictyostelium discoideum OX=44689 GN=dcd2B PE=3 SV=1
A5044	GO:0016567(protein ubiquitination)	-	GO:0016491(oxidoreductase activity),GO:0004842(ubiquitin-protein transferase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	-	-	KOG0167 At5g42340 FOG: Armadillo/beta-catenin-like repeats	TPX74617.1 hypothetical protein CcCBS67573g04104 [Chytridiomycetes confervae]	U-box domain-containing protein 12 OS=Oryza sativa subsp. japonica OX=39947 GN=PUB12 PE=1 SV=1
A5045	GO:0046907(intracellular transport)	-	-	-	-	KOG2724 7304093 Nuclear pore complex component NPAP60L/NU P50	OSC97453.1 hypothetical protein PYCCODRAFT_1454939 [Trametes coccinea BRFM310]	-
A5046	-	-	-	K17435 MRPL54; large subunit ribosomal protein L54	-	-	XP_016610866.1 hypothetical protein SPPG_01908 [Spizellomyces punctatus DAOM BR117]	Large ribosomal subunit protein mL54 OS=Danio rerio OX=7955 GN=mrpl54 PE=3 SV=2
A5047	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K11227 PBS2; mitogen-activated protein kinase kinase [EC:2.7.12.2]	map04139 Mitophagy - yeast;map04011 MAPK signaling pathway - yeast	KOG0581 At5g56580 Mitogen-activated protein kinase kinase (MAP2K)	PIA15783.1 kinase-like protein [Coemansia reversa NRRL 1564]	Mitogen-activated protein kinase kinase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=MKK1 PE=1 SV=1
A5048	-	-	-	-	-	KOG2743 Hs13236499 Cobalamin synthesis protein	OZJ05703.1 hypothetical protein BZG36_01455 [Bifiguratus adalaidae]	Zinc-regulated GTPase metalloprotein activator 1A OS=Homo sapiens OX=9606 GN=ZNG1A PE=1 SV=1
A5049	-	-	-	-	-	-	-	-
A5050	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0029 At3g10390 Amine oxidase	XP_019026647.1 uncharacterized protein SAICODRAFT_33540 [Saitoella complicata NRRL Y-17804]	Protein FLOWERING LOCUS D OS=Arabidopsis thaliana OX=3702 GN=FLD PE=1 SV=1
A5051	-	-	-	-	-	-	-	-

A5052	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	-	-	KOG0054[Hs9955958 Multidrug resistance-associated protein/mitochondrion resistance protein, ABC superfamily]	PJF19609.1 ATP-binding cassette transporter YOR1 [Paramicrosporidium saccamoebae]	Multidrug resistance-associated protein 1 OS=Bos taurus OX=9913 GN=ABCC1 PE=1 SV=1
A5053	GO:0006069(ethanol oxidation)	-	GO:0008270(zinc ion binding);GO:0051903(S-(hydroxymethyl)glutathione dehydrogenase activity);GO:0016491(oxidoreductase activity)	K00121 frmA ADH5, adhC; S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00830 Retinol metabolism;map00680 Methane metabolism;map01220 Degradation of aromatic compounds;map	KOG0022[At5g43940 Alcohol dehydrogenase, class III]	KXS19996.1 alcohol dehydrogenase [Gonapodya prolifera JEL478]	Alcohol dehydrogenase class-3 OS=Oryza sativa subsp. indica OX=39946 GN=ADHIII PE=3 SV=1
A5054	-	-	-	-	-	-	TPX44542.1 hypothetical protein SeMB42_g04292 [Synchytrium endobioticum]	-
A5055	-	-	-	-	-	-	-	-
A5056	-	-	-	-	-	-	-	-
A5057	-	-	-	-	-	-	-	-
A5058	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding);GO:0004672(protein kinase activity)	K11227 PBS2; mitogen-activated protein kinase kinase [EC:2.7.12.2]	map04139 Mitophagy - yeast;map04011 MAPK signaling pathway - yeast	KOG0581[At4g26070 Mitogen-activated protein kinase kinase (MAP2K)]	SCU87678.1 LADA_0E05490g1_1 [Lachancea dasiensis]	Mitogen-activated protein kinase kinase 1a OS=Physcomitrium patens OX=3218 GN=MKK1a PE=2 SV=1
A5059	-	-	-	-	-	-	-	-
A5060	-	-	-	-	-	-	KAF8941231.1 hypothetical protein BGZ58_001035 [Dissophora ornata]	Growth hormone-regulated TBC protein 1 OS=Homo sapiens OX=9606 GN=GRTP1 PE=1 SV=4
A5061	-	-	-	-	-	-	-	-
A5062	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02921 RP-L37Ae, RPL37A; large subunit ribosomal protein L37Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0402[7296944 60S ribosomal protein L37]	KXL50139.1 hypothetical protein FE78DRAFT_27674 [Acidomyces sp. 'richmondensis']	Large ribosomal subunit protein eL43 OS=Gossypium hirsutum OX=3635 GN=RPL37A PE=3 SV=1
A5063	-	-	-	-	-	-	-	-

A5064	-	-	-	K17795 TIM17; mitochondria l import inner membrane translocase subunit TIM17	-	KOG1652 Hs5 454120 Mitochondria l import inner membrane translocase, subunit TIM17	ORX92603.1 mitochondria l import inner membrane translocase, subunit Tim17/22 [Basidiobolus meristosporu s CBS 931.73]	Mitochondrial import inner membrane translocase subunit Tim17-A OS=Mus musculus OX=10090 GN=Timm17a PE=1 SV=1
A5065	-	-	GO:0003924(GT Pase activity),GO:000 5525(GTP binding)	K07904 RAB11A; Ras-related protein Rab- 11A	map04144 Endocytosis;map 04972 Pancreatic secretion;map04 962 Vasopressin- regulated water reabsorption;ma p04961 Endocrine and other factor- regulated calcium reabsorption;ma p05164 Influenza A	KOG0087 At5 g59150 GTPase Rab11/YPT3, small G protein superfamily	XP_00126991. 5.1 Ras GTPase Rab11, putative [Aspergillus clavatus NRRL 1]	Ras-related protein RGP2 OS=Oryza sativa subsp. japonica OX=39947 GN=RGP2 PE=2 SV=2
A5066	-	-	-	-	-	-	-	-
A5067	-	-	-	-	-	-	-	-
A5068	-	-	GO:0008270(zin c ion binding)	K06874 K06874; zinc finger protein	-	KOG2703 Hs4 508021 C4- type Zn- finger protein	KAF3043181. 1 nucleolar zinc-finger protein [Didymella heteroderae]	Zinc finger protein ZPR1 OS=Mus musculus OX=10090 GN=Zpr1 PE=1 SV=1
A5069	-	-	GO:0000166(nu cleotide binding)	K14950 ATP13A1, SPF1; manganese- transporting P-type ATPase [EC:7.2.2.-]	-	KOG0209 At5 g23630 P- type ATPase	KAG4099841. 1 hypothetical protein H8356DRAFT _1273698 [Neocallimast ix sp. JGI- 2020a]	Probable manganese-transporting ATPase PDR2 OS=Arabidopsis thaliana OX=3702 GN=PDR2 PE=1 SV=1
A5070	GO:00070 18(microt ubule- based movemen t),GO:007 2383(plus -end- directed vesicle transport along microtubu le)	-	GO:0005515(pro tein binding),GO:000 3777(microtubul e motor activity),GO:000 5524(ATP binding),GO:000 8017(microtubul e binding)	K10392 KIF1; kinesin family member 1	map04814 Motor proteins	KOG0245 CE 02031 Kinesin-like protein	RKP33473.1 kif1c protein, partial [Dimargaris crystalligena]	Kinesin-like protein KIF13A OS=Mus musculus OX=10090 GN=Kif13a PE=1 SV=1
A5071	-	-	-	-	-	-	-	-
A5072	-	-	GO:0005524(AT P binding)	-	-	-	XP_01660565 4.1 hypothetical protein SPPG_07082 [Spizellomyce s punctatus DAOM BR117]	ABC transporter ATP-binding protein ModF OS=Escherichia coli (strain K12) OX=83333 GN=modF PE=2 SV=2

A5073	-	-	GO:0003924(GTPase activity)	K24104 GPN; GPN-loop GTPase	-	KOG1532 Hs1.4149629 GTPase XAB1, interacts with DNA repair protein XPA	KAF7730575.1 GPN-loop GTPase 1 [Apophysomyces ossiformis]	GPN-loop GTPase 1 OS=Homo sapiens OX=9606 GN=GPN1 PE=1 SV=1
A5074	-	-	-	-	-	-	EPZ35840.1 hypothetical protein O9G_003558 [Rozella allomyces CSF55]	-
A5075	GO:0006412(translation)	GO:0005840(ribosome),GO:0022625(cytosolic large ribosomal subunit)	GO:0003735(structural constituent of ribosome),GO:0003723(RNA binding)	K02885 RP-L19e, RPL19; large subunit ribosomal protein L19e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1696 7291886 60s ribosomal protein L19	ORY02217.1 hypothetical protein K493DRAFT_312122 [Basidiobolus meristosporus CBS 931.73]	Large ribosomal subunit protein eL19 OS=Drosophila melanogaster OX=7227 GN=RpL19 PE=1 SV=2
A5076	GO:0006508(proteolysis)	-	GO:0008237(metallopeptidase activity),GO:0004222(metalloendopeptidase activity)	-	-	KOG3538 Hs21265061 Disintegrin metalloproteinases with thrombospondin repeats	-	Zinc metalloproteinase/disintegrin OS=Bothrops jararaca OX=8724 PE=1 SV=1
A5077	-	-	GO:0016491(oxidoreductase activity)	K00326 CYB5R; cytochrome-b5 reductase [EC:1.6.2.2]	map00520 Amino sugar and nucleotide sugar metabolism	KOG0534 At5g20080 NADH-cytochrome b-5 reductase	PVV02679.1 hypothetical protein BB560_002861 [Smittium megazygosporum]	NADH-cytochrome b5 reductase-like protein OS=Arabidopsis thaliana OX=3702 GN=CBR2 PE=1 SV=2
A5078	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A5079	-	-	-	-	-	-	KAF9145130.1 hypothetical protein BGX30_010209 [Mortierella sp. GBA39]	Transmembrane protein 180 OS=Bos taurus OX=9913 GN=MFS13A PE=2 SV=1
A5080	-	-	-	-	-	-	-	-
A5081	-	-	-	-	-	-	-	-
A5082	GO:0009107(lipoate biosynthetic process)	-	GO:0016992(lipoate synthase activity),GO:0051539(4 iron, 4 sulfur cluster binding),GO:0003824(catalytic activity),GO:0051536(iron-sulfur cluster binding)	K03644 lipA, LIA5, LIP1, LIP5; lipoyl synthase [EC:2.8.1.8]	map00785 Lipoic acid metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	-	XP_018982341.1 uncharacterized protein BABINDRAFT_163908 [Babjeviella inositovora NRRL Y-12698]	Lipoyl synthase 1, mitochondrial OS=Phaeodactylum tricornutum (strain CCAP 1055/1) OX=556484 GN=PHATR18029 PE=3 SV=1

A5083	GO:0006508(proteolysis)	GO:0005838(proteasome regulatory particle)	-	K03031 PSMD8, RPN12; 26S proteasome regulatory subunit N12	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG3151 At1g64520 26S proteasome regulatory complex, subunit RPN12/PSMD8	ORX82899.1 proteasome 26S subunit [Basidiobolus meristosporus CBS 931.73]	26S proteasome non-ATPase regulatory subunit 8 homolog A OS=Arabidopsis thaliana OX=3702 GN=RPN12A PE=1 SV=1
A5084	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	-	-	KOG0544 7302498 FKBP-type peptidyl-prolyl cis-trans isomerase	TPX71669.1 hypothetical protein CcCBS67573_g06057 [Chytridiomycetes confervae]	FK506-binding protein 1 OS=Dictyostelium discoideum OX=44689 GN=fkbp1 PE=3 SV=1
A5085	GO:0006298(mismatch repair)	-	GO:0005524(ATP binding);GO:0030983(mismatched DNA binding)	K08735 MSH2; DNA mismatch repair protein MSH2	map01524 Platinum drug resistance;map05210 Colorectal cancer;map05200 Pathways in cancer;map03430 Mismatch repair	-	XP_003867187.1 Msh2 DNA mismatch repair factor [Candida orthopsilosis Co 90-125]	DNA mismatch repair protein MutS OS=Listeria innocua serovar 6a (strain ATCC BAA-680 / CLIP 11262) OX=272626 GN=mutS PE=3 SV=1
A5086	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K08850 AURKK; aurora kinase, other [EC:2.7.11.1]	-	KOG0583 Hs5453964 Serine/threonine protein kinase	XP_018294424.1 hypothetical protein PHYBLDRAFT_109842 [Phycomycetes blakesleeanus NRRL 1555(-)]	Serine/threonine protein kinase OSK1 OS=Oryza sativa subsp. japonica OX=39947 GN=OSK1 PE=1 SV=1
A5087	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5088	-	-	-	-	-	-	OUM63396.1 hypothetical protein PIROE2DRAFT_61295 [Piromyces sp. E2]	-
A5089	-	-	-	-	-	-	-	-
A5090	-	-	-	-	-	-	-	-
A5091	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity);GO:0005524(ATP binding);GO:0008017(microtubule binding)	-	-	KOG0241 HsM19923582 Kinesin-like protein	EOD50042.1 putative kinesin family protein [Neofusicoccum parvum UCRNP2]	Kinesin-like protein KIF16B OS=Homo sapiens OX=9606 GN=KIF16B PE=1 SV=2

A5092	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs6005990 Sulfatase	XP_033661590.1 uncharacterized protein M409DRAFT_28840 [Zasmidium cellare ATCC 36951]	Arylsulfatase A OS=Homo sapiens OX=9606 GN=ARSA PE=1 SV=3
A5093	-	-	GO:0004045(aminoacyl-tRNA hydrolase activity)	K04794 PTH2, PTRH2; peptidyl-tRNA hydrolase, PTH2 family [EC:3.1.1.29]	-	KOG3282 YBL057c Uncharacterized conserved protein	KAE8191646.1 hypothetical protein CF328_g5616 [Tilletia controversa]	Peptidyl-tRNA hydrolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PTH2 PE=1 SV=2
A5094	GO:0006355(regulation of transcription, DNA-templated),GO:0009873(ethylene-activated signaling pathway)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	Ethylene-responsive transcription factor WR11 OS=Arabidopsis thaliana OX=3702 GN=WR11 PE=1 SV=1
A5095	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K01551 arsA, ASNA1, GET3; arsenite/tail-anchored protein-transporting ATPase [EC:7.3.2.7 7.3.-.-]	-	KOG2825 Hs14759477 Putative arsenite-translocating ATPase	XP_019014267.1 ATPase GET3 [Kwoniella pini CBS 10737]	ATPase ASNA1 homolog OS=Culex quinquefasciatus OX=7176 GN=CPIJ005690 PE=3 SV=1
A5096	-	-	-	-	-	-	KAF9938159.1 hypothetical protein BGZ65_000282 [Modicella reniformis]	Probable transporter MCH1 OS=Yarrowia lipolytica (strain CLIB 122 / E150) OX=284591 GN=MCH1 PE=3 SV=1
A5097	GO:0055085(transmembrane transport),GO:0006811(ion transport)	GO:0016020(membrane),GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity),GO:0015377(cation:chloride symporter activity)	K14429 SLC12A9, CCC6; solute carrier family 12 (potassium/chloride transporters), member 9	-	KOG2082 At1g30450_1 K+/Cl-cotransporter KCC1 and related transporters	RUP46529.1 amino acid permease-domain-containing protein [Jimgerdennia flammicorona]	Cation-chloride cotransporter 1 OS=Oryza sativa subsp. japonica OX=39947 GN=CCC1 PE=2 SV=1
A5098	-	-	-	-	-	KOG1030 Hs21362014 Predicted Ca2+-dependent phospholipid-binding protein	-	Multiple C2 and transmembrane domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Mctp1 PE=1 SV=4
A5099	-	-	-	-	-	-	-	-

A5100	GO:0007165(signal transduction),GO:007186(G-protein-coupled receptor signaling pathway)	-	GO:0003924(GTPase activity),GO:0019001(guanylnucleotide binding),GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04730 Long-term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082 CE08571 G-protein alpha subunit (small G protein superfamily)	XP_009269255.1 Guanine nucleotide-binding protein subunit alpha-1 subunit [Wallemia ichthyophaga EXF-994]	Guanine nucleotide-binding protein subunit alpha OS=Colletotrichum trifolii OX=5466 GN=CTG1 PE=2 SV=3
A5101	-	-	-	-	-	-	-	-
A5102	-	-	GO:0016491(oxidoreductase activity),GO:0005515(protein binding)	-	-	-	OMH80362.1 Rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] reductase [Zancudomyces culisetiae]	Rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] reductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=rhIG PE=1 SV=1
A5103	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG0779 Hs7662312 Protease, Ulp1 family	ORZ25337.1 hypothetical protein BCR42DRAFT_445125 [Absidia repens]	Sentrin-specific protease 6 OS=Homo sapiens OX=9606 GN=SEN6 PE=1 SV=2
A5104	-	-	-	K07019 K07019; uncharacterized protein	-	KOG1838 At3g50790 Alpha/beta hydrolase	PAV20004.1 lipid metabolism [Pyrrhoderma noxium]	Monoacylglycerol lipase ABHD2 OS=Mus musculus OX=10090 GN=Abhd2 PE=1 SV=1
A5105	-	-	-	K07019 K07019; uncharacterized protein	-	KOG1838 7303936 Alpha/beta hydrolase	KZT68995.1 AB-hydrolase YheT [Daedalea quercina L-15889]	Protein ABHD1 OS=Bos taurus OX=9913 GN=ABHD1 PE=2 SV=1
A5106	GO:0006508(proteolysis)	-	GO:0008237(metallopeptidase activity),GO:0008270(zinc ion binding)	K13721 APE2; aminopeptidase 2 [EC:3.4.11.-]	-	KOG1046 7292091 Puromycin-sensitive aminopeptidase and related aminopeptidases	KAF2221602.1 peptidase family M1-domain-containing protein [Elsinoe ampelina]	Aminopeptidase M1-B OS=Oryza sativa subsp. japonica OX=39947 GN=Os08g0398700 PE=2 SV=1
A5107	-	-	GO:0003725(double-stranded RNA binding)	K07566 tsaC, rimN, SUA5, YRDC; L-threonylcarbamoyladenylate synthase [EC:2.7.7.87]	-	KOG3051 ECU09g1610 RNA binding/translational regulation protein of the SUA5 family	AYO42227.1 tRNA threonylcarbamoyladenylate biosynthesis protein sua5 [Malassezia restricta CBS 7877]	Threonylcarbamoyl-AMP synthase OS=Pyrococcus abyssi (strain GE5 / Orsay) OX=272844 GN=sua5 PE=1 SV=1
A5108	-	-	-	K22483 HMO1; transcriptional regulator HMO1	-	KOG0381 Hs4885421 HMG box-containing protein	EED79332.1 predicted protein [Postia placenta Mad-698-R]	High mobility group protein B3 OS=Homo sapiens OX=9606 GN=HMG3 PE=1 SV=4

A5109	-	-	-	-	-	KOG1786[7292461 Lysosomal trafficking regulator LYST and related BEACH and WD40 repeat proteins	ORX99376.1 beach-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	BEACH domain-containing protein B OS=Arabidopsis thaliana OX=3702 GN=BCHB PE=4 SV=1
A5110	-	-	GO:0005096(GTPase activator activity)	-	-	-	-	-
A5111	GO:0006694(steroid biosynthetic process)	-	GO:0008168(methyltransferase activity)	K00559 SMT1, ERG6; sterol 24-C-methyltransferase [EC:2.1.1.41]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG1269[At5g13710 SAM-dependent methyltransferases	XP_024666435.1 Sterol 24-C-methyltransferase [Wickerhamia sorbophila]	Probable cycloartenol-C-24-methyltransferase 1 OS=Dictyostelium discoideum OX=44689 GN=smt1 PE=1 SV=1
A5112	-	-	-	-	-	-	-	-
A5113	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	-
A5114	-	-	-	-	-	-	-	-
A5115	GO:0001522(pseudouridine synthesis), GO:0009451(RNA modification)	-	GO:0003723(RNA binding),GO:0009982(pseudouridine synthase activity)	K01855 PUS3, DEG1; tRNA pseudouridine synthase [EC:5.4.99.45]	-	KOG2554[Hs13775234 Pseudouridylate synthase	RUS20895.1 pseudouridine synthase [Endogone sp. FLAS-F59071]	tRNA pseudouridine(38/39) synthase OS=Bos taurus OX=9913 GN=PUS3 PE=2 SV=1
A5116	GO:0007018(microtubule-based movement),GO:0072383(plus-end-directed vesicle transport along microtubule)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	-	-	KOG0245[CE29235 Kinesin-like protein	KAG0154633.1 hypothetical protein PDIDSM_201 [Penicillium digitatum]	Kinesin-like protein KIF13A OS=Mus musculus OX=10090 GN=Kif13a PE=1 SV=1
A5117	-	-	-	-	-	-	-	-
A5118	-	-	-	K07107 ybgC; acyl-CoA thioester hydrolase [EC:3.1.2.-]	-	-	KIL68419.1 hypothetical protein M378DRAFT_158217 [Amanita muscaria Koide BX008]	-
A5119	-	-	GO:0005515(protein binding)	K13026 DHX57; ATP-dependent RNA helicase DHX57 [EC:3.6.4.13]	-	KOG0920[At2g01130 ATP-dependent RNA helicase A	XP_016604277.1 hypothetical protein SPPG_08391 [Spizellomyces punctatus DAOM BR117]	Dynein axonemal assembly factor 4 OS=Rattus norvegicus OX=10116 GN=Dnaaf4 PE=1 SV=1
A5120	-	-	-	-	-	-	-	-
A5121	-	-	-	K24939 CWF19L1, DRN1; CWF19-like protein 1	-	KOG2476[Hs20149652 Uncharacterized conserved protein	CCA71590.1 hypothetical protein PIIN_05527 [Serendipita indica DSM 11827]	CWF19-like protein 1 OS=Mus musculus OX=10090 GN=Cwf19l1 PE=1 SV=2

A5122	GO:0006412(translation)	GO:0005840(ribosome),GO:0015935(small ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02998 RP-SAE, RPSA; small subunit ribosomal protein SAE	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0830 Hs9845502 40S ribosomal protein SA (P40)/Laminin receptor 1	TPX78724.1 hypothetical protein CcCBS67573_g00003 [Chytridiomycota confervae]	Small ribosomal subunit protein uS2 OS=Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC MYA-4618 / FGSC 9003) OX=240176 GN=RPS0 PE=3 SV=1
A5123	GO:0006511(ubiquitin-dependent protein catabolic process)	GO:0031464(Cul4A-RING E3 ubiquitin ligase complex)	GO:0046872(metal ion binding)	-	-	-	-	Short transient receptor potential channel 4-associated protein OS=Homo sapiens OX=9606 GN=TRPC4AP PE=1 SV=2
A5124	-	-	-	-	-	-	-	-
A5125	-	-	-	-	-	KOG2223 Hs14745035 Uncharacterized conserved protein, contains TBC domain	KNE70568.1 hypothetical protein AMAG_14690 [Allomyces macrogynus ATCC 38327]	TBC1 domain family member 12 OS=Xenopus tropicalis OX=8364 GN=tbcl12 PE=2 SV=1
A5126	GO:0006281(DNA repair),GO:0006284(base-excision repair)	-	GO:0004844(uracil DNA N-glycosylase activity),GO:0016799(hydrolase activity, hydrolyzing N-glycosyl compounds)	K03648 UNG UDG; uracil-DNA glycosylase [EC:3.2.2.27]	map03410 Base excision repair;map05340 Primary immunodeficiency	KOG2994 Hs6224979 Uracil DNA glycosylase	KAF9115664.1 hypothetical protein BGX30_006197, partial [Mortierella sp. GBA39]	Uracil-DNA glycosylase OS=Pseudomonas fluorescens (strain Pf0-1) OX=205922 GN=ung PE=3 SV=1
A5127	GO:0006468(protein phosphorylation),GO:0007165(signal transduction)	GO:0000159(protein phosphatase type 2A complex)	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0019888(protein phosphatase regulator activity)	K06276 PDPK1; 3-phosphoinositide dependent protein kinase-1 [EC:2.7.1.1.1]	map04360 Axon guidance;map03320 PPAR signaling pathway;map05417 Lipid and atherosclerosis;map04140 Autophagy - animal;map05223 Non-small cell lung cancer;map04722 Neurotrophin signaling pathway;map04510 Focal adhesion;map04210 Apoptosis;map04071 Shingolipid signaling pathway;map01524 Platinum drug resistance;map04919 Thyroid hormone signaling	KOG0592 Hs4505695 3-phosphoinositide-dependent protein kinase (PDK1)	RKP27530.1 phosphoinositide-dependent kinase-1, partial [Syncephalis pseudoplumigaleata]	Putative 3-phosphoinositide-dependent protein kinase 2 OS=Homo sapiens OX=9606 GN=PDPK2P PE=5 SV=1
A5128	-	GO:0005737(cytoplasm)	GO:0005515(protein binding),GO:0016462(pyrophosphatase activity)	-	-	KOG4129 YH R201c Exopolyphosphatases and related proteins	KAF9936951.1 Exopolyphosphatase [Mortierella alpina]	Polyphosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PPX1 PE=1 SV=1
A5129	GO:0006511(ubiquitin-dependent protein catabolic process),GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	-	-	KOG1864 Hs20483065 Ubiquitin-specific protease	KAF9277414.1 Ubiquitin carboxyl-terminal hydrolase 35 [Mortierella alpina]	Ubiquitin carboxyl-terminal hydrolase 35 OS=Homo sapiens OX=9606 GN=USP35 PE=1 SV=3
A5130	-	-	-	-	-	-	-	-

A5131	-	-	GO:0008270(zinc ion binding),GO:0005515(protein binding)	K11419 SUV39H, CLR4; [histone H3]-lysine9 N-trimethyltransferase SUV39H [EC:2.1.1.355]	map00310 Lysine degradation;map01100 Metabolic pathways	KOG1080 At4g15180 Histone H3 (Lys4) methyltransferase complex, subunit SET1 and related methyltransferases	KAF1833031.1 SET domain-containing protein [Decorospora gaudefroyi]	Histone-lysine N-methyltransferase ATXR3 OS=Arabidopsis thaliana OX=3702 GN=ATXR3 PE=2 SV=2
A5132	-	-	GO:0003824(catalytic activity)	K13239 ECI2, PECI; Delta3-Delta2-enoyl-CoA isomerase [EC:5.3.3.8]	map04146 Peroxisome;map00071 Fatty acid degradation	KOG0016 Hs5174625_2 Enoyl-CoA hydratase/isomerase	ORZ22109.1 ClpP/crotonase-like domain-containing protein [Absidia repens]	Enoyl-CoA delta isomerase 2 OS=Rattus norvegicus OX=10116 GN=Eci2 PE=1 SV=1
A5133	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K19584 PRKX; protein kinase X [EC:2.7.11.11]	-	KOG0603 Hs7657526 Ribosomal protein S6 kinase	PJF17839.1 Protein kinase, catalytic domain-containing protein [Paramicrosporidium saccamoebae]	Ribosomal protein S6 kinase alpha-6 OS=Mus musculus OX=10090 GN=Rps6ka6 PE=1 SV=2
A5134	GO:0006396(RNA processing)	GO:0005634(nucleus),GO:1990904(ribonucleoprotein complex)	GO:0003723(RNA binding)	K11090 LA, SSB; lupus La protein	map05322 Systemic lupus erythematosus	KOG4213 7298671 RNA-binding protein La	TPX70844.1 hypothetical protein SpCBS45565_g01418 [Spizellomyces sp. 'palustris']	La protein homolog OS=Aedes albopictus OX=7160 PE=1 SV=1
A5135	-	-	-	-	-	-	-	-
A5136	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0619 7300644_2 FOG; Leucine rich repeat	-	Cyclic GMP-binding protein C OS=Dictyostelium discoideum OX=44689 GN=gbpC PE=1 SV=1
A5137	GO:0019752(carboxylic acid metabolic process)	-	GO:0003824(catalytic activity),GO:0016830(carbon-carbon lyase activity),GO:0030170(pyridoxal phosphate binding)	-	-	KOG0629 CE20226 Glutamate decarboxylase and related proteins	ORY51356.1 PLP-dependent transferase [Rhizoclostridium globosum]	Aspartate 1-decarboxylase OS=Aliivibrio fischeri (strain ATCC 700601 / ES114) OX=312309 GN=panP PE=1 SV=1
A5138	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1198 At4g21580 Zinc-binding oxidoreductase	KAG0190104.1 hypothetical protein DFQ28_002467 [Apophysomyces sp. BC1034]	Quinone oxidoreductase PIG3 OS=Homo sapiens OX=9606 GN=TP5313 PE=1 SV=2
A5139	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 YKL091c Phosphatidylinositol transfer protein SEC14 and related proteins	KAF7354694.1 CRAL-TRIO domain-containing protein [Mycena sanguinolenta]	SEC14 cytosolic factor OS=Eremothecium gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=SEC14 PE=3 SV=2
A5140	-	-	-	-	-	-	-	-

A5141	-	-	GO:0003824(catalytic activity),GO:0031419(cobalamin binding),GO:0046872(metal ion binding),GO:0004494(methylmalonyl-CoA mutase activity),GO:0016866(intramolecular transferase activity),GO:0016853(isomerase activity)	-	-	-	KAG0225216.1 hypothetical protein BGW42_004598 [Actinomortierella wolffii]	Methylmalonyl-CoA mutase, mitochondrial OS=Mus musculus OX=10090 GN=Mmut PE=1 SV=2
A5142	-	-	-	-	-	-	-	-
A5143	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5144	GO:0010960(magnesium ion homeostasis)	-	-	K16302 CNNM; metal transporter CNNM	-	KOG2118 At5g52790 Predicted membrane protein, contains two CBS domains	ORX81142.1 DUF21-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	DUF21 domain-containing protein At5g52790 OS=Arabidopsis thaliana OX=3702 GN=CBSDUF5 PE=2 SV=2
A5145	GO:0006813(potassium ion transport)	GO:0008076(voltage-gated potassium channel complex)	GO:0005249(voltage-gated potassium channel activity)	-	-	-	-	-
A5146	-	-	-	-	-	-	-	-
A5147	-	-	GO:0003724(RNA helicase activity),GO:0005524(ATP binding),GO:0003676(nucleic acid binding)	K13179 DDX18, HAS1; ATP-dependent RNA helicase DDX18/HAS1 [EC:3.6.4.13]	-	KOG0342 YMR290c ATP-dependent RNA helicase HAS1 pitchoune	ORY75855.1 ATP-dependent RNA helicase HAS1 [Neocallimastix californiae]	ATP-dependent RNA helicase has1 OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1 / QM 1276 / 107) OX=344612 GN=has1 PE=3 SV=1
A5148	-	-	-	-	-	-	KNE55341.1 hypothetical protein, variant [Allomyces macrogynus ATCC 38327]	-
A5149	GO:0034729(histone H3-K79 methylation),GO:0051726(regulation of cell cycle)	-	GO:0031151(histone methyltransferase activity (H3-K79 specific)),GO:0018024(histone-lysine N-methyltransferase activity)	-	-	KOG3924 YDR440w Putative protein methyltransferase involved in meiosis and transcriptional silencing (Dot1)	-	-
A5150	-	-	GO:0016301(kinase activity)	-	-	-	CDS14367.1 hypothetical protein LRAMOS06536 [Lichtheimia ramosa]	Sphingoid long chain base kinase 4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=lcb4 PE=3 SV=1

A5151	-	-	GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding),GO:0004499(N,N-dimethylaniline monooxygenase activity)	K00485 FMO; dimethylaniline monooxygenase (N-oxide forming) / hypotaurine monooxygenase [EC:1.14.13.8 1.8.1.-]	map00982 Drug metabolism - cytochrome P450;map00430 Taurine and hypotaurine metabolism;map01100 Metabolic pathways	KOG1399 Hs4503761 Flavin-containing monooxygenase	PUU76745.1 flavin monooxygenase-like protein [Tuber borchii]	Flavin-containing monooxygenase 5 OS=Cavia porcellus OX=10141 GN=FMO5 PE=1 SV=2
A5152	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	AP2/ERF and B3 domain-containing transcription repressor RAV2 OS=Arabidopsis thaliana OX=3702 GN=RAV2 PE=1 SV=1
A5153	-	-	-	-	-	-	-	-
A5154	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K14539 LSG1; large subunit GTPase 1 [EC:3.6.1.-]	map03008 Ribosome biogenesis in eukaryotes	KOG1424 Hs20555662 Predicted GTP-binding protein MMR1	KAG0213339.1 Guanine nucleotide-binding-like protein 1 [Mortierella sp. GBA30]	Guanine nucleotide-binding protein-like 1 OS=Macaca fascicularis OX=9541 GN=GNL1 PE=2 SV=1
A5155	GO:0016567(protein ubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	-	-	KOG4345 Hs2049829_1 NF-kappa B regulator AP20/Cezanne	-	Deubiquitinating protein VCIPI1 OS=Homo sapiens OX=9606 GN=VCIPI1 PE=1 SV=2
A5156	GO:0006629(lipid metabolic process)	-	-	-	-	KOG2088 At1g05790 Predicted lipase/calmodulin-binding heat-shock protein	XP_037223977.1 Lipase-3 domain-containing protein [Mycena indigotica]	-
A5157	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5158	GO:0032981(mitochondrial respiratory chain complex I assembly)	GO:0016020(membrane)	-	-	-	KOG3382 Hs10092657 NADH:ubiquinone oxidoreductase, B17.2 subunit	ORY05604.1 NDUFA12-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Dictyostelium discoideum OX=44689 GN=ndufa12 PE=2 SV=2
A5159	-	-	GO:0005515(protein binding)	-	-	-	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A5160	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0603 Hs7657526 Ribosomal protein S6 kinase	RKP17416.1 Pkinase-domain-containing protein [Rozella allomyces CSF55]	Ribosomal protein S6 kinase alpha-6 OS=Homo sapiens OX=9606 GN=RPS6KA6 PE=1 SV=1
A5161	GO:0009058(biosynthetic process), GO:0016117(carotenoid biosynthetic process)	-	GO:0016491(oxidoreductase activity),GO:0004311(farnesyltransferase activity),GO:0016872(intramolecular lyase activity)	K15745 AL1; phytoene desaturase (3,4-didehydrolycopene-forming) [EC:1.3.99.30]	map01110 Biosynthesis of secondary metabolites;map00906 Carotenoid biosynthesis;map01100 Metabolic pathways	KOG1459 At5g17230 Squalene synthetase	PLW05152.1 hypothetical protein PCANC_2672.2 [Puccinia coronata f. sp. avenae]	Carotenoid 3,4-desaturase OS=Haloarcula japonica (strain ATCC 49778 / DSM 6131 / JCM 7785 / NBRC 101032 / NCIMB 13157 / TR-1) OX=1227453 GN=crtD PE=1 SV=1
A5162	-	-	-	-	-	-	-	-

A5163	-	-	GO:0003824(catalytic activity)	-	-	KOG3957 7300628 Predicted L-carnitine dehydratase/alpha-methylacyl-CoA racemase	OZJ03066.1 hypothetical protein BZG36_03786 [Bifiguratus adalaidae]	Succinyl-CoA--D-citramalate CoA-transferase OS=Chloroflexus aurantiacus (strain ATCC 29366 / DSM 635 / J-10-fl) OX=324602 GN=Caur_2266 PE=3 SV=1
A5164	GO:0006412(translation)	GO:0015935(small ribosomal subunit)	GO:0019843(rRNA binding),GO:0003723(RNA binding),GO:0003735(structural constituent of ribosome)	-	-	KOG3301 At5g39850 Ribosomal protein S4	RKP35296.1 hypothetical protein BJ085DRAFT_39117 [Dimargaris cristalligena]	Small ribosomal subunit protein uS4y OS=Arabidopsis thaliana OX=3702 GN=RPS9C PE=1 SV=1
A5165	-	-	-	-	-	-	RCI06474.1 hypothetical protein CU098_012695 [Rhizopus stolonifer]	-
A5166	-	-	GO:0016491(oxidoreductase activity),GO:0016628(oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor)	-	-	KOG1196 At1g65560 Predicted NAD-dependent oxidoreductase	KAF9994455.1 hypothetical protein BGZ79_000789 [Entomortierella chlamydispora]	Putative NADP-dependent oxidoreductase YfmJ OS=Bacillus subtilis (strain 168) OX=224308 GN=yfmJ PE=2 SV=1
A5167	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9976048.1 hypothetical protein BGZ73_009207 [Actinomortierella ambigua]	Bifunctional serine/threonine-protein kinase/NEDD4-like E3 ubiquitin-protein ligase OS=Dictyostelium discoideum OX=44689 GN=DDB_G0276527 PE=3 SV=2
A5168	-	-	-	-	-	-	-	-
A5169	-	-	GO:0005515(protein binding)	K20520 DBNL, ABP1; drebrin-like protein	-	KOG1029 Hs20544596 Endocytic adaptor protein intersectin	THH27533.1 hypothetical protein EUX98_g6653 [Antridiella citrinella]	Protein app1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=app1 PE=2 SV=1
A5170	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5171	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A5172	-	-	GO:0005509(calcium ion binding)	K19327 ANO10, TMEM16K; anoctamin-10	-	KOG2514 7294638 Uncharacterized conserved protein	KAF9923562.1 Anoctamin-7 [Linnemannia zychae]	Anoctamin-7 OS=Mus musculus OX=10090 GN=Ano7 PE=1 SV=2

A5173	GO:0044571([2Fe-2S] cluster assembly)	-	GO:0030170(pyridoxal phosphate binding);GO:0031071(cysteine desulfurase activity);GO:0003824(catalytic activity)	K04487 iscS, NFS1; cysteine desulfurase [EC:2.8.1.7]	map00730 Thiamine metabolism;map01240 Biosynthesis of cofactors;map04122 Sulfur relay system;map01100 Metabolic pathways	KOG1549 7297897 Cysteine desulfurase NFS1	XP_016609867.1 cysteine desulfurase, mitochondria l [Spizellomyces punctatus DAOM BR117]	Cysteine desulfurase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=Nfs1 PE=1 SV=1
A5174	-	-	GO:0005515(protein binding)	-	-	-	KAF8316837.1 hypothetical protein DL93DRAFT_2056052 [Clavulina sp. PMI_390]	General transcription factor 3C polypeptide 2 OS=Mus musculus OX=10090 GN=Gtf3c2 PE=2 SV=2
A5175	-	-	-	K15436 TRPO3, MTR10; transportin-3	map03250 Viral life cycle - HIV-1;map03013 Nucleocytoplasmic transport	KOG2081 Hs6912734 Nuclear transport regulator	KAG2181691.1 hypothetical protein INT44_008506 [Umbelopsis vinacea]	Transportin-3 OS=Mus musculus OX=10090 GN=Tnpo3 PE=1 SV=1
A5176	-	-	-	-	-	-	-	-
A5177	GO:0043161(proteasome-mediated ubiquitin-dependent protein catabolic process)	-	GO:0004842(ubiquitin-protein transferase activity)	K23333 RMND5; E3 ubiquitin-protein transferase RMND5 [EC:2.3.2.27]	-	KOG2817 Hs21362098 Predicted E3 ubiquitin ligase	KAF8590578.1 hypothetical protein K439DRAFT_1403750 [Ramaria rubella]	E3 ubiquitin-protein transferase RMND5B OS=Mus musculus OX=10090 GN=Rmnd5b PE=2 SV=1
A5178	-	-	-	-	-	-	-	-
A5179	GO:0006166(purine ribonucleoside salvage)	-	GO:0016773(phosphotransferase activity, alcohol group as acceptor);GO:0004001(adenosine kinase activity)	K00856 ADK, adok; adenosine kinase [EC:2.7.1.20]	map00230 Purine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG2854 At3g09820 Possible pfkB family carbohydrate kinase	OUM59583.1 hypothetical protein PIROE2DRAFT_67672 [Piromyces sp. E2]	Adenosine kinase 1 OS=Arabidopsis thaliana OX=3702 GN=ADK1 PE=1 SV=1
A5180	-	-	-	-	-	-	KZT58401.1 hypothetical protein CALCODRAFT_508138 [Calocera cornea HHB12733]	-
A5181	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1

A5182	-	-	GO:0005509(cal- cium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04 022 cGMP-PKG signaling pathway;map04 020 Calcium signaling pathway;map05 417 Lipid and atherosclerosis; map05133 Pertussis;map04 722 Neurotrophin signaling pathway;map04 218 Cellular senescence;map 04070 Phosphatidyli- nitro signaling system;map0491 5 Estrogen signaling pathway;map04 912 GnRH signaling pathway;map04 910 Insulin	KOG0027 729 6957 Calmodulin and related proteins (EF- Hand superfamily)	KAF8652900. 1 hypothetical protein AX16_004088 [Volvariella volvacea WC 439]	Probable calcium-binding protein CML18 OS=Oryza sativa subsp. japonica OX=39947 GN=CML18 PE=2 SV=1
A5183	-	-	GO:0005515(pro- tein binding)	-	-	-	-	-
A5184	GO:00064 68(protein phosphor- ylation)	-	GO:0004672(pro- tein kinase activity)	-	-	-	KAG0095046. 1 hypothetical protein BGZ93_00640 0 [Podila epicladia]	-
A5185	-	-	-	-	-	-	-	-
A5186	GO:00450 48(protein insertion into ER membran- e)	-	GO:0005515(pro- tein binding)	K23387 GET4; golgi to ER traffic protein 4	-	KOG3024 Hs2 0543598 Uncharacteriz- ed conserved protein	KAG0054785. 1 hypothetical protein BGZ83_01046 1 [Gryganskiell a cystojenkini]	Golgi to ER traffic protein 4 homolog OS=Dictyostelium discoideum OX=44689 GN=DDB_G0281815 PE=3 SV=1
A5187	GO:00064 68(protein phosphor- ylation)	-	GO:0004672(pro- tein kinase activity);GO:000 5524(ATP binding)	-	-	KOG0192 At5 g03730 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	ORZ30046.1 kinase-like domain- containing protein [Catenaria anguillulae PL171]	Serine/threonine-protein kinase CTR1 OS=Arabidopsis thaliana OX=3702 GN=CTR1 PE=1 SV=1
A5188	GO:00325 08(DNA duplex unwindin- g);GO:000 6260(DNA replicatio- n);GO:000 6270(DNA replicatio- n initiation)	GO:00425 55(MCM complex)	GO:0003677(DN- A binding);GO:000 5524(ATP binding)	K02541 MCM3; DNA replication licensing factor MCM3 [EC:5.6.2.3]	map03030 DNA replication;map0 4113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	-	KAF9978267. 1 MCM DNA helicase complex subunit [Actinomyces ambigua]	DNA replication licensing factor MCM3 homolog 1 OS=Zea mays OX=4577 GN=ROA1 PE=2 SV=2
A5189	GO:00064 68(protein phosphor- ylation)	-	GO:0004672(pro- tein kinase activity);GO:000 5524(ATP binding)	K08838 STK24_25_MS T4; serine/threon- ine-protein kinase 24/25/MST4 [EC:2.7.11.1]	-	KOG0574 Hs1 6178962 STE20-like serine/threon- ine kinase MST	ORY08629.1 serine/threon- ine kinase 3 [Neocallimast- ix californiae]	Serine/threonine-protein kinase 3 OS=Rattus norvegicus OX=10116 GN=Stk3 PE=1 SV=1
A5190	-	-	-	-	-	-	-	-
A5191	GO:00065 08(proteo- lysis)	-	GO:0004181(me- tallocalcarboxypep- tidase activity);GO:000 8270(zinc ion binding)	-	-	KOG3641 Hs7 662452_3 Zinc carboxypepti- dase	TPX65802.1 hypothetical protein CcBS67573_ g08015 [Chytridiomyc- es confervae]	Cytosolic carboxypeptidase 2 OS=Mus musculus OX=10090 GN=Agbl2 PE=1 SV=1

A5192	GO:0043087(regulation of GTPase activity),GO:0048193(Golgi vesicle transport)	-	-	K20304 TRAPPC6, TRS33; trafficking protein particle complex subunit 6	-	KOG3316 At3g05000 Transport protein particle (TRAPP) complex subunit	RCH95496.1 Trafficking protein particle complex subunit 33 [Rhizopus stolonifer]	Trafficking protein particle complex subunit 6b OS=Danio rerio OX=7955 GN=trappc6b PE=2 SV=1
A5193	-	-	-	-	-	-	-	-
A5194	-	-	-	-	-	KOG1429 At5g28840 dTDP-glucose 4-6-dehydratase/UDP-glucuronic acid decarboxylase	RIB27940.1 hypothetical protein C2G38_1952547 [Gigaspora rosea]	GDP-mannose 3,5-epimerase OS=Arabidopsis thaliana OX=3702 GN=At5g28840 PE=1 SV=1
A5195	-	-	-	-	-	-	-	-
A5196	-	-	-	-	-	-	-	-
A5197	GO:0005975(carbohydrate metabolic process)	-	GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	-	-	-	-	-
A5198	-	-	-	-	-	-	-	-
A5199	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0070588(calcium ion transmembrane transport)	GO:0016020(membrane)	GO:0005216(ion channel activity),GO:0005262(calcium channel activity)	-	-	-	-	Short transient receptor potential channel 6 OS=Bos taurus OX=9913 GN=TRPC6 PE=2 SV=2
A5200	GO:0006352(DNA-templated transcription, initiation)	-	GO:0003676(nucleic acid binding)	K03015 RPB7 POLR2G; DNA-directed RNA polymerase II subunit RPB7	map03420 Nucleotide excision repair;map03020 RNA polymerase;map05016 Huntington disease	KOG3298 At5g59180 DNA-directed RNA polymerase subunit E'	EEQ42992.1 DNA-directed RNA polymerase II 19 kDa polypeptide [Candida albicans WO-1]	DNA-directed RNA polymerase II subunit RPB7 OS=Glycine max OX=3847 PE=2 SV=1
A5201	-	-	-	-	-	-	-	-
A5202	-	-	GO:0005515(protein binding)	K13108 SNIP1; smad nuclear-interacting protein 1	-	KOG1880 Hs13699256 Nuclear inhibitor of phosphatase -1	XP_007725125.1 hypothetical protein A1O1_06055 [Capronia coronata CBS 617.96]	Nuclear inhibitor of protein phosphatase 1 OS=Bos taurus OX=9913 GN=PPP1R8 PE=1 SV=1
A5203	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0030117(membrane coat),GO:0030131(cathrin adaptor complex)	-	K12392 AP1B1; AP-1 complex subunit beta-1	map04142 Lysosome;map05170 Human immunodeficiency virus 1 infection	KOG1061 At4g23460 Vesicle coat complex AP-1/AP-2/AP-4, beta subunit	RIA95100.1 Adaptor protein complex beta subunit [Glomus cerebriforme]	Beta-adaptin-like protein C OS=Arabidopsis thaliana OX=3702 GN=BETAC-AD PE=1 SV=2
A5204	-	-	-	K19658 ECH2; peroxisomal enoyl-CoA hydratase 2 [EC:4.2.1.119]	-	KOG1206 CE01215 Peroxisomal multifunctional beta-oxidation protein and related enzymes	TPX66506.1 hypothetical protein SpCBS45565_g04438 [Spizellomyces sp. 'palustris']	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=3
A5205	-	-	-	-	-	-	-	-

A5206	-	-	-	-	-	-	KAF7724311.1 hypothetical protein EC973_001157 [Apophysomyces ossiformis]	Uncharacterized membrane protein C365.16 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC365.16 PE=4 SV=1
A5207	GO:0006807(nitrogen compound metabolic process)	-	GO:0016151(nickel cation binding)	K03188 ureF; urease accessory protein	-	-	KAF0524590.1 urease accessory protein UreF [Gigaspora margarita]	Urease accessory protein F OS=Arabidopsis thaliana OX=3702 GN=UREF PE=2 SV=1
A5208	GO:0006807(nitrogen compound metabolic process)	-	GO:0016151(nickel cation binding)	K03190 ureD, ureH; urease accessory protein	-	-	KDQ12931.1 hypothetical protein BOTBODRAFT_34072 [Botryobasidium botryosum FD-172 SS1]	Urease accessory protein D OS=Arabidopsis thaliana OX=3702 GN=URED PE=2 SV=1
A5209	-	-	-	-	-	-	-	-
A5210	-	-	-	-	-	-	-	-
A5211	-	GO:0005669(transcription factor TFIIID complex)	-	K03128 TAF2; transcription initiation factor TFIIID subunit 2	map03022 Basal transcription factors	KOG1932[Hs4507347 TATA binding protein associated factor	KIY52676.1 hypothetical protein FISHEDRAFT_63651 [Fistulina hepatica ATCC 64428]	Transcription initiation factor TFIIID subunit 2 OS=Danio rerio OX=7955 GN=taf2 PE=2 SV=2
A5212	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG2852[At5g67290 Possible oxidoreductase	OZJ02579.1 hypothetical protein BZG36_04186 [Bifiguratus adelaidae]	Putative oxidoreductase C1F5.03c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC1F5.03c PE=3 SV=1
A5213	-	-	-	-	-	-	XP_025173902.1 kinase-like domain-containing protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	-
A5214	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1203[At5g02240_1 Predicted dehydrogenase	KAF9120638.1 hypothetical protein BGX30_003073 [Mortierella sp. GBA39]	Sanguinarine reductase OS=Eschscholzia californica OX=3467 GN=SARED1 PE=1 SV=1
A5215	-	-	-	-	-	-	-	-
A5216	-	-	GO:0005515(protein binding)	-	-	KOG2130[At5g06550 Phosphatidylinositol-specific receptor PtdSerR, contains JmjC domain	KAF9423959.1 hypothetical protein BGZ94_008115 [Podila epigama]	Arginine-specific demethylase JM22 OS=Arabidopsis thaliana OX=3702 GN=JM22 PE=1 SV=1

A5217	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	KOG0108 At1g71800 mRNA cleavage and polyadenylation factor I complex, subunit RNA15	RPB29072.1 hypothetical protein L211DRAFT_77228 [Terfezia boudieri ATCC MYA-4762]	Cleavage stimulation factor subunit 2 OS=Bos taurus OX=9913 GN=CSTF2 PE=2 SV=1
A5218	-	-	-	K20242 EVI5; ecotropic viral integration site 5 protein	-	KOG1102 At5g15930 Rab6 GTPase activator GAPCenA and related TBC domain proteins	KZV95128.1 RabGAP/TBC [Exidia glandulosa HHB12029]	Rab GTPase-activating protein eat-17 OS=Caenorhabditis elegans OX=6239 GN=eat-17 PE=1 SV=1
A5219	-	-	-	K15303 AKR7; aflatoxin B1 aldehyde reductase	map00980 Metabolism of xenobiotics by cytochrome P450	-	KIL92279.1 hypothetical protein FAVG1_04688 [Fusarium avenaceum]	Aflatoxin B1 aldehyde reductase member 3 OS=Rattus norvegicus OX=10116 GN=Akr7a3 PE=1 SV=2
A5220	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity),GO:0004965(G protein-coupled GABA receptor activity)	-	-	KOG1055 7300772 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	KNE67424.1 hypothetical protein AMAG_11885 [Allomyces macrogynus ATCC 38327]	Metabotropic glutamate receptor-like protein E OS=Dictyostelium discoideum OX=44689 GN=grlE PE=2 SV=2
A5221	-	-	-	-	-	-	-	-
A5222	-	-	-	-	-	-	-	-
A5223	GO:0045116(protein neddylation)	-	GO:0019781(NEDD8 activating enzyme activity),GO:0008641(ubiquitin-like modifier activating enzyme activity)	K04532 NAE1, APPBP1; NEDD8-activating enzyme E1 regulatory subunit	map05010 Alzheimer disease	KOG2016 Hs4502169 NEDD8-activating complex, APP-BP1/UBA5 component	XP_01660797.6.1 hypothetical protein SPPG_05308 [Spizellomyces punctatus DAOM BR117]	NEDD8-activating enzyme E1 regulatory subunit OS=Xenopus laevis OX=8355 GN=nae1 PE=2 SV=1
A5224	-	-	-	-	-	KOG4825 Hs7662180 Component of synaptic membrane glycine-, glutamate- and thienylcyclohexylpiperidine-binding glycoprotein (43kDa)	XP_01660692.1.1 hypothetical protein SPPG_09321 [Spizellomyces punctatus DAOM BR117]	Centrosomal protein of 104 kDa OS=Homo sapiens OX=9606 GN=CEP104 PE=1 SV=1
A5225	-	-	-	-	-	-	XP_031027353.1 uncharacterized protein SmJEL517_g00745 [Synchytrium microbalum]	-

A5226	GO:0051560(mitochondrial calcium ion homeostasis)	-	GO:0005509(calcium ion binding)	K20858 MCU; calcium uniporter protein, mitochondria	map05014 Amyotrophic lateral sclerosis;map04020 Calcium signaling pathway;map04218 Cellular senescence;map04621 NOD-like receptor signaling pathway;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia	KOG2966[Hs2051015 Uncharacterized conserved protein	XP_016606747.1 hypothetical protein SPPG_06385 [Spizellomyces punctatus DAOM BR117]	Calcium uniporter protein, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=DDB0186972 PE=1 SV=1
A5227	-	GO:0071203(WASH complex)	GO:0005515(protein binding)	-	-	-	XP_007001593.1 uncharacterized protein TREMEDRAFT_59272 [Tremella mesenterica DSM 1558]	Formin-like protein 3 OS=Oryza sativa subsp. japonica OX=39947 GN=FH3 PE=2 SV=2
A5228	-	-	-	-	-	KOG3734[At3g60420 Predicted phosphoglycerate mutase	KAG1467185.1 hypothetical protein G6F56_004550 [Rhizopus deleamar]	Steroid-phosphate phosphatase OS=Caenorhabditis elegans OX=6239 GN=T07F12.1 PE=1 SV=2
A5229	-	-	-	-	-	KOG4039[CE27103 Serine/threonine kinase TIP30/CC3	XP_022456456.1 uncharacterized protein KUUA_T00000401001 [Kuraishia capsulata CBS 1993]	Protein FMP52-1, mitochondrial OS=Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) OX=322104 GN=FMP521 PE=3 SV=1
A5230	-	-	GO:0005096(GTPase activator activity);GO:0005515(protein binding)	K14319 RANGAP1; Ran GTPase-activating protein 1	map03013 Nucleocytoplasmic transport	KOG1909[At5g19320_2 Ran GTPase-activating protein	KAG2194727.1 hypothetical protein INT47_012098 [Mucor saturninus]	RAN GTPase-activating protein 2 OS=Arabidopsis thaliana OX=3702 GN=RANGAP2 PE=1 SV=2
A5231	GO:0007017(microtubule-based process)	GO:0030286(dynein complex)	-	-	-	KOG3430[Hs5031667 Dynein light chain type 1	KAG4101912.1 dynein, axonemal, light polypeptide 4 [Neocallimastix sp. JGI-2020a]	Dynein axonemal light chain 4 OS=Bos taurus OX=9913 GN=DNAL4 PE=3 SV=1

A5232	GO:0005975(carbohydrate metabolic process)	-	-	K01057 PGLS, pgl, devB; 6-phosphogluconolactonase [EC:3.1.1.31]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG3147 Hs6912586 6-phosphogluconolactonase - like protein	KAG2177111.1 hypothetical protein INT43_007767 [Umbelopsis isabellina]	6-phosphogluconolactonase OS=Rattus norvegicus OX=10116 GN=Pgls PE=1 SV=1
A5233	-	-	-	-	-	KOG0417 YDR059c Ubiquitin-protein ligase	KAF8479080.1 ubiquitin-conjugating enzyme [Russula ochroleuca]	Ubiquitin conjugating enzyme E2 B OS=Dictyostelium discoideum OX=44689 GN=ubcB PE=1 SV=1
A5234	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG2733 CE17691 Uncharacterized membrane protein	KAG2178993.1 hypothetical protein INT43_001842 [Umbelopsis isabellina]	Putative trans-acting enoyl reductase Rv2449c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2449c PE=1 SV=3
A5235	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG2733 CE17691 Uncharacterized membrane protein	KAG2178993.1 hypothetical protein INT43_001842 [Umbelopsis isabellina]	Putative trans-acting enoyl reductase Rv2449c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2449c PE=1 SV=3
A5236	GO:0016192(vesicle-mediated transport)	-	GO:0005085(guananyl-nucleotide exchange factor activity)	K20131 RABGEF1; Rab5 GDP/GTP exchange factor	-	KOG2319 At3g19770 Vacuolar assembly/sorting protein VPS9	RKP39955.1 hypothetical protein BJ085DRAFT_9944, partial [Dimargaris cristalligena]	Vacuolar protein sorting-associated protein 9A OS=Arabidopsis thaliana OX=3702 GN=VPS9A PE=1 SV=1
A5237	-	-	GO:0005515(protein binding)	-	-	KOG3765 Hs20557116 Predicted glycosyltransferase	KAF9330958.1 hypothetical protein BG006_006125 [Podila minutissima]	Xylosyl- and glucuronyltransferase LARGE2s OS=Gallus gallus OX=9031 GN=LARGE2 PE=2 SV=1
A5238	-	-	-	-	-	-	-	-
A5239	-	-	-	-	-	-	TPX55112.1 hypothetical protein PhCBS80983_g05589 [Powellomyces hirtus]	Uncharacterized protein SCO2049 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2049 PE=4 SV=2

A5240	GO:0030163(protein catabolic process)	GO:0005737(cytoplasm)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0036402(proteasome-activating activity)	K03063 PSMC4, RPT3; 26S proteasome regulatory subunit T3	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG0727 At5g58290 26S proteasome regulatory complex, ATPase RPT3	KNE60286.1 26S protease regulatory subunit 6B [Allomyces macrogynus ATCC 38327]	26S proteasome regulatory subunit 6B homolog OS=Arabidopsis thaliana OX=3702 GN=RPT3 PE=1 SV=1
A5241	-	-	GO:0046872(metal ion binding)	K17732 PMPCB, MAS1; mitochondria l-processing peptidase subunit beta [EC:3.4.24.64]	-	KOG0959 At5g56730 N-arginine dibasic convertase NRD1 and related Zn2+-dependent endopeptidases, insulinase superfamily	RC12296.1 hypothetical protein L249_0272 [Ophiocordyceps polyrhachis-furcata BCC 54312]	Probable zinc protease PqqL OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=pqqL PE=3 SV=1
A5242	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0159 Hs4503211 Cytochrome P450 CYP11/CYP12/CYP24/CYP27 subfamilies	KAG2111524.1 cytochrome P450 [Suillus discolor]	Sterol 26-hydroxylase, mitochondrial OS=Oryctolagus cuniculus OX=9986 GN=CYP27A1 PE=1 SV=1
A5243	-	-	-	-	-	-	KXS08892.1 hypothetical protein M427DRAFT_50230 [Gonapodya prolifera JEL478]	-
A5244	-	-	-	-	-	-	-	-

A5245	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0159 Hs4503205 Cytochrome P450 CYP11/CYP12/CYP24/CYP27 subfamilies	KAF1831638.1 cytochrome P450 [Decorospora gaudefroyi]	Cytochrome P450 CYP12A2 OS=Musca domestica OX=7370 GN=CYP12A2 PE=2 SV=1
A5246	-	-	-	-	-	-	-	-
A5247	-	-	-	-	-	KOG1672 At3g50960 ATP binding protein	XP_035372301.1 GTPase inhibitor [Lasiodiplodia theobromae]	Thioredoxin domain-containing protein PLP3A OS=Arabidopsis thaliana OX=3702 GN=PLP3A PE=1 SV=1
A5248	GO:0006656(phosphatidylcholine biosynthetic process)	-	GO:0008757(S-adenosylmethionine-dependent methyltransferase activity)	-	-	-	-	Phosphatidyl-N-methylethanolamine N-methyltransferase OS=Arabidopsis thaliana OX=3702 GN=PLMT PE=2 SV=1
A5249	GO:0007264(small GTPase mediated signal transduction),GO:0016192(vesicle-mediated transport)	-	GO:0005085(guananyl-nucleotide exchange factor activity)	-	-	-	-	-
A5250	-	-	-	-	-	-	-	-
A5251	-	-	-	-	-	-	-	-
A5252	-	-	-	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG1113 Hs4506063 cAMP-dependent protein kinase types I and II, regulatory subunit	PVU93691.1 hypothetical protein BB559_003200 [Furculomyces boomerangs]	cAMP-dependent protein kinase regulatory subunit OS=Aplysia californica OX=6500 PE=2 SV=2
A5253	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A5254	-	-	-	-	-	-	-	-
A5255	-	-	-	-	-	KOG2497 7293566 Predicted methyltransferase	OQD72588.1 hypothetical protein PENDEC_c020G04922 [Penicillium decumbens]	Protein N-lysine methyltransferase METTL21A OS=Danio rerio OX=7955 GN=mettl21a PE=2 SV=1
A5256	-	-	-	K03142 TFIH2, GTF2H2, SSL1; transcription initiation factor TFIH subunit 2	map03420 Nucleotide excision repair;map03022 Basal transcription factors;map05203 Viral carcinogenesis	KOG2807 At1g05050 RNA polymerase II transcription initiation/nucleotide excision repair factor TFIH, subunit SSL1	KAG4094491.1 TFIH basal transcription factor complex, subunit SSL1 [Neocallimastix sp. JGI-2020a]	General transcription factor IIF subunit 2 OS=Arabidopsis thaliana OX=3702 GN=GTF2H2 PE=1 SV=1

A5257	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K08856 STK16; serine/threonine kinase 16 [EC:2.7.11.1]	-	KOG2345 Hs4505837 Serine/threonine protein kinase/TGF-beta stimulated factor	KAG2199806.1 hypothetical protein INT47_009419 [Mucor saturninus]	Serine/threonine-protein kinase 16 OS=Rattus norvegicus OX=10116 GN=Stk16 PE=2 SV=2
A5258	GO:0016192(vesicle-mediated transport);GO:0006887(exocytosis);GO:0006886(intracellular protein transport)	GO:0016020(membrane)	GO:0005484(SNAP receptor activity)	K08486 STX1B_2_3; syntaxin 1B/2/3	map04130 SNARE interactions in vesicular transport;map04721 Synaptic vesicle cycle	KOG0810 Hs4759184 SNARE protein Syntaxin 1 and related proteins	RKO97242.1 t-SNARE [Caulochytrium protostelioides]	Syntaxin-3 OS=Homo sapiens OX=9606 GN=STX3 PE=1 SV=3
A5259	-	-	-	-	-	-	-	-
A5260	GO:0006457(protein folding)	-	-	K14002 SCJ1; DnaJ-related protein SCJ1	map04141 Protein processing in endoplasmic reticulum	KOG0722 At1g61770 Molecular chaperone (DnaJ) superfamily)	XP_004178709.1 hypothetical protein TBLA_0B03490 [Tetrapispora blattae CBS 6284]	DnaJ homolog subfamily C member 25 OS=Xenopus tropicalis OX=8364 GN=dnaJc25 PE=2 SV=1
A5261	GO:0000387(spliceosomal snRNP assembly)	GO:0005681(spliceosomal complex)	-	-	-	KOG1780 At2g23930 Small Nuclear ribonucleoprotein G	KAG2177463.1 hypothetical protein INT44_007974 [Umbelopsis vinacea]	Probable small nuclear ribonucleoprotein G OS=Dictyostelium discoideum OX=44689 GN=snrpG PE=3 SV=1
A5262	-	-	GO:0008168(methyltransferase activity)	K15336 TRDMT1, DNMT2; tRNA (cytosine38-C5)-methyltransferase [EC:2.1.1.204]	-	-	XP_013023584.1 DNA methyltransferase [Schizosaccharomyces cryophilus OY26]	tRNA (cytosine(38)-C(5))-methyltransferase OS=Rattus norvegicus OX=10116 GN=Trdmt1 PE=2 SV=1
A5263	-	-	GO:0070403(NAD+ binding)	K11121 SIR2; NAD-dependent protein deacetylase SIR2 [EC:2.3.1.286]	map04213 Longevity regulating pathway - multiple species;map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	-	KAG1734500.1 Sir2 family histone deacetylase Hst2 [Suillus lakei]	NAD-dependent protein deacetylase sirtuin-2 OS=Danio rerio OX=7955 GN=sirt2 PE=1 SV=1
A5264	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	K15628 PXA; ATP-binding cassette, subfamily D (ALD), peroxisomal long-chain fatty acid import protein [EC:7.6.2.4]	map04146 Peroxisome;map02010 ABC transporters	KOG0064 Hs7262393 Peroxisomal long-chain acyl-CoA transporter, ABC superfamily	EJT99192.1 hypothetical protein DACRYDRAFT_82277 [Dacryopinax primogenitus]	ABC transporter D family member 2 OS=Dictyostelium discoideum OX=44689 GN=abcD2 PE=3 SV=1
A5265	-	-	-	K11407 HDAC6; histone deacetylase 6 [EC:3.5.1.98]	map05014 Amyotrophic lateral sclerosis;map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG1343 At4g33470 Histone deacetylase complex, catalytic component HDA1	KII91458.1 hypothetical protein PLICRDRAFT_173305 [Plicaturopsis crispa FD-325 SS-3]	Histone deacetylase-like amidohydrolase OS=Alcaligenes sp. (strain DSM 11172) OX=242601 GN=hdaH PE=1 SV=3

A5266	-	-	GO:0003723(RNA binding)	K17943 PUM; pumilio RNA-binding family	map05017 Spinocerebellar ataxia	KOG1488 CE05044 Translational repressor Pumilio/PUF3 and related RNA-binding proteins (Puf superfamily)	KAF8495613.1 armadillo-type protein [Gautieria morchelliformis]	Pumilio domain-containing protein C6G9.14 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC6G9.14 PE=4 SV=1
A5267	-	-	-	-	-	-	-	-
A5268	-	-	GO:0008237(metallopeptidase activity)	-	-	-	-	-
A5269	GO:0016310(phosphorylation),GO:0006355(regulation of transcription, DNA-templated),GO:0000160(phosphorelay signal transduction system)	-	GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	KOG0519 At2g47430 Sensory transduction histidine kinase	EPZ32364.1 hypothetical protein O9G_002204 [Rozella allomycis CSF55]	Sensory/regulatory protein RpfC OS=Xanthomonas campestris pv. campestris (strain 8004) OX=314565 GN=rpfC PE=1 SV=2
A5270	-	-	-	-	-	-	-	ATP-dependent dethiobiotin synthetase BioD OS=Cyanotheca sp. (strain PCC 7425 / ATCC 29141) OX=395961 GN=bioD PE=3 SV=1
A5271	-	-	-	-	-	KOG0756 YMR241w Mitochondrial tricarboxylate/dicarboxylate carrier proteins	TPX62883.1 hypothetical protein PhCBS80983_g00164 [Powellomyces hirtus]	Citrate/oxoglutarate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHM2 PE=1 SV=1
A5272	GO:0006508(proteolysis)	-	GO:0005515(protein binding),GO:0008236(serine-type peptidase activity)	-	-	-	-	Tricorn protease homolog 1 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=tri1 PE=1 SV=1
A5273	-	-	-	-	-	-	-	-
A5274	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG2504 Hs20559959 Monocarboxylate transporter	ORY03792.1 MFS general substrate transporter [Basidiobolus meristosporus CBS 931.73]	MFS-type transporter 1 OS=Ophiocordyceps sp. (strain BCC 1869) OX=1590024 GN=MFS1 PE=1 SV=1
A5275	-	GO:0005856(cytoskeleton),GO:0016459(myosin complex)	GO:0005515(protein binding),GO:0003774(motor activity),GO:0005524(ATP binding)	-	-	KOG0160 At4g28710 Myosin class V heavy chain	KAE9397351.1 hypothetical protein BT96DRAFT_823455 [Gymnopus androsaceus JB14]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1
A5276	-	-	-	-	-	-	-	-
A5277	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5278	GO:0006811(ion transport)	-	-	-	-	-	-	Probable ion channel CASTOR OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0843600 PE=2 SV=1

A5279	GO:0006400(tRNA modification)	-	GO:0003824(catalytic activity),GO:0051536(iron-sulfur cluster binding),GO:0051539(4 iron, 4 sulfur cluster binding),GO:0035596(methylthio transferase activity),GO:0016740(transferase activity)	-	-	KOG2492 At4g36390 CDK5 activator-binding protein	KAG0037371.1 CDK5 regulatory subunit associated protein 1 [Podilla clonocystis]	Mitochondrial tRNA methylthiotransferase CDK5RAP1 OS=Homo sapiens OX=9606 GN=CDK5RAP1 PE=1 SV=2
A5280	GO:1902600(proton transmembrane transport)	GO:0033179(proton-transporting V-type ATPase, V0 domain)	GO:0046961(proton-transporting ATPase activity, rotational mechanism)	K02146 ATPeV0D, ATP6D; V-type H+-transporting ATPase subunit d	map04145 Phagosome;map04142 Lysosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation;map05203 Viral carcinogenesis;map05110 Vibrio cholerae infection;map05120 Epithelial cell signaling in Helicobacter pylori infection;map05152 Tuberculosis;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human	KOG2957 At3g28710 Vacuolar H+-ATPase V0 sector, subunit d	OON05763.1 hypothetical protein BSLG_04427 [Batrachochytrium salamandrivorans]	V-type proton ATPase subunit d OS=Dictyostelium discoideum OX=44689 GN=vatD-1 PE=1 SV=2
A5281	-	-	GO:0005515(protein binding)	-	-	-	PTB78247.1 SET domain-containing protein [Trichoderma longibrachiatum ATCC 18648]	-
A5282	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08850 AURKX; aurora kinase, other [EC:2.7.11.1]	-	KOG0192 At5g49470 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF7747845.1 hypothetical protein DSO57_020938 [Entomophthora muscae]	Putative serine/threonine-protein kinase/receptor R831 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_R831 PE=3 SV=2
A5283	GO:0006633(fatty acid biosynthetic process)	-	GO:0050080(malonyl-CoA decarboxylase activity)	-	-	KOG3018 Hs6912498 Malonyl-CoA decarboxylase	OAJ38151.1 hypothetical protein BDEG_22104 [Batrachochytrium dendrobatidis JEL423]	Malonyl-CoA decarboxylase, mitochondrial OS=Anser anser anser OX=8844 GN=MLYCD PE=1 SV=2
A5284	GO:0006886(intracellular protein transport),GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	GO:0030127(COPII vesicle coat)	GO:0008270(zinc ion binding)	K14007 SEC24; protein transport protein SEC24	map04141 Protein processing in endoplasmic reticulum;map05130 Pathogenic Escherichia coli infection	KOG1984 Hs4758634 Vesicle coat complex COPII, subunit SFB3	RIB17889.1 Sec23/Sec24 trunk domain-containing protein [Gigaspora rosea]	Protein transport protein Sec24C OS=Homo sapiens OX=9606 GN=SEC24C PE=1 SV=3

A5285	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02960 RP-S16e, RPS16; small subunit ribosomal protein S16e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1753 Hs4506691.40S ribosomal protein S16	RIA98489.1 ribosomal protein S5 domain 2-type protein [Glomus cerebriforme]	Small ribosomal subunit protein uS9 OS=Gossypium hirsutum OX=3635 GN=RPS16 PE=2 SV=1
A5286	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02873 RP-L13e, RPL13; large subunit ribosomal protein L13e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3295 At3g49010.60S Ribosomal protein L13	KAF9574206.1.60S ribosomal protein L13 [Mortierella alpina]	Large ribosomal subunit protein eL13 OS=Danio rerio OX=7955 GN=rpl13 PE=1 SV=3
A5287	-	-	-	-	-	-	-	-
A5288	-	-	-	-	-	-	-	-
A5289	-	-	-	-	-	-	-	-
A5290	GO:0006508(proteolysis)	GO:0005576(extracellular region)	GO:0005515(protein binding)	-	-	-	-	-
A5291	-	-	-	-	-	-	-	-
A5292	-	-	-	-	-	-	-	-
A5293	-	-	GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	K11884 PNO1, DIM2; RNA-binding protein PNO1	-	-	RKP12285.1 pre-rRNA-processing protein PNO1 [Piptocephalis cylindrospora]	RNA-binding protein pno1 OS=Nematostella vectensis OX=45351 GN=pno1 PE=3 SV=1
A5294	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0000981(DNA-binding transcription factor activity, RNA polymerase II-specific),GO:0008270(zinc ion binding)	-	-	-	RMX72225.1 hypothetical protein D0869_14835 [Hortaea werneckii]	Xylanolytic transcriptional activator xlnR OS=Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / IAM 13836 / NRRL 3357 / JCM 12722 / SRR 167) OX=332952 GN=xlnR PE=3 SV=1
A5295	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	K20520 DBNL, ABP1; drebrin-like protein	-	-	OUM60404.1 hypothetical protein PIROE2DRAFT_52039 [Piromyces sp. E2]	Protein app1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=app1 PE=2 SV=1
A5296	-	-	-	-	-	-	-	-
A5297	-	-	-	-	-	-	-	-
A5298	-	-	-	K24083 ABHD13; abhydrolase domain-containing protein 13 [EC:3.-.-.-]	-	KOG4391 7295869 Predicted alpha/beta hydrolase BEM46	ORY86705.1 Alpha/Beta hydrolase protein [Leucosporidium creatinivorum]	Protein ABHD13 OS=Danio rerio OX=7955 GN=abhd13 PE=2 SV=1
A5299	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5300	-	-	-	-	-	-	-	-
A5301	-	-	GO:0005515(protein binding)	-	-	KOG1337 At3g07670 N-methyltransferase	OVF07500.1 putative protein-lysine N-methyltransferase [Clavispora lusitanae]	SET domain-containing protein 4 OS=Homo sapiens OX=9606 GN=SETD4 PE=1 SV=1
A5302	GO:1901170(naphthalene catabolic process)	-	GO:0018845(2-hydroxychromene-2-carboxylate isomerase activity),GO:0016491(oxidoreductase activity)	-	-	-	GAA96993.1 hypothetical protein E5Q_03668 [Mixia osmundae IAM 14324]	2-hydroxychromene-2-carboxylate isomerase OS=Pseudomonas sp. (strain C18) OX=69011 GN=doxj PE=3 SV=1
A5303	-	-	-	-	-	-	-	-
A5304	-	-	GO:0005515(protein binding)	-	-	-	-	-

A5305	GO:0015940(pantothenate biosynthetic process)	-	GO:0004592(pantoate-beta-alanine ligase activity)	K01918 panC; pantoate--beta-alanine ligase [EC:6.3.2.1]	map00410 beta-Alanine metabolism;map00770 Pantothenate and CoA biosynthesis;map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	-	ORY82686.1 pantoate/beta-alanine ligase [Protomyces lactucaedebilis]	Pantothenate synthetase OS=Chloroflexus aggregans (strain MD-66 / DSM 9485) OX=326427 GN=panC PE=3 SV=1
A5306	GO:0032259(methylation)	-	GO:0008168(methyltransferase activity);GO:0003676(nucleic acid binding)	K19589 N6AMT1; release factor glutamine methyltransferase [EC:2.1.1.297]	-	KOG3191 Hs7019463 Predicted N6-DNA-methyltransferase	RKP07955.1 S-adenosyl-L-methionine-dependent methyltransferase [Thamnocephalis sphaerospora]	Methyltransferase N6AMT1 OS=Homo sapiens OX=9606 GN=N6AMT1 PE=1 SV=4
A5307	GO:0097428(protein maturation by iron-sulfur cluster transfer)	-	GO:0051537(2 iron, 2 sulfur cluster binding)	-	-	KOG3348 At5g09830 BolA (bacterial stress-induced morphogen)-related protein	KAG0734315.1 hypothetical protein G6F23_012510 [Rhizopus oryzae]	Protein BOLA2 OS=Arabidopsis thaliana OX=3702 GN=BOLA2 PE=1 SV=1
A5308	-	-	GO:0005515(protein binding)	-	-	KOG1337 At3g07670 N-methyltransferase	OBZ84508.1 N-lysine methyltransferase SETD6 [Choanephora cucurbitarum]	Actin-histidine N-methyltransferase OS=Gallus gallus OX=9031 GN=SETD3 PE=2 SV=1
A5309	-	-	GO:0005515(protein binding)	K03350 APC3; CDC27; anaphase-promoting complex subunit 3	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	-	PGH23630.1 hypothetical protein AJ80_02236 [Polytolypa hystrix UAMH7299]	Protein bimA OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / IM139) OX=227321 GN=bimA PE=2 SV=1

A5310	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0157 At5g38450 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	RVX66975.1 hypothetical protein B0A52_09189 [Exophiala mesophila]	Cytokinin hydroxylase OS=Arabidopsis thaliana OX=3702 GN=CYP735A1 PE=1 SV=1
A5311	GO:0008380(RNA splicing)	GO:0030532(small nuclear ribonucleoprotein complex)	-	K11096 SNRPD2, SMD2; small nuclear ribonucleoprotein D2	map03040 Spliceosome	KOG3459 CE08945 Small nuclear ribonucleoprotein (snRNP) Sm core protein	PIA19008.1 Sm-like ribonucleoprotein [Coemansia reversa NRRL1564]	Probable small nuclear ribonucleoprotein Sm D2 OS=Dictyostelium discoideum OX=44689 GN=snrpd2 PE=3 SV=1
A5312	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K14439 SMARCA1; SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 [EC:5.6.2.-]	map04550 Signaling pathways regulating pluripotency of stem cells	KOG0389 At2g02090 SNF2 family DNA-dependent ATPase	XP_001731526.1 hypothetical protein MGL_1709 [Malassezia globosa CBS7966]	Protein CHROMATIN REMODELING 19 OS=Arabidopsis thaliana OX=3702 GN=ETL1 PE=1 SV=1
A5313	-	-	GO:0000340(RNA 7-methylguanosine cap binding),GO:0003729(mRNA binding)	-	-	KOG4441 At2g30600 Proteins containing BTB/POZ and Kelch domains, involved in regulatory/signaling transduction processes	KAF9430677.1 hypothetical protein BGZ94_005107 [Podila epigama]	BTB/POZ domain-containing protein At2g30600 OS=Arabidopsis thaliana OX=3702 GN=At2g30600/At2g30610 PE=2 SV=1
A5314	-	-	-	-	-	-	-	-
A5315	-	-	-	-	-	-	-	Ribitol-5-phosphate xylosyltransferase 1 OS=Homo sapiens OX=9606
A5316	GO:0007165(signal transduction)	-	GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity),GO:0008081(phosphoric diester hydrolase activity)	-	-	KOG3689 Hs5453862 Cyclic nucleotide phosphodiesterase	ORZ01631.1 hypothetical protein BCR43DRAFT_487241 [Syncephalaster racemosus]	3',5'-cyclic-AMP phosphodiesterase 4A OS=Mus musculus OX=10090 GN=Pde4a PE=1 SV=2
A5317	-	-	GO:0030246(carbohydrate binding)	-	-	-	-	-
A5318	GO:0006508(proteolysis)	-	GO:0008236(serine-type peptidase activity)	-	-	KOG2183 Hs7019511 Prolylcarboxypeptidase (angiotensinase C)	KAF2111380.1 peptidase S28 [Lophiotrema nucula]	Dipeptidyl peptidase 2 OS=Mus musculus OX=10090 GN=Dpp7 PE=1 SV=2

A5319	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	-	-	-	KAG0288367.1 hypothetical protein BGZ96_00784.1 [Linnemania gamsii]	Prolyl 4-hydroxylase subunit alpha OS=Dictyostelium discoideum OX=44689 GN=phyA PE=1 SV=1
A5320	GO:0006606(protein import into nucleus)	GO:0005737(cytoplasm)	GO:0005515(protein binding),GO:0061608(nuclear import signal receptor activity)	K15042 KPNA5_6; importin subunit alpha-6/7	map03013 Nucleocytoplasmic transport;map05207 Chemical carcinogenesis - receptor activation;map05164 Influenza A	KOG0166 At1g09270 Karyopherin (importin) alpha	RKO85499.1 armadillo-type protein [Blyttomyces helicus]	Importin subunit alpha-4 OS=Arabidopsis thaliana OX=3702 GN=IMPA4 PE=1 SV=1
A5321	GO:0000338(protein deneddylation)	GO:0008180(COP9 signalosome)	GO:0005515(protein binding)	K12175 GPS1, COPS1, CSN1; COP9 signalosome complex subunit 1	-	KOG0686 At3g61140 COP9 signalosome, subunit CSN1	CDH52777.1 cop9 signalosome complex subunit 1 [Lichtheimia corymbifera JMR:FSU:9682]	COP9 signalosome complex subunit 1 OS=Arabidopsis thaliana OX=3702 GN=CSN1 PE=1 SV=2
A5322	GO:0016192(vesicle-mediated transport), GO:0006623(protein targeting to vacuole)	-	-	K20195 MON1; vacuolar fusion protein MON1	map04138 Autophagy - yeast	KOG0997 Hs14150159 Uncharacterized conserved protein Sand	KAF9570612.1 Vacuolar fusion protein mon1b [Mortierella alpina]	Vacuolar fusion protein MON1 OS=Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) OX=321614 GN=MON1 PE=3 SV=1
A5323	-	-	GO:0005515(protein binding)	K13886 CORO1B_1C_6; coronin-1B/1C/6	-	KOG0303 Hs7656991 Actin-binding protein Coronin, contains WD40 repeats	EPZ31343.1 DUF1900 domain-containing protein [Rozella allomyces CSF55]	Coronin-1C OS=Mus musculus OX=10090 GN=Coro1c PE=1 SV=2
A5324	-	-	-	-	-	KOG0911 At4g04950 Glutaredoxin-related protein	XP_01660416.1.1 Grx4 family monothiol glutaredoxin [Spizellomyces punctatus DAOM BR117]	Monothiol glutaredoxin-S17 OS=Arabidopsis thaliana OX=3702 GN=GRXS17 PE=1 SV=1
A5325	-	-	GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor),GO:0016491(oxidoreductase activity)	-	-	-	KAF8156675.1 succinate semialdehyde dehydrogenase [Crassisporium funariophilum]	Succinate-semialdehyde dehydrogenase [NADP(+)] OS=Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / CCUG 27074 / LMG 4051 / NBRC 15346 / NCIMB 9279 / VKM B-1422 / R1) OX=243230 GN=ssdA PE=3 SV=1

A5326	GO:001700(antibiotic biosynthetic process)	-	GO:0016787(hydrolase activity),GO:0016811(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides)	-	-	-	KXS18991.1 N-terminal nucleophile aminohydrolase [Gonapodya prolifera JEL478]	Acyl-homoserine lactone acylase QuiP OS=Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) OX=223283 GN=quiP PE=3 SV=1
A5327	-	-	-	-	-	-	TPX73630.1 hypothetical protein CcCBS67573_g05106 [Chytridiomycetes confervae]	Basal body-orientation factor 1 OS=Danio rerio OX=7955 GN=bbof1 PE=2 SV=2
A5328	-	-	-	-	-	-	-	-
A5329	-	-	GO:0005509(calcium ion binding),GO:0005515(protein binding)	K16466 CETN3, CDC31; centrin-3	-	-	TPX40966.1 hypothetical protein SeMB42_g05806 [Synchytrium endobioticum]	Protein fantom OS=Mus musculus OX=10090 GN=Rpgrip1l PE=1 SV=2
A5330	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 At4g39180 Phosphatidylinositol transfer protein SEC14 and related proteins	ORX94477.1 hypothetical protein K493DRAFT_315461 [Basidiobolus meristosporus CBS 931.73]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana OX=3702 GN=SFH2 PE=3 SV=1
A5331	-	-	GO:0005524(ATP binding),GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding)	K03257 EIF4A; translation initiation factor 4A	-	KOG0327 Hs4503531 Translation initiation factor 4F, helicase subunit (eIF-4A) and related helicases	KAF9792152.1 P-loop containing nucleoside triphosphate hydrolase protein [Thelephora terrestris]	ATP-dependent RNA helicase eIF4A OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) OX=341663 GN=tif1 PE=3 SV=2
A5332	GO:0015031(protein transport)	GO:0030173(integral component of Golgi membrane)	-	K08504 BET1; blocked early in transport 1	map04130 SNARE interactions in vesicular transport	KOG3385 Hs5031611 V-SNARE	KNE63949.1 hypothetical protein AMAG_09012 [Allomyces macrogynus ATCC 38327]	BET1 homolog OS=Rattus norvegicus OX=10116 GN=Bet1 PE=1 SV=1
A5333	-	-	-	-	-	-	-	-
A5334	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG1287 At3g19553 Amino acid transporters	ORZ36023.1 cationic amino acid transporter [Catenaria anguillulae PL171]	Probable polyamine transporter At3g19553 OS=Arabidopsis thaliana OX=3702 GN=At3g19553 PE=3 SV=1
A5335	-	-	-	K22721 CSG1, SUR1, CSH1; inositol phosphorylceramide mannosyltransferase catalytic subunit [EC:2.4.1.370]	-	-	EEB87546.1 hypothetical protein MPER_15070, partial [Moniliophthora perniciosa FA553]	Inositol phosphoceramide mannosyltransferase 3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC17G8.11c PE=1 SV=1

A5336	-	-	-	K11982 RNF115_126; E3 ubiquitin- protein ligase RNF115/126 [EC:2.3.2.27]	-	-	KOG0800 At5 g05810 FOG: Predicted E3 ubiquitin ligase	PKK70360.1 hypothetical protein RhiirC2_4672 22 [Rhizophagus irregularis]	RING-H2 finger protein ATL43 OS=Arabidopsis thaliana OX=3702 GN=ATL43 PE=2 SV=2
A5337	-	-	-	-	-	-	-	-	-
A5338	-	-	-	-	-	-	-	EPZ32445.1 NAD(P)- binding domain - containing protein [Rozella allomyces CSF55]	NAD(P)H azoreductase OS=Xenophilus azovorans OX=151755 GN=azoB PE=1 SV=2
A5339	-	GO:00160 21(integra l compone nt of membra ne)	GO:0003779(acti n binding)	-	-	-	-	-	-
A5340	-	-	-	-	-	-	-	-	-
A5341	-	GO:00164 59(myosin complex)	GO:0003774(mo tor activity),GO:000 5524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04 814 Motor proteins	KOG0160 At3 g58160 Myosin class V heavy chain	XP_01659728 2.1 Dilute [Penicillium expansum]	Myosin-16 OS=Arabidopsis thaliana OX=3702 GN=XI-J PE=2 SV=1	
A5342	GO:00063 55(regulat ion of transcrip tion, DNA- templated)	-	GO:0003700(DN A-binding transcription factor activity),GO:004 3565(sequence- specific DNA binding)	-	-	KOG0627 At5 g45710 Heat shock transcription factor	KXN69427.1 winged helix DNA-binding domain - containing protein [Conidiobolu s coronatus NRRL 28638]	Heat stress transcription factor A-4c OS=Arabidopsis thaliana OX=3702 GN=HSFA4C PE=2 SV=1	
A5343	-	-	-	-	-	-	-	-	-
A5344	-	-	-	-	-	-	-	RKO87368.1 hypothetical protein BDK51DRAFT _38375 [Blyttiomycet helicus]	-
A5345	-	GO:00058 71(kinesin complex)	GO:0005515(pro tein binding)	-	-	-	-	ORY31577.1 TPR-like protein [Rhizoclosma tium globosum]	-
A5346	-	GO:00160 21(integra l compone nt of membra ne)	-	-	-	-	-	-	-
A5347	-	GO:00160 21(integra l compone nt of membra ne)	-	K17086 TM9SF2_4; transmembra ne 9 superfamily member 2/4	-	KOG1278 At3 g13772 Endosomal membrane proteins, EMP70	TPX61961.1 hypothetical protein PhCBS80983 g00813 [Powellomyce s hirtus]	Transmembrane 9 superfamily member 7 OS=Arabidopsis thaliana OX=3702 GN=TMN7 PE=2 SV=1	
A5348	-	-	GO:0008239(dip eptidyl- peptidase activity),GO:001 6787(hydrolase activity)	K06978 K06978; uncharacteriz ed protein	-	-	-	KPM36175.1 hypothetical protein AK830_g1039 8 [Neonectria ditissima]	Cocaine esterase OS=Rhodococcus sp. (strain MB1 Bresler) OX=104109 GN=cocE PE=1 SV=1

A5349	GO:0000398(mRNA splicing, via spliceosome)	GO:0005681(spliceosomal complex)	GO:0003723(RNA binding),GO:0030623(U5 snRNA binding),GO:0005515(protein binding),GO:0008233(peptidase activity),GO:0008237(metalloproteinase activity),GO:0017070(U6 snRNA binding)	K12856 PRPF8, PRPF8; pre-mRNA-processing factor 8	map03040 Spliceosome	KOG1795 At1g80070 U5 snRNP spliceosome subunit	KAG2180580.1 hypothetical protein [INT44_003584 [Umbelopsis vinacea]	Pre-mRNA-processing-splicing factor 8 OS=Mus musculus OX=10090 GN=Prpf8 PE=1 SV=2
A5350	-	-	GO:0005515(protein binding)	K02180 BUB3; cell cycle arrest protein BUB3	map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG1036 Hs4757880 Mitotic spindle checkpoint protein BUB3, WD repeat superfamily	ORX90961.1 mitotic checkpoint protein BUB3-like protein [Basidiobolus meristosporus CBS 931.73]	Mitotic checkpoint protein BUB3 OS=Bos taurus OX=9913 GN=BUB3 PE=2 SV=1
A5351	GO:0043087(regulation of GTPase activity)	-	GO:0005515(protein binding),GO:0005096(GTPase activator activity)	-	-	KOG1450 Hs20558968 Predicted Rho GTPase-activating protein	-	Rho GTPase-activating protein 27 OS=Rattus norvegicus OX=10116 GN=Arhgap27 PE=1 SV=1
A5352	-	-	-	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis -	KOG0867 7302617 Glutathione S-transferase	KXS11468.1 glutathione S-transferase [Gonapodya prolifera JEL478]	Glutathione S-transferase theta-2B OS=Homo sapiens OX=9606 GN=GSTT2B PE=1 SV=1
A5353	-	-	-	-	-	-	-	-
A5354	-	-	-	K09425 K09425; Myb-like DNA-binding protein FIBD	-	KOG0048 Hs13641706_1 Transcription factor, Myb superfamily	KAF9958436.1 hypothetical protein BGZ72_000355 [Mortierella alpina]	Transforming protein Myb OS=Avian myeloblastosis virus OX=11866 GN=V-MYB PE=1 SV=2
A5355	-	-	-	-	-	-	KAF9272511.1 hypothetical protein BGZ74_005221, partial [Mortierella antarctica]	-

A5356	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K18738 HEK; heterogeneo us nuclear rmp K-like protein	-	KOG2191 At5g04430 RNA-binding protein NOVA1/PAS1LLA and related KH domain proteins	KAF9936893.1 hypothetical protein BGZ67_001910 [Mortierella alpina]	Protein BTR1 OS=Arabidopsis thaliana OX=3702 GN=BTR1 PE=1 SV=1
A5357	-	-	-	-	-	-	EPZ34889.1 hypothetical protein O9G_002020 [Rozella allomycis CSF55]	Spindle assembly abnormal protein 6 homolog OS=Xenopus laevis OX=8355 GN=sas6 PE=2 SV=1
A5358	-	-	-	-	-	-	-	-
A5359	GO:0006106(fumarate metabolic process), GO:0006099(tricarboxylic acid cycle)	GO:0045239(tricarboxylic acid cycle enzyme complex)	GO:0004333(fumarate hydratase activity),GO:0003824(catalytic activity),GO:0016829(lyase activity)	K01679 E4.2.1.2B, fumC, FH; fumarate hydratase, class II [EC:4.2.1.2]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map05211 Renal cell carcinoma;map00720 Carbon fixation pathways in prokaryotes;map00020 Citrate cycle (TCA cycle);map05200 Pathways in cancer;map04934 Cushing syndrome;map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG1317 Hs19743875 Fumarase	XP_02346691.6.1 fumarate hydratase precursor rhizopus oryzae [Rhizopus microsporus ATCC 52813]	Fumarate hydratase, mitochondrial OS=Rhizopus oryzae OX=64495 GN=FUMR PE=3 SV=1
A5360	GO:0006468(protein phosphorylation),GO:0006914(autophagy)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0008270(zinc ion binding),GO:0004674(protein serine/threonine kinase activity)	K20872 NEK2; serine/threonine-protein kinase Nek2 [EC:2.7.11.1]	-	KOG0589 Hs20547878 Serine/threonine protein kinase	EJD36028.1 kinase-like protein [Auricularia subglabra TFB-10046 SS5]	Probable serine/threonine-protein kinase DDB_G0278521 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0278521 PE=3 SV=1
A5361	-	-	-	-	-	-	-	-
A5362	-	-	GO:0016787(hydrolase activity)	K01438 argE; acetylornithine deacetylase [EC:3.5.1.16]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00220 Arginine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG2276 At4g17830 Metalloexopeptidases	TDZ22622.1 Peptidase M20 domain-containing protein [Colletotrichum orbiculare MAFF 240422]	Acetylornithine deacetylase OS=Arabidopsis thaliana OX=3702 GN=At4g17830 PE=2 SV=1
A5363	-	-	GO:0005515(protein binding)	-	-	-	-	-

A5364	GO:0009083(branch ed-chain amino acid catabolic process)	-	GO:0016624(oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor),GO:003863(3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity)	K00166 BCKDHA, bkdA1; 2-oxoisovalerate dehydrogenase E1 component subunit alpha [EC:1.2.4.4]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map00640 Propanoate metabolism;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG1182[Hs1386135 Branched chain alpha-keto acid dehydrogenase complex, alpha subunit]	XP_006675089.1 uncharacterized protein BATDEDRAFT_9167 [Batrachochytrium dendrobatidis JAM81]	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Macaca fascicularis OX=9541 GN=BCKDHA PE=2 SV=1
A5365	GO:0006207('de novo' pyrimidine nucleobase biosynthetic process), GO:0006221(pyrimidine nucleotide biosynthetic process)	-	GO:0004590(ornithine-5'-phosphate decarboxylase activity),GO:0004588(ornotate phosphoribosyltransferase activity)	-	-	KOG1377[YM R271c Uridine 5'-monophosphate synthase/ornotate phosphoribosyltransferase	ORY07841.1 orotate phosphoribosyltransferase [Basidiobolus meristosporus CBS 931.73]	Orotate phosphoribosyltransferase OS=Cronobacter sakazakii (strain ATCC BAA-894) OX=290339 GN=pyrE PE=3 SV=1
A5366	GO:0006099(tricarboxylic acid cycle)	-	GO:0004591(oxoglutarate dehydrogenase (succinyl-transferring) activity),GO:0030976(thiamine pyrophosphate binding),GO:0016624(oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor)	K00164 OGDH, sucA; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0450[At3g55410 2-oxoglutarate dehydrogenase, E1 subunit]	CCJ30874.1 unnamed protein product, partial [Pneumocystis jirovecii]	2-oxoglutarate dehydrogenase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=ogdh PE=3 SV=1

A5367	GO:0006099(tricarboxylic acid cycle)	-	GO:0004591(oxoglutarate dehydrogenase (succinyl-transferring) activity),GO:0030976(thiamine pyrophosphate binding)	K15791 DHKTD1; 2-oxoadipate dehydrogenase E1 component [EC:1.2.4.-]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map00310 Lysine degradation;map00380 Tryptophan metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0450[Hs20541592 2-oxoglutarate dehydrogenase, E1 subunit	KNE58704.1 oxoglutarate dehydrogenase (succinyl-transferring), E1 component [Allomyces macrogynus ATCC 38327]	2-oxoglutarate dehydrogenase complex component E1 OS=Bos taurus OX=9913 GN=OGDH PE=1 SV=1
A5368	GO:0042147(retrograde transport, endosome to Golgi)	GO:0000938(GARP complex)	-	K20299 VPS53; vacuolar protein sorting-associated protein 53	-	KOG2180[At1g50500 Late Golgi protein sorting complex, subunit Vps53	KAG0320866.1 Vacuolar protein sorting-associated protein 53 [Dissophora globulifera]	Vacuolar protein sorting-associated protein 53 A OS=Arabidopsis thaliana OX=3702 GN=VPS53 PE=1 SV=1
A5369	GO:0005975(carbohydrate metabolic process)	-	GO:0030246(carbohydrate binding)	-	-	-	KAG1469147.1 hypothetical protein G6F57_012302 [Rhizopus oryzae]	Uncharacterized glycosidase Rv0584 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv0584 PE=3 SV=1
A5370	GO:0000493(box H/ACA snoRNP assembly),GO:004254(ribosome biogenesis),GO:0001522(pseudouridine synthesis)	GO:0005732(sno(s)RNA-containing ribonucleoprotein complex)	GO:0003723(RNA binding)	K14763 NAF1; H/ACA ribonucleoprotein complex non-core subunit NAF1	-	-	KIP11145.1 hypothetical protein PHLGIDRAFT_83936, partial [Phlebiopsis gigantea 11061_1 CR5-6]	H/ACA ribonucleoprotein complex non-core subunit NAF1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=naf1 PE=1 SV=1
A5371	-	-	-	-	-	-	-	-
A5372	-	GO:0016020(membrane)	-	-	-	KOG4267[YJR085c Predicted membrane protein	RKP07887.1 transmembrane proteins 14C-domain-containing protein [Thamnocephalus sphaerospora]	TMEM14 protein homolog YJR085C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YJR085C PE=1 SV=1
A5373	-	-	-	-	-	-	-	-
A5374	-	-	GO:0005509(calcium ion binding)	K02908 RP-L30e, RPL30; large subunit ribosomal protein L30e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0032[Hs4757908 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	RKP02706.1 hypothetical protein CXG81DRAFT_29455 [Caulochytrium protostelioides]	Calcyphosin OS=Canis lupus familiaris OX=9615 GN=CAPS PE=1 SV=1
A5375	-	-	GO:0008484(sulfuric ester hydrolase activity)	K01133 betC; choline-sulfatase [EC:3.1.6.6]	-	KOG3731[7292365 Sulfatases	ORY85670.1 sulfatase [Protomyces lactucaedebilis]	Ulván-active sulfatase OS=Formosa agariphila (strain DSM 15362 / KCTC 12365 / LMG 23005 / KMM 3901 / M-2A/g 35-1) OX=1347342 GN=BN863_22000 PE=1 SV=1

A5376	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3731 7292365 Sulfatases	RJE26985.1 Sulfatase [Aspergillus sclerotialis]	Ulván-active sulfatase OS=Formosa agariphila (strain DSM 15362 / KCTC 12365 / LMG 23005 / KMM 3901 / M-2Alg 35-1) OX=1347342 GN=BN863_22000 PE=1 SV=1
A5377	GO:0016973(poly(A) + mRNA export from nucleus)	GO:0005643(nuclear pore)	-	-	-	-	-	-
A5378	-	-	GO:0008484(sulfuric ester hydrolase activity)	K01133 betC; choline-sulfatase [EC:3.1.6.6]	-	KOG3867 Hs4557659 Sulfatase	KAB5515376.1 alkaline-phosphatase-like protein [Coniochaeta sp. 2T2.1]	Ulván-active sulfatase OS=Formosa agariphila (strain DSM 15362 / KCTC 12365 / LMG 23005 / KMM 3901 / M-2Alg 35-1) OX=1347342 GN=BN863_22070 PE=1 SV=2
A5379	-	-	-	-	-	-	-	-
A5380	GO:0006468(protein phosphorylation)	-	GO:0004222(metalloendopeptidase activity),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K18156 ATP23, XRCC6BP1; mitochondria l inner membrane protease ATP23 [EC:3.4.24.-]	-	KOG3314 Hs18579834 Ku70-binding protein	EJD37083.1 hypothetical protein AURDEDRAFT_139909 [Auricularia subglabra TFB-10046 SS5]	Mitochondrial inner membrane protease ATP23 homolog OS=Xenopus laevis OX=8355 GN=atp23 PE=2 SV=1
A5381	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5382	GO:0006281(DNA repair),GO:0006310(DNA recombination),GO:0071897(DNA biosynthetic process)	-	GO:0003910(DNA ligase (ATP activity),GO:0005524(ATP binding),GO:0003677(DNA binding),GO:0003909(DNA ligase activity)	K10747 LIG1; DNA ligase 1 [EC:6.5.1.1 6.5.1.6 6.5.1.7]	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03430 Mismatch repair	KOG0967 7291668 ATP-dependent DNA ligase I	XP_038919907.1 ATP-dependent DNA ligase [Cantharellus anzutake]	DNA ligase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=cdc17 PE=3 SV=1
A5383	-	-	GO:0005515(protein binding)	K09527 DNAJC7; DnaJ homolog subfamily C member 7	-	-	XP_017993561.1 tpr-like protein [Malassezia pachydermatis]	DnaJ homolog subfamily C member 3 homolog OS=Dictyostelium discoideum OX=44689 GN=dnajc3 PE=3 SV=1
A5384	-	GO:0008180(COP9 signalosome)	-	K12176 COPS2, CSN2, TRIP15; COP9 signalosome complex subunit 2	-	KOG1464 At2g26990 COP9 signalosome, subunit CSN2	KAF9971767.1 COP9/signalosome complex subunit Csn2 [Actinomyces rella ambigua]	COP9 signalosome complex subunit 2 OS=Arabidopsis thaliana OX=3702 GN=CSN2 PE=1 SV=1
A5385	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:1902600(proton transmembrane transport)	GO:0016020(membrane),GO:0005887(integral component of plasma membrane)	GO:0005216(ion channel activity),GO:0030171(voltage-gated proton channel activity)	-	-	-	KZ095024.1 hypothetical protein CALVIDRAFT_538501 [Calocera viscosa TUFC12733]	-
A5386	-	GO:0016021(integral component of membrane)	-	K13348 MPV17; protein Mpv17	map04146 Peroxisome	KOG1944 7290167 Peroxisomal membrane protein MPV17 and related proteins	XP_016612459.1 hypothetical protein SPPG_00149 [Spizellomyces punctatus DAOM BR117]	PXMP2/4 family protein 2 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0278529 PE=3 SV=1

A5387	-	-	GO:0016787(hydrolase activity)	K22390 ACP7; acid phosphatase type 7	-	KOG1378 At1g13750 Purple acid phosphatase	CCE29616.1 related to acid phosphatase precursor [Claviceps purpurea 20.1]	Probable inactive purple acid phosphatase 24 OS=Arabidopsis thaliana OX=3702 GN=PAP24 PE=2 SV=1
A5388	-	-	-	K11493 RCC1; regulator of chromosome condensation	-	KOG1426 At5g63860 FOG: RCC1 domain	XP_007911975.1 putative rcc1 domain-containing protein [Phaeoacremonium minimum UCRPA7]	Ultraviolet-B receptor UVR8 OS=Arabidopsis thaliana OX=3702 GN=UVR8 PE=1 SV=1
A5389	-	-	GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	K11294 NCL, NSR1; nucleolin	map05130 Pathogenic Escherichia coli infection	KOG0118 At5g50250 FOG: RRM domain	OON04828.1 hypothetical protein BSLG_05151 [Batrachochytrium salamandrivorans]	28 kDa ribonucleoprotein, chloroplastic OS=Spinacia oleracea OX=3562 PE=1 SV=1
A5390	-	-	GO:0005515(protein binding)	K12562 AMPH; amphiphysin	map04144 Endocytosis;map04666 Fc gamma R-mediated phagocytosis	KOG3601 CE01784 Adaptor protein GRB2 contains SH2 and SH3 domains	XP_016607795.1 hypothetical protein SPPG_05133 [Spizellomyces punctatus DAOM BR117]	Protein DD3-3 OS=Dictyostelium discoideum OX=44689 GN=DD3-3 PE=2 SV=1
A5391	GO:0072488(ammonium transmembrane transport)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 CE06770 Ammonia permease	KAF9121223.1 hypothetical protein BGX30_002722 [Mortierella sp. GBA39]	Putative ammonium transporter sli0108 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=sli0108 PE=3 SV=1
A5392	-	-	-	-	-	-	-	-
A5393	-	-	-	K00344 qor, CRYZ; NADPH:quinone reductase [EC:1.6.5.5]	-	-	XP_019042976.1 NADPH2:quinone reductase [Kwoniella bestiolae CBS 10118]	Prostaglandin reductase-3 OS=Mus musculus OX=10090 GN=Ptgr3 PE=1 SV=1
A5394	GO:0071569(protein ufmylation)	-	-	-	-	KOG3483 CE00449 Uncharacterized conserved protein	-	Ubiquitin-fold modifier 1 OS=Caenorhabditis elegans OX=6239 GN=ufr-1 PE=1 SV=1
A5395	GO:0006357(regulation of transcription by RNA polymerase II)	GO:0016592(mediator complex)	GO:0003712(transcription coregulator activity)	K15156 MED14, RGR1; mediator of RNA polymerase II transcription subunit 14	map04919 Thyroid hormone signaling pathway	KOG1875 Hs4758102 Thyroid hormone receptor-associated coactivator complex component (TRAP170)	KAG0184516.1 mediator complex subunit [Apophysomycetes sp. BC1034]	Mediator of RNA polymerase II transcription subunit 14 OS=Mus musculus OX=10090 GN=Med14 PE=1 SV=1
A5396	GO:0006364(rRNA processing)	-	-	-	-	KOG2974 Hs7705620 Uncharacterized conserved protein	KNE57604.1 hypothetical protein AMAG_03294 [Allomyces macrogynus ATCC 38327]	RRP15-like protein OS=Rattus norvegicus OX=10116 GN=Rrp15 PE=1 SV=1
A5397	-	-	-	-	-	-	-	-

A5398	GO:0015703(chromate transport)	-	GO:0015109(chromate transmembrane transporter activity)	-	-	-	OAI36654.1 hypothetical protein BDEG_20806 [Batrachochytrium dendrobatidis JEL423]	Chromate transport protein OS=Pseudomonas aeruginosa OX=287 GN=chrA PE=2 SV=1
A5399	-	-	GO:0016746(acyltransferase activity)	K13509 AGPAT1_2; lysophosphatidate acyltransferase [EC:2.3.1.51]	map01110 Biosynthesis of secondary metabolites;map04072 Phospholipase D signaling pathway;map04975 Fat digestion and absorption;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	KOG2848[At4g30580 1-acyl-sn-glycerol-3-phosphate acyltransferase	KAG1445960.1 hypothetical protein G6F57_017445 [Rhizopus oryzae]	1-acyl-sn-glycerol-3-phosphate acyltransferase BAT2, chloroplastic OS=Brassica napus OX=3708 GN=BAT2 PE=1 SV=2
A5400	-	-	-	-	-	-	-	-
A5401	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5402	-	-	-	-	-	-	-	-
A5403	-	-	-	-	-	-	-	-
A5404	-	-	-	-	-	-	-	-
A5405	GO:0006493(protein O-linked glycosylation)	-	GO:0005515(protein binding),GO:0016757(glycosyltransferase activity)	-	-	KOG4626[At3g04240 O-linked N-acetylglucosamine transferase OGT	KAF8527916.1 glycosyltransferase family 41-domain-containing protein [Hysterangium stoloniferum]	Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC OS=Arabidopsis thaliana OX=3702 GN=SEC PE=1 SV=1
A5406	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5407	-	-	-	-	-	KOG1552[At1g66900 Predicted alpha/beta hydrolase	-	Alpha/beta hydrolase domain-containing protein 17B OS=Xenopus tropicalis OX=8364 GN=abhd17b PE=2 SV=1
A5408	-	-	-	-	-	-	-	-
A5409	-	-	-	-	-	-	RKP20762.1 hypothetical protein ROZALSC1DRAFT_21121 [Rozella allomycis CSF55]	CDAN1-interacting nuclease 1 OS=Xenopus laevis OX=8355 PE=2 SV=2
A5410	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	-	-	KOG0907[Hs14740408 Thioredoxin	KAF8557885.1 hypothetical protein OG21DRAFT_1504871 [Xerocomus badius]	Thioredoxin OS=Echinococcus granulosus OX=6210 GN=TRX PE=3 SV=2

A5411	-	-	GO:0005515(protein binding)	K14026 SEL1, SEL1L; SEL1 protein	map04141 Protein processing in endoplasmic reticulum	KOG1550 CE16043 Extracellular protein SEL-1 and related proteins	RKP26333.1 hypothetical protein SYNPS1DRAFT_14339, partial [Syncephalis pseudoplumigaleata]	Protein sel-1 homolog 2 OS=Homo sapiens OX=9606 GN=SEL1L2 PE=2 SV=2
A5412	-	-	GO:0005525(GTP binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K19788 OLA1; obg-like ATPase 1	-	KOG1491 At1g56050 Predicted GTP-binding protein (ODN superfamily)	KAG1469661.1 hypothetical protein G6F57_012096 [Rhizopus oryzae]	Ribosome-binding ATPase YchF OS=Escherichia coli O157:H7 OX=83334 GN=ychF PE=3 SV=2
A5413	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	K11968 ARIH1; ariadne-1 [EC:2.3.2.31]	-	-	KAG2223426.1 hypothetical protein INT45_001732 [Mucor circinatus]	E3 ubiquitin-protein ligase dbf4 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=dbf4 PE=3 SV=1
A5414	GO:0006807(nitrogen compound metabolic process)	-	GO:0016811(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides)	K13566 NIT2, yafV; omega-amidase [EC:3.5.1.3]	map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG0806 Hs910460 Carbon-nitrogen hydrolase	KAF9944528.1 hypothetical protein BGZ72_002310 [Mortierella alpina]	Omega-amidase NIT2 OS=Bos taurus OX=9913 GN=NIT2 PE=2 SV=1
A5415	-	-	-	-	-	-	-	-
A5416	-	-	-	K22696 EEF2KMT; protein-lysine N-methyltransferase EEF2KMT [EC:2.1.1.-]	-	KOG2793 CE02891_1 Putative N2,N2-dimethylguanosine tRNA methyltransferase	XP_006678250.1 uncharacterized protein BATDEDRAFT_87678 [Batrachochytrium dendrobatidis JAM81]	Protein N-lysine methyltransferase METTL21A OS=Mus musculus OX=10090 GN=Mettl21A PE=2 SV=1
A5417	-	-	-	-	-	-	-	-
A5418	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 ECU03g0170 Uncharacterized conserved protein	KAF9076349.1 magnesium transporter NIPA-domain-containing protein [Rhodocollybia butyracea]	Probable magnesium transporter NIPA2 OS=Arabidopsis thaliana OX=3702 GN=At4g13800 PE=2 SV=1
A5419	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02920 RP-L36e, RPL36; large subunit ribosomal protein L36e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3452 At5g02450 60S ribosomal protein L36	GAV30344.1 60S ribosomal protein [Pichia membranifaciens]	Large ribosomal subunit protein eL36x OS=Arabidopsis thaliana OX=3702 GN=RPL36C PE=3 SV=1
A5420	-	-	-	-	-	-	-	-
A5421	GO:0006357(regulation of transcription by RNA polymerase II)	GO:0016592(mediator complex)	GO:0003712(transcription coregulator activity)	-	-	-	-	-
A5422	-	-	-	-	-	-	-	-
A5423	GO:0006508(proteolysis)	-	GO:0008236(serine-type peptidase activity),GO:0016787(hydrolase activity)	-	-	KOG2100 At2g47390 Dipeptidyl aminopeptidase	KAG1255201.1 hypothetical protein G6F68_010489 [Rhizopus microsporus]	Probable glutamyl endopeptidase, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=GEP PE=2 SV=1
A5424	-	-	-	-	-	-	-	-

A5425	-	-	GO:0005515(protein binding)	K13342 PEX5, PXR1; peroxin-5	map04146 Peroxisome	KOG1125 At5g56290 TPR repeat-containing protein	KXN70555.1 TPR-like protein [Conidiobolus coronatus NRRL 28638]	Peroxisome biogenesis protein 5 OS=Arabidopsis thaliana OX=3702 GN=PEX5 PE=1 SV=1
A5426	-	-	-	-	-	-	-	-
A5427	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02912 RP-L32e, RPL32; large subunit ribosomal protein L32e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0878 Hs4506635 60S ribosomal protein L32	ORX62389.1 50S ribosomal protein L32 [Hesseltinella vesiculosa]	Large ribosomal subunit protein eL32 OS=Canis lupus familiaris OX=9615 GN=RPL32 PE=1 SV=1
A5428	-	-	GO:0005515(protein binding)	-	-	KOG4018 Hs20551750 Uncharacterized conserved protein, contains RWD domain	XP_018297003.1 hypothetical protein PHYBLDRAFT_122243 [Phycomyces blakesleeanus NRRL 1555(-)]	RWD domain-containing protein 1 OS=Rattus norvegicus OX=10116 GN=Rwdd1 PE=2 SV=1
A5429	GO:0055085(transmembrane transport), GO:0080162(intracellular auxin transport)	GO:0016021(integral component of membrane)	-	K24139 PILS, ECM3; auxin efflux carrier family protein	-	-	VUG19812.1 DEBR0S6_00386g1.1 [Brettanomyces bruxellensis]	-
A5430	-	-	GO:0010181(FMN binding),GO:0051287(NAD binding),GO:0051539(4 iron, 4 sulfur cluster binding),GO:0008137(NADH dehydrogenase (ubiquinone) activity)	K03942 NDUFV1; NADH dehydrogenase (ubiquinone) flavoprotein 1 [EC:7.1.1.2]	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG2658 At5g08530 NADH:ubiquinone oxidoreductase, NDUFV1/51kDa subunit	KAF8929859.1 NADH dehydrogenase flavoprotein subunit 1 [Dissophoromata]	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At5g08530 PE=1 SV=1
A5431	-	-	GO:0004386(helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K12815 DHX38, PRP16; pre-mRNA-splicing factor ATP-dependent RNA helicase DHX38/PRP16 [EC:3.6.4.13]	map03040 Spliceosome	KOG0924 At5g13010 mRNA splicing factor ATP-dependent RNA helicase	TPX50854.1 hypothetical protein SeLEV6574_g00656 [Synchytrium endobioticum]	Pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH7 OS=Arabidopsis thaliana OX=3702 GN=CUV PE=1 SV=1
A5432	-	-	GO:0051015(actin filament binding)	K05768 GSN; gelsolin	map04810 Regulation of actin cytoskeleton;map04666 Fc gamma R-mediated phagocytosis;map05203 Viral carcinogenesis	KOG0443 7296888 Actin regulatory proteins (gelsolin/villin family)	XP_006679594.1 uncharacterized protein BATDEDRAFT_37025 [Batrachochytrium dendrobatidis JAM81]	Gelsolin-like protein 2 OS=Lumbricus terrestris OX=6398 GN=gelsolin PE=1 SV=1

A5433	-	-	-	K24205 TMBIM, LFG; protein lifeguard	-	KOG2322 730 3389 N- methyl-D- aspartate receptor glutamate- binding subunit	CCG81377.1 Bax Inhibitor family protein [Taphrina deformans PYCC 5710]	Protein lifeguard 1 OS=Bos taurus OX=9913 GN=GRINA PE=2 SV=1
A5434	-	-	GO:0005515(pro tein binding)	-	-	-	-	-
A5435	-	-	-	-	-	-	-	-
A5436	-	-	-	-	-	-	-	-
A5437	-	-	GO:0005515(pro tein binding)	-	-	-	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A5438	GO:00063 55(regulat ion of transcripti on, DNA- templated)	-	GO:0003700(DN A-binding transcription factor activity);GO:004 3565(sequence- specific DNA binding)	-	-	KOG0627 Hs4 758568 Heat shock transcription factor	ONH66541.1 Heat shock transcription factor [Cyberlindner a fabianii]	Heat shock factor protein 2 OS=Mus musculus OX=10090 GN=Hsf2 PE=1 SV=2
A5439	GO:00550 85(transm embrane transport)	GO:00160 21(integra l compone nt of membran e)	GO:0005524(AT P binding);GO:014 0359(ABC-type transporter activity)	K05643 ABCA3; ATP- binding cassette, subfamily A (ABC1), member 3	map02010 ABC transporters	KOG0059 Hs1 4550412 Lipid exporter ABCA1 and related proteins, ABC superfamily	RKP23674.1 P-loop containing nucleoside triphosphate hydrolase protein, partial [Syncephalis pseudoplumi galeata]	ABC transporter A family member 8 OS=Arabidopsis thaliana OX=3702 GN=ABCA8 PE=2 SV=3
A5440	GO:00165 79(protein deubiquiti nation);G O:000651 1(ubiquiti n- dependen t protein catabolic process)	-	GO:0008270(zin c ion binding);GO:000 4843(thiol- dependent deubiquitinase); GO:0005515(pro tein binding)	K11836 USP5_13, UBP14; ubiquitin carboxyl- terminal hydrolase 5/13 [EC:3.4.19.12]	-	KOG0944 Hs4 507855 Ubiquitin- specific protease UBP14	XP_03102647 0.1 uncharacteriz ed protein SmJEL517_g0 1651 [Synchytrium microbalum]	Ubiquitin carboxyl-terminal hydrolase 5 OS=Mus musculus OX=10090 GN=Usp5 PE=1 SV=1
A5441	GO:00193 46(transsu lfuration)	-	GO:0030170(pyr idoxal phosphate binding);GO:000 3824(catalytic activity)	K01739 metB; cystathionine gamma- synthase [EC:2.5.1.48]	map01110 Biosynthesis of secondary metabolites;map 01230 Biosynthesis of amino acids;map00920 Sulfur metabolism;map 01100 Metabolic pathways;map00 450 Selenocompoun d metabolism;map 00270 Cysteine and methionine metabolism	KOG0053 At3 g57050 Cystathionine beta- lyases/cystath ionine gamma- synthases	ORY51013.1 cystathionine gamma- synthase [Rhizoclosma tium globosum]	Cystathionine beta-lyase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=At3g57050 PE=1 SV=1
A5442	GO:00066 29(lipid metabolic process)	-	GO:0008081(ph osphoric diester hydrolase activity)	K18694 PGC1; phosphatidyl glycerol phospholipas e C [EC:3.1.4.-]	map00564 Glycerophospho lipid metabolism	KOG2258 CE 11152 Glycerophosp horyl diester phosphodiester erase	TGJ78796.1 hypothetical protein E0Z10_g9962 , partial [Xylaria hypoxylon]	Phosphatidylglycerol phospholipase C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGC1 PE=1 SV=1

A5443	-	-	-	-	-	KOG3170 Hs1 3129044 Conserved phosducin- like protein	PIA15324.1 thioredoxin- like protein [Coemansia reversa NRRL 1564]	Phosducin-like protein 3 OS=Danio rerio OX=7955 GN=pdcl3 PE=2 SV=1
A5444	-	-	GO:0008939(nic otinate- nucleotide- dimethylbenzimi dazole phosphoribosylt ransferase activity)	-	-	-	TPX69513.1 nicotinate- nucleotide-- - dimethylbenz imidazole phosphoribos yltransferase [Chytriomyc s confervae]	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase OS=Pseudomonas fluorescens (strain ATCC BAA-477 / NRRL B-23932 / Pf-5) OX=220664 GN=cobT PE=3 SV=1
A5445	-	-	GO:0008818(co balamin 5'- phosphate synthase activity),GO:005 1073(adenosylc obinamide-GDP ribazoletransfer ase activity)	-	-	-	ORZ35075.1 cobalamin- 5-phosphate synthase- domain- containing protein [Catenaria anguillulae PL171]	Adenosylcobinamide-GDP ribazoletransferase OS=Aromatoleum aromaticum (strain EbN1) OX=76114 GN=cobS PE=3 SV=1
A5446	-	-	-	K14572 MDN1, REA1; midasin	map03008 Ribosome biogenesis in eukaryotes	KOG1808 Hs2 0552711 AAA ATPase containing von Willebrand factor type A (vWA) domain	RKP04693.1 hypothetical protein THASP1DRAF T_20843 [Thamnoceph alis sphaerospora]	-
A5447	-	-	GO:0000062(fatt y-acyl-CoA binding)	-	-	KOG1205 730 1818 Predicted dehydrogena se	KAF4511539. 1 hypothetical protein G6O67_0033 23 [Ophiocordyc eps sinensis]	Fatty acyl-CoA reductase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=acr1 PE=1 SV=2
A5448	GO:00311 45(anaph ase- promotin g complex- dependen t catabolic process)	GO:00056 80(anaph ase- promotin g complex)	GO:0008270(zin c ion binding),GO:006 1630(ubiquitin protein ligase activity),GO:009 7602(cullin family protein binding)	-	-	KOG2502 Hs1 9923167 Tub family proteins	PKY23519.1 hypothetical protein RhiirB3_4119 35 [Rhizophagus irregularis]	Tubby protein OS=Mus musculus OX=10090 GN=Tub PE=1 SV=1
A5449	-	GO:00160 20(memb rane)	-	-	-	KOG2718 Hs4 506973 Na+- bile acid cotransporter	-	Sodium-dependent organic anion transporter OS=Bos taurus OX=9913 GN=SLC10A6 PE=2 SV=2
A5450	-	GO:00056 34(nucleu s)	GO:0005515(pro tein binding),GO:000 3676(nucleic acid binding)	K12830 SF3B3, SAP130, RSE1; splicing factor 3B subunit 3	map03040 Spliceosome	KOG1898 Hs1 1034823 Splicing factor 3b, subunit 3	KAG0237415. 1 pre- mRNA- splicing factor rse1 [Actinomortie rella wolfii]	Splicing factor 3B subunit 3 OS=Bos taurus OX=9913 GN=SF3B3 PE=2 SV=1
A5451	-	-	-	-	-	-	-	-
A5452	-	-	-	-	-	-	-	-
A5453	-	-	-	-	-	-	-	-

A5454	-	-	-	K23469 CLB2; G2/mitotic-specific cyclin 2	map04011 MAPK signaling pathway - yeast;map04111 Cell cycle - yeast	KOG0656[Hs4502619 G1/S-specific cyclin D	TPX67271.1 hypothetical protein SpCBS45565_g03980 [Spizellomyces sp. 'palustris']	G1/S-specific cyclin-D2 OS=Mus musculus OX=10090 GN=Ccnd2 PE=1 SV=1
A5455	-	-	-	-	-	-	-	-
A5456	-	-	-	-	-	-	-	-
A5457	GO:0016567(protein ubiquitination)	-	GO:0005515(protein binding)	-	-	KOG1987[At3g43700 Speckle-type POZ protein SPOP and related proteins with TRAF, MATH and BTB/POZ domains	-	BTB/POZ and MATH domain-containing protein 6 OS=Arabidopsis thaliana OX=3702 GN=BPM6 PE=1 SV=1
A5458	-	-	-	-	-	KOG4249[At3g45890 Uncharacterized conserved protein	ORZ36603.1 vitamin B6 photo-protection and homoeostasis -domain-containing protein [Catenaria anguillulae PL171]	Protein root UVB sensitive 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=RUS1 PE=1 SV=1
A5459	-	-	-	-	-	-	-	-
A5460	-	-	-	-	-	-	-	-
A5461	-	-	-	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis -	-	KAG1273186.1 hypothetical protein G6F65_011214 [Rhizopus oryzae]	Disulfide-bond oxidoreductase YfcG OS=Escherichia coli (strain K12) OX=83333 GN=yfcG PE=1 SV=1
A5462	-	-	GO:0003723(RNA binding);GO:0003676(nucleic acid binding)	K12837 U2AF2; splicing factor U2AF 65 kDa subunit	map03040 Spliceosome	KOG0120[7291545 Splicing factor U2AF, large subunit (RRM superfamily)	PKC01855.1 hypothetical protein RhiirA5_298045 [Rhizophagus irregularis]	Splicing factor U2af large subunit B OS=Arabidopsis thaliana OX=3702 GN=U2AF65B PE=1 SV=2
A5463	GO:0000398(mRNA splicing, via spliceosome)	GO:0071013(catalytic step 2 spliceosome)	GO:0005515(protein binding)	K12816 CDC40, PRP17; pre-mRNA-processing factor 17	map03040 Spliceosome	KOG0282[At1g10580 mRNA splicing factor	KAF9214564.1 pre-mRNA-processing factor 17 [Podila verticillata]	Pre-mRNA-processing factor 17 OS=Mus musculus OX=10090 GN=Cdc40 PE=1 SV=1

A5464	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG4280[Hs4758646 Kinesin-like protein	KXS10018.1 kinesin-domain-containing protein, partial [Gonapodya prolifera JEL478]	Kinesin-like protein KIF3B OS=Mus musculus OX=10090 GN=Kif3b PE=1 SV=1
A5465	-	-	-	-	-	-	-	-
A5466	-	-	-	-	-	-	-	-
A5467	-	-	-	-	-	KOG3213[7297698 Transcription factor IIB	KNE73049.1 hypothetical protein AMAG_17318 [Allomyces macrogynus ATCC 38327]	Cilia- and flagella-associated protein 20 OS=Bos taurus OX=9913 GN=CFAP20 PE=1 SV=1
A5468	GO:0006099(tricarboxylic acid cycle),GO:0019752(carboxylic acid metabolic process)	-	GO:0016491(oxidoreductase activity),GO:0030060(L-malate dehydrogenase activity),GO:0003824(catalytic activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)	K00026 MDH2; malate dehydrogenase [EC:1.1.1.37]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00710 Carbon fixation in photosynthetic organisms;map00620 Pyruvate metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism;map00630 Glyoxylate and dicarboxylate metabolism	KOG1494[At3g47520 NAD-dependent malate dehydrogenase	XP_019009315.1 malate dehydrogenase, NAD-dependent [Kwoniella pini CBS 10737]	Malate dehydrogenase, glyoxysomal OS=Glycine max OX=3847 PE=2 SV=2
A5469	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08842 TESK2; testis-specific kinase 2 [EC:2.7.12.1]	-	KOG0192[At4g31170 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KU25238.1 hypothetical protein M422DRAFT_118874, partial [Sphaerobolus stellatus SS14]	RasGEF domain-containing serine/threonine-protein kinase X OS=Dictyostelium discoideum OX=44689 GN=gefX PE=2 SV=1
A5470	-	-	-	-	-	-	-	-
A5471	-	-	-	-	-	-	-	-

A5472	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	-	-	KOG1591 At3g28480 Prolyl 4-hydroxylase alpha subunit	-	Probable prolyl 4-hydroxylase 7 OS=Arabidopsis thaliana OX=3702 GN=P4H7 PE=2 SV=1
A5473	-	-	-	-	-	-	-	-
A5474	GO:0008295(spermidine biosynthetic process), GO:0006597(spermine biosynthetic process)	-	GO:0004014(adenosylmethionine decarboxylase activity)	K01611 speD, AMD1; S-adenosylmethionine decarboxylase [EC:4.1.1.50]	map00330 Arginine and proline metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG0788 7297665 S-adenosylmethionine decarboxylase	RKP04746.1 S-adenosylmethionine decarboxylase [Thamnocephalis sphaerospora]	S-adenosylmethionine decarboxylase proenzyme OS=Dictyostelium discoideum OX=44689 GN=amd1 PE=3 SV=3
A5475	GO:0036211(protein modification process)	-	-	-	-	KOG2156 Hs7661970 Tubulin-tyrosine ligase-related protein	TPX76176.1 hypothetical protein CcCBS67573_g02572 [Chytridiomycetes confervae]	Tubulin--tyrosine ligase OS=Bos taurus OX=9913 GN=TTL PE=1 SV=1
A5476	-	-	GO:0005515(protein binding)	-	-	KOG1337 At3g07670 N-methyltransferase	XP_024666594.1 SET domain-containing protein 8 [Wickerhamiella sorbophila]	Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplastic OS=Pisum sativum OX=3888 GN=RBCMT PE=1 SV=1
A5477	-	-	-	K10765 ALKBH1; alkylated DNA repair protein alkB homolog 1 [EC:1.14.11.5 1 4.2.99.18 1.14.11.-]	-	KOG2731 Hs11434914 DNA alkylation damage repair protein	KAF8976710.1 hypothetical protein BGZ52_007698, partial [Haplosporangium bisporeale]	Nucleic acid dioxygenase ALKBH1 OS=Homo sapiens OX=9606 GN=ALKBH1 PE=1 SV=2

A5478	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity);GO:0005524(ATP binding);GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	-	XP_02761289.8.1 Kinesin heavy chain [Sparassis crispa]	Kinesin heavy chain OS=Botryotinia fuckeliana OX=40559 GN=kfp1 PE=3 SV=1
A5479	-	-	GO:0016787(hydrolase activity)	K01515 nudF; ADP-ribose diphosphatase [EC:3.6.1.13 3.6.1.-]	map00230 Purine metabolism;map00740 Riboflavin metabolism;map01100 Metabolic pathways	KOG3041 YBR111c Nucleoside diphosphate-sugar hydrolase of the MutT (NUDIX) family	XP_03102315.5.1 uncharacterized protein SmJEL517_g04943 [Synchytrium microbalum]	ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=1
A5480	-	-	GO:0003677(DNA binding)	-	-	-	-	-
A5481	-	-	-	-	-	KOG3589 CE06948 G protein signaling regulators	-	Regulator of G-protein signaling rgs-6 OS=Caenorhabditis elegans OX=6239 GN=rgs-6 PE=4 SV=4
A5482	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5483	-	-	-	-	-	-	-	-
A5484	-	-	GO:0005524(ATP binding);GO:0008270(zinc ion binding)	K03235 EF3, TEF3; elongation factor 3	-	KOG0062 YPL226w_2 ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	XP_01661052.1.1 hypothetical protein SPPG_02943 [Spizellomyces punctatus DAOM BR117]	Elongation factor 3 OS=Phytophthora infestans (strain T30-4) OX=403677 GN=TEF3 PE=1 SV=1
A5485	-	-	-	-	-	-	-	-
A5486	-	-	-	-	-	-	-	-
A5487	GO:0015031(protein transport)	GO:0016020(membrane)	-	-	-	KOG1373 Hs14589847 Transport protein Sec61, alpha subunit	RKP10621.1 SecY subunit domain-containing protein [Thamnocephalusphaerospora]	Protein transport protein Sec61 subunit alpha isoform 2 OS=Bos taurus OX=9913 GN=SEC61A2 PE=2 SV=3
A5488	GO:0032508(DNA duplex unwinding);GO:0006260(DNA replication);GO:0006270(DNA replication initiation)	GO:0005634(nucleus);GO:0042555(MCM complex)	GO:0003677(DNA binding);GO:0005524(ATP binding);GO:0003688(DNA replication origin binding)	K02209 MCM5, CDC46; DNA replication licensing factor MCM5 [EC:5.6.2.3]	map03030 DNA replication;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0481 At2g07690 DNA replication licensing factor, MCM5 component	RKO89743.1 MCM2/3/5 family-domain-containing protein [Blytiomyces helicus]	DNA replication licensing factor MCM5 OS=Arabidopsis thaliana OX=3702 GN=MCM5 PE=1 SV=1
A5489	-	-	-	-	-	-	TPX58176.1 hypothetical protein PhCBS80983_g03324 [Powellomyces hirtus]	-

A5490	GO:0000467(exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)),GO:0006139(nucleobase-containing compound metabolic process),GO:0044237(cellular	GO:0000176(nuclear exosome (RNase complex))	GO:0000175(3'-5'-exoribonuclease activity),GO:0003676(nucleic acid binding),GO:0008408(3'-5'-exonuclease activity),GO:0001666(nucleotide binding)	K12591 RRP6, EXOSC10; exosome complex exonuclease RRP6 [EC:3.1.13.-]	map03018 RNA degradation	KOG2206[Hs4505917 Exosome 3'-5' exoribonuclease complex, subunit PM/SCL-100 (Rrp6)	RKP10165.1 ribonuclease H-like domain-containing protein [Thamnocephalis sphaerospora]	Exosome complex component 10 OS=Rattus norvegicus OX=10116 GN=Exosc10 PE=1 SV=2
A5491	-	-	-	-	-	-	TPX53783.1 hypothetical protein PhCBS80983.g06161 [Powellomyces hirtus]	Cilia- and flagella-associated protein 206 OS=Macaca fascicularis OX=9541 GN=CFAP206 PE=2 SV=1
A5492	-	-	GO:0003824(catalytic activity),GO:0008483(transaminase activity),GO:0030170(pyridoxal phosphate binding)	K01845 hemL; glutamate-1-semialdehyde 2.1-aminomutase [EC:5.4.3.8]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG1401 At3g48730 Acetylornithine aminotransferase	KAG1270972.1 hypothetical protein G6F65_012724 [Rhizopus oryzae]	Mycosubtilin synthase subunit A OS=Bacillus subtilis OX=1423 GN=mycA PE=1 SV=1
A5493	GO:0015693(magnesium ion transport),GO:0000278(mitotic cell cycle)	GO:0016021(integral component of membrane),GO:0000775(chromosome, centromeric region),GO:0005634(nucleus)	GO:0015095(magnesium ion transmembrane transporter activity)	-	-	-	-	-
A5494	-	-	-	-	-	KOG0048[Hs4505293_1 Transcription factor, Myb superfamily	KAF9780729.1 Homeodomain-like protein, partial [Thelephora terrestris]	Myb-related protein A OS=Gallus gallus OX=9031 GN=MYBL1 PE=2 SV=1
A5495	GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	-	RIB24834.1 Co/Zn/Cd cation transporter-like protein, partial [Gigaspora rosea]	Transmembrane protein 163b OS=Danio rerio OX=7955 GN=tmem163b PE=2 SV=1
A5496	-	-	-	-	-	-	-	-

A5497	-	-	-	K23469 CLB2; G2/mitotic-specific cyclin 2	map04011 MAPK signaling pathway - yeast; map04111 Cell cycle - yeast	KOG0654 At1g44110 G2/Mitotic-specific cyclin A	KAF3909905.1 Cyclin-B2-2 [Drechslerella brochopaga]	Cyclin-A1-4 OS=Oryza sativa subsp. japonica OX=39947 GN=CYCA1-4 PE=2 SV=2
A5498	-	-	-	-	-	-	-	Regulator of G-protein signaling 4 OS=Gallus gallus OX=9031
A5499	-	-	-	K15109 SLC25A20_29, CACT, CACL, CRC1; solute carrier family 25 (mitochondrial carnitine/acyl carnitine transporter), member 20/29	map04714 Thermogenesis	KOG0758 YP R058w Mitochondrial carnitine-acylcarnitine carrier protein	TPX75266.1 hypothetical protein CcCBS67573_g03462 [Chytridiomycetes confervae]	Solute carrier family 25 member 45 OS=Mus musculus OX=10090 GN=Slc25a45 PE=1 SV=1
A5500	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0500 CE27352 Cyclic nucleotide-gated cation channel CNGA1-3 and related proteins	KNE66921.1 hypothetical protein AMAG_11395 [Allomyces macrogynus ATCC 38327]	Cyclic nucleotide-gated cation channel beta-3 OS=Mus musculus OX=10090 GN=Cngb3 PE=1 SV=1
A5501	-	-	-	-	-	KOG0498 7302693 K+-channel ERG and related proteins, contain PAS/PAC sensor domain	-	Potassium voltage-gated channel subfamily H member 2 OS=Mus musculus OX=10090 GN=Kcnh2 PE=1 SV=2
A5502	-	-	GO:0004497(monoxygenase activity), GO:0005506(iron ion binding), GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen), GO:0020037(heme binding)	-	-	KOG0157 At2g27690 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	KAB5580547.1 cytochrome P450 4A12A [Coniochaeta sp. 2T2.1]	Cytochrome P450 4B1 OS=Rattus norvegicus OX=10116 GN=Cyp4b1 PE=1 SV=3
A5503	-	-	-	-	-	-	-	-
A5504	GO:000469(cleavage involved in rRNA processing), GO:0042274(ribosomal subunit biogenesis)	-	GO:0004521(endoribonuclease activity)	K11883 NOB1; RNA-binding protein NOB1	map03008 Ribosome biogenesis in eukaryotes	KOG2463 At5g41190 Predicted RNA-binding protein Nob1p involved in 26S proteasome assembly	TPX69551.1 hypothetical protein SpCBS45565_g02250 [Spizellomyces sp. 'palustris']	RNA-binding NOB1-like protein OS=Arabidopsis thaliana OX=3702 GN=NOB1 PE=1 SV=1
A5505	GO:000958(biosynthetic process)	-	GO:0016740(transferase activity), GO:0005515(protein binding), GO:0016779(nucleotidyl transferase activity)	K03240 EIF2B5; translation initiation factor eIF-2B subunit epsilon	map05168 Herpes simplex virus 1 infection	-	RIA92604.1 nucleotide-diphosphosugar transferase [Glomus cerebriforme]	Translation initiation factor eIF2B subunit epsilon OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=tif225 PE=1 SV=1

A5506	-	-	-	K10355 ACTF; actin, other eukaryote	map04814 Motor proteins	KOG0676 CE12358 Actin and related proteins	RKO99664.1 hypothetical protein CXG81DRAFT_27595 [Caulochytrium protostelioides]	Actin OS=Achlya bisexualis OX=4766 PE=3 SV=1
A5507	-	-	-	K10355 ACTF; actin, other eukaryote	map04814 Motor proteins	KOG0676 Hs4501887 Actin and related proteins	RKP27433.1 actin-2 [Syncephalis pseudoplumigaleata]	Actin-1 OS=Phytophthora infestans OX=4787 GN=ACTA PE=2 SV=1
A5508	-	-	-	-	-	-	-	-
A5509	-	-	-	K23518 MACROD. ymdB; O-acetyl-ADP-ribose deacetylase [EC:3.1.1.106]	-	KOG2633 At1g69340 Hismacro and SEC14 domain-containing proteins	PHH79388.1 hypothetical protein CDD80_4947 [Ophiocordyceps camponoti-rufipedis]	Protein GDAP2 homolog OS=Nematostella vectensis OX=45351 GN=gdap2 PE=3 SV=1
A5510	-	-	-	-	-	KOG0914 Hs7705726 Thioredoxin-like protein	ORX80562.1 hypothetical protein K493DRAFT_412123 [Basidiobolus meristosporus CBS 931.73]	Thioredoxin-related transmembrane protein 2 OS=Homo sapiens OX=9606 GN=TMX2 PE=1 SV=1
A5511	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5512	-	-	GO:0005515(protein binding)	K14961 RBBP5, SWD1, CPS50; COMPASS component SWD1	map04934 Cushing syndrome	KOG0275 Hs8922679 Conserved WD40 repeat-containing protein	KAF9433925.1 Serine/threonine-protein kinase smu1 [Entomortierella beljakovae]	WD40 repeat-containing protein SMU1 OS=Xenopus laevis OX=8355 GN=smu1 PE=2 SV=1
A5513	-	-	GO:0005509(cal cium ion binding)	K16466 CETN3, CDC31; centrin-3	-	KOG0028 7289491 Ca2+ -binding protein (centrin/caltr actin), EF-Hand superfamily protein	TPX67250.1 hypothetical protein SpCBS45565_g03964 [Spizellomyces sp. 'palustris']	Centrin-2 OS=Toxoplasma gondii (strain ATCC 50611 / Me49) OX=508771 GN=CEN2 PE=1 SV=1
A5514	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG0198 At2g40560 MEKK and related serine/threonine protein kinases	KAF9976048.1 hypothetical protein BGZ73_009207 [Actinomortierella ambigua]	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1 OS=Arabidopsis thaliana OX=3702 GN=RLK1 PE=2 SV=2
A5515	-	-	-	K01922 PPCS, COAB; phosphopant othenate---cysteine ligase (ATP) [EC:6.3.2.51]	map00770 Pantothenate and CoA biosynthesis;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG2728 At5g02080 Uncharacterized conserved protein with similarity to phosphopant othenoylcysteine synthetase/d ecarboxylase	KZO91610.1 DFP-domain-containing protein [Calocera viscosa TUFC12733]	Phosphopantothenate--cysteine ligase 2 OS=Arabidopsis thaliana OX=3702 GN=PPCS2 PE=2 SV=2
A5516	-	-	-	-	-	-	-	-

A5517	GO:0006629(lipid metabolic process)	-	-	-	-	-	XP_033563364.1 uncharacterized protein BU25DRAFT_337858 [Macroventuria anomochaeta]	-
A5518	GO:0006508(proteolysis)	-	GO:0008236(serine-type peptidase activity),GO:0004252(serine-type endopeptidase activity)	-	-	KOG2237 At1g50380 Predicted serine protease	TPX77576.1 hypothetical protein CcCBS67573_g01165 [Chytridiomycetes confervae]	Protease 2 OS=Moraxella lacunata OX=477 GN=ptrB PE=3 SV=1
A5519	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K13093 HTATSF1; HIV Tat-specific factor 1	-	KOG1548 HsM7657637 Transcription elongation factor TAT-SF1	KAG0171699.1 hypothetical protein DFQ30_000533 [Apophysomyces sp. BC1015]	17S U2 SnRNP complex component HTATSF1 OS=Pongo abelii OX=9601 GN=HTATSF1 PE=2 SV=1
A5520	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5521	-	-	-	-	-	KOG4511 Hs18087843 Uncharacterized conserved protein	-	Cilia- and flagella-associated protein 36 OS=Xenopus tropicalis OX=8364 GN=cfap36 PE=2 SV=2
A5522	-	-	-	-	-	-	-	-
A5523	-	-	-	K17491 SMEK, PPP4R3; protein phosphatase 4 regulatory subunit 3	map04212 Longevity regulating pathway - worm;map04922 Glucagon signaling pathway	KOG2175 Hs14725277 Protein predicted to be involved in carbohydrate metabolism	ORY03121.1 DUF625-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Serine/threonine-protein phosphatase 4 regulatory subunit 3 OS=Xenopus tropicalis OX=8364 GN=ppp4r3b PE=2 SV=1
A5524	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5525	-	-	-	K17278 PGRMC1_2; membrane-associated progesterone receptor component	map04080 Neuroactive ligand-receptor interaction	KOG1110 At2g24940 Putative steroid membrane receptor Hpr6.6/25-Dx	XP_033594523.1 cytochrome b5-like heme/steroid binding domain-containing protein, partial [Neohortaea acidophila]	Probable steroid-binding protein 3 OS=Arabidopsis thaliana OX=3702 GN=MP3 PE=1 SV=1
A5526	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K20872 NEK2; serine/threonine-protein kinase Nek2 [EC:2.7.11.1]	-	KOG1826 Hs4505373 Ras GTPase activating protein RasGAP/neurofibromin	KXS15482.1 kinase-like protein [Gonapodya prolifera JEL478]	Probable serine/threonine-protein kinase nek2 OS=Dictyostelium discoideum OX=44689 GN=nek2 PE=1 SV=1
A5527	-	-	-	-	-	-	-	-

A5528	-	-	-	K20523 SH3YL1; SH3 domain- containing YSC84-like protein 1	-	KOG1843 YH R016c Uncharacteriz ed conserved protein	SMN19250.1 similar to Saccharomyc es cerevisiae YHR016C YSC84 Actin- binding protein involved in bundling of actin filaments and endocytosis of actin cortical patches [Kazachstania saulegensis]	Protein YSC84 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YSC84 PE=1 SV=2
A5529	GO:0042254(ribosome biogenesis);GO:0006364(rRNA processing)	-	GO:0005515(protein binding)	K14824 ERB1, BOP1; ribosome biogenesis protein ERB1	-	KOG0650 Hs21327667 WD40 repeat nucleolar protein Bop1, involved in ribosome biogenesis	ORY07319.1 BOP1NT-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Ribosome biogenesis protein BOP1 homolog OS=Monosiga brevicollis OX=81824 GN=37129 PE=3 SV=1
A5530	-	-	GO:0000166(nucleotide binding)	-	-	KOG2741 At4g09670 Dimeric dihydrodiol dehydrogenase	ORY51383.1 NAD(P)-binding protein [Rhizoclostium globosum]	Uncharacterized oxidoreductase At4g09670 OS=Arabidopsis thaliana OX=3702 GN=At4g09670 PE=1 SV=1
A5531	-	-	GO:0000166(nucleotide binding)	-	-	KOG2741 At4g09670 Dimeric dihydrodiol dehydrogenase	ORY51383.1 NAD(P)-binding protein [Rhizoclostium globosum]	Uncharacterized oxidoreductase At4g09670 OS=Arabidopsis thaliana OX=3702 GN=At4g09670 PE=1 SV=1
A5532	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A5533	-	-	-	-	-	KOG4356 Hs20270333 Uncharacterized conserved protein	-	-
A5534	-	-	-	-	-	-	-	-
A5535	GO:0006511(ubiquitin-dependent protein catabolic process)	-	-	K14016 UFD1; ubiquitin fusion degradation protein 1	map04141 Protein processing in endoplasmic reticulum	KOG1816 At2g21270 Ubiquitin fusion-degradation protein	KAA8909204.1 ubiquitin fusion degradation protein UFD1-domain-containing protein [Sphaerospora brunnea]	Ubiquitin fusion degradation protein 1 homolog OS=Dictyostelium discoideum OX=44689 GN=ufd1 PE=3 SV=1
A5536	-	-	-	-	-	-	-	-
A5537	GO:0006364(rRNA processing)	-	GO:0019843(rRNA binding)	K14859 SSF1_2; ribosome biogenesis protein SSF1/2	-	-	KAG1052211.1 hypothetical protein G6F43_005642 [Rhizopus delemar]	Suppressor of SWI4 1 homolog OS=Mus musculus OX=10090 GN=Ppan PE=1 SV=2
A5538	GO:0007165(signal transduction)	GO:0000159(protein phosphatase type 2A complex)	GO:0019888(protein phosphatase regulator activity)	-	-	-	-	Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' kappa isoform OS=Oryza sativa subsp. japonica OX=39947 GN=B'KAPPA PE=1 SV=1
A5539	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5540	-	-	-	-	-	-	-	-
A5541	-	-	-	-	-	-	-	-

A5542	GO:0000154(rRNA modification),GO:0006364(rRNA processing)	-	GO:0000179(rRNA (adenine-N6,N6-)-dimethyltransferase activity),GO:0008649(rRNA methyltransferase activity)	K14191 DIM1; 18S rRNA (adenine1779-N6/adenine1780-N6)-dimethyltransferase [EC:2.1.1.183]	-	KOG0820 Hs7657198 Ribosomal RNA adenine dimethylase	RKP05804.1 putative dimethyladenosine transferase-like protein [Thamnocephalus sphaerospora]	Probable dimethyladenosine transferase OS=Bos taurus OX=9913 GN=DIMT1 PE=2 SV=1
A5543	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	CEH12291.1 hypothetical protein CBOM_00290 [Ceraceosorus bombacis]	E3 ubiquitin-protein ligase SlrP OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=slrP PE=1 SV=1
A5544	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0192 At2g35050_2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	OJT05228.1 MAP kinase kinase kinase mkh1 [Trametes pubescens]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei brucei OX=5702 GN=CRK2 PE=3 SV=1
A5545	-	-	-	-	-	-	-	-
A5546	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity)	-	-	-	KAG0095046.1 hypothetical protein BGZ93_006400 [Podila epiciadia]	-
A5547	-	-	-	-	-	-	-	-
A5548	GO:0009072(aromatic amino acid family metabolic process)	GO:0005737(cytoplasm)	GO:0003824(catalytic activity)	K01800 malA, GSTZ1; maleylacetate isomerase [EC:5.2.1.2]	map01120 Microbial metabolism in diverse environments;map00643 Styrene degradation;map00350 Tyrosine metabolism;map01100 Metabolic pathways	KOG0868 7299184 Glutathione S-transferase	KAF9157681.1 Glutathione S-transferase zeta-1 [Actinomortierella ambigua]	Maleylacetate isomerase OS=Rattus norvegicus OX=10116 GN=Gstz1 PE=1 SV=2
A5549	-	-	-	-	-	-	-	-
A5550	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K16196 EIF2AK4; eukaryotic translation initiation factor 2-alpha kinase 4 [EC:2.7.11.1]	map04140 Autophagy - animal;map04138 Autophagy - yeast;map05160 Hepatitis C;map05162 Measles;map05168 Herpes simplex virus 1 infection	KOG0198 At2g40560 MEKK and related serine/threonine protein kinases	XP_008717248.1 hypothetical protein HMPREF1541_04682 [Cyphellophora europaea CBS 101466]	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase wee-1.3 OS=Caenorhabditis elegans OX=6239 GN=wee-1.3 PE=1 SV=1
A5551	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	KAF8726638.1 hypothetical protein AX14_007619 [Amanita brunnescens Koide BX004]	-
A5552	-	-	-	-	-	-	-	-

A5553	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0589 At1g54510 Serine/threonine protein kinase	OJT05228.1 MAP kinase kinase mkh1 [Trametes pubescens]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei brucei OX=5702 GN=CRK2 PE=3 SV=1
A5554	-	-	-	-	-	-	-	-
A5555	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0192 At2g35050.2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	XP_025533287.1 kinase-like protein [Aspergillus japonicus CBS 114.51]	Probable serine/threonine-protein kinase PkwA OS=Thermomonospora curvata OX=2020 GN=pkwA PE=1 SV=1
A5556	-	-	-	-	-	-	-	-
A5557	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity),GO:0005515(protein binding)	K06641 CHEK2; serine/threonine-protein kinase CHEK2 [EC:2.7.11.1]	map04218 Cellular senescence;map04115 p53 signaling pathway;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG0032 Hs9966875 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORX91130.1 Pkinase-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Probable serine/threonine-protein kinase fhkC OS=Dictyostelium discoideum OX=44689 GN=fhkC PE=3 SV=2
A5558	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K20098 ERCC6L2; DNA excision repair protein ERCC-6-like 2 [EC:5.6.2.-]	-	KOG0387 At1g03750 Transcription-coupled repair protein CSB/RAD26 (contains SNF2 family DNA-dependent ATPase domain)	TPX57534.1 hypothetical protein PhCBS80983_g03788 [Powellomyces hirtus]	Switch 2 OS=Arabidopsis thaliana OX=3702 GN=SWI2 PE=3 SV=1
A5559	-	-	GO:0003824(catalytic activity),GO:0004802(transketolase activity)	K00615 E2.2.1.1, tktA, tktB; transketolase [EC:2.2.1.1]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map01051 Biosynthesis of ansamycins;map00710 Carbon fixation in photosynthetic organisms;map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG0523 YP074c Transketolase	KNE55313.1 transketolase, variant [Allomyces macrogynus ATCC 38327]	Transketolase OS=Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) OX=103690 GN=tkt PE=1 SV=1
A5560	-	-	-	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698 At5g36250 Serine/threonine protein phosphatase	RKP05315.1 phosphatase 2C-like domain-containing protein, partial [Thamnocephalus sphaerospora]	Probable protein phosphatase 2C 73 OS=Arabidopsis thaliana OX=3702 GN=PPC6-7 PE=2 SV=1

A5561	GO:0006811(ion transport);GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005216(ion channel activity)	K10273 FBXL7; F-box and leucine-rich repeat protein 7	-	KOG0498 Hs4557729 K+-channel ERG and related proteins, contain PAS/PAC sensor domain	KNE63751.1 hypothetical protein AMAG_08834 [Allomyces macrogynus ATCC 38327]	Cyclic nucleotide-gated channel cone photoreceptor subunit alpha OS=Gallus gallus OX=9031 PE=2 SV=1
A5562	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A5563	GO:0070286(axonemal dynein complex assembly)	-	GO:0051087(chaperone binding)	-	-	-	TPX56427.1 hypothetical protein SpCBS45565_g08417 [Spizellomyces sp. 'palustris']	Dynein axonemal assembly factor 6 OS=Homo sapiens OX=9606 GN=DNAAF6 PE=1 SV=1
A5564	GO:0006396(RNA processing)	-	GO:0008173(RNA methyltransferase activity)	K15331 TRMT2B, TRMT2; tRNA (uracil-5-)-methyltransferase [EC:2.1.1.35]	-	KOG2187 HsM12232381 tRNA uracil-5-methyltransferase and related tRNA-modifying enzymes	EPB89308.1 hypothetical protein HMPREF1544_03817 [Mucor circinelloides 1006PhL]	tRNA (uracil-5-)-methyltransferase homolog A OS=Homo sapiens OX=9606 GN=TRMT2A PE=1 SV=2
A5565	-	-	GO:0003824(catalytic activity)	K12663 ECH1; Delta3,5-Delta2,4-dienoyl-CoA isomerase [EC:5.3.3.21]	map04146 Peroxisome	KOG1681 Hs1433007 Enoyl-CoA isomerase	KXS18520.1 enoyl CoA hydratase 1 [Gonapodya prolifera JEL478]	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Rattus norvegicus OX=10116 GN=Ech1 PE=1 SV=2
A5566	-	-	-	K03686 dnaJ; molecular chaperone DnaJ	-	KOG0714 Hs9558755 Molecular chaperone (DnaJ superfamily)	KIK71338.1 hypothetical protein GYMLUDRAFT_33489 [Gymnopus luxurians FD-317 M1]	DnaJ homolog subfamily B member 9 OS=Homo sapiens OX=9606 GN=DNAJB9 PE=1 SV=1
A5567	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A5568	GO:0032508(DNA duplex unwinding)	-	GO:0003677(DNA binding);GO:0005524(ATP binding)	K02540 MCM2; DNA replication licensing factor MCM2 [EC:5.6.2.3]	map03030 DNA replication;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0477 At2g14050 DNA replication licensing factor, MCM2 component	RKP36181.1 MCM2/3/5 family-domain-containing protein [Dimargaris cristalligena]	DNA helicase MCM9 OS=Xenopus tropicalis OX=8364 GN=mcm9 PE=3 SV=1
A5569	-	-	-	-	-	-	-	-
A5570	-	-	-	-	-	-	-	-
A5571	-	-	-	-	-	-	-	-
A5572	GO:0006397(mRNA processing)	-	GO:0016788(hydrolase activity, acting on ester bonds);GO:0016787(hydrolase activity)	K18328 DBR1; lariat debranching enzyme [EC:3.1.-.-]	-	KOG2863 At4g31770 RNA lariat debranching enzyme	ORX71148.1 hypothetical protein DL89DRAFT_222148 [Linderina pennisporea]	Lariat debranching enzyme OS=Danio rerio OX=7955 GN=dbr1 PE=1 SV=1

A5573	GO:0006796(phosphate-containing compound metabolic process)	GO:0005737(cytoplasm)	GO:0000287(magnesium ion binding);GO:0004427(inorganic diphosphatase activity)	K01507 ppa; inorganic pyrophosphatase [EC:3.6.1.1]	map00190 Oxidative phosphorylation	-	XP_003658795.1 uncharacterized protein MYCTH_2295040 [Thermothelomyces thermophilus ATCC 42464]	Inorganic pyrophosphatase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ppa1 PE=3 SV=2
A5574	-	-	-	-	-	-	-	-
A5575	-	-	-	-	-	-	-	-
A5576	GO:0006465(signal peptide processing);GO:0006508(protolysis)	GO:0016020(membrane)	GO:0004252(serine-type endopeptidase activity);GO:0008236(serine-type peptidase activity)	K09647 IMP1; mitochondrial inner membrane protease subunit 1 [EC:3.4.21.-]	map03060 Protein export	KOG0171 Hs21450679 Mitochondrial inner membrane protease, subunit IMP1	KNE55016.1 hypothetical protein AMAG_00953 [Allomyces macrogynus ATCC 38327]	Mitochondrial inner membrane protease subunit 1 OS=Homo sapiens OX=9606 GN=IMMP1L PE=2 SV=1
A5577	-	-	-	-	-	-	-	-
A5578	-	-	-	K15015 SLC32A, VGAT; solute carrier family 32 (vesicular inhibitory amino acid transporter)	map04727 GABAergic synapse;map04721 Synaptic vesicle cycle;map04723 Retrograde endocannabinoid signaling;map05033 Nicotine addiction;map05032 Morphine addiction	KOG1303 At5g02170 Amino acid transporters	RKP28136.1 transmembrane amino acid transporter protein-domain-containing protein [Syncephalis pseudoplumigaleata]	Amino acid transporter AVT1E OS=Arabidopsis thaliana OX=3702 GN=AVT1E PE=2 SV=1
A5579	-	-	-	K03456 PPP2R1; serine/threonine-protein phosphatase 2A regulatory subunit A	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04730 Long-term depression;map04350 TGF-beta signaling pathway;map04071 Sphingolipid signaling pathway;map04728 Dopaminergic synapse;map0460 T cell receptor signaling pathway;map04261 Adrenergic signaling in cardiomyocytes; map05142 Chagas disease;map04530 Tight junction;map03015 mRNA	KOG0211 Hs11386167 Protein phosphatase 2A regulatory subunit A and related proteins	KAG1757558.1 ARM repeat-containing protein [Suillus lakei]	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens OX=9606 GN=PPP2R1B PE=1 SV=3

A5580	GO:0006006(glucose metabolic process), GO:0001678(cellular glucose homeostasis), GO:0005975(carbohydrate metabolic process)	-	GO:0004345(glucose-6-phosphate dehydrogenase activity), GO:00050661(NADP binding), GO:0004396(hexokinase activity), GO:0005524(ATP binding), GO:0005536(glucose binding), GO:0016773(phosphotransferase activity, alcohol group as acceptor), GO:0016614(oxidoreductase activity, acting on CH-OH group of donors)	K00844 HK; hexokinase [EC:2.7.1.1]	map01250 Biosynthesis of nucleotide sugars; map05131 Shigellosis; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map04910 Insulin signaling pathway; map00010 Glycolysis / Gluconeogenesis; map01120 Microbial metabolism in diverse environments; map00052 Galactose metabolism; map00051 Fructose and mannose metabolism; map00500 Starch and sucrose	KOG1369 Hs15967161 Hexokinase	RKO87403.1 hypothetical protein BDK51DRAFT_16571 [Blyttiomycetes helicis]	Hexokinase-4 OS=Homo sapiens OX=9606 GN=GCK PE=1 SV=1
A5581	-	GO:0016459(myosin complex), GO:0005856(cytoskeleton)	GO:0003774(motor activity), GO:0005524(ATP binding), GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection; map04814 Motor proteins	KOG0160 At2g33240 Myosin class V heavy chain	RCH86216.1 Myosin type-2 heavy chain 1, partial [Rhizopus azygosporus]	Myosin-I heavy chain OS=Dictyostelium discoideum OX=44689 GN=myol PE=1 SV=1
A5582	GO:0036211(protein modification process), GO:0016925(protein sumoylation)	-	GO:0008641(ubiquitin-like modifier activating enzyme activity), GO:0019948(SUMO activating enzyme activity)	K10685 UBL1B, SAE2, UBA2; ubiquitin-like 1-activating enzyme E1 B [EC:6.2.1.45]	map04120 Ubiquitin mediated proteolysis	KOG2013 At2g21470 SMT3/SUMO-activating complex, catalytic component UBA2	KAG0286959.1 E1 ubiquitin-activating protein uba2 [Linnemania gamsii]	SUMO-activating enzyme subunit 2 OS=Arabidopsis thaliana OX=3702 GN=SAE2 PE=1 SV=1
A5583	GO:0000226(microtubule cytoskeleton organization), GO:0007020(microtubule nucleation)	GO:0000922(spindle pole), GO:0005815(microtubule organizing center)	GO:0043015(gamma-tubulin binding)	K16570 TUBGCP3, GCP3; gamma-tubulin complex component 3	-	KOG2000 At5g06680 Gamma-tubulin complex, DGRIP91/SPC98 component	KAG0048645.1 Gamma-tubulin complex component 3 [Gryganskiella cystojenkinii]	Gamma-tubulin complex component 3 OS=Arabidopsis thaliana OX=3702 GN=GCP3 PE=1 SV=1
A5584	-	-	GO:0005515(protein binding)	-	-	KOG0504 Hs13899267.1 FOG: Ankyrin repeat	-	NAD-capped RNA hydrolase NUDT12 OS=Homo sapiens OX=9606 GN=NUDT12 PE=1 SV=1
A5585	-	-	GO:0015643(toxic substance binding)	-	-	-	-	-
A5586	-	-	GO:0016614(oxidoreductase activity, acting on CH-OH group of donors), GO:00050660(flavin adenine dinucleotide binding)	-	-	KOG1238 Hs18556423 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	KAG1469234.1 hypothetical protein G6F57_012272 [Rhizopus oryzae]	Oxygen-dependent choline dehydrogenase OS=Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000) OX=223283 GN=betA PE=3 SV=1
A5587	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5588	-	-	GO:0003756(protein disulfide isomerase activity)	K09584 PDIA6, TXNDC7; protein disulfide-isomerase A6 [EC:5.3.4.1]	map04141 Protein processing in endoplasmic reticulum	KOG0191 At2g47470 Thioredoxin/protein disulfide isomerase	XP_018033129.1 disulfide isomerase [Paraphaeosphaeria sporulosa]	Protein disulfide-isomerase-like protein EhSep2 OS=Emiliania huxleyi OX=2903 GN=SEP2 PE=1 SV=2

A5589	GO:0006614(SRP-dependent cotranslational protein targeting to membrane)	GO:0048500(signal recognition particle)	GO:0005525(GTP binding),GO:0008312(7S RNA binding),GO:0003924(GTPase activity)	K03106 SRP54, ffh; signal recognition particle subunit SRP54 [EC:3.6.5.4]	map03070 Bacterial secretion system;map03060 Protein export;map02024 Quorum sensing	KOG0780 CE09524 Signal recognition particle, subunit Srp54	PIA13770.1 signal recognition particle 54 [Coemansia reversa NRRL 1564]	Signal recognition particle subunit SRP54 2 OS=Solanum lycopersicum OX=4081 PE=2 SV=1
A5590	GO:0006298(mismatch repair)	GO:0032300(mismatch repair complex)	GO:0016887(ATP hydrolysis activity),GO:0005524(ATP binding),GO:0030983(mismatched DNA binding)	K08734 MLH1; DNA mismatch repair protein MLH1	map01524 Platinum drug resistance;map05210 Colorectal cancer;map05226 Gastric cancer;map05200 Pathways in cancer;map03430 Mismatch repair;map03460 Fanconi anemia pathway	KOG1979 Hs4557757 DNA mismatch repair protein - MLH1 family	ORY04078.1 MutL-like protein 1, colon cancer, nonpolyposis type 2 [Basidiobolus meristosporus CBS 931.73]	DNA mismatch repair protein Mlh1 OS=Mus musculus OX=10090 GN=Mlh1 PE=1 SV=2
A5591	GO:0006099(tricarboxylic acid cycle)	-	GO:0003824(catalytic activity)	K01900 LSC2; succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00020 Citrate cycle (TCA cycle);map01100 Metabolic pathways	KOG1447 7295455 GTP-specific succinyl-CoA synthetase, beta subunit	ORY00690.1 Sclg2 protein, partial [Basidiobolus meristosporus CBS 931.73]	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=scsB PE=3 SV=1
A5592	-	-	-	-	-	-	ELQ39347.1 hypothetical protein OOU_Y34scaffold00502g23 [Pyricularia oryzae Y34]	-
A5593	-	-	-	-	-	-	-	-
A5594	-	-	GO:0005515(protein binding)	-	-	KOG0619 730644_2 FOG; Leucine rich repeat	-	Probable serine/threonine-protein kinase roco5 OS=Dictyostelium discoideum OX=44689 GN=roco5 PE=3 SV=1

A5595	GO:0009102(biotin biosynthetic process)	-	GO:0003824(catalytic activity),GO:0008483(transaminase activity),GO:0030170(pyridoxal phosphate binding),GO:0004015(adenosylmethionine-8-amino-7-oxononanoate transaminase activity)	-	-	KOG1401 YNR058w Acetylornithine aminotransferase	KGQ11298.1 Adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Beauveria bassiana D1-5]	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase OS=Pseudoscherichia vulneris OX=566 GN=bioA PE=3 SV=1
A5596	-	-	GO:0005509(calcium ion binding)	K19932 NCS1; neuronal calcium sensor	-	KOG0034 At4g33000 Ca2+/calmodulin-dependent protein phosphatase (calcineurin subunit B), EF-Hand superfamily protein	CDH54383.1 calcium calmodulin-dependent protein phosphatase [Lichtheimia corymbifera JMRC.FSU:9682]	Calcineurin B-like protein 10 OS=Arabidopsis thaliana OX=3702 GN=CBL10 PE=1 SV=1
A5597	-	-	-	-	-	-	-	-
A5598	GO:0006606(protein import into nucleus)	-	-	K18752 TNPO1, IPO2, KPNB2; transportin-1	map03013 Nucleocytoplasmic transport	KOG2023 Hs4504907 Nuclear transport receptor Karyopherin-beta2/Transportin (importin beta superfamily)	POY71472.1 hypothetical protein BMF94_5785 [Rhodotorula taiwanensis]	Transportin-1 OS=Mus musculus OX=10090 GN=Tnp1 PE=1 SV=2
A5599	-	-	-	-	-	-	KAF7725059.1 hypothetical protein EC973_000466 [Apophysomyces ossiformis]	-
A5600	-	-	-	-	-	-	-	-
A5601	-	-	-	-	-	-	-	-
A5602	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K06660 CDC5; cell cycle serine/threonine-protein kinase CDC5/MSD2 [EC:2.7.11.21]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG1151 Hs18677726 Tousled-like protein kinase	KXS13327.1 kinase-like protein [Gonapodya prolifera JEL478]	Serine/threonine-protein kinase tousled-like 1-B OS=Danio rerio OX=7955 GN=tlk1b PE=2 SV=1
A5603	GO:0006355(regulation of transcription, DNA-templated),GO:0007165(signal transduction),GO:0001601(phosphorelay signal transduction system),GO:0016310(phosphorylation)	-	GO:0005515(protein binding),GO:0000155(phosphorelay sensor kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	-	KAF2682689.1 putative histidine kinase group protein-like protein [Lentithecium fluviatile CBS 122367]	Autoinducer 2 sensor kinase/phosphatase LuxQ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) OX=223926 GN=luxQ PE=3 SV=1

A5604	-	GO:0005956 (protein kinase CK2 complex)	GO:0019887 (protein kinase regulator activity)	K03115 CSNK2B; casein kinase II subunit beta	map04310 Vhl signaling pathway; map04139 Mitophagy - yeast; map04137 Mitophagy - animal; map04712 Circadian rhythm - plant; map03083 Polycomb repressive complex; map05020 Prion disease; map05022 Pathways of neurodegeneration - multiple diseases; map05010 Alzheimer disease; map05235 PD-L1 expression and PD-1 checkpoint pathway in cancer; map04520 Adherens junction; map03008 Ribosome biogenesis in	KOG3092 7292695 Casein kinase II, beta subunit	NP_001342935.1 CK2 family regulatory subunit Ckb1 [Schizosaccharomyces pombe]	Casein kinase II subunit beta OS=Spodoptera frugiperda OX=7108 PE=2 SV=1
A5605	-	-	GO:0003950 (NAD+ ADP-ribosyltransferase activity), GO:0005515 (protein binding)	K10798 PARP2_3_4; poly [ADP-ribose] polymerase 2/3/4 [EC:2.4.2.30]	map04210 Apoptosis; map04212 Longevity regulating pathway - worm; map03410 Base excision repair	KOG1037 CE25556 NAD+ ADP-ribosyltransferase Parp, required for poly-ADP ribosylation of nuclear proteins	ORX86892.1 PARP-domain-containing protein [Anaeromyxetes robustus]	Poly [ADP-ribose] polymerase 2 OS=Homo sapiens OX=9606 GN=PARP2 PE=1 SV=2
A5606	-	-	-	-	-	-	-	-
A5607	GO:0006370 (7-methylguanosine mRNA capping)	-	GO:0004484 (mRNA guanylyltransferase activity), GO:0005524 (ATP binding), GO:0004482 (mRNA (guanine-N7-)-methyltransferase activity)	-	-	KOG1975 At3g20650 mRNA cap methyltransferase	XP_016604488.1 hypothetical protein SPPG_08040 [Spizellomyces punctatus DAOM BR117]	mRNA cap guanine-N7 methyltransferase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os08g0180000 PE=2 SV=1
A5608	-	-	-	-	-	-	-	-
A5609	GO:0006508 (proteolysis)	-	GO:0004181 (metallocarboxypeptidase activity), GO:0008270 (zinc ion binding), GO:0016788 (hydrolase activity, acting on ester bonds)	-	-	-	-	Aspartoacylase OS=Homo sapiens OX=9606 GN=ASPA PE=1 SV=1
A5610	GO:0007018 (microtubule-based movement)	-	GO:0003777 (microtubule motor activity), GO:0005524 (ATP binding), GO:0008017 (microtubule binding)	K10398 KIF11, EG5; kinesin family member 11	map04814 Motor proteins	KOG0245 7301599 Kinesin-like protein	ORX74357.1 kinesin-domain-containing protein [Linderina pennisporea]	Osmotic avoidance abnormal protein 3 OS=Caenorhabditis elegans OX=6239 GN=osm-3 PE=1 SV=4
A5611	-	-	-	-	-	-	-	-
A5612	-	-	-	-	-	-	-	-
A5613	-	-	-	-	-	-	-	-
A5614	-	-	GO:0047429 (nucleoside-triphosphate diphosphatase activity)	K06287 yhdE; nucleoside triphosphate pyrophosphatase [EC:3.6.1.-]	map00240 Pyrimidine metabolism; map01232 Nucleotide metabolism; map01100 Metabolic pathways	KOG1509 Hs20554409_1 Predicted nucleic acid-binding protein ASMTL	XP_021879597.1 acetylserotonin O-methyltransferase-like protein [Lobosporangium transversale]	dTTP/UTP pyrophosphatase OS=Clostridium perfringens (strain SM101 / Type A) OX=289380 GN=CPR_2112 PE=3 SV=1

A5615	-	-	-	-	-	-	ORY43044.1 hypothetical protein BCR33DRAFT_660405 [Rhizoclostium globosum]	Intraflagellar transport protein 20 homolog OS=Xenopus tropicalis OX=8364 GN=ift20 PE=2 SV=1
A5616	-	-	-	-	-	-	-	-
A5617	-	-	GO:0016491(oxidoreductase activity)	K16066 ydfG; 3-hydroxy acid dehydrogenase / malonic semialdehyde reductase [EC:1.1.1.381 1.1.1.-]	map00240 Pyrimidine metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG1205 7301818 Predicted dehydrogenase	SAL96717.1 hypothetical protein [Absidia glauca]	Dehydrogenase/reductase SDR family protein 7-like OS=Drosophila melanogaster OX=7227 GN=CG7601 PE=2 SV=1
A5618	-	-	GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity)	K03695 clpB; ATP-dependent Clp protease ATP-binding subunit ClpB	map04213 Longevity regulating pathway - multiple species	-	OWB54418.1 hypothetical protein B5S28_g265 [[Candida boidinii]	Chaperone protein ClpB OS=Agrobacterium fabrum (strain C58 / ATCC 33970) OX=176299 GN=clpB PE=3 SV=2
A5619	-	-	-	-	-	-	-	-
A5620	-	-	GO:0016757(glycosyltransferase activity)	-	-	KOG4698 At5g55500 Uncharacterized conserved protein	KXG47967.1 Glycosyltransferase AER61, uncharacterized [Penicillium griseofulvum]	Beta-1,2-xylosyltransferase RCN11 OS=Oryza sativa subsp. japonica OX=39947 GN=RCN11 PE=1 SV=1
A5621	-	-	-	-	-	-	-	-
A5622	-	-	-	K10134 El24; etoposide-induced 2.4 mRNA	map04115 p53 signaling pathway	KOG3966 Hs631104 p53-mediated apoptosis protein El24/PIG8	TPX58496.1 hypothetical protein PhCBS80983_g03074 [Powellomyces hirtus]	Protein El24 homolog OS=Dictyostelium discoideum OX=44689 GN=DDB_G0284253 PE=3 SV=1
A5623	GO:0042073(intracellular transport);GO:0060271(cilium assembly)	GO:0030992(intracellular transport particle B)	GO:0015631(tubulin binding)	-	-	-	KAG4096729.1 hypothetical protein H8356DRAFT_1425994 [Neocallimastix sp. JGI-2020a]	Intraflagellar transport protein 81 homolog OS=Rattus norvegicus OX=10116 GN=ift81 PE=2 SV=1
A5624	-	GO:0016020(membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	K05681 ABCG2, CD338; ATP-binding cassette, subfamily G (WHITE), member 2	map01523 Antifolate resistance;map04976 Bile secretion;map02010 ABC transporters	KOG0061 Hs4757850 Transporter, ABC superfamily (Breast cancer resistance protein)	RKP21732.1 hypothetical protein ROZALSC1DR_AFT_26874 [Rozella allomycis CSF55]	Broad substrate specificity ATP-binding cassette transporter ABCG2 OS=Macaca mulatta OX=9544 GN=ABCG2 PE=2 SV=1

A5625	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map04972 Pancreatic secretion;map04080 Neuroactive ligand-receptor interaction;map05164 Influenza A	KOG3627 7289776 Trypsin	KAG1271466.1 hypothetical protein G6F65_012377 [Rhizopus oryzae]	Chymotrypsin-like protease CTRL-1 OS=Homo sapiens OX=9606 GN=CTRL PE=1 SV=1
A5626	-	-	-	-	-	KOG3589 Hs4506519 G protein signaling regulators	KAF9354390.1 hypothetical protein BGX26_007784 [Mortierella sp. AD094]	Regulator of G-protein signaling 21 OS=Homo sapiens OX=9606 GN=RGS21 PE=2 SV=1
A5627	-	-	-	-	-	-	-	-
A5628	-	-	GO:0019901(protein kinase binding)	K09554 CDC37; cell division cycle protein 37	map04151 PI3K-Akt signaling pathway	KOG2260 Hs5901922 Cell division cycle 37 protein, CDC37	KAF9429020.1 hsp90 co-chaperone Cdc37, partial [Entomortierella beljakovae]	Hsp90 co-chaperone Cdc37 OS=Mus musculus OX=10090 GN=Cdc37 PE=1 SV=1
A5629	GO:0006265(DNA topological change),GO:0006259(DNA metabolic process)	-	GO:0003677(DNA binding),GO:0003918(DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity),GO:0005524(ATP binding)	K03164 TOP2; DNA topoisomerase II [EC:5.6.2.2]	map01524 Platinum drug resistance	KOG0355 ECU04g0350 DNA topoisomerase type II	ORY19637.1 type II DNA topoisomerase [Neocallimastix californiae]	DNA topoisomerase 2 OS=Arabidopsis thaliana OX=3702 GN=TOP2 PE=2 SV=2
A5630	GO:0016192(vesicle-mediated transport)	-	GO:0016021(integral component of membrane)	-	-	KOG0859 At5g22360 Synaptobrevin/VAMP-like protein	XP_016610698.1 hypothetical protein SPPG_01745 [Spizellomyces punctatus DAOM BR117]	Vesicle-associated membrane protein 714 OS=Arabidopsis thaliana OX=3702 GN=VAMP714 PE=1 SV=1
A5631	GO:0009058(biosynthetic process)	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups)	K00641 metX; homoserine O-acetyltransferase/O-succinyltransferase [EC:2.3.1.31 2.3.1.46]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00920 Sulfur metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	-	OZJ06494.1 hypothetical protein BZG36_00558 [Bifiguratus adalaidae]	Homoserine O-acetyltransferase OS=Chlorobium chlorochromatii (strain CaD3) OX=340177 GN=metXA PE=3 SV=1
A5632	-	-	-	-	-	-	-	-

A5633	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08838 STK24_25_MS T4; serine/threonine-protein kinase 24/25/MST4 [EC:2.7.11.1]	-	KOG0581 At5g40440 Mitogen-activated protein kinase kinase (MAP2K)	PVZ96484.1 hypothetical protein BB558_007636 [Smittium angustum]	Mitogen-activated protein kinase kinase 3 OS=Arabidopsis thaliana OX=3702 GN=MKK3 PE=1 SV=1
A5634	GO:0006508(proteolysis)	-	GO:0004185(serine-type carboxypeptidase activity)	K13289 CTSA, CPY; cathepsin A (carboxypeptidase C) [EC:3.4.16.5]	map04142 Lysosome;map04614 Renin-angiotensin system	KOG1282 At3g25420 Serine carboxypeptidases (lysosomal cathepsin A)	KAA8916903.1 hypothetical protein TRICL001022 [Trichomonas cucurbitae]	Serine carboxypeptidase-like 20 OS=Arabidopsis thaliana OX=3702 GN=SCPL20 PE=2 SV=2
A5635	-	-	-	-	-	-	-	-
A5636	GO:0006361(transcription initiation from RNA polymerase II promoter)	-	GO:0001181(RNA polymerase I general transcription initiation factor activity)	-	-	KOG2434 Hs21361631 RNA polymerase I transcription factor	TPX63592.1 hypothetical protein SpCBS45565.5g06491 [Spizellomyces sp. 'palustris']	RNA polymerase I-specific transcription initiation factor RRN3 OS=Homo sapiens OX=9606 GN=RRN3 PE=1 SV=1
A5637	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0598 YKL126w Ribosomal protein S6 kinase and related proteins	KAF8271939.1 Pkinase-domain-containing protein [Lactarius quietus]	Serine/threonine-protein kinase YPK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPK1 PE=1 SV=2
A5638	GO:0006979(response to oxidative stress),GO:0034599(cellular response to oxidative stress)	-	GO:0004601(peroxidase activity),GO:0020037(heme binding)	K00428 E1.1.1.1.5; cytochrome c peroxidase [EC:1.11.1.5]	-	-	RMJ22353.1 cytochrome c peroxidase [Aspergillus sp. HF37]	Probable L-ascorbate peroxidase 5, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=APX5 PE=2 SV=1
A5639	-	-	-	K18443 GBF1; golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	map04144 Endocytosis	KOG0928 At1g13980 Pattern-formation protein/guanine nucleotide exchange factor	KAF9052720.1 Sec7-domain-containing protein [Panaeolus papilionaceus]	ARF guanine-nucleotide exchange factor GNOM OS=Arabidopsis thaliana OX=3702 GN=GN PE=1 SV=1
A5640	GO:0032012(regulation of ARF protein signal transduction)	-	GO:0005085(guanine-nucleotide exchange factor activity)	K18443 GBF1; golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	map04144 Endocytosis	KOG0928 At1g13980 Pattern-formation protein/guanine nucleotide exchange factor	KXS16367.1 Sec7-domain-containing protein [Gonapodya prolifera JEL478]	ARF guanine-nucleotide exchange factor GNOM OS=Arabidopsis thaliana OX=3702 GN=GN PE=1 SV=1
A5641	-	-	GO:0005085(guanine-nucleotide exchange factor activity)	K10733 GINS2, PSF2; GINS complex subunit 2	-	KOG4071 At3g12530 Uncharacterized conserved protein	KAF0451687.1 Dbl-like domain-containing protein [Gigaspora margarita]	Myosin-M heavy chain OS=Dictyostelium discoideum OX=44689 GN=myoM PE=1 SV=1
A5642	-	-	-	-	-	-	-	-
A5643	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	-	KXS12596.1 Formate/nitrite transporter [Gonapodya prolifera JEL478]	Probable formate transporter OS=Methanothermobacter thermotrophicus OX=145262 GN=fdhC PE=3 SV=1

A5644	-	-	-	-	-	KOG0814 CE15664 Glyoxylase	ORX51371.1 Metallo-hydrolase/oxidoreductase [Piromyces finnis]	Hydroxyacylglutathione hydrolase GloC OS=Escherichia coli (strain K12) OX=83333 GN=gloC PE=1 SV=1
A5645	-	-	-	-	-	-	-	-
A5646	-	-	-	-	-	-	-	-
A5647	GO:0006562(proline catabolic process)	-	GO:0004657(proline dehydrogenase activity)	K00318 PRODH, fadM, putB; proline dehydrogenase [EC:1.5.5.2]	map01110 Biosynthesis of secondary metabolites;map00330 Arginine and proline metabolism;map01100 Metabolic pathways	KOG0186 Hs19924111 Proline oxidase	KAG0170358.1 hypothetical protein DFQ30_002606 [Apophysom yces sp. BC1015]	Proline dehydrogenase 1, mitochondrial OS=Homo sapiens OX=9606 GN=PRODH PE=1 SV=3
A5648	GO:0006811(ion transport), GO:0055085(transmembrane transport), GO:0006813(potassium ion transport)	GO:0016020(membrane)	GO:0005216(ion channel activity),GO:0005249(voltage-gated potassium channel activity)	K10273 FBXL7; F-box and leucine-rich repeat protein 7	-	KOG0498 Hs4885407 K+-channel ERG and related proteins, contain PAS/PAC sensor domain	KNE71946.1 hypothetical protein AMAG_16369 [Allomyces macrogynus ATCC 38327]	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 3 OS=Rattus norvegicus OX=10116 GN=Hcn3 PE=1 SV=1
A5649	-	-	-	-	-	-	-	-
A5650	-	-	-	-	-	-	-	-
A5651	GO:0017186(peptidyl-pyroglutamic acid biosynthetic process, using glutaminy l-peptide cyclotransferase)	-	GO:0005515(protein binding),GO:0016603(glutaminy l-peptide cyclotransferase activity)	-	-	-	KZM27602.1 hypothetical protein ST47_g1307 [Ascochyta rabiei]	Glutaminy l-peptide cyclotransferase OS=Arabidopsis thaliana OX=3702 GN=QCT PE=1 SV=1
A5652	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin---tyrosine ligase [EC:6.3.2.25]	-	KOG2156 7297795 Tubulin-tyrosine ligase-related protein	XP_016608407.1 hypothetical protein SPPG_04692 [Spizellomyces punctatus DAOM BR117]	Protein polyglycyase TTL10 OS=Macaca fascicularis OX=9541 GN=TTL10 PE=2 SV=1
A5653	-	-	-	-	-	-	-	-
A5654	-	GO:0005634(nucleus)	-	-	-	-	-	-
A5655	-	-	-	-	-	-	-	-
A5656	-	GO:0016459(myosin complex)	GO:0005515(protein binding),GO:0003774(motor activity),GO:0005524(ATP binding)	-	-	KOG0162 Hs4826844 Myosin class I heavy chain	KAG4091241.1 heavy chain, unconventional myosin family member-like protein [Neocallimastix sp. JGI-2020a]	Unconventional myosin-le OS=Rattus norvegicus OX=10116 GN=Myo1e PE=1 SV=1
A5657	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K25079 RBM42; RNA-binding protein 42	-	KOG0226 HsM13236563 RNA-binding proteins	RKP38969.1 hypothetical protein BJ085DRAFT_11423, partial [Dimargaris cristalligena]	RNA-binding protein 42 OS=Xenopus tropicalis OX=8364 GN=rbm42 PE=2 SV=1

A5658	GO:0006099(tricarboxylic acid cycle),GO:0006108(malate metabolic process),GO:0019752(carboxylic acid metabolic process)	-	GO:0003824(catalytic activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0030060(L-malate dehydrogenase activity),GO:0016615(malate dehydrogenase activity),GO:0016491(oxidoreductase activity)	K00026 MDH2; malate dehydrogenase [EC:1.1.1.37]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00710 Carbon fixation in photosynthetic organisms;map00620 Pyruvate metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism;map00630 Glyoxylate and dicarboxylate metabolism	KOG1494 Hs21735621 NAD-dependent malate dehydrogenase	OUM64508.1 hypothetical protein PIROE2DRAFT_51257 [Piromyces sp. E2]	Malate dehydrogenase, mitochondrial OS=Mus musculus OX=10090 GN=Mdh2 PE=1 SV=3
A5659	-	-	-	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1235 At5g24810 Predicted unusual protein kinase	KXS09410.1 beta-lactamase/transpeptidase-like protein [Gonapodya prolifera JEL478]	Protein ACTIVITY OF BC1 COMPLEX KINASE 8, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ABC1K8 PE=2 SV=1
A5660	-	-	GO:0004420(hydroxymethylglutaryl-CoA reductase (NADPH) activity)	-	-	-	-	-
A5661	-	-	-	-	-	-	-	-
A5662	GO:0006259(DNA metabolic process)	GO:0005694(chromosome)	GO:0003677(DNA binding),GO:0003918(DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity),GO:0003824(catalytic activity),GO:0005524(ATP binding)	K10878 SPO11; meiotic recombination protein SPO11	map04113 Meiosis - yeast	KOG2795 At1g63990 Catalytic subunit of the meiotic double strand break transesterase	XP_025348150.1 DNA topoisomerase IV, alpha subunit [Pseudomicrostroma glucosiphilum]	Meiotic recombination protein SPO11-2 OS=Oryza sativa subsp. japonica OX=39947 GN=SPO11-2 PE=2 SV=1
A5663	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5664	GO:0007264(small GTPase mediated signal transduction)	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K04392 RAC1; Ras-related C3 botulinum toxin substrate 1	map04360 Axon guidance;map04361 Axon regeneration;map05014 Amyotrophic lateral sclerosis;map04024 cAMP signaling pathway;map05415 Diabetic cardiomyopathy;map05417 Lipid and atherosclerosis;map05416 Viral myocarditis;map04145 Phagosome;map05135 Yersinia infection;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04810 Regulation	KOG0393 Hs9845511 Ras-related small GTPase, Rho type	KNE55842.1 small GTP-binding protein domain [Allomyces macrogynus ATCC 38327]	Ras-related C3 botulinum toxin substrate 1 OS=Bos taurus OX=9913 GN=RAC1 PE=1 SV=1

A5665	GO:0006355(regulation of transcription, DNA-templated)	-	-	-	-	-	XP_031025403.1 uncharacterized protein SmJEL517_g02736 [Synchytrium microbalum]	Probable serine/threonine-protein kinase DDB_G0280133 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0280133 PE=3 SV=1
A5666	-	-	GO:0005515(protein binding)	-	-	-	XP_025601020.1 hypothetical protein FA09DRAFT_112792 [Tilletiopsis washingtonensis]	-
A5667	-	GO:0008537(proteasome activator complex)	-	K06698 PSME3; proteasome activator subunit 3 (PA28 gamma)	map04612 Antigen processing and presentation;map03050 Proteasome;map05160 Hepatitis C	KOG4470[CE28807 Proteasome activator subunit	EPZ32152.1 Proteasome activator pa28, REG alpha/beta subunit domain-containing protein [Rozella allomyces CSF55]	Proteasome activator complex subunit 3 OS=Gallus gallus OX=9031 GN=PSME3 PE=1 SV=1
A5668	-	-	-	-	-	KOG1192[At1g43620 UDP-glucuronosyl and UDP-glucosyl transferase	KAF2036520.1 putative glucosyl/glucuronosyl transferase [Setomelanomma holmii]	Sterol 3-beta-glucosyltransferase UGT80B1 OS=Arabidopsis thaliana OX=3702 GN=UGT80B1 PE=1 SV=1
A5669	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015267(channel activity)	-	-	KOG0224[CE04707 Aquaporin (major intrinsic protein family)	ORY45159.1 putative glycerol uptake facilitator protein [Rhizoclostium globosum]	Glycerol uptake facilitator protein OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=glpF PE=3 SV=2
A5670	-	-	GO:0005515(protein binding)	-	-	-	TPX75281.1 hypothetical protein CcCBS67573_g03448 [Chytridiomycetes confervae]	-
A5671	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015267(channel activity)	-	-	KOG0224[CE04707 Aquaporin (major intrinsic protein family)	TPX48008.1 hypothetical protein SeMB42_g03148 [Synchytrium endobioticum]	Glycerol uptake facilitator protein OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=glpF PE=3 SV=2
A5672	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015267(channel activity)	-	-	KOG0224[CE04707 Aquaporin (major intrinsic protein family)	ORY45159.1 putative glycerol uptake facilitator protein [Rhizoclostium globosum]	Glycerol uptake facilitator protein OS=Escherichia coli O157:H7 OX=83334 GN=glpF PE=3 SV=1
A5673	-	-	GO:0005515(protein binding)	-	-	-	-	-

A5674	-	-	-	K17361 ACOT9; acyl-coenzyme A thioesterase 9 [EC:3.1.2.-]	-	KOG2763 At5g48370 Acyl-CoA thioesterase	KNE61261.1 hypothetical protein AMAG_07004 [Allomyces macrogynus ATCC 38327]	Acyl-coenzyme A thioesterase 4, mitochondrial OS=Humulus lupulus OX=3486 GN=TE4 PE=1 SV=1
A5675	-	-	GO:0003824(catalytic activity),GO:0004488(methylene tetrahydrofolate dehydrogenase (NADP+) activity)	K00288 MTHFD; methylenetetrahydrofolate dehydrogenase (NADP+)/methylenetetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase [EC:1.5.1.5,3.5.4.9,6.3.4.3]	map00670 One carbon pool by folate;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG0089 At3g12290 Methylenetetrahydrofolate dehydrogenase/methylene tetrahydrofolate cyclohydrolase	XP_018290800.1 hypothetical protein PHYBLDRAFT_113185 [Phycomyces blakesleeanus NRRL 1555(-)]	Bifunctional protein FOLD 2 OS=Arabidopsis thaliana OX=3702 GN=FOLD2 PE=2 SV=1
A5676	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K12614 DDX6, RCK, DHH1; ATP-dependent RNA helicase DDX6/DHH1 [EC:3.6.4.13]	map03018 RNA degradation	KOG0326 At3g61240 ATP-dependent RNA helicase	XP_016606024.1 ATP-dependent RNA helicase dhh1 [Spizellomyces punctatus DAOM BR117]	DEAD-box ATP-dependent RNA helicase 6 OS=Oryza sativa subsp. japonica OX=39947 GN=Os04g0533000 PE=2 SV=1
A5677	-	-	GO:0020037(heme binding)	K23490 CYB5; cytochrome b5	-	KOG0537 CE14418 Cytochrome b5	KAF8916553.1 hypothetical protein BGZ58_00527.1, partial [Dissophora ornata]	Cytochrome b5 OS=Rhizopus stolonifer OX=4846 PE=2 SV=1
A5678	-	-	GO:0003824(catalytic activity)	K07511 ECHS1; enoyl-CoA hydratase [EC:4.2.1.17]	map00410 beta-Alanine metabolism;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00930 Caprolactam degradation;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00062 Fatty acid elongation;map00627 Aminobenzoate	KOG1683 Hs2068528 Hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase	TPX61615.1 hypothetical protein PhCBS80983_g01002 [Powellomyces hirtus]	Enoyl-CoA delta isomerase 1, mitochondrial OS=Mus musculus OX=10090 GN=Eci1 PE=1 SV=2
A5679	GO:0006259(DNA metabolic process), GO:0006265(DNA topological change)	-	GO:0003677(DNA binding),GO:0003918(DNA topoisomerase type II (double strand cut, ATP-hydrolyzing activity),GO:0005524(ATP binding)	K03164 TOP2; DNA topoisomerase II [EC:5.6.2.2]	map01524 Platinum drug resistance	KOG0355 At3g23890 DNA topoisomerase type II	ORY19637.1 type II DNA topoisomerase [Neocallimastix californiae]	DNA topoisomerase 2 OS=Arabidopsis thaliana OX=3702 GN=TOP2 PE=2 SV=2

A5680	-	-	GO:0008757(S-adenosylmethionine-dependent methyltransferase activity)	-	-	-	XP_503586.1 YALIOE05467p [Yarrowia lipolytica CLIB122]	Probable thiopurine S-methyltransferase OS=Danio rerio OX=7955 GN=tpmt PE=2 SV=1
A5681	GO:0006420(arginyl-tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation)	GO:0005737(cytoplasm)	GO:0004814(arginine-tRNA ligase activity),GO:0005524(ATP binding),GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity)	K01887 RARS, argS: arginyl-tRNA synthetase [EC:6.1.1.19]	map00970 Aminoacyl-tRNA biosynthesis	KOG4426 7293140 Arginyl-tRNA synthetase	KXS11511.1 arginyl-tRNA synthetase [Gonapodya prolifera JEL478]	Probable arginine--tRNA ligase, cytoplasmic OS=Drosophila melanogaster OX=7227 GN=ArgRS PE=2 SV=1
A5682	-	-	GO:0008757(S-adenosylmethionine-dependent methyltransferase activity)	-	-	-	KAG5356810.1 putative thiopurine S-methyltransferase [Yarrowia sp. E02]	Thiopurine S-methyltransferase OS=Pseudomonas aeruginosa (strain PA7) OX=381754 GN=tpm PE=3 SV=1
A5683	-	-	-	-	-	-	TPX60914.1 hypothetical protein PhCBS80983.g01465 [Powellomyces hirtus]	Cilia- and flagella-associated protein 300 OS=Xenopus tropicalis OX=8364 GN=cfap300 PE=2 SV=1
A5684	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0598 At3g08720 Ribosomal protein S6 kinase and related proteins	XP_007304880.1 AGC/Akt protein kinase [Sterium hirsutum FP-91666 SS1]	Protein kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pkgB PE=1 SV=2
A5685	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity),GO:0004672(protein kinase activity)	K08793 STK32, YANK; serine/threonine kinase 32 [EC:2.7.11.1]	-	KOG0986 Hs4504101 G protein-coupled receptor kinase	TFK32792.1 kinase-like domain-containing protein [Crucibulum laeve]	G protein-coupled receptor kinase 6 OS=Homo sapiens OX=9606 GN=GRK6 PE=1 SV=2
A5686	-	-	-	-	-	-	-	-
A5687	-	-	-	-	-	-	-	-
A5688	-	-	-	-	-	-	-	-
A5689	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K18664 SLH1; antiviral helicase SLH1 [EC:3.6.4.13]	-	KOG0952 Hs14747366 DNA/RNA helicase MER3/SLH1, DEAD-box superfamily	OZJ04536.1 hypothetical protein BZG36_03995 [Bifiguratus adalaidae]	DExH-box ATP-dependent RNA helicase DExH14 OS=Arabidopsis thaliana OX=3702 GN=BRR2C PE=2 SV=1
A5690	-	-	-	K25201 IPO11, RANBP11; importin-11	map03013 Nucleocytoplasmic transport	KOG1993 7303045_2 Nuclear transport receptor KAP120 (importin beta superfamily)	KXS11401.1 ARM repeat-containing protein [Gonapodya prolifera JEL478]	Importin beta-like protein KAP120 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAP120 PE=1 SV=1

A5691	-	-	-	-	-	KOG1256 Hs20070257 Long-chain acyl-CoA synthetases (AMP-forming)	KZM27732.1 hypothetical protein ST47_g1294 [Ascochyta rabiei]	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Gallus gallus OX=9031 GN=ACSBG2 PE=2 SV=2
A5692	-	-	GO:0005515(protein binding)	-	-	KOG0266 Hs21450820 WD40 repeat-containing protein	TPX70450.1 hypothetical protein SpCBS45565_g01836 [Spizellomyces sp. 'palustris']	Cilia- and flagella-associated protein 52 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP52 PE=1 SV=1
A5693	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027 Hs22068637 Calmodulin and related proteins (EF-Hand superfamily)	TPX56243.1 hypothetical protein SpCBS45565_g08440 [Spizellomyces sp. 'palustris']	Calcium-binding protein 7 OS=Homo sapiens OX=9606 GN=CABP7 PE=1 SV=1
A5694	-	-	-	K01251 AHCY, ahcY; adenosylhomocysteinase [EC:3.13.2.1]	map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG1370 At4g13940 S-adenosylhomocysteine hydrolase	KAG0323276.1 hypothetical protein BGZ97_011027 [Linnemannia gamsii]	Adenosylhomocysteinase OS=Nicotiana sylvestris OX=4096 GN=SAHH PE=2 SV=1
A5695	-	-	-	-	-	-	-	-
A5696	-	-	-	-	-	-	ORZ38127.1 hypothetical protein BCR44DRAFT_66373 [Catenaria anguillulae PL171]	Cilia- and flagella-associated protein 100 OS=Chlamydomonas reinhardtii OX=3055 GN=FAP100 PE=1 SV=1
A5697	-	-	-	-	-	-	-	-
A5698	-	-	GO:0005515(protein binding)	-	-	-	XP_037168343.1 uncharacterized protein HO173_002919 [Letharia columbiana]	-

A5699	-	-	GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0028 7298440 Ca2+-binding protein (centrin/caltractin), EF-Hand superfamily protein	CAE6474361.1 unnamed protein product, partial [Rhizoctonia solani]	-
A5700	-	-	-	-	-	-	-	-
A5701	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08827 PRPF4B; serine/threonine-protein kinase PRP4 [EC:2.7.11.1]	-	KOG0670 At1g13350 U4/U6-associated splicing factor PRP4	RIB20934.1 kinase-like domain-containing protein [Gigaspora rosea]	Serine/threonine-protein kinase PRP4 homolog OS=Pongo abelii OX=9601 GN=PRPF4B PE=2 SV=1
A5702	-	-	-	-	-	-	-	-
A5703	GO:0001510(RNA methylation),GO:0009452(7-methylguanosine RNA capping)	-	GO:0008168(methyltransferase activity)	K14292 TGS1; trimethylguanosine synthase [EC:2.1.1.-]	-	KOG2730 Hs19923661 Methylase	KNE55434.1 hypothetical protein AMAG_17786 [Allomyces macrogynus ATCC 38327]	Uncharacterized protein L320 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_L320 PE=4 SV=1
A5704	-	-	GO:0005515(protein binding)	-	-	KOG0543 Hs4758384 FKBP-type peptidyl-prolyl cis-trans isomerase	TPX71669.1 hypothetical protein CcCBS67573_g06057 [Chytridiomycetes confervae]	Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Saguinus oedipus OX=9490 GN=FKBP5 PE=2 SV=2
A5705	GO:0006396(RNA processing),GO:0000398(mRNA splicing, via spliceosome),GO:0000956(nuclear-transcribed mRNA catabolic process)	-	-	K12623 LSM4; U6 snRNA-associated Sm-like protein LSM4	map03040 Spliceosome;map03018 RNA degradation	KOG3293 Hs6912486 Small nuclear ribonucleoprotein (snRNP)	KZS87802.1 Sm-like ribonucleo protein [Sistotremastrum niveocremaum HHB9708]	Probable U6 snRNA-associated Sm-like protein LSM4 OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0256900 PE=2 SV=1
A5706	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity)	-	-	KOG0698 7291977 Serine/threonine protein phosphatase	TPX71020.1 hypothetical protein CcCBS67573_g06331 [Chytridiomycetes confervae]	Probable protein phosphatase 2C 45 OS=Oryza sativa subsp. japonica OX=39947 GN=Os04g0659500 PE=2 SV=2
A5707	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 At4g39180 Phosphatidylinositol transfer protein SEC14 and related proteins	KAF8324063.1 hypothetical protein DL93DRAFT_91013 [Clavulina sp. PMI_390]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana OX=3702 GN=SFH2 PE=3 SV=1
A5708	-	-	-	-	-	-	-	-

A5709	-	-	-	-	-	-	-	-
A5710	-	-	-	K03939 NDUFS6; NADH dehydrogenase (ubiquinone) Fe-S protein 6	map05014 Amyotrophic lateral sclerosis;map054 15 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04 714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map050 22 Pathways of neurodegenerati on - multiple diseases;map052 08 Chemical carcinogenesis - reactive oxygen species;map049 32 Non- alcoholic fatty liver disease;map050	KOG3456 729 6948 NADH:ubiqui none oxidoreducta se, NDUFS6/13 kDa subunit	KAF7320346. 1 Lactobacillus shifted protein [Mycena kentingensis]	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Gorilla gorilla gorilla OX=9595 GN=NDUFS6 PE=2 SV=1
A5711	GO:00065 37(glutam ate biosynthe tic process), GO:00068 07(nitroge n compoun d metabolic process)	-	GO:0015930(glu tamate synthase activity),GO:001 6638(oxidoredu ctase activity, acting on the CH-NH2 group of donors),GO:001 6491(oxidoredu ctase activity)	-	-	KOG0399 At5 g53460 Glutamate synthase	RKO91909.1 hypothetical protein BDK51DRAFT _18838 [Blyttiomycet helicus]	Glutamate synthase 1 [NADH], chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0681900 PE=2 SV=1
A5712	GO:00065 37(glutam ate biosynthe tic process)	-	GO:0051536(iron-sulfur cluster binding),GO:001 6639(oxidoredu ctase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor),GO:00 16491(oxidoredu ctase activity)	K00264 GLT1; glutamate synthase (NADH) [EC:1.4.1.14]	map00910 Nitrogen metabolism;map 01110 Biosynthesis of secondary metabolites;map 01120 Microbial metabolism in diverse environments;map 01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map 01100 Metabolic pathways	KOG0399 At5 g53460 Glutamate synthase	RCH79684.1 glutamate synthase [NADH], partial [Rhizopus stolonifer]	Glutamate synthase 1 [NADH], chloroplastic OS=Arabidopsis thaliana OX=3702 GN=GLT1 PE=1 SV=2

A5713	GO:0009058(biosynthetic process), GO:0006520(cellular amino acid metabolic process)	-	GO:0003824(catalytic activity), GO:0030170(pyridoxal phosphate binding), GO:0008483(transaminase activity)	K00815 TAT; tyrosine aminotransferase [EC:2.6.1.5]	map00950 Isoquinoline alkaloid biosynthesis;map01110 Biosynthesis of secondary metabolites;map00960 Tropane, piperidine and pyridine alkaloid biosynthesis;map00401 Novobiocin biosynthesis;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map00360 Phenylalanine metabolism;map00130 Ubiquinone and other terpenoid-quinone biosynthesis;map00350 Tyrosine metabolism;map	KOG0259[Hs4507369 Tyrosine aminotransferase	RKP07642.1 tyrosine aminotransferase [Thamnocephalis sphaerospora]	Tyrosine aminotransferase OS=Mus musculus OX=10090 GN=Tat PE=1 SV=1
A5714	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3731[7292365 Sulfatases	RCI11935.1 hypothetical protein L249_4576 [Ophiocordyceps polyrhachis-furcata BCC 54312]	Ulvian-active sulfatase OS=Formosa agariphila (strain DSM 15362 / KCTC 12365 / LMG 23005 / KMM 3901 / M-2Alg 35-1) OX=1347342 GN=BN863_22000 PE=1 SV=1
A5715	GO:0006629(lipid metabolic process)	-	-	-	-	KOG2088[Hs21040277 Predicted lipase/calmodulin-binding heat-shock protein	TPX65219.1 hypothetical protein SpCBS45565_g05341 [Spizellomyces sp. 'palustris']	Diacylglycerol lipase-alpha OS=Homo sapiens OX=9606 GN=DAGLA PE=1 SV=3
A5716	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5717	-	-	GO:0035091(phosphatidylinositol binding)	K17887 SNX25, MDM1; sorting nexin-25	-	-	KUI52992.1 Structural protein MDM1 [Valsamali var. pyri]	Sorting nexin-13 OS=Mus musculus OX=10090 GN=Snx13 PE=2 SV=1
A5718	-	GO:0005639(integral component of nuclear inner membrane)	-	-	-	KOG2687[Hs14778953 Spindle pole body protein, contains UNC-84 domain	RKP17111.1 hypothetical protein ROZALSC1DR AFT_16738 [Rozella allomycis CSF55]	SUN domain-containing protein 3 OS=Mus musculus OX=10090 GN=Sun3 PE=1 SV=1
A5719	-	-	-	-	-	-	KXS14081.1 phosphoglycerate mutase-like protein [Gonapodya prolifera JEL478]	Phosphoglycerate mutase-like protein AT74H OS=Arabidopsis thaliana OX=3702 GN=At1g08940 PE=3 SV=2
A5720	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02899 RP-L27, MRPL27, rpmA; large subunit ribosomal protein L27	map03010 Ribosome	KOG4600[At2g16930 Mitochondrial ribosomal protein MRP7 (L2)	RKP13501.1 ribosomal protein L27, partial [Piptocephalis cylindrospora]	Large ribosomal subunit protein bL27 OS=Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966) OX=402881 GN=rpmA PE=3 SV=1
A5721	-	-	-	-	-	-	-	-

A5722	-	-	GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG1198 At4g13010 Zinc-binding oxidoreductase	XP_017990789.1 nadph:quinone reductase [Malassezia pachydermatis]	Quinone-oxidoreductase homolog, chloroplastic OS=Spinacia oleracea OX=3562 GN=QOR PE=1 SV=1
A5723	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A5724	GO:0006044(N-acetylglucosamine metabolic process)	-	GO:0008448(N-acetylglucosamine-6-phosphate deacetylase activity),GO:0016810(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds),GO:0016787(hydrolase activity)	K01443 nagA,AMDHD2; N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]	map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG3892 7295614 N-acetylglucosamine-6-phosphate deacetylase	ORX93959.1 hypothetical protein K493DRAFT_315720 [Basidiobolus meristosporus CBS 931.73]	N-acetylglucosamine-6-phosphate deacetylase OS=Danio rerio OX=7955 GN=amdhd2 PE=2 SV=1
A5725	-	-	GO:0005524(ATP binding),GO:0035299(inositol pentakisphosphate 2-kinase activity)	K10572 IPPK; inositol-pentakisphosphate 2-kinase [EC:2.7.1.158]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG4749 At1g22100 Inositol polyphosphate kinase	KAF9959964.1 Inositol-pentakisphosphate 2-kinase [Mortierella alpina]	Inositol-pentakisphosphate 2-kinase IPK1 OS=Oryza sativa subsp. indica OX=39946 GN=IPK1 PE=3 SV=1
A5726	-	-	GO:0016787(hydrolase activity)	-	-	KOG2679 At3g17790 Purple (tartrate-resistant) acid phosphatase	ORY30966.1 Metallo-dependent phosphatase [Rhizoclostium globosum]	Purple acid phosphatase 17 OS=Arabidopsis thaliana OX=3702 GN=PAP17 PE=2 SV=1
A5727	GO:0006914(autophagy)	-	GO:0005515(protein binding)	-	-	KOG2109 At1g03380 WD40 repeat protein	-	Autophagy-related protein 18f OS=Arabidopsis thaliana OX=3702 GN=ATG18F PE=2 SV=1
A5728	-	-	-	-	-	-	XP_016612258.1 hypothetical protein SPPG_01651 [Spizellomyces punctatus DAOM BR117]	Uncharacterized signaling protein PA1727 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA1727 PE=1 SV=1
A5729	-	-	-	-	-	-	TPX68705.1 hypothetical protein SpCBS45565_g02947 [Spizellomyces sp. 'palustris']	Centrosomal protein of 290 kDa OS=Danio rerio OX=7955 GN=cep290 PE=2 SV=1

A5730	GO:0008299(isoprenoid biosynthetic process)	-	-	K00804 GGPS1; geranylgeranyl diphosphate synthase, type III [EC:2.5.1.1 2.5.1.10 2.5.1.29]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis;map01100 Metabolic pathways	KOG0777 Hs4758430 Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase	XP_031027449.1 uncharacterized protein SmJEL517_g00639 [Synchytrium microbalum]	Geranylgeranyl pyrophosphate synthase OS=Mus musculus OX=10090 GN=Ggps1 PE=1 SV=1
A5731	-	-	-	-	-	-	-	-
A5732	-	-	-	-	-	-	-	-
A5733	-	-	-	-	-	-	RYO87457.1 hypothetical protein DL763_006327 [Monosporascus cannonballus]	Uncharacterized protein MT1414 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=MT1414 PE=4 SV=2
A5734	-	-	-	-	-	-	-	-
A5735	-	-	GO:0005515(protein binding)	-	-	KOG0472 HsM20127578 Leucine-rich repeat protein	XP_001226734.1 hypothetical protein CHGG_08807 [Chaetomium globosum CBS 148.51]	Adenylate cyclase OS=Podospora anserina OX=2587412 PE=3 SV=1
A5736	GO:0006783(heme biosynthetic process)	-	GO:0004325(ferrochelatase activity)	K01772 hemH, FECH; protoporphyrin/coprotoporphyrin ferrochelatase [EC:4.98.1.1 4.99.1.9]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	-	XP_016269583.1 ferrochelatase [Rhodotorula toruloides NP11]	Ferrochelatase, mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=hem15 PE=3 SV=2
A5737	-	-	-	-	-	-	-	-
A5738	-	-	GO:0004089(carbonate dehydratase activity),GO:0008270(zinc ion binding)	-	-	KOG0382 7301545 Carbonic anhydrase	OSS46254.1 hypothetical protein B5807_07980 [Epicoccum nigrum]	Putative carbonic anhydrase 5 OS=Caenorhabditis elegans OX=6239 GN=cah-5 PE=3 SV=3
A5739	GO:0046855(inositol phosphate dephosphorylation)	-	GO:0008934(inositol monophosphate 1-phosphatase activity)	K01092 E3.1.3.25, IMPA, suhB; myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]	map01110 Biosynthesis of secondary metabolites;map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map00521 Streptomycin biosynthesis;map01100 Metabolic pathways	KOG2951 At3g02870 Inositol monophosphatase	ORY45140.1 inositol monophosphatase [Rhizoclostridium globosum]	Inositol monophosphatase 2 OS=Solanum lycopersicum OX=4081 GN=IMP2 PE=1 SV=1

A5740	GO:0006364(rRNA processing)	GO:0032040(small-subunit processome)	-	K14567 UTP14; U3 small nucleolar RNA-associated protein 14	map03008 Ribosome biogenesis in eukaryotes	-	KAG2185968.1 hypothetical protein INT43_002406 [Umbelopsis isabellina]	Uncharacterized protein C57A7.06 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC57A7.06 PE=1 SV=1
A5741	-	-	GO:0005509(calcium ion binding)	K19525 VPS13A_C; vacuolar protein sorting-associated protein 13A/C	-	KOG0696[Hs4506067 Serine/threonine protein kinase	KZO93498.1 vacuolar protein sorting-associated protein 13 [Calocera viscosa TUFC12733]	Protein kinase C alpha type OS=Homo sapiens OX=9606 GN=PRKCA PE=1 SV=4
A5742	GO:0000413(protein peptidyl-prolyl isomerization)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K05864 PPID; CYPD; peptidyl-prolyl isomerase D [EC:5.2.1.8]	map05131 Shigellosis;map04217 Necroptosis;map04218 Cellular senescence;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease	KOG0865[At2g21130 Cyclophilin type peptidyl-prolyl cis-trans isomerase	CDS03415.1 Putative Peptidyl-prolyl cis-trans isomerase cyp5 [Lichtheimia ramosa]	Peptidyl-prolyl cis-trans isomerase cyp5 OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) OX=246409 GN=cyp5 PE=3 SV=1
A5743	-	-	GO:0005515(protein binding)	-	-	KOG2796[Hs21361635 Uncharacterized conserved protein	KAE9985643.1 hypothetical protein BLS_006726 [Venturia inaequalis]	Trafficking protein particle complex subunit 12 OS=Homo sapiens OX=9606 GN=TRAPPC12 PE=1 SV=3
A5744	-	-	-	-	-	-	-	-
A5745	GO:0006072(glycerol-3-phosphate metabolic process)	GO:0009331(glycerol-3-phosphate dehydrogenase complex)	GO:0016491(oxidoreductase activity),GO:0004368(glycerol-3-phosphate dehydrogenase (quinone) activity)	K00111 glpA; glpD; glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism	KOG0042[CE14180 Glycerol-3-phosphate dehydrogenase	OLL22121.1 Glycerol-3-phosphate dehydrogenase, mitochondrial [Neoelecta irregularis DAH-3]	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mesocricetus auratus OX=10036 GN=GPD2 PE=1 SV=1
A5746	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K06961 KRR1; ribosomal RNA assembly protein	-	-	CDS14066.1 Putative Ribosomal RNA assembly protein mis3 [Lichtheimia ramosa]	KRR1 small subunit processome component homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=mis3 PE=3 SV=1

A5747	GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0005839(proteasome core complex)	GO:0004298(threonine-type endopeptidase activity)	K02737 PSMB5; 20S proteasome subunit beta 5 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0175[Hs4506201 20S proteasome, regulatory subunit beta type PSMB5/PSMB8/PRE2	KXS12386.1 LMP7-like protein [Gonapodya prolifera JEL478]	Proteasome subunit beta type-5 OS=Dictyostelium discoideum OX=44689 GN=psmB5 PE=1 SV=1
A5748	GO:0006813(potassium ion transport)	GO:0016021(integral component of membrane)	GO:0005242(inward rectifier potassium channel activity)	-	-	KOG3827[Hs4504835 Inward rectifier K+ channel	KXS20929.1 E set domain-containing protein [Gonapodya prolifera JEL478]	ATP-sensitive inward rectifier potassium channel 12 OS=Gallus gallus OX=9031 GN=KCNJ12 PE=1 SV=1
A5749	-	-	-	K22684 MCA1; metacaspase -1 [EC:3.4.22.-]	-	-	OUM65244.1 hypothetical protein PIROE2DRAFT_25262, partial [Piromyces sp. E2]	Metacaspase III c OS=Phaeodactylum tricornutum (strain CCAP 1055/1) OX=556484 GN=MCA-IIIc PE=1 SV=2
A5750	-	-	GO:0005509(calcium ion binding)	-	-	-	GFZ51889.1 Calcium-binding protein NCS-1 [Saitozyma sp. JCM 24511]	-
A5751	-	-	-	K22684 MCA1; metacaspase -1 [EC:3.4.22.-]	-	KOG1546[YO R197w Metacaspase involved in regulation of apoptosis	ONH66585.1 Metacaspase -1 [Cyberlindnera fabianii]	Metacaspase III c OS=Phaeodactylum tricornutum (strain CCAP 1055/1) OX=556484 GN=MCA-IIIc PE=1 SV=2
A5752	-	-	-	K11407 HDAC6; histone deacetylase 6 [EC:3.5.1.98]	map05014 Amyotrophic lateral sclerosis;map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG1343[Hs13128864 Histone deacetylase complex, catalytic component HDA1	PJF19637.1 hypothetical protein PSACC_00555 [Paramicrosporidium saccamoebae]	Histone deacetylase 6 OS=Mus musculus OX=10090 GN=Hdac6 PE=1 SV=3
A5753	GO:0015937(coenzyme A biosynthetic process)	-	GO:0004140(dephospho-CoA kinase activity);GO:0005524(ATP binding)	K00859 coaE; dephospho-CoA kinase [EC:2.7.1.24]	map00770 Pantothenate and CoA biosynthesis;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG3220[At2g27490 Similar to bacterial dephospho-CoA kinase	KAF9113107.1 hypothetical protein BGX27_002217 [Mortierella sp. AM989]	Dephospho-CoA kinase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) OX=169963 GN=coaE PE=3 SV=1
A5754	-	-	-	-	-	-	-	-

A5755	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004707(MAP kinase activity)	K04441 P38; p38 MAP kinase [EC:2.7.11.24]	map04361 Axon regeneration;map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map05417 Lipid and atherosclerosis;map05135 Yersinia infection;map05132 Salmonella infection;map05133 Pertussis;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04722 Neurotrophin signaling pathway;map04933 AGE-RAGE signaling pathway in	KOG0660 At4g01370 Mitogen-activated protein kinase	KAG0212781.1 Mitogen-activated protein kinase [Mortierella sp. GBA30]	Mitogen-activated protein kinase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=MPK1 PE=1 SV=1
A5756	-	-	-	-	-	-	-	-
A5757	-	-	-	-	-	KOG0800 At4g26580 FOG: Predicted E3 ubiquitin ligase	EPZ35251.1 hypothetical protein O9G_000647 [Rozella allomyces CSF55]	E3 ubiquitin ligase BIG BROTHER-related OS=Arabidopsis thaliana OX=3702 GN=BBR PE=2 SV=1
A5758	-	-	-	-	-	-	-	-
A5759	-	-	-	-	-	KOG4256 CE07281 Kinetochore component	TPX40326.1 hypothetical protein SeLEV6574_g06674, partial [Synchytrium endobioticum]	Kinetochore-associated protein rod-1 OS=Caenorhabditis elegans OX=6239 GN=rod-1 PE=1 SV=1
A5760	GO:0006457(protein folding)	-	GO:0000774(adenyl-nucleotide exchange factor activity),GO:0042803(protein homodimerization activity),GO:0051087(chaperone binding)	K03687 GRPE; molecular chaperone GrpE	-	KOG3003 At4g26780 Molecular chaperone of the GrpE family	RKO97227.1 GrpE nucleotide exchange factor [Caulochytrium protostelioides]	Protein GrpE OS=Brucella melitensis biotype 1 (strain 16M / ATCC 23456 / NCTC 10094) OX=224914 GN=grpE PE=3 SV=2
A5761	-	-	-	-	-	-	-	-
A5762	GO:0006418(tRNA aminoacylation for protein translation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding)	K01883 CARS, cysS; cysteinyl-tRNA synthetase [EC:6.1.1.16]	map00970 Aminoacyl-tRNA biosynthesis	KOG2007 YNL247w Cysteinyl-tRNA synthetase	KIK60442.1 hypothetical protein GYMLUDRAFT_43756 [Gymnopus luxurians FD-317 M1]	Cysteine--tRNA ligase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YNL247W PE=1 SV=1
A5763	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K14805 DDX24, MAK5; ATP-dependent RNA helicase DDX24/MAK5 [EC:3.6.4.13]	-	KOG0347 At3g16840 RNA helicase	OAC98153.1 hypothetical protein MUCCIDRAFT_128375, partial [Mucor lusitanicus CBS 277.49]	ATP-dependent RNA helicase MAK5 OS=Cryptococcus neoformans var. neoformans serotype D (strain B-3501A) OX=283643 GN=MAK5 PE=3 SV=1
A5764	-	-	-	-	-	-	-	-

A5765	-	-	-	-	-	KOG0861 At5g58060 SNARE protein YKT6, synaptobrevin/VAMP superfamily	XP_02534041.1.1 hypothetical protein CXQ85_003317 [[Candida] haemulonii]	VAMP-like protein YKT61 OS=Arabidopsis thaliana OX=3702 GN=YKT61 PE=1 SV=1
A5766	GO:0007021(tubulin complex assembly),GO:0007023(post-chaperonin tubulin folding pathway)	-	GO:0048487(beta-tubulin binding)	K17292 TBCA; tubulin-specific chaperone A	-	KOG3470 Hs4759212 Beta-tubulin folding cofactor A	KAG5173762.1 hypothetical protein JR316_000419 [Psilocybe cubensis]	Tubulin-specific chaperone A OS=Oryctolagus cuniculus OX=9986 GN=TBCA PE=1 SV=2
A5767	-	-	-	-	-	KOG2296 7299174 Integral membrane protein	KXS12200.1 LMBR1-domain-containing protein, partial [Gonapodya prolifera JEL478]	G-protein coupled receptor-associated protein LMBRD2 OS=Gallus gallus OX=9031 GN=LMBRD2 PE=2 SV=1
A5768	-	-	GO:0004842(ubiquitin-protein transferase activity)	K12232 HECTD2; E3 ubiquitin-protein ligase HECTD2 [EC:2.3.2.26]	-	KOG0941 Hs7657152 E3 ubiquitin protein ligase	ORX86300.1 HECT-domain-containing protein [Anaeromyces robustus]	Probable E3 ubiquitin-protein ligase HERC4 OS=Rattus norvegicus OX=10116 GN=Herc4 PE=2 SV=1
A5769	GO:0032259(methylation)	-	GO:0008168(methyltransferase activity)	K18203 LCMT1; [phosphatase 2A protein]-leucine-carboxy methyltransferase [EC:2.1.1.233]	-	KOG2918 Hs7662174 Carboxymethyl transferase	TPX51432.1 hypothetical protein SeMB42_g01914 [Synchytrium endobioticum]	Leucine carboxyl methyltransferase 1 homolog OS=Arabidopsis thaliana OX=3702 GN=LCMT1 PE=1 SV=1
A5770	-	-	-	-	-	-	-	-
A5771	-	GO:0034464(BBSome)	GO:0004386(helicase activity)	K12813 DHX16; pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 [EC:3.6.4.13]	map03040 Spliceosome	KOG0923 At1g32490 mRNA splicing factor ATP-dependent RNA helicase	KNE56940.1 hypothetical protein AMAG_02707 [Allomyces macrogynus ATCC 38327]	Pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH1 OS=Arabidopsis thaliana OX=3702 GN=ESP3 PE=1 SV=1
A5772	-	-	-	-	-	-	-	-
A5773	-	GO:0016020(membrane)	-	-	-	-	-	-
A5774	-	GO:0016020(membrane)	-	-	-	-	-	-
A5775	-	-	GO:0008237(metalloproteinase activity)	-	-	KOG3607 Hs11497043 Meltrins, fertilins and related Zn-dependent metalloproteinases of the ADAMs family	XP_022395903.1 hypothetical protein ASPGLDRAFT_70225 [Aspergillus glaucus CBS 516.65]	Disintegrin and metalloproteinase domain-containing protein B OS=Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) OX=554155 GN=ADM-B PE=3 SV=1
A5776	GO:0006508(proteolysis)	-	GO:0004222(metalloendopeptidase activity),GO:0008237(metalloproteinase activity)	-	-	-	XP_022395903.1 hypothetical protein ASPGLDRAFT_70225 [Aspergillus glaucus CBS 516.65]	Disintegrin and metalloproteinase domain-containing protein B OS=Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) OX=554155 GN=ADM-B PE=3 SV=1

A5777	GO:0006508(proteolysis)	-	GO:0008233(peptidase activity)	K05290 PIGK; GPI-anchor transamidase subunit K	map00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis;map01100 Metabolic pathways	KOG1348 At3g20210 Asparaginyl peptidases	KAG0676282.1 glycosylphosphatidylinositol anchor biosynthesis [Kluyveromyces marxianus]	Vacuolar-processing enzyme delta-isozyme OS=Arabidopsis thaliana OX=3702 GN=dVPE PE=1 SV=1
A5778	-	-	-	K21804 METTL21A; protein N-lysine methyltransferase METTL21A [EC:2.1.1.-]	-	KOG2793 CE26910 Putative N2,N2-dimethylguanosine tRNA methyltransferase	XP_028486909.1 putative methyltransferase-domain-containing protein [Byssoschlamys spectabilis]	EEF1A lysine methyltransferase 3 OS=Bos taurus OX=9913 GN=EEF1AKMT3 PE=2 SV=1
A5779	-	-	-	-	-	-	-	-
A5780	-	-	-	-	-	-	-	-
A5781	-	-	-	-	-	-	-	-
A5782	GO:0006813(potassium ion transport)	GO:0016020(membrane)	GO:0005509(calcium ion binding),GO:0005249(voltage-gated potassium channel activity)	-	-	KOG0498 Hs13540549 K+-channel ERG and related proteins, contain PAS/PAC sensor domain	ORY50894.1 voltage-gated potassium channel, partial [Rhizoclostium globosum]	Potassium channel KOR1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os06g0250600 PE=2 SV=1
A5783	-	-	-	K09425 K09425; Myb-like DNA-binding protein FlbD	-	KOG0048 Hs13641706_1 Transcription factor, Myb superfamily	OAG31322.1 myb proto-oncogene protein [Nematocida dispodere]	Myb-related protein A OS=Xenopus laevis OX=8355 GN=myb1 PE=2 SV=1
A5784	-	-	GO:0005525(GTP binding)	K14538 NUG1, GNL3; nuclear GTP-binding protein	map03008 Ribosome biogenesis in eukaryotes	KOG2484 At3g07050 GTPase	TPX65462.1 hypothetical protein SpCBS45565_g05124 [Spizellomyces sp. 'palustris']	Guanine nucleotide-binding protein-like NSN1 OS=Arabidopsis thaliana OX=3702 GN=NSN1 PE=1 SV=1
A5785	-	-	-	-	-	-	KAF7541393.1 hypothetical protein G7054_g553 [Neopestalotiopsis clavispora]	CRAL-TRIO domain-containing protein C3H8.02 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC3H8.02 PE=1 SV=1
A5786	-	-	-	-	-	-	-	-
A5787	GO:0006886(intracellular protein transport), GO:0006611(protein export from nucleus)	-	GO:0031267(small GTPase binding),GO:0005049(nuclear export signal receptor activity)	K14290 XPO1, CRM1; exportin-1	map03250 Viral life cycle - HIV-1;map03013 Nucleocytoplasmic transport;map04013 MAPK signaling pathway - fly;map03008 Ribosome biogenesis in eukaryotes;map05164 Influenza A;map05166 Human T-cell leukemia virus 1 infection	KOG2020 Hs4507943 Nuclear transport receptor CRM1/MSN5 (importin beta superfamily)	RIB27651.1 CRM1 C-terminal-domain-containing protein [Gigaspora rosea]	Exportin-1 OS=Mus musculus OX=10090 GN=Xpo1 PE=1 SV=1

A5788	GO:0006412(translation)	GO:0005840(ribosome)	GO:0005515(protein binding);GO:0003735(structural constituent of ribosome)	K02977 RPS27Ae, RPS27A, UBA80; ubiquitin-small subunit ribosomal protein S27Ae	map04140 Autophagy - animal;map05131 Shigellosis;map05171 Coronavirus disease - COVID-19;map04137 Mitophagy - animal;map04120 Ubiquitin mediated proteolysis;map03010 Ribosome;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease;map05167 Kaposi sarcoma-associated herpesvirus infection	KOG0004[Hs4506713 Ubiquitin/40S ribosomal protein S27a fusion	TPX66255.1 hypothetical protein SpCBS45565.g04583 [Spizellomyces sp. 'palustris']	Ubiquitin-ribosomal protein eS31 fusion protein OS=Gallus gallus OX=9031 GN=RPS27A PE=1 SV=3
A5789	-	-	GO:0016787(hydrolase activity)	-	-	KOG0374[At3g09970 Serine/threonine specific protein phosphatase PP1, catalytic subunit	KTA96519.1 putative metallophosphoesterase [[Candida glabrata]	Tyrosine-protein phosphatase RLP2 OS=Arabidopsis thaliana OX=3702 GN=RLP2 PE=1 SV=1
A5790	-	-	-	-	-	KOG1208[7300387 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	OZJ01686.1 hypothetical protein BZG36_05351 [Bifiguratus adelaidae]	Retinol dehydrogenase 12 OS=Mus musculus OX=10090 GN=Rdh12 PE=2 SV=1
A5791	GO:0006368(transcription elongation from RNA polymerase II promoter);GO:0016570(histone modification)	GO:0016593(Cdc73/Paf1 complex)	-	K15177 LEO1; RNA polymerase-associated protein LEO1	-	KOG2428[Hs20270337_2 Uncharacterized conserved protein	XP_019040568.1 hypothetical protein WICANDRAFT_61917 [Wickerhamomyces anomalus NRRL Y-366-8]	Protein LEO1 homolog OS=Arabidopsis thaliana OX=3702 GN=VIP4 PE=1 SV=1
A5792	GO:0018216(peptidyl-arginine methylation)	-	GO:0016274(protein-arginine N-methyltransferase activity)	K11434 PRMT1; type I protein arginine methyltransferase [EC:2.1.1.319]	map04068 FoxO signaling pathway;map04922 Glucagon signaling pathway	KOG1499[HsM9789979 Protein arginine N-methyltransferase PRMT1 and related enzymes	XP_007397106.1 uncharacterized protein PHACADRAFT_258242 [Phanerochaete carnosae HHB-10118-sp]	Protein arginine N-methyltransferase 8 OS=Homo sapiens OX=9606 GN=PRMT8 PE=1 SV=2
A5793	-	-	-	-	-	-	-	-
A5794	-	-	-	-	-	-	-	-

A5795	GO:0006633(fatty acid biosynthetic process)	-	-	K03955 NDUFB1; NADH dehydrogenase (ubiquinone) 1 alpha/beta subcomplex 1, acyl-carrier protein	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG1748 At1g65290 Acyl carrier protein/NADH-ubiquinone oxidoreductase, NDUFB1/SDAP subunit	KJX92032.1 acyl carrier protein [Zymoseptoria brevis]	Acyl carrier protein 2, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MTACP2 PE=1 SV=1
A5796	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K14416 HBS1; elongation factor 1 alpha-like protein	map05134 Legionellosis;map03015 mRNA surveillance pathway	KOG0458 Hs5729864.2 Elongation factor 1 alpha	CDS12523.1 hypothetical protein LRAMOSA04717 [Lichtheimia ramosa]	HBS1-like protein OS=Pongo abelii OX=9601 GN=HBS1L PE=2 SV=1
A5797	-	GO:0005758(mitochondrial intermembrane space)	-	K17781 TIM13; mitochondrial import inner membrane translocase subunit TIM13	-	KOG1733 Hs11024700 Mitochondrial import inner membrane translocase, subunit TIM13	KAG0027238.1 protein translocase subunit [Podila clonocystis]	Mitochondrial import inner membrane translocase subunit Tim13 OS=Danio rerio OX=7955 GN=timm13 PE=3 SV=1
A5798	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding)	K00249 ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map03320 PPAR signaling pathway;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map04936 Alcoholic liver disease;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG1469 At3g06810 Predicted acyl-CoA dehydrogenase	OON04997.1 hypothetical protein BSLG_05023 [Batrachochytrium salamandrivorans]	Probable acyl-CoA dehydrogenase FadE2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=fadE2 PE=1 SV=4
A5799	GO:0043161(proteasome-mediated ubiquitin-dependent protein catabolic process)	-	GO:0004842(ubiquitin-protein transferase activity),GO:0061630(ubiquitin protein ligase activity)	K18624 MAEA, EMP; macrophage erythroblast attacher	-	KOG0396 7301214.1 Uncharacterized conserved protein	OZJ06587.1 hypothetical protein BZG36_00627 [Bifiguratus adalaidae]	E3 ubiquitin-protein transferase MAEA OS=Homo sapiens OX=9606 GN=MAEA PE=1 SV=1
A5800	-	-	-	-	-	-	-	-
A5801	-	-	GO:0016787(hydrolase activity),GO:0003993(acid phosphatase activity)	K22390 ACP7; acid phosphatase type 7	-	KOG1378 Hs2052480 Purple acid phosphatase	OOQ91347.1 metallophosphoesterase [Penicillium brasilianum]	Acid phosphatase OS=Aspergillus ficuum OX=5058 GN=aphA PE=1 SV=1

A5802	-	-	GO:0008195(phosphatidate phosphatase activity)	-	-	-	-	-
A5803	GO:0045116(protein neddylation)	-	GO:0019781(NEDD8 activating enzyme activity).GO:0008641(ubiquitin-like modifier activating enzyme activity)	K10686 UBA3, UBE1C; NEDD8-activating enzyme E1 [EC:6.2.1.64]	map04120 Ubiquitin mediated proteolysis	KOG2015 Hs19923744 NEDD8-activating complex, catalytic component UBA3	RKP20942.1 NEDD8 activating enzyme [Rozella allomyces CSF55]	NEDD8-activating enzyme E1 catalytic subunit OS=Dictyostelium discoideum OX=44689 GN=uba3 PE=1 SV=1
A5804	-	-	GO:0005524(ATP binding)	K09490 HSPA5, BiP; endoplasmic reticulum chaperone BiP [EC:3.6.4.10]	map05014 Amyotrophic lateral sclerosis;map05417 Lipid and atherosclerosis; map04141 Protein processing in endoplasmic reticulum;map04918 Thyroid hormone synthesis;map04612 Antigen processing and presentation;map03060 Protein export;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease	KOG0100 At5g28540 Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily	RFU75793.1 78 kda glucose-regulated [Trichoderma arundinaceum]	Luminal-binding protein 5 OS=Nicotiana tabacum OX=4097 GN=BiP5 PE=2 SV=1
A5805	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02979 RP-S28e, RPS28; small subunit ribosomal protein S28e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3502 Hs4506715 40S ribosomal protein S28 [Wallemia ichthyophaga EXF-994]	XP_009269323.1 40S ribosomal protein S28 [Wallemia ichthyophaga EXF-994]	Small ribosomal subunit protein eS28 OS=Bos taurus OX=9913 GN=RPS28 PE=3 SV=1
A5806	GO:0006886(intracellular protein transport)	GO:0005801(cis-Golgi network), GO:0016020(membrane)	-	K20290 COG3, SEC34; conserved oligomeric Golgi complex subunit 3	-	KOG2604 Hs13899251 Subunit of cis-Golgi transport vesicle tethering complex - Sec34p	KAF0355701.1 Sec34-domain-containing protein [Gigaspora margarita]	Conserved oligomeric Golgi complex subunit 3 OS=Arabidopsis thaliana OX=3702 GN=COG3 PE=1 SV=1
A5807	GO:0046314(phosphocreatine biosynthetic process)	-	GO:0016301(kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups),GO:0004111(creatine kinase activity),GO:0003824(catalytic activity)	-	-	KOG3581 Hs21536286 Creatine kinases	OAL68456.1 putative creatine kinase M-type [Trichophyton violaceum]	Arginine kinase Oct f 2 OS=Amphioctopus fangsiao OX=515817 PE=1 SV=1
A5808	-	-	GO:0005509(calcium ion binding)	-	-	KOG0032 7299682 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	RKO93542.1 hypothetical protein BDK51DRAFT_26340 [Blyttiomycetes helicus]	Crustacean calcium-binding protein 23 OS=Faxonius limosus OX=28379 PE=1 SV=1

A5809	-	-	-	-	-	KOG2607 At5g06830 CDK5 activator-binding protein	-	CDK5RAP3-like protein OS=Arabidopsis thaliana OX=3702 GN=At5g06830 PE=2 SV=2
A5810	-	-	GO:0003723(RNA binding),GO:0004540(ribonuclease activity)	K12585 DIS3, RRP44; exosome complex exonuclease DIS3/RRP44 [EC:3.1.13.-]	map03018 RNA degradation	KOG2102 At2g17510 Exosomal 3'-5' exoribonuclease complex, subunit Rrp44/Dis3	ORX84255.1 RNB-domain-containing protein [Anaeromyces robustus]	Exosome complex exonuclease RRP44 homolog A OS=Arabidopsis thaliana OX=3702 GN=RRP44A PE=2 SV=2
A5811	-	-	GO:0004499(N, N-dimethylaniline monooxygenase activity),GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding)	-	-	KOG1399 At1g19250 Flavin-containing monooxygenase	KXS10400.1 FAD/NAD(P)-binding domain-containing protein [Gonapodya prolifera JEL478]	Probable flavin-containing monooxygenase 1 OS=Arabidopsis thaliana OX=3702 GN=FMO1 PE=2 SV=1
A5812	-	GO:0016020(membrane)	-	-	-	-	KAG1461821.1 hypothetical protein G6F56_005640 [Rhizopus deleamar]	Uncharacterized protein slp1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC3E7.09 PE=3 SV=1
A5813	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05665 ABCC1; ATP-binding cassette, subfamily C (CFTR/MRP), member 1 [EC:7.6.2.3]	map04071 Sphingolipid signaling pathway;map01523 Antifolate resistance;map04977 Vitamin digestion and absorption;map02010 ABC transporters;map05206 MicroRNAs in cancer	KOG0054 At1g30410 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	KAF9181719.1 hypothetical protein BGZ50_005356 [Haplosporangium sp. Z 11]	ABC transporter C family member 12 OS=Arabidopsis thaliana OX=3702 GN=ABCC12 PE=2 SV=1
A5814	GO:0006189('de novo' IMP biosynthetic process)	-	GO:0004642(phosphoribosylformylglycinamidase synthase activity)	K01952 PFAS, purL; phosphoribosylformylglycinamidase synthase [EC:6.3.5.3]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01100 Metabolic pathways	KOG1907 At1g74260 Phosphoribosylformylglycinamidase synthase	KLO16949.1 phosphoribosylformylglycinamidase [Schizopora paradoxa]	Probable phosphoribosylformylglycinamidase synthase, chloroplastic/mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At1g74260 PE=2 SV=3
A5815	-	-	-	-	-	-	TKA49383.1 hypothetical protein B0A54_00049 [Friedmanniomyces endolithicus]	Glyoxalase 3 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GLX3 PE=1 SV=1
A5816	-	-	-	K05925 METTL3; mRNA m6A methyltransferase catalytic subunit [EC:2.1.1.348]	-	KOG2098 HsM9790095 Predicted N6-adenine RNA methylase	KAF1797975.1 MT-A70-domain-containing protein [Mucor lusitanicus]	N6-adenosine-methyltransferase subunit METTL3 OS=Danio rerio OX=7955 GN=mettl3 PE=2 SV=1

A5817	GO:0016255(attachment of GPI anchor to protein);GO:0006508(proteolysis)	GO:0042765(GPI-anchor transamidase complex)	GO:0003923(GPI-anchor transamidase activity);GO:0008233(peptidase activity)	K05290 PIGK; GPI-anchor transamidase subunit K	map00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis;map01100 Metabolic pathways	KOG1349 At1g08750 Gpi-anchor transamidase	XP_018210469.1 uncharacterized protein OGAPODRAFT_37824, partial [Ogataea polymorpha]	GPI-anchor transamidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPI8 PE=1 SV=1
A5818	-	-	-	-	-	-	-	-
A5819	-	-	-	-	-	-	-	-
A5820	-	-	-	-	-	-	-	-
A5821	-	-	GO:0008237(metallopeptidase activity)	-	-	-	-	-
A5822	-	-	-	-	-	-	KJY00171.1 amine oxidase like protein [Zymoseptoria brevis]	-
A5823	GO:0019856(pyrimidine nucleobase biosynthetic process)	-	GO:0016787(hydrolase activity);GO:0004151(dihydroorotase activity);GO:0016812(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides)	K01465 URA4, pyrC; dihydroorotase [EC:3.5.2.3]	map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG2902 At4g22930 Dihydroorotase	KAG0162698.1 hypothetical protein DFQ30_001434 [Apophysomyces sp. BC1015]	Dihydroorotase OS=Cupriavidus necator (strain ATCC 17699 / DSM 428 / KCTC 22496 / NCIMB 10442 / H16 / Stanier 337) OX=381666 GN=pyrC PE=3 SV=1
A5824	-	-	-	-	-	-	-	-
A5825	-	-	-	-	-	-	-	-
A5826	-	-	-	-	-	-	KAF9392138.1 hypothetical protein CPB97_003783 [Podila verticillata]	-
A5827	-	-	-	-	-	-	-	-
A5828	GO:0007165(signal transduction)	-	-	-	-	-	ORY46062.1 hypothetical protein BCR33DRAFT_159571 [Rhizoclostium globosum]	-
A5829	-	-	GO:0005524(ATP binding)	-	-	KOG2372 7296767 Oxidation resistance protein	RGB43741.1 TLD-domain-containing protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	TLD domain-containing protein 2 OS=Bos taurus OX=9913 GN=TLDC2 PE=2 SV=1
A5830	-	-	-	-	-	KOG3918 Hs14765221 Predicted membrane protein	KZV94582.1 hypothetical protein EXIGLDRAFT_736606 [Exidia glandulosa HHB12029]	ER membrane protein complex subunit 5-B OS=Xenopus laevis OX=8355 GN=mmgt1-b PE=2 SV=1
A5831	GO:0009089(lysine biosynthetic process via diaminopimelate)	-	GO:0008839(4-hydroxy-tetrahydrodipicolinate reductase)	-	-	-	-	Probable 4-hydroxy-tetrahydrodipicolinate reductase 2, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=DAPB2 PE=2 SV=1

A5832	-	-	GO:0005515(protein binding)	-	-	-	KXS11606.1 RNI-like protein [Gonapodya prolifera JEL478]	NACHT, LRR and PYD domains-containing protein 1 OS=Homo sapiens OX=9606 GN=NLRP1 PE=1 SV=1
A5833	-	-	-	-	-	-	-	-
A5834	-	-	-	-	-	-	-	-
A5835	-	-	GO:0005524(ATP binding)	K04043 dnaK, HSPA9; molecular chaperone DnaK	map04212 Longevity regulating pathway - worm;map03018 RNA degradation;map05152 Tuberculosis	KOG0102[CE08631 Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	KAG1260073.1 hypothetical protein G6F65_01515.1 [Rhizopus oryzae]	Chaperone protein DnaK OS=Wolbachia pipientis subsp. Culex pipiens (strain wPip) OX=570417 GN=dnaK PE=3 SV=1
A5836	-	-	-	-	-	-	-	-
A5837	-	-	-	-	-	-	-	-
A5838	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004707(MAP kinase activity)	K04371 ERK, MAPK1_3; mitogen-activated protein kinase 1/3 [EC:2.7.11.24]	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map04730 Long-term depression;map05135 Yersinia infection;map05132 Salmonella infection;map05133 Pertussis;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04350 TGF-beta signaling pathway;map04810 Regulation	KOG0660[CE29020 Mitogen-activated protein kinase	TID28610.1 hypothetical protein CANINC_002366 [[Candida] inconspicua]	Extracellular signal-regulated kinase 2 OS=Dictyostelium discoideum OX=44689 GN=erkB PE=1 SV=1
A5839	-	-	-	-	-	KOG1471[Hs14779875 Phosphatidylinositol transfer protein SEC14 and related proteins	TPX67981.1 hypothetical protein CcCBS67573_g07329 [Chytridiomycetes confervae]	SEC14-like protein 5 OS=Homo sapiens OX=9606 GN=SEC14L5 PE=1 SV=3
A5840	GO:0006281(DNA repair)	-	GO:0016779(nucleotidyltransferase activity),GO:0003677(DNA binding),GO:0004061(DNA polymerase activity),GO:0003887(DNA-directed DNA polymerase activity)	K10981 POL4; DNA polymerase IV [EC:2.7.7.7]	map03450 Non-homologous end-joining	-	RKO93586.1 hypothetical protein BDK51DRAFT_24341, partial [Blyttiomycetes helicus]	Coiled-coil domain-containing protein 146 OS=Homo sapiens OX=9606 GN=CCDC146 PE=1 SV=2

A5841	-	-	-	K08341 GABARAP, ATG8, LC3; GABA(A) receptor - associated protein	map04140 Autophagy - animal;map0421 2 Longevity regulating pathway - worm;map04139 Mitophagy - yeast;map04138 Autophagy - yeast;map04137 Mitophagy - animal;map0413 6 Autophagy - other;map04727 GABAergic synapse;map046 21 NOD-like receptor signaling pathway;map04 068 FoxO signaling pathway	-	-	-
A5842	GO:00064 68(protein phosphor ylation)	-	GO:0005524(AT P binding),GO:000 5515(protein binding),GO:000 4672(protein kinase activity)	-	-	KOG0575 Hs2 1359873 Polo-like serine/threon ine protein kinase	ORX87490.1 Pkinase- domain- containing protein [Anaeromyce s robustus]	Probable serine/threonine-protein kinase CCRP1 OS=Zea mays OX=4577 GN=CCRP1 PE=1 SV=1
A5843	-	-	-	-	-	-	-	-
A5844	-	-	-	K12860 CDC5L, CDC5, CEF1; pre-mRNA- splicing factor CDC5/CEF1	map03040 Spliceosome	KOG0050 At1 g09770 mRNA splicing protein CDC5 (Myb superfamily)	OZJ03547.1 hypothetical protein BZG36_04168 [Bifiguratus adelaidae]	Cell division cycle 5-related protein OS=Nematostella vectensis OX=45351 GN=cdc5l PE=3 SV=1
A5845	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	K14758 HRR25; casein kinase I homolog HRR25 [EC:2.7.11.1]	map03008 Ribosome biogenesis in eukaryotes	KOG1164 At4 g26100 Casein kinase (serine/threo nine/tyrosine protein kinase)	RKO83919.1 kinase-like domain- containing protein [Blyttiomycet helicus]	Casein kinase I OS=Toxoplasma gondii OX=5811 PE=2 SV=1
A5846	GO:00064 68(protein phosphor ylation)	-	GO:0005524(AT P binding),GO:000 4672(protein kinase activity)	K14758 HRR25; casein kinase I homolog HRR25 [EC:2.7.11.1]	map03008 Ribosome biogenesis in eukaryotes	KOG1164 At4 g26100 Casein kinase (serine/threo nine/tyrosine protein kinase)	KAF9174511. 1 serine/threon ine protein kinase, partial [Mortierella sp. AD010]	Casein kinase I OS=Toxoplasma gondii OX=5811 PE=2 SV=1
A5847	-	-	GO:0016301(kin ase activity)	-	-	-	-	-
A5848	-	-	-	-	-	-	-	-
A5849	GO:00068 07(nitroge n compoun d metabolic process)	-	GO:0003824(cat alytic activity),GO:000 4356(glutamate -ammonia ligase activity)	-	-	-	RKO97791.1 glutamine synthetase/g uanido kinase [Caulochytriu m protostelioid es]	Type-3 glutamine synthetase OS=Dictyostelium discoideum OX=44689 GN=glnA3 PE=1 SV=1
A5850	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	K08794 CAMK1; calcium/calmo dulin- dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05 214 Glioma;map049 21 Oxytocin signaling pathway;map04 925 Aldosterone synthesis and secretion	KOG0032 Hs4 502553 Ca2+/calmod ulin- dependent protein kinase, EF- Hand protein superfamily	ORX77741.1 Pkinase- domain- containing protein [Anaeromyce s robustus]	Calcium/calmodulin-dependent protein kinase type 1 OS=Homo sapiens OX=9606 GN=CAMK1 PE=1 SV=1

A5851	-	-	GO:0004499(N, N-dimethylaniline monooxygenase activity),GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding)	-	-	KOG1399 Hs4503761 Flavin-containing monooxygenase	XP_009158819.1 cyclohexanone monooxygenase [Exophiala dermatitidis NIH/UT8656]	FAD-binding monooxygenase ktnD OS=Aspergillus niger (strain ATCC MYA-4892 / CBS 513.88 / FGSC A1513) OX=425011 GN=ktnD PE=3 SV=1
A5852	-	-	GO:0070403(NAD+ binding)	K11414 SIRT4, SIRT4L; NAD-dependent protein deacetylase/ipoamidase sirtuin 4 [EC:2.3.1.286 2.3.1.313]	map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	KOG2683 At5g09230 Sirtuin 4 and related class II sirtuins (SIR2 family)	PKK62150.1 DHS-like NAD/FAD-binding domain-containing protein [Rhizophagus irregularis]	NAD-dependent protein deacylase Sirt4 OS=Drosophila melanogaster OX=7227 GN=Sirt4 PE=2 SV=2
A5853	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	-	-	-	-	-
A5854	-	GO:0005634(nucleus)	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0003723(RNA binding)	K14808 DDX54, DBP10; ATP-dependent RNA helicase DDX54/DBP10 [EC:3.6.4.13]	-	KOG0337 Hs19923595 ATP-dependent RNA helicase	TPX76233.1 hypothetical protein CcCBS67573_g02490 [Chytridiomycetes confervae]	Putative DEAD-box ATP-dependent RNA helicase 29 OS=Arabidopsis thaliana OX=3702 GN=RH29 PE=3 SV=1
A5855	GO:0006396(RNA processing),GO:0001522(pseudouridine synthesis),GO:0009451(RNA modification)	-	GO:0003723(RNA binding),GO:0009982(pseudouridine synthase activity)	K11131 DKC1, NOLA4, CBF5; H/ACA ribonucleoprotein complex subunit 4 [EC:5.4.99.-]	map03008 Ribosome biogenesis in eukaryotes	-	ORY07498.1 putative rRNA pseudouridine synthase [Basidiobolus meristosporus CBS 931.73]	H/ACA ribonucleoprotein complex subunit cbf5 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=cbf5 PE=3 SV=1
A5856	-	-	GO:0003723(RNA binding),GO:0004540(ribonuclease activity),GO:0003924(GTPase activity),GO:0005525(GTP binding)	K18748 SSD1; protein SSD1	-	KOG2102 Hs2045556 Exosomal 3'-5' exoribonuclease complex, subunit Rrp44/Dis3	PKY55397.1 RNB-domain-containing protein [Rhizophagus irregularis]	DIS3-like exonuclease 2 OS=Xenopus tropicalis OX=8364 GN=dis3l2 PE=2 SV=2
A5857	-	GO:0016021(integral component of membrane)	-	K05034 SLC6A1, GAT1; solute carrier family 6 (neurotransmitter transporter, GABA) member 1	map04727 GABAergic synapse;map04721 Synaptic vesicle cycle	KOG3659 7302914 Sodium-neurotransmitter symporter	KXS13338.1 Sodium:neurotransmitter symporter [Gonapodya prolifera JEL478]	Sodium- and chloride-dependent taurine transporter OS=Homo sapiens OX=9606 GN=SLC6A6 PE=1 SV=2
A5858	-	GO:0016021(integral component of membrane)	-	K05034 SLC6A1, GAT1; solute carrier family 6 (neurotransmitter transporter, GABA) member 1	map04727 GABAergic synapse;map04721 Synaptic vesicle cycle	KOG3660 Hs5032097 Sodium-neurotransmitter symporter	KKZ61104.1 hypothetical protein EMCG_04300 [Emmonsia crescens UAMH 3008]	Sodium- and chloride-dependent creatine transporter 1 OS=Bos taurus OX=9913 GN=SLC6A8 PE=2 SV=1
A5859	-	-	-	-	-	-	-	-

A5860	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0003995(acyl-CoA dehydrogenase activity),GO:0050660(flavin adenine dinucleotide binding)	K09478 ACADSB; short-chain 2-methylacyl-CoA dehydrogenase [EC:1.3.8.5]	map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG0140 Hs7656849 Medium-chain acyl-CoA dehydrogenase	OON05477.1 hypothetical protein BSLG_04652 [Batrachochytrium salamandrivorans]	Isobutyryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAD8 PE=1 SV=1
A5861	-	-	-	-	-	-	-	-
A5862	-	-	-	-	-	-	-	-
A5863	-	-	-	-	-	-	-	-
A5864	-	-	-	-	-	-	-	-
A5865	-	-	-	-	-	-	-	-
A5866	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K06641 CHEK2; serine/threonine-protein kinase CHEK2 [EC:2.7.11.1]	map04218 Cellular senescence;map04115 p53 signaling pathway;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG0597 At1g50230 Serine-threonine protein kinase FUSED	KAF9153351.1 hypothetical protein DFQ26_000595, partial [Actinomyces rella ambigua]	Putative serine/threonine-protein kinase/receptor R831 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_R831 PE=3 SV=2
A5867	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity),GO:0005515(protein binding)	-	-	KOG0192 Hs4506539 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KDQ14059.1 hypothetical protein BOTBODRAFT_175166 [Botryobasidium botryosum FD-172 SS1]	RGS domain-containing serine/threonine-protein kinase A OS=Dictyostelium discoideum OX=44689 GN=rckA PE=1 SV=1
A5868	-	-	-	-	-	-	-	-
A5869	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG4229 7298201 Myosin VII, myosin IXB and related myosins	XP_016605569.1 hypothetical protein SPPG_07005 [Spizellomyces punctatus DAOM BR117]	Myosin-VIIa OS=Drosophila melanogaster OX=7227 GN=ck PE=1 SV=1
A5870	-	-	-	-	-	-	-	-
A5871	-	-	-	-	-	-	OLL23930.1 hypothetical protein NEOLI_003130 [Neolectia irregularis DAH-3]	-

A5872	GO:0009058(biosynthetic process), GO:0006520(cellular amino acid metabolic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0008483(transaminase activity),GO:0003824(catalytic activity)	K14455 GOT2; aspartate aminotransferase, mitochondrial [EC:2.6.1.1]	map00950 Isoquinoline alkaloid biosynthesis;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00960 Tropane, piperidine and pyridine alkaloid biosynthesis;map00330 Arginine and proline metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map04975 Fat	KOG1411 CE02477 Aspartate aminotransferase/Glutamic oxaloacetic transaminase AAT1/GOT2	KAG0227779.1 aspartate transaminase aat1 [Actinomyces rella wolffii]	Aspartate aminotransferase, mitochondrial OS=Oryctolagus cuniculus OX=9986 GN=GOT2 PE=1 SV=2
A5873	GO:0000209(protein polyubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity),GO:0061630(ubiquitin protein ligase activity)	K10589 UBE3C; ubiquitin-protein ligase E3 C [EC:2.3.2.26]	map04120 Ubiquitin mediated proteolysis	KOG0942 Hs7661856 E3 ubiquitin protein ligase	EJT98849.1 HECT-domain-containing protein [Dacryopinax primogenitus]	Ubiquitin-protein ligase E3C OS=Mus musculus OX=10090 GN=Ube3c PE=1 SV=2
A5874	-	-	-	-	-	KOG4840 At5g19050 Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	RUS15049.1 hypothetical protein BC937DRAFT_92965 [Endogone sp. FLAS-F59071]	UPF0613 protein PB24D3.06c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAPB24D3.06c PE=3 SV=1
A5875	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0163 Hs4826846 Myosin class VI heavy chain	TGZ81077.1 putative class V myosin [Ascodesmis nigricans]	Unconventional myosin-VI OS=Bos taurus OX=9913 GN=MYO6 PE=1 SV=4
A5876	GO:0006470(protein dephosphorylation), GO:0016311(dephosphorylation)	-	GO:0008138(protein tyrosine/serine/threonine phosphatase activity),GO:0016791(phosphatase activity)	-	-	KOG1717 7293827 Dual specificity phosphatase	KAF0556690.1 dual specificity protein phosphatase 19 [Gigaspora margarita]	Dual specificity protein phosphatase Mpk3 OS=Drosophila melanogaster OX=7227 GN=Mkp3 PE=1 SV=2

A5877	-	-	-	K03946 NDUFA2; NADH dehydrogena se (ubiquinone) 1 alpha subcomplex subunit 2	map05014 Amyotrophic lateral sclerosis;map054 15 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoi d signaling;map04 714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map050 22 Pathways of neurodegenerati on - multiple diseases;map052 08 Chemical carcinogenesis - reactive oxygen species;map049 32 Non- alcoholic fatty liver disease;map050	KOG3446 Hs4 505355 NADH:ubiqui none oxidoreducta se NDUFA2/B8 subunit	RKP07957.1 thioredoxin- like protein [Thamnoceph alis sphaerospora]	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Bos taurus OX=9913 GN=NDUFA2 PE=1 SV=2
A5878	-	-	-	-	-	KOG4157 Hs1 4755576 beta-1,6-N- acetylglucosa minyltransfer ase, contains WSC domain	-	Sialate:O-sulfotransferase 1 OS=Xenopus tropicalis OX=8364 GN=wscd1 PE=2 SV=1
A5879	-	-	-	-	-	-	-	-
A5880	-	-	-	-	-	-	-	-
A5881	-	-	-	-	-	-	-	-
A5882	GO:00065 11(ubiquit in- dependen t protein catabolic process), GO:00165 79(protein deubiquiti nation)	-	GO:0004843(thi ol-dependent deubiquitinase)	K11835 USP4_11, UBP12; ubiquitin carboxyl- terminal hydrolase 4/11 [EC:3.4.19.12]	-	KOG1870 Hs4 758564_2 Ubiquitin C- terminal hydrolase	KAG0263362. 1 CSN- associated deubiquitinati ng enzyme Ubp12 [Mortierella polycephala]	Ubiquitin carboxyl-terminal hydrolase 15 OS=Xenopus tropicalis OX=8364 GN=usp15 PE=2 SV=2
A5883	-	GO:00056 34(nucleu s)	GO:0003677(DN A binding)	-	-	KOG0526 729 1642 Nucleosome- binding factor SPN, POB3 subunit	SGZ40946.1 uncharacteriz ed protein HGUI_03146 [Hanseniastro guilliermondii]	FACT complex subunit Ssrp1 OS=Drosophila melanogaster OX=7227 GN=Ssrp PE=1 SV=2
A5884	-	-	-	-	-	-	-	-
A5885	-	-	GO:0005515(pro tein binding)	-	-	-	-	-
A5886	-	GO:00164 59(myosin complex), GO:00058 56(cytoske leton)	GO:0003774(mo tor activity),GO:000 5524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04 814 Motor proteins	KOG0160 At5 g43900 Myosin class V heavy chain	RKO94560.1 myosin VIIA, isoform CRA_d, partial [Blyttiomycet helicus]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1
A5887	-	-	GO:0003676(nu cleic acid binding),GO:000 8270(zinc ion binding)	-	-	-	-	-
A5888	GO:00001 84(nuclea r- transcribe d mRNA catabolic process, nonsense - mediated decay)	-	GO:0003723(RN A binding),GO:000 5515(protein binding)	K14327 UPF2, RENT2; regulator of nonsense transcripts 2	map03013 Nucleocytoplas mic transport;map03 015 mRNA surveillance pathway	KOG2051 Hs1 1693132 Nonsense- mediated mRNA decay 2 protein	KAG2176994. 1 hypothetical protein INT43_00764 8 [Umbelopsis isabellina]	Regulator of nonsense transcripts 2 OS=Homo sapiens OX=9606 GN=UPF2 PE=1 SV=1

A5889	-	GO:0005789(endoplasmic reticulum membrane),GO:0016021(integral component of membrane)	-	-	-	-	KU69800.1 hypothetical protein HYDPIDRAFT_142411 [Hydnomerulis pinastri MD-312]	Uncharacterized protein C119.09c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC119.09c PE=2 SV=3
A5890	-	-	-	-	-	KOG4081 Hs5730085 Dynein light chain	TPX71942.1 hypothetical protein CcBS67573_g06048 [Chytridiomyces confervae]	Dynein light chain Tctex-type 1 OS=Bos taurus OX=9913 GN=DYNLT1 PE=1 SV=1
A5891	-	-	-	-	-	-	ORY73312.1 hypothetical protein LY90DRAFT_3_22960, partial [Neocallimastix californiae]	-
A5892	-	-	-	-	-	-	-	-
A5893	-	-	-	-	-	-	XP_033656679.1 uncharacterized protein EI97DRAFT_3_43364, partial [Westerdykella ornata]	-
A5894	-	-	GO:0005524(ATP binding)	K06158 ABCF3; ATP-binding cassette, subfamily F, member 3	-	KOG0062 At1g64550 ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	PVV00305.1 hypothetical protein BB560_005319 [Smittium megazygosporum]	ABC transporter F family member 3 OS=Arabidopsis thaliana OX=3702 GN=ABCF3 PE=1 SV=1
A5895	GO:0007156(homophilic cell adhesion via plasma membrane adhesion molecules)	GO:0016020(membrane)	GO:0005509(calcium ion binding),GO:0005515(protein binding)	-	-	KOG3594 Hs16507962 FOG: Cadherin repeats	KUL84836.1 hypothetical protein ZTR_08225 [Talaromyces verruculosus]	Protocadherin Fat 4 OS=Homo sapiens OX=9606 GN=FAT4 PE=1 SV=2
A5896	-	-	-	-	-	-	-	-
A5897	GO:0006486(protein glycosylation)	-	GO:0004378(GDP-Mann:Man1GlcNAc2-PP-Dol alpha-1,3-mannosyltransferase activity),GO:0016757(glycosyltransferase activity),GO:0005515(protein binding)	K03843 ALG2; alpha-1,3/alpha-1,6-mannosyltransferase [EC:2.4.1.132,2.4.1.257]	map00513 Various types of N-glycan biosynthesis;map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG0853 Hs14861836 Glycosyltransferase	ORY98211.1 alpha-1,3/1,6-mannosyltransferase ALG2 [Syncephalastrium racemosum]	Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Homo sapiens OX=9606 GN=ALG2 PE=1 SV=1
A5898	-	-	GO:0005515(protein binding)	-	-	KOG0504 Hs20476895 FOG: Ankyrin repeat	KAF7722493.1 hypothetical protein DSO57_000084, partial [Entomophthora muscae]	SH3 and multiple ankyrin repeat domains protein 2 OS=Homo sapiens OX=9606 GN=SHANK2 PE=1 SV=4

A5899	GO:0006623(protein targeting to vacuole)	-	GO:0005515(protein binding)	K20178 VPS8; vacuolar protein sorting-associated protein 8	map04138 Autophagy - yeast	KOG2079 7295341 Vacuolar assembly/sorting protein VPS8	XP_016607060.1 hypothetical protein SPPG_05970 [Spizellomyces punctatus DAOM BR117]	Vacuolar protein sorting-associated protein 8 homolog OS=Mus musculus OX=10090 GN=Vps8 PE=1 SV=1
A5900	-	GO:0005680(anaphase-promoting complex)	-	K03348 APC1, ANAPC1; anaphase-promoting complex subunit 1	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG1858 Hs12056971 Anaphase-promoting complex (APC), subunit 1 (meiotic check point regulator/Tsg 24)	ORY08304.1 hypothetical protein K493DRAFT_29218 [Basidiobolus meristosporus CBS 931.73]	Anaphase-promoting complex subunit 1 OS=Homo sapiens OX=9606 GN=ANAPC1 PE=1 SV=1
A5901	GO:0007017(microtubule-based process)	GO:0030286(dynein complex)	-	-	-	-	-	-
A5902	-	-	GO:0005515(protein binding)	K13341 PEX7, PTS2R; peroxin -7	map04146 Peroxisome	KOG0305 7290520 Anaphase promoting complex, Cdc20, Cdh1, and Ama1 subunits	PWY98354.1 WD40 repeat-like protein [Testicularia cyper]	WD repeat-containing protein 17 OS=Homo sapiens OX=9606 GN=WDR17 PE=2 SV=2
A5903	-	-	-	-	-	-	-	-
A5904	-	-	-	-	-	KOG1398 At5g51150 Uncharacterized conserved protein	XP_031024551.1 uncharacterized protein SmJEL517_g03584 [Synchytrium microbalum]	Transmembrane protein 135 OS=Xenopus laevis OX=8355 GN=tmem135 PE=2 SV=1
A5905	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0019773(proteasome core complex, alpha-subunit complex), GO:0005839(proteasome core complex)	-	K02730 PSMA6; 20S proteasome subunit alpha 1 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0182 Hs14749945 20S proteasome, regulatory subunit alpha type PSMA6/SCL1	KAG2211346.1 hypothetical protein INT46_002044 [Mucor plumbeus]	Proteasome subunit alpha type-6 OS=Bos taurus OX=9913 GN=PSMA6 PE=1 SV=1

A5906	GO:0042176(regulation of protein catabolic process)	GO:0000502(proteasome complex)	GO:0030234(enzyme regulator activity)	K03032 PSMD1, RPN2; 26S proteasome regulatory subunit N2	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG2062 At2g32730 26S proteasome regulatory complex, subunit RPN2/PSMD1	ORY92164.1 armadillo-type protein [Syncephalastrum racemosum]	26S proteasome non-ATPase regulatory subunit 1 homolog A OS=Arabidopsis thaliana OX=3702 GN=RPN2A PE=1 SV=1
A5907	-	-	-	-	-	-	-	-
A5908	GO:0006631(fatty acid metabolic process)	-	GO:0003824(catalytic activity),GO:0016491(oxidoreductase activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0070403(NAD+ binding)	K00022 HADH; 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]	map01110 Biosynthesis of secondary metabolites;map00907 Pinene, camphor and geraniol degradation;map01120 Microbial metabolism in diverse environments;map00930 Caprolactam degradation;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00062 Fatty acid elongation;map00310 Lysine degradation;map00380 Tryptophan metabolism;map	KOG1683 Hs4503497 Hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase	RKL18215.1 hypothetical protein BFJ72_g15243, partial [Fusarium proliferatum]	Peroxisomal bifunctional enzyme OS=Danio rerio OX=7955 GN=ehadh PE=2 SV=1
A5909	-	-	GO:0005515(protein binding)	K09553 STIP1; stress-induced-phosphoprotein 1	map05020 Prion disease	KOG1124 Hs1024639 FOG: TPR repeat	RKO89858.1 hypothetical protein BDK51DRAFT_28191 [Blyttiomycetes helicus]	Sperm-associated antigen 1 OS=Rattus norvegicus OX=10116 GN=Spag1 PE=1 SV=1
A5910	GO:0006606(protein import into nucleus)	-	-	K20222 IPO5, KPNB3, RANBP5; importin-5	map03013 Nucleocytoplasmic transport	KOG2171 At5g19820 Karyopherin (importin) beta 3	OLY77768.1 Importin subunit beta-3 [Smittium mucronatum]	Importin-5 OS=Mus musculus OX=10090 GN=Ipo5 PE=1 SV=3
A5911	-	-	-	-	-	-	-	-
A5912	-	-	-	-	-	-	RKO88830.1 hypothetical protein BDK51DRAFT_52216 [Blyttiomycetes helicus]	-
A5913	-	-	-	-	-	KOG0895 Hs10442822_2 Ubiquitin-conjugating enzyme	EEB91238.1 hypothetical protein MPER_10436 [Moniliophthora perniciosa FA553]	Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens OX=9606 GN=BIRC6 PE=1 SV=3

A5914	GO:0006629(lipid metabolic process)	-	GO:0016491(oxidoreductase activity)	-	-	KOG4232 At3g61580 Delta 6-fatty acid desaturase/delta-8 sphingolipid desaturase	PVV02261.1 hypothetical protein BB560_003291 [Smittium megazygosporum]	NADPH-dependent stearyl-CoA 9-desaturase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=desA3 PE=3 SV=1
A5915	-	-	-	-	-	-	-	Uncharacterized protein MJ1566 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440)
A5916	-	-	GO:0051537(2 iron, 2 sulfur cluster binding)	-	-	-	-	-
A5917	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K03083 GSK3B; glycogen synthase kinase 3 beta [EC:2.7.11.26]	map04390 Hippo signaling pathway;map04360 Axon guidance;map05415 Diabetic cardiomyopathy;map05417 Lipid and atherosclerosis;map05135 Yersinia infection;map05131 Shigellosis;map04722 Neurotrophin signaling pathway;map04510 Focal adhesion;map01521 EGFR tyrosine kinase inhibitor resistance;map04919 Thyroid hormone signaling pathway;map04917 Prolactin	KOG0658 At5g14640 Glycogen synthase kinase-3	KAG0359125.1 regulator of ime2 [Podila minutissima]	Glycogen synthase kinase-3 homolog MsK-3 OS=Medicago sativa OX=3879 GN=MSK-3 PE=2 SV=2
A5918	GO:0006890(retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum)	GO:0030126(COPI vesicle coat)	-	K20472 COPZ, RET3; coatamer subunit zeta	-	KOG3343 Hs7706337 Vesicle coat complex COPI, zeta subunit	XP_016609617.1 hypothetical protein SPPG_03376 [Spizellomyces punctatus DAOM BR117]	Coatamer subunit zeta-2 OS=Oryza sativa subsp. japonica OX=39947 GN=COPZ2 PE=2 SV=1
A5919	-	-	GO:0005515(protein binding)	-	-	-	-	-
A5920	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0003169(cation binding)	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG0698 At2g20050 Serine/threonine protein phosphatase	KXN68028.1 camp-dependent protein kinase regulatory subunit [Conidiobolus coronatus NRRL 28638]	Protein phosphatase 2C and cyclic nucleotide-binding/kinase domain-containing protein OS=Arabidopsis thaliana OX=3702 GN=At2g20050/At2g20040 PE=2 SV=2
A5921	-	-	GO:0046872(metal ion binding),GO:0003729(mRNA binding)	-	-	KOG1677 At1g66810 CCCH-type Zn-finger protein	RKP01207.1 hypothetical protein CXG81DRAFT_3782, partial [Caulochytrium protostelioides]	Zinc finger CCCH domain-containing protein 14 OS=Arabidopsis thaliana OX=3702 GN=C3H14 PE=2 SV=1
A5922	GO:0000398(mRNA splicing, via spliceosome)	GO:0005681(spliceosomal complex)	-	-	-	KOG1806 7299528 DEAD box containing helicases	ORX55227.1 P-loop containing nucleoside triphosphate hydrolase protein [Piromyces finnis]	RNA helicase aquarius OS=Homo sapiens OX=9606 GN=AQR PE=1 SV=4

A5923	GO:0006468(protein phosphorylation)	-	GO:0005509(calcium ion binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At1g50700 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	XP_007007876.1 uncharacterized protein TREMEDRAFT_35340, partial [Tremella mesenterica DSM 1558]	Calcium and calcium/calmodulin-dependent serine/threonine-protein kinase OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=CCAMK PE=2 SV=1
A5924	-	-	GO:0003824(catalytic activity)	K11390 CLYBL; citrate lyase subunit beta-like protein [EC:4.1.-.-]	-	-	OAJ41557.1 hypothetical protein BDEG_25133 [Batrachochytrium dendrobatidis JEL423]	(3S)-methyl-CoA thioesterase OS= <i>Cereibacter sphaeroides</i> (strain ATCC 17025 / ATCC 2.4.3) OX=349102 GN=mcl2 PE=3 SV=1
A5925	-	-	-	-	-	KOG2565 CE14390 Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	KAF3226471.1 hypothetical protein TWF191_004733 [Orbilia oligospora]	Putative epoxide hydrolase OS= <i>Stigmatella aurantiaca</i> (strain DW4/3-1) OX=378806 GN=STAU_4299 PE=3 SV=2
A5926	GO:0044237(cellular metabolic process), GO:0044249(cellular biosynthetic process)	-	-	K08963 mtmA; methylthioribose-1-phosphate isomerase [EC:5.3.1.23]	map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG1468 At2g05830 Predicted translation initiation factor related to eIF-2B alpha/beta/delta subunits (CIG2/DI2)	CAE6393118.1 unnamed protein product [Rhizoctonia solani]	Methylthioribose-1-phosphate isomerase OS= <i>Thermosiphon africanus</i> (strain TCF52B) OX=484019 GN=mtmA PE=3 SV=1
A5927	GO:0006084(acetyl-CoA metabolic process), GO:0010142(farnesyl diphosphate biosynthetic process, mevalonate pathway), GO:0008299(isoprenoid biosynthetic process)	-	GO:0004421(hydroxymethylglutaryl-CoA synthase activity),GO:0016746(acyltransferase activity)	-	-	KOG1393 Hs4504429 Hydroxymethylglutaryl-CoA synthase	OUM61884.1 hypothetical protein PIROE2DRAFT_54504 [Piromyces sp. E2]	Hydroxymethylglutaryl-CoA synthase A OS= <i>Dictyostelium discoideum</i> OX=44689 GN=hgsA PE=1 SV=2
A5928	GO:0035556(intracellular signal transduction)	-	GO:0005085(guanylate cyclase activity)	-	-	KOG3519 Hs19882229_1 Invasion-inducing protein TIAM1/CDC24 and related RhoGEF GTPases	KNE61101.1 hypothetical protein AMAG_06855 [Allomyces macrogynus ATCC 38327]	Myosin-M heavy chain OS= <i>Dictyostelium discoideum</i> OX=44689 GN=myoM PE=1 SV=1
A5929	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG0194 CE11430 Protein tyrosine kinase	QRC36148.1 hypothetical protein FDK38_000479 [Candida auris]	Spermatocyte protein spe-8 OS= <i>Caenorhabditis elegans</i> OX=6239 GN=spe-8 PE=1 SV=2

A5930	GO:0006508(proteolysis)	GO:0016021(integral component of membrane)	GO:0016757(glycosyltransferase activity),GO:0004252(serine-type endopeptidase activity)	-	-	-	ORX96694.1 hypothetical protein K493DRAFT_370600 [Basidiobolus meristosporus CBS 931.73]	-
A5931	GO:0046488(phosphatidylinositol metabolic process)	-	GO:0016307(phosphatidylinositol phosphate kinase activity)	K00889 PIP5K; 1-phosphatidylinositol-4-phosphate 5-kinase [EC:2.7.1.68]	map04144 Endocytosis;map05135 Yersinia infection;map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04070 Phosphatidylinositol signaling system;map04072 Phospholipase D signaling pathway;map04139 Mitophagy - yeast;map04666 Fc gamma R-mediated phagocytosis;map00562 Inositol phosphate metabolism;map04011 MAPK signaling pathway - yeast;map05231 Choline metabolism in	-	RCH98441.1 Phosphatidylinositol-4-phosphate 5-kinase [Rhizopus stolonifer]	Phosphatidylinositol 4-phosphate 5-kinase its3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=its3 PE=1 SV=3
A5932	-	-	-	-	-	-	-	-
A5933	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0008569(minus-end-directed microtubule motor activity),GO:0045505(dynein intermediate chain binding),GO:0051959(dynein light intermediate chain binding)	K10413 DYNC1H1; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595 CE05659 Dyneins, heavy chain	XP_01660623.1.1 hypothetical protein SPPG_06593 [Spizellomyces punctatus DAOM BR117]	Cytoplasmic dynein 2 heavy chain 1 OS=Tripneustes gratilla OX=7673 GN=DYH1B PE=2 SV=2
A5934	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0008569(minus-end-directed microtubule motor activity),GO:0045505(dynein intermediate chain binding),GO:0051959(dynein light intermediate chain binding)	-	-	KOG3595 CE05659 Dyneins, heavy chain	TPX70937.1 hypothetical protein SpCBS45565_g01524 [Spizellomyces sp. 'palustris']	Cytoplasmic dynein 2 heavy chain 1 OS=Rattus norvegicus OX=10116 GN=Dync2h1 PE=1 SV=1
A5935	-	-	-	-	-	KOG3832 7296305 Predicted amino acid transporter	-	Transmembrane protein 104 homolog OS=Dictyostelium discoideum OX=44689 GN=tmem104 PE=3 SV=1
A5936	-	-	-	-	-	-	-	-
A5937	-	-	GO:0003950(NAD+ ADP-ribosyltransferase activity)	-	-	-	-	Protein mono-ADP-ribosyltransferase PARP12 OS=Mus musculus OX=10090 GN=Parp12 PE=1 SV=3
A5938	-	-	-	-	-	-	-	-
A5939	-	-	GO:0005515(protein binding)	-	-	-	-	-

A5940	-	-	-	-	-	KOG4249 Hs1 2232403 Uncharacterized conserved protein	TPX70465.1 hypothetical protein CcCBS67573_g06553 [Chytriomycetes confervae]	Protein root UVB sensitive 3 OS=Arabidopsis thaliana OX=3702 GN=RUS3 PE=2 SV=1
A5941	-	-	-	-	-	-	-	-
A5942	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0157 At2g45970 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	TPX65003.1 hypothetical protein CcCBS67573_g08264 [Chytriomycetes confervae]	Cytochrome P450 CYP94D108 OS=Paris polyphylla OX=49666 GN=CYP94D108 PE=1 SV=1
A5943	-	-	GO:0005515(protein binding)	K13886 CORO1B_1C_6; coronin-1B/1C/6	-	KOG0303 Hs7656991 Actin-binding protein Coronin, contains WD40 repeats	RKP11930.1 hypothetical protein BJ684DRAFT_17533 [Piptocephalis cylindrospora]	Coronin-1C OS=Mus musculus OX=10090 GN=Coro1c PE=1 SV=2
A5944	-	-	-	-	-	KOG1700 7299283 Regulatory protein MLP and related LIM proteins	XP_031025425.1 uncharacterized protein SmJEL517_g02776 [Synchytrium microbalum]	[F-actin]-monooxygenase MICAL1 OS=Bos taurus OX=9913 GN=MICAL1 PE=2 SV=1
A5945	-	-	GO:0016746(acyltransferase activity)	K00624 E2.3.1.7; carnitine O-acetyltransferase [EC:2.3.1.7]	map04146 Peroxisome	KOG3717 Hs21618334 Carnitine O-acetyltransferase CRAT	ORZ39107.1 acyltransferase ChoActase/COT/CPT [Catenaria anguillulae PL171]	Carnitine O-acetyltransferase, mitochondrial OS=Candida tropicalis OX=5482 GN=CAT2 PE=3 SV=1
A5946	GO:0006629(lipid metabolic process)	-	GO:0016491(oxidoreductase activity)	K13076 SLD; sphingolipid 8-(E)-desaturase [EC:1.14.19.18]	-	KOG4232 Hs11181775 Delta 6-fatty acid desaturase/delta-8 sphingolipid desaturase	KAG0259277.1 hypothetical protein BG011_002742 [Mortierella polycephala]	Acyl-lipid (8-3)-desaturase OS=Thraustochytrium sp. OX=145168 GN=Fad5 PE=1 SV=1
A5947	-	-	GO:0005544(calcium-dependent phospholipid binding)	-	-	KOG1327 Hs4503015 Copine	XP_016609497.1 hypothetical protein SPPG_03260 [Spizellomyces punctatus DAOM BR117]	Copine-3 OS=Homo sapiens OX=9606 GN=CPNE3 PE=1 SV=1
A5948	-	-	-	-	-	-	-	-
A5949	-	-	GO:0016787(hydrolase activity)	-	-	-	KAG0164461.1 hypothetical protein DFQ30_009930 [Apophysomyces sp. BC1015]	Hippurate hydrolase OS=Campylobacter jejuni subsp. jejuni serotype O:2 (strain ATCC 700819 / NCTC 11168) OX=192222 GN=hipO PE=1 SV=2

A5950	-	-	-	K09529 DNAJC9; DnaJ homolog subfamily C member 9	-	KOG0719 At5 g06910 Molecular chaperone (DnaJ superfamily)	XP_02466352 9.1 DnaJ subfamily C member 9 [Wickerhamia lla sorbophila]	Chaperone protein dnaJ 6 OS=Arabidopsis thaliana OX=3702 GN=ATJ6 PE=2 SV=1
A5951	-	-	-	-	-	-	-	-
A5952	-	-	GO:0046982(pro tein heterodimerizati on activity)	K08066 NFYC, HAP5; nuclear transcription factor Y, gamma	map04612 Antigen processing and presentation;ma p05152 Tuberculosis	KOG1657 At1 g56170 CCAAT- binding factor, subunit C (HAP5)	XP_01798754 6.1 HDL194Wp [Erethocium sinicaudum]	Nuclear transcription factor Y subunit C-2 OS=Arabidopsis thaliana OX=3702 GN=NFYC2 PE=1 SV=2
A5953	-	-	-	-	-	-	EPZ32450.1 RIB43A domain- containing protein [Rozella allomyces CSF55]	RIB43A-like with coiled-coils protein 2 OS=Bos taurus OX=9913 GN=RIBC2 PE=1 SV=2
A5954	-	-	-	-	-	-	ORY35145.1 hypothetical protein BCR33DRAFT _503794 [Rhizoclosma tium globosum]	Protein FAM184A OS=Homo sapiens OX=9606 GN=FAM184A PE=1 SV=3
A5955	-	-	-	-	-	-	RDB20542.1 hypothetical protein Hypma_0124 51 [Hypsizygus marmoreus]	-
A5956	-	-	-	-	-	-	-	-
A5957	GO:00066 29(lipid metabolic process)	-	GO:0016491(oxi doreductase activity)	-	-	-	RYO83630.1 hypothetical protein DL763_00775 4 [Monosporas cus cannonballus]	Alkane 1-monooxygenase 2 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=alkB2 PE=1 SV=1
A5958	GO:00512 60(protein homoolig omerizati on)	-	GO:0005525(GT P binding)	-	-	KOG2723 Hs1 9923973 Uncharacteriz ed conserved protein, contains BTB/POZ domain	RUS16366.1 BTB/POZ protein [Endogone sp. FLAS- F59071]	BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens OX=9606 GN=KCTD12 PE=1 SV=1
A5959	GO:00163 11(depho sphorylati on)	-	GO:0016791(ph osphatase activity)	-	-	-	XP_00786752 7.1 hypothetical protein GLOTRDRAFT _116807 [Gloeophyllu m trabeum ATCC 11539]	Paladin OS=Gallus gallus OX=9031 GN=PALD1 PE=2 SV=2
A5960	-	-	-	-	-	-	-	-
A5961	-	-	-	-	-	-	-	-
A5962	-	GO:00160 21(integra l compone nt of membran e),GO:000 5887(inte gral compone nt of plasma membran e)	-	-	-	-	XP_03102321 7.1 uncharacteriz ed protein SmJEL517_g0 4855 [Synchytrium microbalum]	-

A5963	-	-	GO:0003824(catalytic activity)	-	-	KOG1018 YOL066c.2 Cytosine deaminase FCY1 and related enzymes	OUM66539.1 hypothetical protein PIR0E2DRAFT_59279 [Piromyces sp. E2]	tRNA (32'-2'-O)-methyltransferase regulator THADA OS=Gallus gallus OX=9031 GN=THADA PE=2 SV=1
A5964	-	-	-	-	-	-	XP_660192.1 hypothetical protein AN2588.2 [Aspergillus nidulans FGSC A4]	-
A5965	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 At3g24840 Phosphatidylinositol transfer protein SEC14 and related proteins	TPX64796.1 hypothetical protein CcCBS67573_g08312 [Chytridiomycota confervae]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH9 OS=Arabidopsis thaliana OX=3702 GN=SFH9 PE=2 SV=1
A5966	GO:0007094(mitotic spindle assembly checkpoint signaling)	-	-	K02178 BUB1; checkpoint serine/threonine-protein kinase [EC:2.7.11.1]	map04914 Progesterone-mediated oocyte maturation;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG1166 Hs20149509 Mitotic checkpoint serine/threonine protein kinase	RKP08328.1 mitotic checkpoint complex, partial [Thamnocephalus sphaerosporus]	Probable inactive serine/threonine-protein kinase bub1 OS=Dictyostelium discoideum OX=44689 GN=bub1 PE=3 SV=1
A5967	GO:0006811(ion transport), GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015075(ion transmembrane transporter activity)	K23503 SFXN5; sideroflexin-5	-	KOG3767 Hs21389351 Sideroflexin	ORZ35516.1 Tricarboxylate/iron carrier [Catenaria anguillulae PL171]	Sideroflexin-5 OS=Homo sapiens OX=9606 GN=SFXN5 PE=1 SV=1
A5968	-	-	-	-	-	-	-	-
A5969	-	-	-	-	-	-	-	-
A5970	GO:0000776(DNA replication checkpoint signaling), GO:0006974(cellular response to DNA damage stimulus), GO:0048478(replication fork protection)	GO:0005634(nucleus)	-	-	-	-	-	-
A5971	-	-	-	-	-	-	PVU85490.1 hypothetical protein BB560_007009 [Smittium megazygosporum]	-
A5972	GO:0042254(ribosome biogenesis)	-	-	K14771 NOC4, UTP19; U3 small nucleolar RNA-associated protein 19	-	-	ORX56974.1 CBF-domain-containing protein [Hesseltinella vesiculosa]	Nucleolar complex protein 4 homolog OS=Mus musculus OX=10090 GN=Noc4I PE=2 SV=1

A5973	GO:0009298(GDP-mannose biosynthetic process)	-	GO:0004615(phosphomannomutase activity)	K17497 PMM; phosphomannomutase [EC:5.4.2.8]	map01250 Biosynthesis of nucleotide sugars;map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00051 Fructose and mannose metabolism;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG3189 At2g45790 Phosphomannomutase	CAE6508780.1 unnamed protein product [Rhizoctonia solani]	Phosphomannomutase OS=Oryza sativa subsp. indica OX=39946 GN=PMM PE=3 SV=1
A5974	GO:0007034(vacuolar transport)	-	-	K12191 CHMP2A; charged multivesicular body protein 2A	map04144 Endocytosis;map04217 Necroptosis	KOG3230 CE21987 Vacuolar assembly/sorting protein DID4	RIB30950.1 charged multivesicular body protein 2a [Gigaspora rosea]	Charged multivesicular body protein 2a OS=Xenopus tropicalis OX=8364 GN=chmp2a PE=2 SV=1
A5975	GO:0016226(iron-sulfur cluster assembly)	-	-	K22069 LYRM4; LYR motif-containing protein 4	-	-	THZ84605.1 hypothetical protein D6C84_04028 [Aureobasidium pullulans]	Protein ISD11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ISD11 PE=1 SV=1
A5976	-	-	-	-	-	-	-	-
A5977	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0008569(minus-end-directed microtubule motor activity);GO:0005524(ATP binding)	K10413 DYNC1H1; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595 7292540 Dyneins, heavy chain	ORX99360.1 dynein heavy chain [Basidiobolus meristosporus CBS 931.73]	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus OX=10116 GN=Dync1h1 PE=1 SV=1
A5978	GO:0007165(signal transduction)	-	GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity);GO:0008081(phosphoric diester hydrolase activity)	-	-	KOG3689 7290408 Cyclic nucleotide phosphodiesterase	TPX65455.1 hypothetical protein SpCBS45565_g05142 [Spizellomyces sp. 'palustris']	High affinity cGMP-specific 3',5'-cyclic phosphodiesterase 9A OS=Mus musculus OX=10090 GN=Pde9a PE=1 SV=1
A5979	-	-	GO:0005515(protein binding)	-	-	-	KDQ16399.1 hypothetical protein BOTBODRAFT_130203, partial [Botryobasidium botryosum FD-172 SS1]	Transient receptor potential cation channel subfamily A member 1 OS=Rattus norvegicus OX=10116 GN=Trpa1 PE=2 SV=1

A5980	GO:0006013(mannose metabolic process), GO:0005975(carbohydrate metabolic process)	-	GO:0004559(alpha-mannosidase activity),GO:0003824(catalytic activity),GO:0030246(carbohydrate binding)	-	-	KOG1959 At5g66150 Glycosyl hydrolase, family 38 - alpha-mannosidase	ORX67622.1 hypothetical protein DL89DRAFT_47974 [Linderina pennisporea]	Probable alpha-mannosidase At5g66150 OS=Arabidopsis thaliana OX=3702 GN=At5g66150 PE=3 SV=1
A5981	-	-	-	-	-	-	-	-
A5982	-	-	-	-	-	-	-	-
A5983	-	-	-	-	-	KOG4288 At1g32220 Predicted oxidoreductase	RPA87868.1 NAD(P)-binding protein [Ascobolus immersus RN42]	Uncharacterized protein At1g32220, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=At1g32220 PE=1 SV=1
A5984	GO:0006260(DNA replication)	-	GO:0003677(DNA binding)	K02321 POLA2; DNA polymerase alpha subunit B	map03030 DNA replication	KOG1625 Hs20127448 DNA polymerase alpha-primase complex, polymerase-associated subunit B	KAG2174107.1 hypothetical protein INT43_004127 [Umbelopsis isabellina]	DNA polymerase alpha subunit B OS=Homo sapiens OX=9606 GN=POLA2 PE=1 SV=2
A5985	-	-	-	K23469 CLB2; G2/mitotic-specific cyclin 2	map04011 MAPK signaling pathway - yeast;map04111 Cell cycle - yeast	KOG0655 Hs17318561 G1/S-specific cyclin E	EPZ34375.1 Cyclin domain-containing protein [Rozella allomycis CSF55]	G1/S-specific cyclin-E1 OS=Danio rerio OX=7955 GN=ccne1 PE=2 SV=1
A5986	-	-	-	-	-	-	-	-
A5987	-	-	-	-	-	-	-	-
A5988	-	-	GO:0005524(ATP binding)	K03283 HSPA1_6_8; heat shock 70kDa protein 1/6/8	map03040 Spliceosome;map05417 Lipid and atherosclerosis; map04144 Endocytosis;map04141 Protein processing in endoplasmic reticulum;map05134 Legionellosis;map04213 Longevity regulating pathway - multiple species;map04915 Estrogen signaling pathway;map04612 Antigen processing and presentation;map05145 Toxoplasmosis; map05020 Prion disease;map04010 MAPK	KOG0101 CE09682 Molecular chaperones HSP70/HSC70, HSP70 superfamily	RHZ71095.1 hypothetical protein Glove_262g20 [Diversispora epigaea]	Heat shock 70 kDa protein OS=Achlya klebsiana OX=4767 GN=HSP70 PE=2 SV=1
A5989	GO:0006412(translation)	GO:0005840(ribosome),GO:0005761(mitochondrial ribosome)	GO:0003735(structural constituent of ribosome)	K17428 MRPL47, NCM1; large subunit ribosomal protein L47	-	KOG3331 At1g07830 Mitochondrial/chloroplast ribosomal protein L4/L29	KNE56218.1 hypothetical protein AMAG_02052 [Allomyces macrogynus ATCC 38327]	Large ribosomal subunit protein uL29m OS=Bos taurus OX=9913 GN=MRPL47 PE=2 SV=1
A5990	GO:0006508(proteolysis)	-	GO:0004222(metalloendopeptidase activity),GO:0046872(metal ion binding)	K01408 IDE, ide; insulysin [EC:3.4.24.56]	map05010 Alzheimer disease;map03266 Virion - Herpesvirus	KOG0959 7296294 N-arginine dibasic convertase NRD1 and related Zn2+-dependent endopeptidases, insulinase superfamily	KAG0267649.1 Insulinase (Peptidase M16) [Actinomortierella ambigua]	Insulin-degrading enzyme OS=Drosophila melanogaster OX=7227 GN=Ide PE=1 SV=4

A5991	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	K05665 ABCC1; ATP-binding cassette, subfamily C (CFTR/MRP), member 1 [EC:7.6.2.3]	map04071 Sphingolipid signaling pathway;map01523 Antifolate resistance;map04977 Vitamin digestion and absorption;map02010 ABC transporters;map05206 MicroRNAs in cancer	KOG0054 Hs9955958 Multidrug resistance-associated protein/mitochondrion resistance protein, ABC superfamily	ORZ19904.1 multi drug resistance-associated protein MRP [Absidia repens]	Multidrug resistance-associated protein 1 OS=Macaca fascicularis OX=9541 GN=ABCC1 PE=1 SV=1
A5992	-	-	-	-	-	KOG1791 At4g27010 Uncharacterized conserved protein	TPX38943.1 hypothetical protein SeLEV6574_g07500 [Synchytrium endobioticum]	Nucleolar pre-ribosomal-associated protein 1 OS=Mus musculus OX=10090 GN=Urb1 PE=1 SV=2
A5993	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity);GO:0005524(ATP binding);GO:0008017(microtubule binding)	K11498 CENPE, KIF10; centromeric protein E	map04814 Motor proteins	KOG0242 At1g59540 Kinesin-like protein	RKP39116.1 P-loop containing nucleoside triphosphate hydrolase protein, partial [Dimargaris cristalligena]	Kinesin-like protein KIN-7L OS=Oryza sativa subsp. japonica OX=39947 GN=KIN7L PE=2 SV=1
A5994	-	-	GO:0003676(nucleic acid binding)	K01148 PARN, PNLD1; poly(A)-specific ribonuclease [EC:3.1.13.4]	map03018 RNA degradation	KOG1990 At1g55870 Poly(A)-specific exoribonuclease PARN	CDS09676.1 hypothetical protein LRAMOSA02353 [Lichtheimia ramosa]	Poly(A)-specific ribonuclease PARN OS=Xenopus laevis OX=8355 GN=parn PE=1 SV=1
A5995	-	-	-	-	-	KOG4300 Hs13378141 Predicted methyltransferase	PWA01527.1 hypothetical protein BB558_002359 [Smittium angustum]	Thiol S-methyltransferase TMT1B OS=Rattus norvegicus OX=10116 GN=Tmt1b PE=1 SV=1
A5996	-	-	-	-	-	-	-	-
A5997	-	-	GO:0005524(ATP binding)	K06158 ABCF3; ATP-binding cassette, subfamily F, member 3	-	KOG0062 ECU05g1190 ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	OBT43011.1 hypothetical protein VE00_07354 [Pseudogymnoascus sp. WSF 3629]	Probable ATP-binding cassette sub-family F member 3 homolog OS=Encephalitozoon cuniculi (strain GB-M1) OX=284813 GN=ECU05_1190 PE=3 SV=1
A5998	-	-	GO:0016491(oxidoreductase activity);GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	K00130 betB, gbsA; betaine-aldehyde dehydrogenase [EC:1.2.1.8]	map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG2450 Hs4502047 Aldehyde dehydrogenase	KAG1716754.1 hypothetical protein ID866.448 [Astraeus odoratus]	Betaine aldehyde dehydrogenase OS=Brucella anthropi (strain ATCC 49188 / DSM 6882 / CCUG 24695 / JCM 21032 / LMG 3331 / NBRC 15819 / NCTC 12168 / Alc 37) OX=439375 GN=betB PE=3 SV=1

A5999	GO:0006412(translation)	GO:0005840(ribosome),GO:015935(small ribosomal subunit)	GO:0003723(RNA binding),GO:0003735(structural constituent of ribosome)	K02981 RP-S2e, RPS2; small subunit ribosomal protein S2e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0877 7297568 40S ribosomal protein S2/30S ribosomal protein S5	RKP39767.1 ribosomal protein S5, N-terminal domain-containing protein [Dimargaris cristalligena]	Small ribosomal subunit protein uS5 OS=Drosophila melanogaster OX=7227 GN=RpS2 PE=1 SV=2
A6000	-	-	-	-	-	-	-	-
A6001	GO:0055085(transmembrane transport)	-	-	K15275 SLC35B1; solute carrier family 35 (UDP-galactose transporter), member B1	-	KOG1580 Hs5032213 UDP-galactose transporter related protein	KAF9585894.1 UDP-galactose transporter [Lunasporea selenosporea]	Solute carrier family 35 member B1 OS=Xenopus laevis OX=8355 GN=slc35b1 PE=2 SV=1
A6002	-	-	-	-	-	-	-	-
A6003	GO:0006468(protein phosphorylation),GO:0006397(mRNA processing),GO:0030968(endoplasmic reticulum unfolded protein response)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding),GO:0004540(ribonuclease activity),GO:0004521(endoribonuclease activity),GO:0004674(protein serine/threonine kinase activity)	K08852 ERN1; serine/threonine-protein kinase/endoribonuclease IRE1 [EC:2.7.11.1 3.1.26.-]	map05014 Amyotrophic lateral sclerosis;map05417 Lipid and atherosclerosis;map04140 Autophagy - animal;map04141 Protein processing in endoplasmic reticulum;map04210 Apoptosis;map05022 Pathways of neurodegeneration - multiple diseases;map04932 Non-alcoholic fatty liver disease;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spino cerebellar	KOG1027 YH079c Serine/threonine protein kinase and endoribonuclease ERN1/IRE1, sensor of the unfolded protein response pathway	KAG0679978.1 bifunctional endoribonuclease/protein kinase ire1 [[Candida] californica]	Serine/threonine-protein kinase/endoribonuclease IRE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IRE1 PE=1 SV=2
A6004	-	-	-	-	-	-	-	-
A6005	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4557659 Sulfatase	KJZ77521.1 hypothetical protein HIM_03245 [Hirsutella minnesotensis 3608]	Ulvian-active sulfatase OS=Formosa agariphila (strain DSM 15362 / KCTC 12365 / LMG 23005 / KMM 3901 / M-2Alg 35-1) OX=1347342 GN=BN863_22000 PE=1 SV=1
A6006	GO:0007264(small GTPase mediated signal transduction)	-	GO:0005509(calcium ion binding),GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07870 RHOT1, ARHT1; mitochondrial Rho GTPase 1 [EC:3.6.5.-]	map04214 Apoptosis - fly;map04137 Mitophagy - animal	KOG1707 At3g63150 Predicted Ras related/Rac-GTP binding protein	KXS11950.1 mitochondrial Rho GTPase [Gonapodya prolifera JEL478]	Mitochondrial Rho GTPase 2 OS=Arabidopsis thaliana OX=3702 GN=MIRO2 PE=2 SV=1
A6007	-	-	GO:0000062(fatty-acyl-CoA binding),GO:0005515(protein binding)	K08762 DBI, ACBP; diazepam-binding inhibitor (GABA receptor modulator, acyl-CoA-binding protein)	map03320 PPAR signaling pathway	KOG0817 At5g53470 Acyl-CoA-binding protein	XP_018285591.1 hypothetical protein PHYBLDRAFT_189028, partial [Phycomyces blakesleeana NRRL 1555(-)]	Acyl-CoA-binding domain-containing protein 1 OS=Arabidopsis thaliana OX=3702 GN=ACBP1 PE=1 SV=2
A6008	-	-	-	K24121 MPO1; 2-hydroxy fatty acid dioxygenase [EC:1.14.18.1 2]	-	-	XP_024679636.1 DUF962-domain-containing protein [Aspergillus novofumigatus IBT 16806]	-

A6009	GO:0000105(histidine biosynthetic process)	-	GO:0016763(peptidyl transferase activity),GO:00010107(imidazole glycerol-phosphate synthase activity)	K01663 HIS7; imidazole glycerol-phosphate synthase [EC:4.3.2.10]	map00340 Histidine metabolism;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways	KOG0623 At4g26900 Glutamine amidotransferase/cyclase	KAG0225151.1 Histidine biosynthesis bifunctional protein hisB [Actinomyces rella wolffii]	Imidazole glycerol phosphate synthase hisHF, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=HISN4 PE=2 SV=1
A6010	-	-	GO:0003824(catalytic activity),GO:0050660(flavin adenine dinucleotide binding),GO:0071949(FAD binding)	K21618 DLD3; (R)-2-hydroxyglutarate-pyruvate transhydrogenase [EC:1.1.99.40]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG1232 At4g36400 Proteins containing the FAD binding domain	KAG0262968.1 hypothetical protein BGZ95_003911 [Linnemania exigua]	D-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Danio rerio OX=7955 GN=d2hgdh PE=2 SV=1
A6011	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0006813(potassium ion transport)	GO:0016020(membrane)	GO:0005216(ion channel activity),GO:0005249(voltage-gated potassium channel activity)	K10273 FBXL7; F-box and leucine-rich repeat protein 7	-	KOG0500 Hs4502917 Cyclic nucleotide-gated cation channel CNGA1-3 and related proteins	ORZ39155.1 hypothetical protein BCR44DRAFT_1427319 [Catenaria anguillulae PL171]	Cyclic nucleotide-gated channel cone photoreceptor subunit alpha OS=Gallus gallus OX=9031 PE=2 SV=1
A6012	GO:0035721(intracellular retrograde transport),GO:0035735(intracellular transport involved in cilium assembly)	GO:0005868(cytoplasmic dynein complex)	-	-	-	KOG3929 Hs7706300 Uncharacterized conserved protein	ORY39938.1 hypothetical protein BCR33DRAFT_719748 [Rhizoclostium globosum]	Cytoplasmic dynein 2 light intermediate chain 1 OS=Danio rerio OX=7955 GN=dync2li1 PE=2 SV=1
A6013	GO:0009058(biosynthetic process),GO:0033014(tetrapyrrole biosynthetic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0016740(transferase activity),GO:0003824(catalytic activity),GO:0003870(5-aminolevulinic acid synthase activity)	K00643 E2.3.1.37, ALAS; 5-aminolevulinic acid synthase [EC:2.3.1.37]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG1360 Hs4502025 5-aminolevulinic acid synthase	KAF9158507.1 mitochondria l 5-aminolevulinic acid synthase [Actinomyces rella ambigua]	5-aminolevulinic acid synthase OS=Rhizobium radiobacter OX=358 GN=hema PE=3 SV=1
A6014	-	-	-	-	-	-	ORY20141.1 hypothetical protein LY90DRAFT_517048 [Neocallimastix californiae]	-

A6015	GO:0006508(proteolysis)	-	GO:0046872(metal ion binding)	K06972 PITRM1, PreP, CYM1; presequence protease [EC:3.4.24.-]	-	KOG2019 Hs7 657343 Metalloendo protease HMP1 (insulinase superfamily)	OBZ86830.1 Mitochondria l presequence protease [Choanephora cucurbitarum]	Presequence protease, mitochondrial OS=Danio rerio OX=7955 GN=pitrm1 PE=2 SV=1
A6016	-	-	-	-	-	-	-	Protein ApaG OS=Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)
A6017	GO:0006520(cellular amino acid metabolic process)	-	GO:0016491(oxidoreductase activity),GO:0016639(oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor)	K00262 E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	map00910 Nitrogen metabolism;map 01120 Microbial metabolism in diverse environments;map 00250 Alanine, aspartate and glutamate metabolism;map 00220 Arginine biosynthesis;map 01100 Metabolic pathways	KOG2250 Hs4 885281 Glutamate/leucine/phenyl alanine/valine dehydrogenases	KAG1527947.1 hypothetical protein G6F52_001085 [Rhizopus delemar]	Glutamate dehydrogenase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=gluD PE=1 SV=1
A6018	GO:000077(DNA damage checkpoint signaling)	-	-	K02830 HRAD1, RAD17; cell cycle checkpoint protein [EC:3.1.11.2]	map04218 Cellular senescence;map 04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG3194 Hs4 506385 Checkpoint 9-1-1 complex, RAD1 component	OON08414.1 hypothetical protein BSLG_02310 [Batrachochytrium salamandrivorans]	Cell cycle checkpoint protein RAD1 OS=Homo sapiens OX=9606 GN=RAD1 PE=1 SV=1
A6019	-	-	GO:0030234(enzyme regulator activity)	K03037 PSMD6, RPN7; 26S proteasome regulatory subunit N7	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG0687 At4 g24820 26S proteasome regulatory complex, subunit RPN7/PSMD6	KAG0747884.1 hypothetical protein G6F23_002371 [Rhizopus oryzae]	26S proteasome non-ATPase regulatory subunit 6 homolog OS=Arabidopsis thaliana OX=3702 GN=RPN7 PE=1 SV=1
A6020	-	-	-	-	-	-	-	-
A6021	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0616 YKL 166c cAMP- dependent protein kinase catalytic subunit (PKA)	OAG32185.1 protein kinase X [Nematocida displodere]	cAMP-dependent protein kinase type 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPK3 PE=1 SV=2
A6022	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0192 At2 g35050_2 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9976048.1 hypothetical protein BGZ73_009207 [Actinomortierella ambigua]	Probable serine/threonine-protein kinase PkwA OS=Thermomonospora curvata OX=2020 GN=pkwA PE=1 SV=1
A6023	-	-	-	-	-	-	-	-

A6024	-	-	-	-	-	-	KIM52504.1 hypothetical protein SCLCIDRAFT 1223705 [Scleroderma citrinum Foug A]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces ribosidificus OX=80859 GN=rbmC PE=3 SV=1
A6025	-	-	GO:0016787(hy drolase activity)	K15498 PPP6C; serine/threon ine-protein phosphatase 6 catalytic subunit [EC:3.1.3.16]	-	KOG0373 At3 g19980 Serine/threon ine specific protein phosphatase involved in cell cycle control, PP2A-related	KAG2180507. 1 hypothetical protein INT44_00351 1 [Umbelopsis vinacea]	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Dictyostelium discoideum OX=44689 GN=ppp6c PE=2 SV=2
A6026	GO:00065 06(GPI anchor biosynthe tic process)	GO:00057 89(endopl asmic reticulum membran e),GO:001 6021(inte gral compo nent of membran e)	GO:0016740(tra nsferase activity),GO:000 8484(sulfuric ester hydrolase activity),GO:005 1377(mannose- ethanolamine phosphotransfer ase activity)	K05285 PIGN; GPI ethanolamine phosphate transferase 1 [EC:2.7.-.-]	map00563 Glycosylphosphat idylinositol (GPI)-anchor biosynthesis;map 01100 Metabolic pathways	KOG2124 Hs6 912500 Glycosylphosphat idylinositol anchor synthesis protein	RKP36392.1 GPI ethanolamine phosphate transferase [Dimargaris crystalligena]	GPI ethanolamine phosphate transferase 1 OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=MCD4 PE=3 SV=1
A6027	-	-	GO:0005524(AT P binding),GO:001 6887(ATP hydrolysis activity)	K08900 BCS1; mitochondria l chaperone BCS1	-	KOG0743 At5 g17730 AAA+-type ATPase	XP_00121643 9.1 conserved hypothetical protein [Aspergillus terreus NIH2624]	AAA-ATPase At5g17730 OS=Arabidopsis thaliana OX=3702 GN=At5g17730 PE=3 SV=1
A6028	-	-	GO:0005524(AT P binding),GO:001 6887(ATP hydrolysis activity)	K08900 BCS1; mitochondria l chaperone BCS1	-	KOG0743 At5 g17730 AAA+-type ATPase	RGB35364.1 P-loop containing nucleoside triphosphate hydrolase protein, partial [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	AAA-ATPase At5g17730 OS=Arabidopsis thaliana OX=3702 GN=At5g17730 PE=3 SV=1
A6029	-	-	-	K01697 CBS; cystathionine beta- synthase [EC:4.2.1.22]	map01110 Biosynthesis of secondary metabolites;map 01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map 01100 Metabolic pathways;map00 270 Cysteine and methionine metabolism	KOG1252 YG R155w Cystathionine beta- synthase and related enzymes	ONH73330.1 Cysteine synthase [Pichia kudriavzevii]	Putative cystathionine beta-synthase MT1108 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=cbs PE=3 SV=1

A6030	-	-	-	-	-	-	TPX57582.1 hypothetical protein PhCBS80983. g03759 [Powellomyces hirtus]	tRNA uridine(34) hydroxylase OS=Enterococcus faecalis (strain ATCC 700802 / V583) OX=226185 GN=trhO PE=3 SV=1
A6031	-	-	-	K26544 SEC14, SEC14L; phosphatidyl inositol/phosph atidylcholine transfer protein	-	KOG1471 YKL 091c Phosphatidyl inositol transfer protein SEC14 and related proteins	ORZ29452.1 CRAL-TRIO domain- containing protein [Catenaria anguillulae PL171]	CRAL-TRIO domain-containing protein YKL091C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YKL091C PE=1 SV=2
A6032	-	-	GO:0005544(cal cium- dependent phospholipid binding)	-	-	KOG1031 Hs1 4764556 Predicted Ca2+- dependent phospholipid -binding protein	KAF9355095. 1 hypothetical protein BGX26_00700 0 [Mortierella sp. AD094]	C2 domain-containing protein 5 OS=Homo sapiens OX=9606 GN=C2CD5 PE=1 SV=1
A6033	-	-	-	-	-	-	-	-
A6034	-	-	-	-	-	-	ORY93520.1 hypothetical protein BCR43DRAFT _497075 [Syncephalast rum racemosum]	-
A6035	-	-	-	K10750 CHAF1A; chromatin assembly factor 1 subunit A	-	KOG4364 729 0959 Chromatin assembly factor-1	CCO28062.1 hypothetical protein BN14_02054 [Rhizoctonia solani AG-1 IB]	Chromatin assembly factor 1 subunit A OS=Gallus gallus OX=9031 GN=CHAF1A PE=1 SV=1
A6036	-	-	-	-	-	-	-	-
A6037	-	-	GO:0005515(pro tein binding)	-	-	KOG4003 730 0541 Pyrazinamida se/nicotinami dase PNC1	XP_01866343 5.1 hypothetical protein TGAM01_v20 5213 [Trichoderma gamsii]	Nicotinamidase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=pncA PE=1 SV=1
A6038	-	-	GO:0009055(ele ctron transfer activity)	K03521 fixA, etfb; electron transfer flavoprotein beta subunit	-	KOG3180 Hs4 503609 Electron transfer flavoprotein, beta subunit	RKP06732.1 hypothetical protein THASP1DRAF T_31459 [Thamnoceph alis sphaerospora]	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus OX=10116 GN=Etfb PE=1 SV=3
A6039	GO:00163 10(phosphorylation)	-	GO:0004672(pro tein kinase activity),GO:001 6772(transferase activity, transferring phosphorus- containing groups)	K00898 PDK2_3_4; pyruvate dehydrogenase kinase 2/3/4 [EC:2.7.11.2]	map05415 Diabetic cardiomyopathy	KOG0787 At3 g06483 Dehydrogenase kinase	KAF8992734. 1 mitochondria l pyruvate dehydrogenase [Cyathus striatus]	[Pyruvate dehydrogenase (acetyl-transferring)] kinase, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=PDK PE=1 SV=1
A6040	-	-	GO:0003824(cat alytic activity)	-	-	KOG1075 CE 04575 FOG: Reverse transcriptase	OMJ10672.1 RNA- directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polypeptide from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1

A6041	-	GO:0000786(nucleosome)	GO:0046982(protein heterodimerization activity),GO:0003677(DNA binding),GO:000527(structural constituent of chromatin)	K11495 CENPA; histone H3-like centromeric protein A	-	KOG1745 At1g75600 Histones H3 and H4	PPQ99034.1 hypothetical protein CVT24_003594 [Panaeolus cyanescens]	Histone H3-like centromeric protein CSE4 OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=CSE4 PE=3 SV=1
A6042	-	-	-	-	-	KOG0725 Hs10190704 Reductases with broad range of substrate specificities	KAF9128005.1 hypothetical protein BGX30_014505 [Mortierella sp. GBA39]	Uncharacterized oxidoreductase UxuB OS=Bacillus subtilis (strain 168) OX=224308 GN=uxuB PE=2 SV=1
A6043	-	-	GO:0016787(hydrolase activity)	K04382 PPP2C; serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16]	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04140 Autophagy - animal;map04730 Long-term depression;map04350 TGF-beta signaling pathway;map04071 Sphingolipid signaling pathway;map04138 Autophagy - yeast;map04136 Autophagy - other;map04728 Dopaminergic synapse;map04660 T cell receptor signaling pathway;map04261 Adrenergic signaling in	KOG0371 Hs4758952 Serine/threonine protein phosphatase 2A, catalytic subunit	CRG83916.1 protein phosphatase 2 (formerly 2A), catalytic subunit [Talaromyces islandicus]	Serine/threonine-protein phosphatase PP2A catalytic subunit OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=pphA PE=3 SV=2
A6044	-	-	-	-	-	-	-	-
A6045	GO:0005975(carbohydrate metabolic process)	-	GO:0003824(catalytic activity),GO:00030246(carbohydrate binding),GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	K05546 GANAB; mannosyl-oligosaccharide alpha-1,3-glucosidase [EC:3.2.1.207]	map04141 Protein processing in endoplasmic reticulum;map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG1066 Hs21361456 Glucosidase II catalytic (alpha) subunit and related enzymes, glycosyl hydrolase family 31	KAF9971179.1 hypothetical protein BGZ73_005916 [Actinomortierella ambigua]	Neutral alpha-glucosidase AB OS=Dictyostelium discoideum OX=44689 GN=modA PE=3 SV=1
A6046	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0005524(ATP binding),GO:0019205(nucleobase-containing compound kinase activity)	K00939 adk, AK; adenylate kinase [EC:2.7.4.3]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map00730 Thiamine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3078 At2g37250 Adenylate kinase	KAG0163675.1 hypothetical protein DFQ30_011193 [Apophysomyces sp. BC1015]	Adenylate kinase OS=Thermodesulfovibrio yellowstonii (strain ATCC 51303 / DSM 11347 / YP87) OX=289376 GN=adk PE=3 SV=1

A6047	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6048	-	-	-	-	-	KOG0048 Hs13641706.1 Transcription factor, Myb superfamily	ORX94530.1 hypothetical protein K493DRAFT_30240 [Basidiobolus meristosporus CBS 931.73]	Transcriptional activator Myb OS=Xenopus laevis OX=8355 GN=myb PE=2 SV=1
A6049	-	-	-	-	-	KOG0614 Hs5453978 cGMP-dependent protein kinase	KAG5362384.1 cAMP-dependent protein kinase regulatory subunit [Yarrowia sp. C11]	cAMP-dependent protein kinase regulatory subunit OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=PKAR PE=3 SV=1
A6050	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0619 7300644_2 FOG: Leucine rich repeat	KAG0151365.1 hypothetical protein CROQUODRAFT_651184 [Cronartium quercuum f. sp. fusiforme G11]	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A6051	GO:0045892(negative regulation of transcription, DNA-templated)	GO:0005634(nucleus)	GO:0005515(protein binding)	-	-	-	KAG2173657.1 hypothetical protein INT43_005077 [Umbelopsis isabellina]	Negative elongation factor B OS=Drosophila melanogaster OX=7227 GN=NELF-B PE=1 SV=1
A6052	-	-	-	-	-	-	-	-
A6053	-	-	-	-	-	-	-	-
A6054	GO:0001522(pseudouridine synthesis), GO:0009451(RNA modification)	-	GO:0003723(RNA binding),GO:0009982(pseudouridine synthase activity)	K06173 truA, PUS1; tRNA pseudouridine synthase [EC:5.4.99.12]	-	KOG2553 At2g30320 Pseudouridylate synthase	RPA78946.1 pseudouridine synthase [Ascobolus immersus RN42]	Putative tRNA pseudouridine synthase OS=Arabidopsis thaliana OX=3702 GN=At2g30320 PE=3 SV=1
A6055	-	-	-	-	-	-	-	-
A6056	-	-	-	-	-	-	-	-
A6057	GO:0006470(protein dephosphorylation), GO:0016311(dephosphorylation)	-	GO:0004725(protein tyrosine phosphatase activity),GO:0016791(phosphatase activity)	K01104 E3.1.3.48; protein-tyrosine phosphatase [EC:3.1.3.48]	-	KOG0791 Hs18860900 Protein tyrosine phosphatase, contains fn3 domain	RKO92216.1 protein-tyrosine phosphatase -like protein, partial [Blyttiomycetes helicus]	Tyrosine-protein phosphatase non-receptor type 1 OS=Rattus norvegicus OX=10116 GN=Ptpn1 PE=1 SV=1
A6058	-	-	-	-	-	-	-	-
A6059	-	-	-	-	-	-	-	-
A6060	-	-	-	-	-	-	KAG4084717.1 hypothetical protein H8356DRAFT_1743360 [Neocallimastix sp. JGI-2020a]	Zinc finger MYND domain-containing protein 10 OS=Danio rerio OX=7955 GN=zmynd10 PE=2 SV=1
A6061	-	-	-	-	-	-	-	-

A6062	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0157 7293040 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	XP_031025487.1 uncharacterized protein SmJEL517_g02588 [Synchytrium microbalum]	Probable cytochrome P450 4s3 OS=Drosophila melanogaster OX=7227 GN=Cyp4s3 PE=3 SV=1
A6063	-	-	-	-	-	-	-	-
A6064	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K19800 SCH9; serine/threonine protein kinase SCH9 [EC:2.7.11.1]	map04213 Longevity regulating pathway - multiple species;map04138 Autophagy - yeast	-	ORX94730.1 Pkinase-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Protein kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pkgB PE=1 SV=2
A6065	-	-	GO:0005515(protein binding)	-	-	KOG1987 Hs4507183 Speckle-type POZ protein SPOP and related proteins with TRAF, MATH and BTB/POZ domains	XP_033408175.1 uncharacterized protein GIQ15_03597 [Arthroderma uncinatum]	Speckle-type POZ protein-like B OS=Danio rerio OX=7955 GN=spoplb PE=2 SV=2
A6066	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	-	-	KOG0986 Hs4501971 G protein-coupled receptor kinase	KWU42216.1 kinase-like protein, partial [Rhodotorula sp. JG-1b]	G protein-coupled receptor kinase 3 OS=Bos taurus OX=9913 GN=GRK3 PE=2 SV=1
A6067	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6068	GO:0006414(translational elongation)	-	GO:0003924(GTPase activity),GO:0005525(GTP binding),GO:0003746(translation elongation factor activity)	K02358 tuf, TUFM; elongation factor Tu	map04626 Plant-pathogen interaction	KOG0460 At4g02930 Mitochondrial translation elongation factor Tu	GAT46923.1 elongation factor [Mycena chlorophos]	Elongation factor Tu OS=Novosphingobium aromaticivorans (strain ATCC 700278 / DSM 12444 / CCUG 56034 / CIP 105152 / NBRC 16084 / F199) OX=279238 GN=tuf PE=3 SV=1
A6069	-	-	-	-	-	-	-	-
A6070	-	-	-	-	-	-	-	-

A6071	GO:0046034(ATP metabolic process), GO:1902600(proton transmembrane transport)	-	GO:0005524(ATP binding)	K02132 ATPeF1A, ATP5A1, ATP1; F-type H+-transporting ATPase subunit alpha	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05008 Chemical carcinogenesis - reactive oxygen species;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease;map01100 Metabolic pathways	KOG1353 CE18826 F0F1-type ATP synthase, alpha subunit	XP_006687583.1 uncharacterized protein CANTEDRAFT_124062 [Yamadazyma tenuis ATCC 10573]	ATP synthase subunit alpha OS=Rickettsia canadensis (strain McKiel) OX=293613 GN=atpA PE=3 SV=1
A6072	-	-	GO:0005515(protein binding)	-	-	KOG1080 At4g15180 Histone H3 (Lys4) methyltransferase complex, subunit SET1 and related methyltransferases	KIY67062.1 SET domain-containing protein [Cylindrobacterium torrendii FP15055 ss-10]	Histone-lysine N-methyltransferase ATXR3 OS=Arabidopsis thaliana OX=3702 GN=ATXR3 PE=2 SV=2
A6073	-	-	-	-	-	-	XP_016612258.1 hypothetical protein SPPG_01651 [Spizellomyces punctatus DAOM BR117]	Uncharacterized signaling protein PA1727 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA1727 PE=1 SV=1
A6074	-	-	-	-	-	-	KAG0195475.1 hypothetical protein BGX28_001302, partial [Mortierella sp. GBA30]	-
A6075	-	-	GO:0005542(folic acid binding),GO:0016740(transferase activity)	-	-	-	-	Formiminotransferase cyclodeaminase-like protein OS=Arabidopsis thaliana OX=3702 GN=FTCD-L PE=2 SV=2
A6076	-	-	-	-	-	-	-	-
A6077	GO:0044237(cellular metabolic process), GO:0006310(DNA recombination)	-	GO:0000166(nucleotide binding),GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0004386(helicase activity)	K10901 BLM, RECQL3, SGS1; bloom syndrome protein [EC:5.6.2.4]	map03440 Homologous recombination; map03460 Fanconi anemia pathway	KOG0351 ECU07g1130 ATP-dependent DNA helicase	KZP29982.1 ATP-dependent DNA helicase [Fibularhizoctonia sp. CBS 109695]	ATP-dependent DNA helicase RecQ OS=Pasteurella multocida (strain Pm70) OX=272843 GN=recQ PE=3 SV=1
A6078	-	-	GO:0005515(protein binding)	-	-	-	OON09526.1 hypothetical protein BSLG_01446 [Batrachochytrium salamandrivorans]	Flagellar WD repeat-containing protein Pf20 OS=Chlamydomonas reinhardtii OX=3055 GN=PF20 PE=1 SV=1
A6079	-	-	-	-	-	-	-	-
A6080	-	-	-	-	-	-	-	-
A6081	-	-	-	-	-	-	-	-
A6082	-	-	-	-	-	-	-	-

A6083	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0054 CE26370 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	RIA93900.1 ATP-binding cassette transporter 1 [Glomus cerebriforme]	ABC transporter C family member 3 OS=Dictyostelium discoideum OX=44689 GN=abcC3 PE=3 SV=1
A6084	GO:0006281(DNA repair)	-	GO:0003824(catalytic activity),GO:0051536(iron-sulfur cluster binding)	K07739 ELP3, KAT9; elongator complex protein 3 (tRNA carboxymethyluridine synthase) [EC:2.3.1.311]	-	KOG2535 At5g50320 RNA polymerase II elongator complex, subunit ELP3/histone acetyltransferase	TIA91776.1 hypothetical protein E3P99_00921 [Wallemia hederae]	tRNA uridine(34) acetyltransferase OS=Methanocaldococcus infernus (strain DSM 11812 / JCM 15783 / ME) OX=573063 GN=Metin_0452 PE=1 SV=1
A6085	-	-	-	-	-	-	-	-
A6086	GO:0015986(ATP synthesis coupled proton transport)	GO:0045261(proton-transporting ATP synthase complex, catalytic core F1)	GO:0046933(proton-transporting ATP synthase activity, rotational mechanism)	K02136 ATPeF1G, ATP5C1, ATP3; F-type H+-transporting ATPase subunit gamma	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease;map01100 Metabolic pathways	KOG1531 7301823 F0F1-type ATP synthase, gamma subunit	KAG2076394.1 ATP synthase F1 gamma [Suillus decipiens]	ATP synthase subunit gamma, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ATPsyngamma PE=2 SV=2
A6087	-	-	-	-	-	-	KAG0958818.1 hypothetical protein G6F31_012271 [Rhizopus oryzae]	Formylglycine-generating enzyme OS=Bos taurus OX=9913 GN=SUMF1 PE=2 SV=1
A6088	-	-	GO:0005515(protein binding)	K14818 SQT1; ribosome assembly protein SQT1	-	KOG0296 Hs4557229 Angio-associated migratory cell protein (contains WD40 repeats)	KAG4103738.1 WD40 repeat-like protein [Neocallimastix sp. JGI-2020a]	Angio-associated migratory cell protein OS=Bos taurus OX=9913 GN=AAMP PE=2 SV=1
A6089	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K07893 RAB6A; Ras-related protein Rab-6A	-	KOG0094 At5g10260 GTPase Rab6/YPT6/Ryh1, small G protein superfamily	XP_006681351.1 uncharacterized protein BATDEDRAFT_20546 [Batrachochytrium dendrobatidis JAM81]	Ras-related protein RABH1e OS=Arabidopsis thaliana OX=3702 GN=RABH1E PE=2 SV=1
A6090	-	-	GO:0008239(dipeptidyl-peptidase activity),GO:0016787(hydrolase activity)	-	-	-	CEL01030.1 hypothetical protein ASPCAL00622 [Aspergillus calidoustus]	Cocaine esterase OS=Rhodococcus sp. (strain MB1 Bresler) OX=104109 GN=cocE PE=1 SV=1

A6091	GO:0006418(tRNA aminoacylation for protein translation),GO:0006435(threonyl-tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004829(threonine-tRNA ligase activity)	K01868 TARS, thrS; threonyl-tRNA synthetase [EC:6.1.1.3]	map00970 Aminoacyl-tRNA biosynthesis	KOG1637 At5g26830 Threonyl-tRNA synthetase	KAG0687716.1 threonyl-tRNA synthetase [[Candida] californica]	Probable threonine--tRNA ligase 1, cytoplasmic OS=Dictyostelium discoideum OX=44689 GN=thrS1 PE=3 SV=1
A6092	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K15628 PXA; ATP-binding cassette, subfamily D (ALD), peroxisomal long-chain fatty acid import protein [EC:7.6.2.4]	map04146 Peroxisome;map02010 ABC transporters	KOG0060 At4g39850 Long-chain acyl-CoA transporter, ABC superfamily (involved in peroxisome organization and biogenesis)	CRK33215.1 hypothetical protein BN1723_003909 [Verticillium longisporum]	ABC transporter D family member 1 OS=Arabidopsis thaliana OX=3702 GN=ABCD1 PE=1 SV=1
A6093	-	-	-	-	-	-	-	-
A6094	-	-	-	-	-	-	-	-
A6095	GO:0055085(transmembrane transport)	GO:0016020(membrane)	-	-	-	-	KAF9145128.1 hypothetical protein BGX30_010207 [Mortierella sp. GBA39]	Small-conductance mechanosensitive channel MscMJ OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ0170 PE=1 SV=1
A6096	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A6097	-	-	-	-	-	-	-	-
A6098	-	-	-	-	-	-	-	-
A6099	GO:0006207('de novo' pyrimidine nucleobase biosynthetic process)	GO:0005737(cytoplasm),GO:0016020(membrane)	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0004152(dihydroorotate dehydrogenase activity)	K00254 DHODH, pyrD; dihydroorotate dehydrogenase [EC:1.3.5.2]	map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG1436 Hs16753223 Dihydroorotate dehydrogenase	RKP08042.1 mitochondria l Dihydroorotate dehydrogenase, partial [Thamnocephalus sphaerospora]	Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Rattus norvegicus OX=10116 GN=Dhodh PE=1 SV=1
A6100	-	-	GO:0016301(kinase activity)	K04718 SPHK; sphingosine kinase [EC:2.7.1.91]	map04020 Calcium signaling pathway;map04071 Sphingolipid signaling pathway;map04072 Phospholipase D signaling pathway;map00600 Sphingolipid metabolism;map04666 Fc gamma R-mediated phagocytosis;map04371 Apelin signaling pathway;map04370 VEGF signaling pathway;map05152 Tuberculosis;map01100 Metabolic pathways	KOG1115 Hs20336726 Ceramide kinase	KAF9436251.1 hypothetical protein BGZ76_004479 [Entomortierella beljakovae]	Ceramide kinase OS=Mus musculus OX=10090 GN=Cerk PE=1 SV=2

A6101	-	-	-	K13535 CLD1; cardiolipin- specific phospholipase [EC:3.1.1.-]	map00564 Glycerophospholipid metabolism	KOG4409 At4g24160 Predicted hydrolase/acyltransferase (alpha/beta hydrolase superfamily)	KAF0491965.1 alpha/beta-hydrolase [Gigaspora margarita]	Probable 1-acylglycerol-3-phosphate O-acyltransferase OS= <i>Oryza sativa</i> subsp. japonica OX=39947 GN=Os09g0520200 PE=3 SV=3
A6102	-	-	-	-	-	-	-	-
A6103	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map04972 Pancreatic secretion;map04080 Neuroactive ligand-receptor interaction;map05164 Influenza A	KOG3627 7294373 Trypsin	BCS20308.1 hypothetical protein APUU_20740 S [Aspergillus puulaauensis]	Trypsin-7 OS= <i>Anopheles gambiae</i> OX=7165 GN=TRYP7 PE=2 SV=2
A6104	GO:0006508(proteolysis),GO:0042256(mature ribosome assembly)	-	GO:0004252(serine-type endopeptidase activity),GO:0043022(ribosome binding)	K03264 EIF6; translation initiation factor 6	map03008 Ribosome biogenesis in eukaryotes	KOG3185 At3g55620 Translation initiation factor 6 (eIF-6)	KAF7747685.1 eukaryotic translation initiation factor 6 [Entomophthora muscae]	Eukaryotic translation initiation factor 6-2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=EIF6-2 PE=2 SV=1
A6105	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A6106	-	GO:0016021(integral component of membrane)	-	-	-	-	KAF9123946.1 hypothetical protein BGX30_001169 [Mortierella sp. GBA39]	Probable membrane transporter protein YunE OS= <i>Bacillus subtilis</i> (strain 168) OX=224308 GN=yunE PE=3 SV=1
A6107	-	GO:0016021(integral component of membrane)	-	-	-	KOG3669 7293668 Uncharacterized conserved protein, contains dysferlin, TECPR and PH domains	KAG5363668.1 Vacuolar protein sorting-associated protein 13 [Yarrowia sp. B02]	Intermembrane lipid transfer protein VPS13 OS= <i>Chaetomium thermophilum</i> (strain DSM 1495 / CBS 144.50 / IMI 039719) OX=759272 GN=VPS13 PE=1 SV=1
A6108	GO:0019346(transsulfuration)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	K01760 metC; cysteine-S-conjugate beta-lyase [EC:4.4.1.13]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways;map00450 Selenocompound metabolism;map00270 Cysteine and methionine metabolism	KOG0053 At3g57050 Cystathionine beta-lyases/cystathionine gamma-synthases	ORY03016.1 cystathionine beta-lyase [Basidiobolus meristosporus CBS 931.73]	Cystathionine beta-lyase, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At3g57050 PE=1 SV=1

A6109	-	-	GO:0005515(protein binding)	K23314 WRAP53, TCAB1; telomerase Cajal body protein 1	-	KOG2919[Hs8922396 Guanine nucleotide-binding protein	ORY06980.1 WD40 repeat-like protein [Basidiobolus meristosporus CBS 931.73]	Telomerase Cajal body protein 1 OS=Bos taurus OX=9913 GN=WRAP53 PE=2 SV=1
A6110	GO:0006396(RNA processing)	GO:0000178(exosome (RNase complex))	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K07573 CSL4, EXOSC1; exosome complex component CSL4	map03018 RNA degradation	KOG3409[At5g38890.1 Exosomal 3'-5' exoribonuclease complex, subunit ski4 (Csl4)	KAG2185853.1 hypothetical protein [INT43_002291 [Umbelopsis isabellina]	Exosome complex component CSL4 OS=Homo sapiens OX=9606 GN=EXOSC1 PE=1 SV=1
A6111	GO:0007186(G protein-coupled receptor signaling pathway), GO:0019236(response to pheromone)	-	-	-	-	KOG4290[7291350 Predicted membrane protein	-	Transmembrane protein 145 OS=Xenopus laevis OX=8355 GN=tmem145 PE=2 SV=1
A6112	-	-	-	-	-	-	-	-
A6113	-	-	GO:0003677(DNA binding)	K10301 FBXO21; F-box protein 21	-	-	TKA47491.1 hypothetical protein B0A54_01863 [Friedmanniomyces endolithicus]	F-box only protein 21 OS=Mus musculus OX=10090 GN=Fbxo21 PE=1 SV=1
A6114	GO:0006508(proteolysis),GO:0016192(vesicle-mediated transport),GO:0070286(axonemal dynein complex assembly)	GO:0016020(membrane),GO:0005858(axonemal dynein complex)	GO:0004252(serine-type endopeptidase activity)	-	-	-	ORX43304.1 hypothetical protein BCR36DRAFT_586780 [Piromyces finnis]	Dynein regulatory complex subunit 2 OS=Chlamydomonas reinhardtii OX=3055 GN=DRC2 PE=1 SV=2
A6115	-	-	-	-	-	-	-	-
A6116	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A6117	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	-	CBQ72270.1 related to mfs-multidrug-resistance transporter [Sporisorium reilianum SRZ2]	Tetracycline resistance protein, class A OS=Escherichia coli OX=562 GN=tetA PE=3 SV=2
A6118	-	-	-	-	-	-	-	-
A6119	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG2816[Hs20533609 Predicted transporter ADD1 (major facilitator superfamily)	-	Tetracycline resistance protein, class A OS=Escherichia coli OX=562 GN=tetA PE=3 SV=2
A6120	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	Tetracycline resistance protein, class A OS=Escherichia coli OX=562 GN=tetA PE=3 SV=2
A6121	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG2615[CE04352 Permease of the major facilitator superfamily	KGQ13597.1 Tetracycline resistance protein, class A [Beauveria bassiana D1-5]	Tetracycline resistance protein, class A OS=Escherichia coli OX=562 GN=tetA PE=3 SV=2

A6122	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	Tetracycline resistance protein, class A OS=Escherichia coli OX=562 GN=tetA PE=3 SV=2
A6123	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG2615[CE04352 Permease of the major facilitator superfamily	XP_018148892.1 MFS transporter [Pochonia chlamydosporia 170]	Tetracycline resistance protein, class A OS=Escherichia coli OX=562 GN=tetA PE=3 SV=2
A6124	-	-	-	-	-	-	-	-
A6125	-	-	-	-	-	-	-	-
A6126	-	-	-	K16536 HOOK3; protein HOOK3	map04814 Motor proteins	-	-	-
A6127	-	-	-	-	-	-	-	-
A6128	-	-	-	-	-	-	-	-
A6129	-	-	-	-	-	-	-	-
A6130	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08856 STK16; serine/threonine kinase 16 [EC:2.7.11.1]	-	KOG2345[Hs17445015 Serine/threonine protein kinase/TGF-beta stimulated factor	ORX56050.1 kinase-like protein [Piromyces finnis]	Serine/threonine-protein kinase 16 OS=Rattus norvegicus OX=10116 GN=Stk16 PE=2 SV=2
A6131	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	K00643 E2.3.1.37, ALAS; 5-aminolevulinic acid synthase [EC:2.3.1.37]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG1359[7294669 Glycine C-acetyltransferase/2-amino-3-ketobutyrate-CoA ligase	KAG0033975.1 hypothetical protein BGZ81_006643 [Podila clonocystis]	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial OS=Homo sapiens OX=9606 GN=GCAT PE=1 SV=1
A6132	-	-	-	-	-	-	-	-
A6133	-	-	-	-	-	-	-	-
A6134	GO:0006265(DNA topological change)	-	GO:0003677(DNA binding),GO:0003916(DNA topoisomerase activity),GO:0003917(DNA topoisomerase type I (single strand cut, ATP-independent) activity)	K03165 TOP3; DNA topoisomerase III [EC:5.6.2.1]	map03440 Homologous recombination; map03460 Fanconi anemia pathway	KOG1956[At5g63920 DNA topoisomerase III alpha	RUP50984.1 hypothetical protein BC936DRAFT_136729 [Jimgerdmania flammicorona]	DNA topoisomerase 3-alpha OS=Arabidopsis thaliana OX=3702 GN=TOP3A PE=1 SV=1
A6135	-	-	GO:0005507(copper ion binding),GO:0016491(oxidoreductase activity)	K08100 E1.3.3.5; bilirubin oxidase [EC:1.3.3.5]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism	-	TPX65528.1 hypothetical protein CcCB567573_g08089 [Chytridiomycota confervae]	Multicopper oxidase CueO OS=Escherichia coli O157:H7 OX=83334 GN=cueO PE=3 SV=1
A6136	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	K12306 MSFD7, SLC49A4; MFS transporter, FLVCR family, MFS-domain-containing protein 7	-	KOG2563[Hs8923350 Permease of the major facilitator superfamily	KAG0337829.1 hypothetical protein BG004_007482 [Podila humilis]	Solute carrier family 49 member A3 OS=Xenopus tropicalis OX=8364 GN=slc49a3 PE=2 SV=2
A6137	-	-	-	-	-	-	-	-

A6138	-	-	-	-	-	-	-	-
A6139	GO:001626(iron-sulfur cluster assembly)	-	GO:0008199(ferric iron binding)	-	-	-	-	-
A6140	-	-	GO:0005515(protein binding)	-	-	KOG0619[Hs20550607 FOG: Leucine rich repeat	EPZ32441.1 hypothetical protein O9G_001343 [Rozella allomycis CSF55]	Dynein regulatory complex subunit 5 OS=Chlamydomonas reinhardtii OX=3055 GN=DRC5 PE=1 SV=1
A6141	-	-	-	-	-	-	-	-
A6142	GO:0007264(small GTPase mediated signal transduction),GO:0015031(protein transport)	-	GO:0005092(GDP-P-dissociation inhibitor activity),GO:0005515(protein binding),GO:0005093(Rab GDP-dissociation inhibitor activity)	-	-	-	XP_019022654.1 rab GDP-dissociation inhibitor [Saitoella complicata NRRL Y-17804]	Probable secretory pathway GDP dissociation inhibitor 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=gdi1 PE=3 SV=1
A6143	-	-	-	-	-	-	-	-
A6144	GO:0055085(transmembrane transport)	-	-	K15110 SLC25A21, ODC; solute carrier family 25 (mitochondrial 2-oxodicarboxylate transporter), member 21	-	KOG0754[YO R222w Mitochondrial oxodicarboxylate carrier protein	XP_019023559.1 mitochondrial carrier [Saitoella complicata NRRL Y-17804]	Mitochondrial citrate transporter D OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ctpD PE=3 SV=1
A6145	-	-	-	-	-	-	-	-
A6146	-	GO:0005743(mitochondrial inner membrane)	GO:0005509(calcium ion binding),GO:0043022(ribosome binding)	-	-	KOG1043[At1g65540 Ca2+-binding transmembrane protein LETM1/MRS7	KAG0005737.1 hypothetical protein BGZ79_002268 [Entomortierella chlamydispora]	Mitochondrial proton/calcium exchanger protein OS=Bos taurus OX=9913 GN=LETM1 PE=2 SV=1
A6147	GO:0009165(nucleotide biosynthetic process)	-	GO:0000287(magnesium ion binding),GO:0004749(ribose phosphate diphosphokinase activity)	K00948 PRPS, prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG1448[At2g35390 Ribose-phosphate pyrophosphokinase	KGQ02247.1 Ribose-phosphate pyrophosphokinase [Beauveria bassiana D1-5]	Ribose-phosphate pyrophosphokinase OS=Desulfotalea psychrophila (strain LSV54 / DSM 12343) OX=177439 GN=prs PE=3 SV=1
A6148	GO:0006886(intracellular protein transport),GO:0006606(protein import into nucleus)	-	GO:0031267(smooth muscle GTPase binding)	K14293 KPNB1, IPO1; importin subunit beta-1	map03013 Nucleocytoplasmic transport;map05207 Chemical carcinogenesis - receptor activation	KOG1241[At5g53480 Karyopherin (importin) beta 1	PWN46943.1 putative karyopherin beta-1 subunit [Violaceomyces palustris]	Importin subunit beta-1 OS=Arabidopsis thaliana OX=3702 GN=KPNB1 PE=1 SV=1

A6149	GO:0008299(isoprenoid biosynthetic process)	-	-	-	-	KOG0776 At3g29430 Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase	RDB27174.1 Geranylgeranyl diphosphate synthase [Hypsizygus marmoreus]	Short chain isoprenyl diphosphate synthase OS=Methanothermobacter marburgensis (strain ATCC BAA-927 / DSM 2133 / JCM 14651 / NBRC 100331 / OCM 82 / Marburg) OX=79929 GN=idsA PE=1 SV=3
A6150	-	-	-	-	-	-	KZM27564.1 hypothetical protein ST47_g1178 [Ascochyta rabiei]	Putative carbamate hydrolase RutD OS=Methylorubrum populi (strain ATCC BAA-705 / NCIMB 13946 / BJ001) OX=441620 GN=rutD PE=3 SV=1
A6151	-	-	-	-	-	-	KAF5345350.1 hypothetical protein D9758_008466 [Tetrapyrgos nigripes]	L-threonine 3-dehydrogenase OS=Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087) OX=3042615 GN=tdh PE=3 SV=1
A6152	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6153	-	-	-	-	-	-	-	-
A6154	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239 At5g27550 Kinesin (KAR3 subfamily)	ORX55269.1 kinesin-domain-containing protein [Piromyces finnis]	Kinesin-like protein KIN-14E OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14E PE=2 SV=1
A6155	GO:0006508(proteolysis)	-	GO:0004488(methylenetetrahydrofolate dehydrogenase (NADP+) activity),GO:0003824(catalytic activity),GO:0008236(serine-type peptidase activity)	K00288 MTHFD; methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase [EC:1.5.1.5 3.5.4.9 6.3.4.3]	map00670 One carbon pool by folate;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG0089 At4g00620 Methylenetetrahydrofolate dehydrogenase/methylene tetrahydrofolate cyclohydrolase	KAG1104644.1 hypothetical protein G6F42_017057 [Rhizopus oryzae]	Bifunctional protein FOLD 4, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=FOLD4 PE=1 SV=1
A6156	-	-	GO:0005515(protein binding)	-	-	-	KAF4494158.1 kinesin [Fusarium agapanthi]	-
A6157	-	-	GO:0003676(nucleic acid binding)	K14785 ESF2, ABT1; ESF2/ABP1 family protein	-	-	RKP08844.1 hypothetical protein THASP1DRAFT_15081 [Thamnocephalis spherospora]	Pre-rRNA-processing protein ESF2 OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=ESF2 PE=3 SV=1

A6158	GO:0006096(glycolytic process)	-	GO:0000287(magnesium ion binding),GO:0004743(pyruvate kinase activity),GO:0030955(potassium ion binding),GO:0003824(catalytic activity)	K00873 PK, pyk; pyruvate kinase [EC:2.7.1.40]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map05203 Viral carcinogenesis; map04930 Type II diabetes mellitus;map00620 Pyruvate metabolism;map05230 Central carbon metabolism in cancer;map01110 Metabolic	KOG2323 At5g63680 Pyruvate kinase	XP_01323703.2.1 pyruvate kinase [Mitosporidium daphniae]	Pyruvate kinase OS=Eimeria tenella OX=5802 GN=PYK PE=2 SV=1
A6159	GO:000629(lipid metabolic process)	-	-	-	-	-	-	-
A6160	GO:0000413(protein peptidyl-prolyl isomerization),GO:006457(protein folding)	-	GO:0005515(protein binding),GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K12736 PPWD1; peptidylprolyl isomerase domain and WD repeat-containing protein 1 [EC:5.2.1.8]	-	KOG0882 At3g44600 Cyclophilin-related peptidyl-prolyl cis-trans isomerase	KAG0238919.1 hypothetical protein BGW42_000080 [Actinomyces rella wolfii]	Peptidyl-prolyl cis-trans isomerase CYP71 OS=Arabidopsis thaliana OX=3702 GN=CYP71 PE=1 SV=1
A6161	-	-	GO:0003824(catalytic activity)	-	-	KOG2840 CE29003 Uncharacterized conserved protein with similarity to predicted ATPase of the PP-loop superfamily	RSH82897.1 hypothetical protein EHS25_005887 [Saitozyma podzolica]	tRNA-cytidine(32) 2-sulfurtransferase OS=Geobacter metallireducens (strain ATCC 53774 / DSM 7210 / GS-15) OX=269799 GN=ttcA PE=3 SV=2
A6162	-	-	-	-	-	-	-	-
A6163	-	-	GO:0016301(kinase activity)	-	-	KOG1116 7292647 Sphingosine kinase, involved in sphingolipid metabolism	ORX70183.1 hypothetical protein DL89DRAFT_257453 [Linderina pennisporea]	Sphingosine kinase 1 OS=Arabidopsis thaliana OX=3702 GN=SPHK1 PE=1 SV=1
A6164	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6165	GO:0030026(cellular manganese ion homeostasis)	-	GO:0005384(manganese ion transmembrane transporter activity)	K22736 VIT; vacuolar iron transporter family protein	-	KOG4473 At2g01770 Uncharacterized membrane protein	ORY96329.1 VIT family-domain-containing protein [Syncephalastrium racemosum]	Vacuolar iron transporter OS=Toxoplasma gondii (strain ATCC 50861 / VEG) OX=432359 GN=VIT PE=1 SV=1
A6166	-	-	GO:0008113(peptide-methionine (S)-S-oxide reductase activity)	K07304 msrA; peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]	-	KOG1635 At4g25130 Peptide methionine sulfoxide reductase	RKP10251.1 peptide methionine sulfoxide reductase MsrA [Thamnocephalus sphaerospora]	Peptide methionine sulfoxide reductase A2-1 OS=Oryza sativa subsp. japonica OX=39947 GN=MSRA2-1 PE=2 SV=2

A6167	GO:0006814(sodium ion transport), GO:0006885(regulation of pH), GO:0055085(transmembrane transport), GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0015385(sodium:proton antiporter activity), GO:0015299(solute:proton antiporter activity)	K12041 SLC9A6_7, NHE6_7; solute carrier family 9 (sodium/hydrogen exchanger), member 6/7	map04260 Cardiac muscle contraction	-	TPX60708.1 hypothetical protein PhCBS80983_g01591 [Powellomyces hirtus]	Uncharacterized Na(+)/H(+) antiporter C15A10.06 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC15A10.06 PE=1 SV=3
A6168	GO:0006189('de novo' IMP biosynthetic process), GO:0006164(purine nucleotide biosynthetic process)	-	GO:0005524(ATP binding), GO:0004638(phosphoribosylaminoimidazole carboxylase activity), GO:0004639(phosphoribosylaminoimidazole succinocarboxamide synthase activity), GO:0046872(metal ion binding)	K11808 ADE2; phosphoribosylaminoimidazole carboxylase [EC:4.1.1.21]	map00230 Purine metabolism; map01110 Biosynthesis of secondary metabolites; map01100 Metabolic pathways	KOG2835 At2g37690 Phosphoribosylaminoimidazole-succinocarboxamide synthase	ORY03395.1 phosphoribosylaminoimidazole carboxylase [Basidiobolus meristosporus CBS 931.73]	Phosphoribosylaminoimidazole carboxylase OS=Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) OX=214684 GN=ADE2 PE=3 SV=1
A6169	-	-	-	-	-	-	-	-
A6170	-	-	GO:0016787(hydrolase activity)	-	-	KOG3043 At2g32520 Predicted hydrolase related to diene lactone hydrolase	XP_016609915.1 hypothetical protein SPPG_03665 [Spizellomyces punctatus DAOM BR117]	-
A6171	-	-	-	K10866 RAD50; DNA repair protein RAD50 [EC:3.6.-.-]	map04218 Cellular senescence; map03450 Non-homologous end-joining; map03440 Homologous recombination	KOG0962 At2g31970 DNA repair protein RAD50, ABC-type ATPase/SMC superfamily	XP_016604561.1 rad50 [Spizellomyces punctatus DAOM BR117]	DNA repair protein RAD50 OS=Arabidopsis thaliana OX=3702 GN=RAD50 PE=1 SV=2
A6172	-	-	-	-	-	-	-	-
A6173	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	-	KAG2212356.1 hypothetical protein INT47_001717 [Mucor saturninus]	Probable tubulin--tyrosine ligase C12B10.04 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC12B10.04 PE=3 SV=1
A6174	-	-	GO:0005515(protein binding)	K18696 GDE1; glycerophosphodiester phosphodiesterase [EC:3.1.4.46]	map00564 Glycerophospholipid metabolism	KOG0509 7294202 Ankyrin repeat and DHHC-type Zn-finger domain containing proteins	KDQ13936.1 hypothetical protein BOTBODRAFT_81080, partial [Botryobasidium botryosum FD-172 SS1]	-
A6175	-	-	-	-	-	-	RUP49012.1 hypothetical protein BC936DRAFT_143479 [Jimgerdmania flammicorona]	-
A6176	-	-	-	-	-	-	-	-
A6177	-	-	-	-	-	-	-	-

A6178	-	-	-	-	-	KOG2365 Hs14042923 Uncharacterized membrane protein	-	-
A6179	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY43997.1 TPR-like protein, partial [Rhizoclostium globosum]	-
A6180	-	GO:0030014(CCR4-NOT complex)	GO:0003723(RNA binding),GO:0003676(nucleic acid binding),GO:0004842(ubiquitin-protein transferase activity)	K10643 CNOT4, NOT4, MOT2; CCR4-NOT transcription complex subunit 4 [EC:2.3.2.27]	map03018 RNA degradation	KOG2068 At3g45630.1 MOT2 transcription factor	RIA82336.1 RING/Ubox like zinc-binding domain-containing protein [Glomus cerebriforme]	CCR4-NOT transcription complex subunit 4 OS=Homo sapiens OX=9606 GN=CNOT4 PE=1 SV=3
A6181	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	-	K13754 SLC24A6, NCKX6; solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	-	KOG1307 Hs10190740 K+-dependent Ca2+/Na+ exchanger NCKX1 and related proteins	PPQ67479.1 hypothetical protein CVT25_006020 [Psilocybe cyanescens]	Sodium/potassium/calcium exchanger 3 (Fragment) OS=Rattus norvegicus OX=10116 GN=Slc24a3 PE=1 SV=1
A6182	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02870 RP-L12e, RPL12; large subunit ribosomal protein L12e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0886 CE17986_40S ribosomal protein S2	KAF9427639.1 60S ribosomal protein L12 [Entomortierella beljakovae]	Large ribosomal subunit protein uL11A OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rpl1201 PE=3 SV=1
A6183	-	-	GO:0016491(oxidoreductase activity),GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor)	K00128 ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]	map00410 beta-Alanine metabolism;map00981 Insect hormone biosynthesis;map00770 Pantothenate and CoA biosynthesis;map00340 Histidine metabolism;map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map00903 Limonene degradation;map01240 Biosynthesis of cofactors;map00330 Arginine and proline metabolism;map01120 Microbial metabolism in	KOG2450 At3g48170 Aldehyde dehydrogenase	KAF8625142.1 hypothetical protein AX17_006920 [Amanita inopinata Kibby_2008]	Aminoaldehyde dehydrogenase 2, peroxisomal OS=Pisum sativum OX=3888 GN=AMADH2 PE=1 SV=2
A6184	-	-	-	-	-	-	-	-
A6185	-	-	-	-	-	-	-	-
A6186	-	-	-	-	-	KOG2226 7303477 Proteins containing regions of low-complexity	XP_018297679.1 hypothetical protein PHYBLDRAFT_35188 [Phycomyces blakesleeanus NRRL 1555(-)]	Protein HID1 OS=Mus musculus OX=10090 GN=Hid1 PE=1 SV=1

A6187	-	-	GO:0008962(phosphatidylglycerophosphatase activity)	K01094 GEP4; phosphatidylglycerophosphatase GEP4 [EC:3.1.3.27]	map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG2961 At3g58830 Predicted hydrolase (HAD superfamily)	ORZ02691.1 mitochondria PGP phosphatase -domain-containing protein [Syncephalastrium racemosum]	Phosphatidylglycerophosphate phosphatase 1, chloroplastic/mitochondrial OS=Arabidopsis thaliana OX=3702 GN=PGPP1 PE=1 SV=1
A6188	-	-	-	-	-	KOG1929 Hs5902138 Nucleotide excision repair factor NEF2, RAD4/CUT5 component	XP_016608672.1 hypothetical protein SPPG_03760 [Spizellomyces punctatus DAOM BR117]	DNA topoisomerase 2-binding protein 1 OS=Mus musculus OX=10090 GN=Topbp1 PE=1 SV=2
A6189	GO:0005975(carbohydrate metabolic process)	-	-	-	-	-	XP_025597723.1 hypothetical protein FA09DRAFT_339442 [Tilletiopsis washingtonensis]	Uncharacterized glycosidase Rv0584 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv0584 PE=3 SV=1
A6190	-	-	-	-	-	KOG2490 7300336 Predicted membrane protein	RGB36651.1 eukaryotic membrane protein family-domain-containing protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Transmembrane anterior posterior transformation protein 1 homolog OS=Homo sapiens OX=9606 GN=TAPT1 PE=1 SV=1
A6191	-	-	-	K23643 LSM12; protein LSM12	map04711 Circadian rhythm - fly	KOG4401 At1g24050 Uncharacterized conserved protein	XP_026608900.1 Uncharacterized protein DSM5745_01039 [Aspergillus mulundensis]	-
A6192	-	-	-	-	-	-	-	-
A6193	-	-	-	K24083 ABHD13; abhydrolase domain-containing protein 13 [EC:3.-.-.-]	-	KOG4391 Hs14249592 Predicted alpha/beta hydrolase BEM46	XP_022462057.1 hypothetical protein KNAG_0A01220 [Kazachstania naganishii CBS 8797]	Multifunctional-autoprocessing repeats-in-toxin OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) OX=243277 GN=rtxA PE=1 SV=2
A6194	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin---tyrosine ligase [EC:6.3.2.25]	-	KOG2156 Hs7661970 Tubulin-tyrosine ligase-related protein	KNE60360.1 hypothetical protein AMAG_05755 [Allomyces macrogynus ATCC 38327]	Tubulin monoglutamylase TTL4 OS=Homo sapiens OX=9606 GN=TTL4 PE=1 SV=2

A6195	GO:0006468(protein phosphorylation),GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0006813(potassium ion transport)	GO:0016020(membrane)	GO:0005524(ATP binding),GO:0004672(protein kinase activity),GO:0005216(ion channel activity),GO:0005249(voltage-gated potassium channel activity),GO:0004707(MAP kinase activity)	K04371 ERK, MAPK1_3; mitogen-activated protein kinase 1/3 [EC:2.7.11.24]	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map04730 Long-term depression;map05135 Yersinia infection;map05132 Salmonella infection;map05133 Pertussis;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04350 TGF-beta signaling pathway;map04810 Regulation of	KOG0660 At4g01370 Mitogen-activated protein kinase	RIA82975.1 mitogen-activated protein kinase [Glomus cerebriiforme]	Extracellular signal-regulated kinase 1 OS=Dictyostelium discoideum OX=44689 GN=erkA PE=2 SV=2
A6196	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6197	GO:0016559(peroxisome fission)	GO:0005779(integral component of peroxisomal membrane)	-	-	-	-	-	-
A6198	GO:0006614(SRP-dependent cotranslational protein targeting to membrane)	GO:0048500(signal recognition particle)	GO:0008312(7S RNA binding)	-	-	KOG3198 7295253 Signal recognition particle, subunit Srp19	ORX74793.1 signal recognition particle, SRP19 subunit [Linderina pennisporea]	Signal recognition particle 19 kDa protein OS=Drosophila melanogaster OX=7227 GN=Srp19 PE=2 SV=2
A6199	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2157 7297165 Predicted tubulin-tyrosine ligase	KAG4093002.1 tubulin-tyrosine ligase family-domain-containing protein [Neocallimastix sp. JGI-2020a]	Tubulin tyrosine ligase 3 OS=Xenopus tropicalis OX=8364 GN=ttl3 PE=1 SV=1
A6200	-	-	-	K14544 UTP22, NOL6; U3 small nucleolar RNA-associated protein 22	map03008 Ribosome biogenesis in eukaryotes	KOG2054 Hs18644728 Nucleolar RNA-associated protein (NRAP)	KAF9097926.1 hypothetical protein BGX23_007632 [Mortierella sp. AD031]	Nucleolar protein 6 OS=Mus musculus OX=10090 GN=Nol6 PE=2 SV=2
A6201	-	GO:0016021(integral component of membrane)	GO:0000166(nucleotide binding),GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K14802 DRS2, ATP8A; phospholipid-transporting ATPase [EC:7.6.2.1]	-	-	OAV94616.1 phospholipid-transporting ATPase [Puccinia tritici Race 1]	Phospholipid-transporting ATPase C887.12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC887.12 PE=3 SV=1
A6202	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0404 At4g35460 Thioredoxin reductase	QEU62494.1 hypothetical protein KDRO_F04230 [Kluyveromyces fragilis]	Thioredoxin reductase glIT OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=glIT PE=1 SV=1

A6203	GO:0007005(mitochondrion organization)	GO:0005739(mitochondrion)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	-	-	KOG0742 At5g16930 AAA+ -type ATPase	KZV88919.1 AAA-domain-containing protein [Exidia glandulosa HHB12029]	ATPase family AAA domain-containing protein 3 OS=Xenopus tropicalis OX=8364 GN=atad3 PE=2 SV=1
A6204	-	-	-	-	-	-	-	-
A6205	-	-	-	-	-	-	-	-
A6206	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	K23665 FMQA; fumiquinazoline F synthetase [EC:6.3.2.-]	map01110 Biosynthesis of secondary metabolites;map00997 Biosynthesis of various other secondary metabolites;map01100 Metabolic pathways	KOG1543 At3g49340 Cysteine proteinase Cathepsin L	KFH62689.1 hypothetical protein MVEG_12081 [Podila verticillata NRRL 6337]	Cysteine endopeptidase RepA OS=Oryza sativa subsp. japonica OX=39947 GN=REPA PE=2 SV=1
A6207	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6208	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs4502553 Ca2+ /calmodulin-dependent protein kinase, EF-Hand protein superfamily	KAF0441368.1 Pkinase-domain-containing protein [Gigaspora margarita]	Calcium/calmodulin-dependent protein kinase type 1 OS=Homo sapiens OX=9606 GN=CAMK1 PE=1 SV=1
A6209	-	-	GO:0005515(protein binding)	K03671 trxA; thioredoxin 1	map05132 Salmonella infection;map05418 Fluid shear stress and atherosclerosis; map04621 NOD-like receptor signaling pathway;map05012 Parkinson disease	KOG0910 Hs21361403 Thioredoxin-like protein	KAG1265185.1 hypothetical protein G6F65_014225 [Rhizopus oryzae]	Thioredoxin OS=Chloroflexus aurantiacus (strain ATCC 29366 / DSM 635 / J-10-fl) OX=324602 GN=trxA PE=1 SV=3
A6210	-	-	-	-	-	KOG1937 Hs7661844 Uncharacterized conserved protein	-	Coiled-coil domain-containing protein 22 OS=Homo sapiens OX=9606 GN=CCDC22 PE=1 SV=1
A6211	-	-	-	-	-	-	-	-
A6212	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0725 At3g51680 Reductases with broad range of substrate specificities	KAF1798160.1 hypothetical protein FB192DRAFT_1397963 [Mucor lusitanicus]	3-oxoacyl-[acyl-carrier-protein] reductase FabG OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=fabG PE=3 SV=1
A6213	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1200 Hs15277342 Mitochondrial beta-ketoacyl-ACP reductase	KAF1798160.1 hypothetical protein FB192DRAFT_1397963 [Mucor lusitanicus]	3-oxoacyl-[acyl-carrier-protein] reductase FabG OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=fabG PE=3 SV=1

A6214	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0725 At3g26770 Reductases with broad range of substrate specificities	KAF1798160.1 hypothetical protein FB192DRAFT_1397963 [Mucor lusitanicus]	3-oxoacyl-[acyl-carrier-protein] reductase FabG OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=fabG PE=3 SV=1
A6215	-	-	GO:0003724(RNA helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K12812 DDX39B, UAP56, SUB2, ATP-dependent RNA helicase UAP56/SUB2 [EC:3.6.4.13]	map03040 Spliceosome;map03013 Nucleocytoplasmic transport;map03015 mRNA surveillance pathway	KOG0329 Hs4758112 ATP-dependent RNA helicase	ORX92692.1 putative ATP-dependent RNA helicase [Basidiobolus meristosporus CBS 931.73]	Spliceosome RNA helicase DDX39B OS=Canis lupus familiaris OX=9615 GN=DDX39B PE=3 SV=1
A6216	-	-	-	K18168 SDHAF2, SDH5; succinate dehydrogenase assembly factor 2	-	KOG3326 CE22606 Uncharacterized conserved protein	XP_021877692.1 Flavinator of succinate dehydrogenase-domain-containing protein, partial [Lobosporangium transversale]	Succinate dehydrogenase assembly factor 2, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=DDB_G0293946 PE=3 SV=1
A6217	-	-	GO:0050660(flavin adenine dinucleotide binding),GO:0016614(oxidoreductase activity, acting on CH-OH group of donors)	-	-	KOG1238 7293017 Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	XP_016611424.1 hypothetical protein SPPG_00874 [Spizellomyces punctatus DAOM BR117]	Choline oxidase OS=Arthrobacter globiformis OX=1665 GN=codA PE=1 SV=1
A6218	-	-	-	-	-	-	-	-
A6219	-	-	-	-	-	-	-	-
A6220	GO:0000398(mRNA splicing, via spliceosome)	-	GO:0030628(pre-mRNA 3'-splice site binding)	K12819 SLU7; pre-mRNA-processing factor SLU7	map03040 Spliceosome	KOG2560 Hs20127501 RNA splicing factor - Slu7p	KAF8313436.1 pre-mRNA-splicing factor SLU7 [Clavulina sp. PML_390]	Pre-mRNA-splicing factor SLU7 OS=Danio rerio OX=7955 GN=slu7 PE=2 SV=1
A6221	-	-	-	-	-	-	-	-
A6222	-	-	GO:0005515(protein binding)	-	-	KOG0510 Hs18571424 Ankyrin repeat protein	KAF9364086.1 hypothetical protein BGX34_002539 [Mortierella sp. NVP85]	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens OX=9606 GN=HECTD1 PE=1 SV=4
A6223	-	-	-	-	-	-	-	-
A6224	GO:0006508(proteolysis)	GO:0005576(extracellular region)	GO:0005515(protein binding)	-	-	-	-	-
A6225	-	-	-	-	-	-	-	-

A6226	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0157 At2g45510 Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	KAG0181675.1 hypothetical protein DFQ29_00751 [Apophysomyces sp. BC1021]	Cytochrome P450 704C1 OS=Pinus taeda OX=3352 GN=CYP704C1 PE=2 SV=1
A6227	-	-	-	-	-	-	-	-
A6228	GO:0006890(retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum)	-	-	-	-	-	KAG2183026.1 hypothetical protein INT44_006007 [Umbelopsis vinacea]	-
A6229	-	-	-	-	-	-	-	Protein ENHANCED DISEASE RESISTANCE 2-like OS=Arabidopsis
A6230	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG2325 Hs2041026 Predicted transporter/transmembrane protein	-	Major facilitator superfamily domain-containing protein 8 OS=Xenopus laevis OX=8355 GN=msd8 PE=2 SV=1
A6231	-	-	-	-	-	-	-	-
A6232	-	-	GO:0016491(oxidoreductase activity)	K04708 KDSR; 3-dehydrosphinganine reductase [EC:1.1.1.102]	map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG1205 Hs5031765 Predicted dehydrogenase	TPX70870.1 hypothetical protein SpCBS45565_g01533 [Spizellomyces sp. 'palustris']	Hydroxysteroid 11-beta-dehydrogenase 1-like protein OS=Xenopus tropicalis OX=8364 GN=hsd11b1l PE=2 SV=1
A6233	-	-	-	K05019 CLNS1A; chloride channel, nucleotide-sensitive, 1A	-	-	TRM64891.1 regulator of volume decrease after cellular swelling-domain-containing protein [Auriculariopsis ampla]	Methylosome subunit pICln OS=Rattus norvegicus OX=10116 GN=Clns1a PE=1 SV=1
A6234	-	-	-	-	-	-	-	-
A6235	GO:0001522(pseudouridine synthesis), GO:0042254(ribosome biogenesis)	-	-	K11128 GAR1, NOLA1; H/ACA ribonucleoprotein complex subunit 1	map03008 Ribosome biogenesis in eukaryotes	KOG3262 At5g18180 H/ACA small nucleolar RNP component GAR1	XP_007400414.1 uncharacterized protein PHACADRAFT_69662, partial [Phanerochaete carnosae HHB-10118-sp]	H/ACA ribonucleoprotein complex subunit GAR1 OS=Cryptococcus neoformans var. neoformans serotype D (strain B-3501A) OX=283643 GN=GAR1 PE=3 SV=1

A6236	GO:0009165(nucleotide biosynthetic process)	-	GO:0000287(magnesium ion binding),GO:0004749(ribose phosphate diphosphokinase activity)	K00948 PRPS, prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG1448 At2g35390 Ribose-phosphate pyrophosphokinase	KAG0194296.1 hypothetical protein DFQ28_000541 [Apophysomycetes sp. BC1034]	Ribose-phosphate pyrophosphokinase 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PRS1 PE=2 SV=2
A6237	GO:0045454(cell redox homeostasis)	-	GO:0016668(oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor),GO:0016491(oxidoreductase activity),GO:0050660(flavin adenine dinucleotide binding)	K00383 GSR, gor; glutathione reductase (NADPH) [EC:1.8.1.7]	map05415 Diabetic cardiomyopathy;map04918 Thyroid hormone synthesis;map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG0405 At3g24170 Pyridine nucleotide-disulphide oxidoreductase	RKP23799.1 glutathione reductase [Syncephalis pseudoplumigaleata]	Glutathione reductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=gor PE=3 SV=1
A6238	-	-	-	-	-	-	-	Regulator of G-protein signaling 16 OS=Mus musculus OX=10090
A6239	-	GO:0016021(integral component of membrane)	GO:0009922(fatty acid elongase activity)	K10246 ELO3, fatty acid elongase 3 [EC:2.3.1.199]	map01110 Biosynthesis of secondary metabolites;map00062 Fatty acid elongation;map01040 Biosynthesis of unsaturated fatty acids;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG3071 Hs8923312 Fatty acyl-CoA elongase/Polynunsaturated fatty acid specific elongation enzyme	KNE60123.1 hypothetical protein AMAG_05546 [Allomyces macrogynus ATCC 38327]	Fatty acid elongase 6 OS=Leishmania major OX=5664 GN=ELO6 PE=3 SV=1

A6240	-	-	GO:0009055(electron transfer activity),GO:0020037(heme binding)	K00413 CYC1, CYT1, petC; ubiquinol-cytochrome c reductase cytochrome c1 subunit	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04260 Cardiac muscle contraction;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map02020 Two-component	KOG3052 At3g27240 Cytochrome c1	KAG2187972.1 hypothetical protein INT44_00072.2 [Umbelopsis vinacea]	Cytochrome c1 1, heme protein, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=CYC1-1 PE=1 SV=1
A6241	GO:0030150(protein import into mitochondrial matrix),GO:0055085(transmembrane transport)	GO:0005741(mitochondrial outer membrane)	GO:0008320(protein transmembrane transporter activity)	K11518 TOM40; mitochondrial import receptor subunit TOM40	map05014 Amyotrophic lateral sclerosis;map05022 Pathways of neurodegeneration - multiple diseases	KOG3296 At3g20000 Translocase of outer mitochondrial membrane complex, subunit TOM40	ORX97654.1 hypothetical protein K493DRAFT_313989 [Basidiobolus meristosporus CBS 931.73]	Mitochondrial import receptor subunit TOM40-1 OS=Arabidopsis thaliana OX=3702 GN=TOM40-1 PE=1 SV=3
A6242	GO:0070476(rRNA (guanine-N7)-methylation)	-	GO:0016435(rRNA (guanine) methyltransferase activity)	K19306 BUD23; 18S rRNA (guanine1575-N7)-methyltransferase [EC:2.1.1.309]	-	KOG1541 YCR047c Predicted protein carboxyl methylase	KFH48725.1 putative methyltransferase-like protein [Acremonium chrysogenum ATCC 11550]	18S rRNA (guanine(1575)-N(7))-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BUD23 PE=1 SV=1
A6243	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	-	XP_003684981.1 hypothetical protein TPHA_0C03970 [Tetrapisispora phaffii CBS 4417]	Sec14 cytosolic factor OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=sec14 PE=4 SV=1
A6244	-	-	GO:0004497(monoxygenase activity),GO:0005507(copper ion binding),GO:0016715(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced ascorbate as one donor, and incorporation of one atom of oxygen),GO:0003824(catalytic activity)	-	-	KOG4293 At5g54830.2 Predicted membrane protein, contains DoH and Cytochrome b-561/ferric reductase transmembrane domains	KNE71661.1 hypothetical protein AMAG_16216 [Allomyces macrogynus ATCC 38327]	Temptin OS=Aplysia californica OX=6500 PE=1 SV=1

A6245	GO:0042073(intracellular transport)	GO:0030992(intracellular transport particle B)	-	-	-	KOG3437 Hs7706383 Anaphase-promoting complex (APC), subunit 10	TPX61718.1 hypothetical protein PhCBS80983.g00998 [Powellomyces hirtus]	Intraflagellar transport protein 25 homolog OS=Homo sapiens OX=9606 GN=IFT25 PE=1 SV=1
A6246	-	-	-	-	-	-	ORX56004.1 hypothetical protein BCR36DRAFT_410040 [Piromyces finnis]	Enkurin OS=Mus musculus OX=10090 GN=Enkur PE=1 SV=1
A6247	GO:0016036(cellular response to phosphate starvation)	-	-	K24195 XPRI, PHO1; xenotropic and polytropic retrovirus receptor 1	-	KOG1161 At5g20150 Protein involved in vacuolar polyphosphate accumulation, contains SPX domain	ORY08265.1 SPX-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	SPX domain-containing protein 1 OS=Arabidopsis thaliana OX=3702 GN=SPX1 PE=1 SV=2
A6248	-	-	-	-	-	-	-	-
A6249	-	-	-	-	-	-	-	Sporulation-control protein spo0M OS=Bacillus subtilis (strain 168)
A6250	-	-	-	-	-	-	-	-
A6251	GO:0043419(urea catabolic process), GO:0006807(nitrogen compound metabolic process)	GO:0035550(urease complex)	GO:0016151(nickel cation binding),GO:0016810(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds),GO:0009039(urease activity),GO:0016787(hydrolase activity)	K01427 URE; urease [EC:3.5.1.5]	map00230 Purine metabolism;map01120 Microbial metabolism in diverse environments;map00220 Arginine biosynthesis;map01100 Metabolic pathways;map00791 Atrazine degradation	-	KAF7727710.1 hypothetical protein EC973_007266 [Apophysomyces ossiformis]	Urease OS=Arabidopsis thaliana OX=3702 GN=URE PE=1 SV=1
A6252	-	-	GO:0016491(oxidoreductase activity)	K00474 TMLHE; trimethyllysine dioxygenase [EC:1.14.11.8]	map00310 Lysine degradation;map01100 Metabolic pathways	KOG3889 Hs8922625 Predicted gamma-butyrobetaine,2-oxoglutarate dioxygenase	TPX58507.1 trimethyllysine dioxygenase [Powellomyces hirtus]	Trimethyllysine dioxygenase, mitochondrial OS=Mus musculus OX=10090 GN=Tmlhe PE=1 SV=2
A6253	-	-	-	-	-	-	-	-
A6254	-	-	-	K18703 SUGCT; succinate--hydroxymethylglutarate CoA-transferase [EC:2.8.3.13]	-	KOG4299 At4g29940_1 PHD Zn-finger protein	QSZ29087.1 hypothetical protein DSL72_003597 [Monilinia vaccinii-corymbosii]	Homeobox protein HOX1A OS=Zea mays OX=4577 GN=HOX1A PE=2 SV=1

A6255	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07874 RAB1A; Ras-related protein Rab-1A	map05014 Amyotrophic lateral sclerosis;map04140 Autophagy - animal;map05134 Legionellosis;map05130 Pathogenic Escherichia coli infection;map05022 Pathways of neurodegeneration - multiple diseases	KOG0084[Hs4758988 GTPase Rab1/YPT1, small G protein superfamily, and related GTP-binding proteins	KAF2671906.1 ras family protein [Microthyrium microscopium]	Ras-related protein Rab-1A OS=Canis lupus familiaris OX=9615 GN=RAB1A PE=1 SV=3
A6256	-	-	-	K10575 UBE2G1, UBC7; ubiquitin-conjugating enzyme E2 G1 [EC:2.3.2.23]	map04141 Protein processing in endoplasmic reticulum;map04120 Ubiquitin mediated proteolysis;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease	-	RDX43694.1 ubiquitin-conjugating enzyme [Polyporus brumalis]	Ubiquitin-conjugating enzyme E2 15 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ubc15 PE=1 SV=1
A6257	GO:0006508(proteolysis)	GO:0005886(plasma membrane)	GO:0004252(serine-type endopeptidase activity),GO:0008233(peptidase activity)	-	-	-	KGQ06050.1 putative protease sohB [Beauveria bassiana D1-5]	Probable protease SohB OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=sohB PE=3 SV=1
A6258	-	-	-	K22696 EEF2KMT; protein-lysine N-methyltransferase EEF2KMT [EC:2.1.1.-]	-	KOG2793[At5g49560 Putative N2,N2-dimethylguanosine tRNA methyltransferase	KIO24686.1 hypothetical protein M407DRAFT_76657 [Tulasnella calospora MUT 4182]	EEF1A lysine methyltransferase 3 OS=Xenopus tropicalis OX=8364 GN=eef1akmt3 PE=2 SV=1
A6259	-	-	-	-	-	-	-	-
A6260	GO:0006431(methionyl-tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation)	-	GO:0004825(methionine-tRNA ligase activity),GO:000166(nucleotide binding),GO:0005524(ATP binding),GO:0004812(aminoacyl-tRNA ligase activity)	K01874 MARS, metG; methionyl-tRNA synthetase [EC:6.1.1.10]	map00970 Aminoacyl-tRNA biosynthesis;map01100 Metabolic pathways;map00450 Selenocompound metabolism	KOG0436[Hs14732427 Methionyl-tRNA synthetase	RKP10661.1 tRNA synthetase class I [Thamnocephalis sphaerospora]	Probable methionine--tRNA ligase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=mmetS PE=3 SV=1
A6261	GO:0006629(lipid metabolic process)	-	-	-	-	-	KAF4973990.1 hypothetical protein FZEAL_9058 [Fusarium zealandicum]	-

A6262	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A6263	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6264	GO:0006811(ion transport); GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015075(ion transmembrane transporter activity)	K23503 SFXN5; sideroflexin-5	-	KOG3767 Hs21389351 Sideroflexin	KAG2178979.1 hypothetical protein INT43_001828 [Umbelopsis isabellina]	Sideroflexin-5 OS=Homo sapiens OX=9606 GN=SFXN5 PE=1 SV=1
A6265	-	-	GO:0000049(tRNA binding)	-	-	-	-	Phenylalanine--tRNA ligase beta subunit OS=Hydrogenovibrio crunogenus (strain DSM 25203 / XCL-2) OX=317025 GN=pheT PE=3 SV=1
A6266	-	-	-	-	-	-	-	-
A6267	-	-	-	-	-	KOG1030 Hs21362014 Predicted Ca2+-dependent phospholipid-binding protein	XP_018656749.1 hypothetical protein TGAM01_v210697 [Trichoderma gamsii]	Multiple C2 and transmembrane domain-containing protein 1 OS=Mus musculus OX=10090 GN=Mctp1 PE=1 SV=1
A6268	-	-	GO:0016746(acyltransferase activity)	K08765 E2.3.1.21;carnitine O-palmitoyltransferase 1 [EC:2.3.1.21]	map00071 Fatty acid degradation	KOG3716 Hs4758050 Carnitine O-acyltransferase CPT1	XP_016608398.1 hypothetical protein SPPG_04683 [Spizellomyces punctatus DAOM BR117]	carnitine O-palmitoyltransferase OS=Sus scrofa OX=9823 GN=CPT1A PE=2 SV=1
A6269	-	GO:0016021(integral component of membrane)	GO:0009922(fatty acid elongase activity)	-	-	KOG3071 At3g06470 Fatty acyl-CoA elongase/Polynunsaturated fatty acid specific elongation enzyme	TPX66262.1 very-long-chain 3-oxoacyl-CoA synthase [Spizellomyces sp. 'palustris']	Putative fatty acid elongase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC1B2.03c PE=1 SV=1
A6270	-	-	-	-	-	-	-	-
A6271	GO:0006659(phosphatidylserine biosynthetic process)	-	GO:0106245(L-serine-phosphatidylethanolamine phosphatidyltransferase activity)	-	-	KOG2735 At1g15110 Phosphatidylserine synthase	GES76742.1 phosphatidylserine synthase 2 [Rhizophagus clarus]	CDP-diacylglycerol--serine O-phosphatidyltransferase 1 OS=Arabidopsis thaliana OX=3702 GN=PSS1 PE=1 SV=1
A6272	GO:0007076(mitotic chromosome condensation)	GO:0000796(condensin complex)	GO:0005515(protein binding)	-	-	KOG2025 Hs21359945 Chromosome condensation complex subunit G	XP_021882980.1 nuclear condensing complex subunit [Lobosporangium transversale]	Condensin complex subunit 3 OS=Homo sapiens OX=9606 GN=NCAPG PE=1 SV=1

A6273	GO:0007165(signal transduction)	GO:0000159(protein phosphatase type 2A complex)	GO:0019888(protein phosphatase regulator activity)	K11584 PPP2R5; serine/threonine-protein phosphatase 2A regulatory subunit B'	map04071 Sphingolipid signaling pathway;map04728 Dopaminergic synapse;map04660 T cell receptor signaling pathway;map04261 Adrenergic signaling in cardiomyocytes;map03015 mRNA surveillance pathway;map04152 AMPK signaling pathway;map04151 PI3K-Akt signaling pathway;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04110 Cell cycle;map05165	KOG2085 At3g26020 Serine/threonine protein phosphatase 2A, regulatory subunit	ORZ33572.1 phosphatase 2A regulatory B subunit-domain-containing protein [Catenaria anguillulae PL171]	Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' eta isoform OS=Arabidopsis thaliana OX=3702 GN=B'ETA PE=1 SV=1
A6274	-	-	-	-	-	-	-	-
A6275	-	GO:0016021(integral component of membrane)	GO:0009922(fatty acid elongase activity)	K10246 ELO3; fatty acid elongase 3 [EC:2.3.1.199]	map01110 Biosynthesis of secondary metabolites;map00062 Fatty acid elongation;map01040 Biosynthesis of unsaturated fatty acids;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG3072 Hs13129088 Long chain fatty acid elongase	KAF7752320.1 hypothetical protein DSO57_016465 [Entomophthora muscae]	Very long chain fatty acid elongase 6 OS=Mus musculus OX=10090 GN=Elov6 PE=1 SV=1
A6276	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015297(antiporter activity);GO:0042910(xenobiotic transmembrane transporter activity)	-	-	-	-	-
A6277	-	-	GO:0016746(acyltransferase activity)	K13507 GAT; glycerol-3-phosphate O-acyltransferase / dihydroxyacetone phosphate acyltransferase [EC:2.3.1.15 2.3.1.42]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	-	KAG2180129.1 hypothetical protein INT43_003917 [Umbelopsis isabellina]	Glycerol-3-phosphate O-acyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCT1 PE=1 SV=3
A6278	GO:0045292(mRNA cis splicing, via spliceosome)	-	GO:0005515(protein binding)	-	-	KOG0155 At3g19840 Transcription factor CA150	-	-

A6279	-	GO:0016021(integral component of membrane)	-	-	-	KOG3195 7295016 Uncharacterized membrane protein NP0008/CGI-148	TPX64920.1 hypothetical protein SpCBS45565-g05561 [Spizellomyces sp. 'palustris']	Uncharacterized Golgi apparatus membrane protein-like protein 2 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0286703 PE=3 SV=1
A6280	GO:0030150(protein import into mitochondrial matrix)	GO:0005744(TIM23 mitochondrial import inner membrane translocase complex)	-	K17805 PAM16, TIM16; mitochondrial import inner membrane translocase subunit TIM16	-	-	RPA77639.1 protein transporter [Ascobolus immersus RN42]	Mitochondrial import inner membrane translocase subunit tim16 OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=un-4 PE=3 SV=1
A6281	-	-	-	-	-	-	-	-
A6282	-	-	-	-	-	-	-	-
A6283	GO:0006508(proteolysis)	GO:0004222(metalloendopeptidase activity),GO:0008237(metalloproteinase activity)	-	-	-	KOG3607 Hs20539131 Meltrins, fertilins and related Zn-dependent metalloproteinases of the ADAMs family	RWA06055.1 hypothetical protein EKO27_g9054 [Xylaria grammica]	Zinc metalloproteinase-disintegrin-like cobrin OS=Naja kaouthia OX=8649 PE=2 SV=1
A6284	-	-	-	-	-	KOG0048 At5g02320 Transcription factor, Myb superfamily	ORE15519.1 hypothetical protein BGV71DRAFT_159810, partial [Rhizopus microsporus]	Transcription factor MYB3R-5 OS=Arabidopsis thaliana OX=3702 GN=MYB3R5 PE=2 SV=1
A6285	-	-	-	-	-	-	-	Protein ENHANCED DISEASE RESISTANCE 2-like OS=Arabidopsis
A6286	-	-	-	-	-	-	-	-
A6287	-	-	-	-	-	-	RHZ75234.1 hypothetical protein Glove_216g152 [Diversispora epigaea]	-
A6288	-	-	-	K20238 E2.1.1.317; sphingolipid C9-methyltransferase [EC:2.1.1.317]	-	-	ORY45462.1 S-adenosyl-L-methionine-dependent methyltransferase [Rhizoclostium globosum]	Sphingolipid C9-methyltransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MTS1 PE=1 SV=1
A6289	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6290	-	-	-	-	-	-	-	-
A6291	-	-	-	K06685 MOB1, Mats; MOB kinase activator 1	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04392 Hippo signaling pathway - multiple species;map04111 Cell cycle - yeast	KOG0440 Hs8922671 Cell cycle-associated protein Mob1-1	KXS17134.1 mps one binder kinase activator-like 1 protein [Gonapodya prolifera JEL478]	MOB kinase activator 1A OS=Homo sapiens OX=9606 GN=MOB1A PE=1 SV=4

A6292	GO:0055085(transmembrane transport),GO:0006857(oligopeptide transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K03305 TC,POT; proton-dependent oligopeptide transporter, POT family	-	KOG1237 At2g02040 H+/oligopeptide symporter	ORY01223.1 PTR2-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Protein NRT1/ PTR FAMILY 8.3 OS=Arabidopsis thaliana OX=3702 GN=NPF8.3 PE=1 SV=1
A6293	GO:0055085(transmembrane transport),GO:0006857(oligopeptide transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K03305 TC,POT; proton-dependent oligopeptide transporter, POT family	-	KOG1237 At2g02020 H+/oligopeptide symporter	ORY01223.1 PTR2-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Protein NRT1/ PTR FAMILY 8.4 OS=Arabidopsis thaliana OX=3702 GN=NPF8.4 PE=2 SV=2
A6294	-	-	-	-	-	KOG1470 At4g08690 Phosphatidylinositol transfer protein PDR16 and related proteins	TPX57783.1 hypothetical protein PhCBS80983g03595 [Powellomyces hirtus]	Protein real-time OS=Anopheles gambiae OX=7165 GN=retm PE=3 SV=4
A6295	GO:0006508(proteolysis)	-	GO:0008236(serine-type peptidase activity),GO:0004252(serine-type endopeptidase activity)	K01280 TPP2; tripeptidyl-peptidase II [EC:3.4.14.10]	-	KOG1114 Hs4507657 Tripeptidyl peptidase II	KAF9152876.1 tripeptidyl-peptidase II Tpp2 [Linnemanna schmuckeri]	Tripeptidyl-peptidase 2 OS=Homo sapiens OX=9606 GN=TPP2 PE=1 SV=4
A6296	GO:0043039(tRNA aminoacylation),GO:0006468(protein phosphorylation),GO:0006419(alanyl-tRNA aminoacylation)	-	GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity),GO:0003676(nucleic acid binding),GO:0004813(alanine-tRNA ligase activity),GO:0000166(nucleotide binding)	-	-	KOG2105 Hs13376886.2 Predicted metal-dependent hydrolase, contains AlaS domain	ORX94571.1 alanyl-tRNA synthetase domain-containing protein 1 [Basidiobolus meristosporus CBS 931.73]	Alanyl-tRNA editing protein Aarsd1 OS=Mus musculus OX=10090 GN=Aarsd1 PE=1 SV=2
A6297	-	-	-	-	-	-	-	-
A6298	GO:0006012(galactose metabolic process)	-	GO:0003978(UDP-glucose 4-epimerase activity)	K01784 galE, GALE; UDP-glucose 4-epimerase [EC:5.1.3.2]	map01250 Biosynthesis of nucleotide sugars;map00541 O-Antigen nucleotide sugar biosynthesis;map00052 Galactose metabolism;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG1371 At4g10960 UDP-glucose 4-epimerase/UDP-sulfoquinovose synthase	KAG2180319.1 hypothetical protein INT44_003321 [Umbelopsis vinacea]	UDP-glucose 4-epimerase OS=Bacillus subtilis (strain 168) OX=224308 GN=galE PE=3 SV=1

A6299	GO:0009086(methionine biosynthetic process)	-	GO:0008168(methyltransferase activity),GO:0008270(zinc ion binding)	-	-	KOG1579 At3g25900 Homocysteine S-methyltransferase	KAF9740891.1 hypothetical protein PMIN01_00430 [Paraphaeosphaeria minitans]	Homocysteine S-methyltransferase 1 OS=Zea mays OX=4577 GN=HMT-1 PE=2 SV=1
A6300	GO:0034220(ion transmembrane transport),GO:0006811(ion transport)	GO:0016021(integral component of membrane)	GO:0004888(transmembrane signaling receptor activity),GO:0005216(ion channel activity),GO:0005230(extracellular ligand-gated ion channel activity)	-	-	-	-	-
A6301	GO:0006811(ion transport),GO:0034220(ion transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005230(extracellular ligand-gated ion channel activity),GO:0004888(transmembrane signaling receptor activity),GO:0005216(ion channel activity)	-	-	-	-	-
A6302	-	-	-	-	-	-	-	-
A6303	-	-	-	-	-	-	-	-
A6304	-	-	-	-	-	-	-	-
A6305	-	-	-	-	-	-	-	-
A6306	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG1286 At3g03720 Amino acid transporters	PJF16920.1 Amino acid permease [Paramicrosporidium saccamoebae]	Methylthioribose transporter OS=Bacillus subtilis (strain 168) OX=224308 GN=mtrA PE=3 SV=1
A6307	GO:0007017(microtubule-based process)	GO:0030286(dynein complex),GO:0005875(microtubule associated complex)	-	K10418 DYNLL; dynein light chain LC8-type	map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3430 7290522 Dynein light chain type 1	KNE69126.1 dynein light chain 2, cytoplasmic [Allomyces macrogynus ATCC 38327]	Dynein light chain 2, cytoplasmic OS=Drosophila melanogaster OX=7227 GN=CdLc2 PE=1 SV=1
A6308	-	-	-	-	-	-	-	-
A6309	-	-	-	-	-	-	XP_007735297.1 hypothetical protein A1O3_06993 [Capronia epimyces CBS 606.96]	-
A6310	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02925 RP-L3e, RPL3; large subunit ribosomal protein L3e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0746 At1g61580 60S ribosomal protein L3 and related proteins	XP_006675627.1 uncharacterized protein BATDEDRAFT_29178 [Batrachochytrium dendrobatidis JAM81]	Large ribosomal subunit protein uL3 OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=rpl3 PE=1 SV=2

A6311	-	-	-	-	-	-	KNE66443.1 PAS domain S-box protein [Allomyces macrogynus ATCC 38327]	Tiny macrocysts protein C OS=Dictyostelium discoideum OX=44689 GN=tmcC PE=2 SV=1
A6312	GO:0006144(purine nucleobase metabolic process)	-	GO:0033971(hydroxyisourate hydrolase activity)	K07127 uraH, pucM, huiH; 5-hydroxyisourate hydrolase [EC:3.5.2.17]	map00230 Purine metabolism:map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	-	ORX66681.1 hydroxyisourate hydrolase [Basidiobolus meristosporus CBS 931.73]	5-hydroxyisourate hydrolase OS=Mus musculus OX=10090 GN=Urah PE=1 SV=1
A6313	-	-	GO:0003824(catalytic activity),GO:0008270(zinc ion binding),GO:0016787(hydrolase activity)	K15441 TAD2, ADAT2; tRNA-specific adenosine deaminase 2 [EC:3.5.4.-]	-	KOG1018[CE01371 Cytosine deaminase FCY1 and related enzymes	SHO76970.1 Similar to S.cerevisiae protein FCY1 (Cytosine deaminase) [Malassezia sympodialis ATCC 42132]	Guanine deaminase OS=Bacillus subtilis (strain 168) OX=224308 GN=guaD PE=1 SV=1
A6314	-	-	GO:0016491(oxidoreductase activity)	K06912 tfdA; alpha-ketoglutarate-dependent 2,4-dichlorophenoxycetate dioxygenase [EC:1.14.11.-]	map01120 Microbial metabolism in diverse environments;map01220 Degradation of aromatic compounds;map00361 Chlorocyclohexane and chlorobenzene degradation	-	XP_013284005.1 hypothetical protein Z517_06812 [Fonsecaea pedrosoi CBS 271.37]	(3R)-3-[(carboxymethyl)amino]fatty acid oxygenase/decarboxylase OS=Streptomyces coeruleorubidus OX=116188 GN=ScoE PE=1 SV=2
A6315	-	-	GO:0004620(phospholipase activity)	-	-	KOG3774[Hs13376232 Uncharacterized conserved protein Lama	-	Phospholipase B-like 1 OS=Bos taurus OX=9913 GN=PLBD1 PE=1 SV=2
A6316	-	-	-	-	-	KOG1895[Hs4759196 mRNA cleavage and polyadenylation factor II complex, subunit PTA1	KIY64034.1 hypothetical protein CYLTODRAFT_402460 [Cylindrobacterium torrendii FP15055 ss-10]	Symplekin OS=Homo sapiens OX=9606 GN=SYMPK PE=1 SV=2
A6317	-	-	-	-	-	KOG3869[Hs8923271 Uncharacterized conserved protein	RKP25955.1 Pre-mRNA splicing factor-domain-containing protein, partial [Syncephalis pseudoplumi galeata]	Pre-mRNA-splicing factor CWC25 homolog OS=Mus musculus OX=10090 GN=Cwc25 PE=2 SV=2
A6318	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity),GO:0030170(pyridoxal phosphate binding)	-	-	KOG0634[7294778 Aromatic amino acid aminotransferase and related proteins	ORY48137.1 PLP-dependent transferase [Rhizoclostium globosum]	Aromatic-amino-acid aminotransferase 1 OS=Thermococcus litoralis (strain ATCC 51850 / DSM 5473 / JCM 8560 / NS-C) OX=523849 GN=OCC_04335 PE=1 SV=1

A6319	-	-	GO:0005515(protein binding),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	-	-	-	-	-
A6320	-	-	-	-	-	-	-	-
A6321	-	-	GO:0004377(GDP-Man:Man3GlcNAc2-PP-Dol alpha-1,2-mannosyltransferase activity),GO:0016757(glycosyltransferase activity)	K03844 ALG11; alpha-1,2-mannosyltransferase [EC:2.4.1.131]	map00513 Various types of N-glycan biosynthesis;map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG1387 7296469 Glycosyltransferase	RCH83696.1 asparagine-linked glycosylation protein [Rhizopus stolonifer]	GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase OS=Xenopus laevis OX=8355 GN=alg11 PE=2 SV=2
A6322	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0005794(Golgi apparatus),GO:0030121(AP-1 adaptor complex),GO:0030117(membrane coat)	-	K12391 AP1G1; AP-1 complex subunit gamma-1	map04142 Lysosome;map05170 Human immunodeficiency virus 1 infection	KOG1062 Hs18104998 Vesicle coat complex AP-1, gamma subunit	PKC75369.1 gamma-adaptin [Rhizophagus irregularis]	AP-1 complex subunit gamma-1 OS=Homo sapiens OX=9606 GN=AP1G1 PE=1 SV=5
A6323	GO:0080162(intracellular auxin transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	-	K24139 PILS, ECM3; auxin efflux carrier family protein	-	KOG2722 At1g71090 Predicted membrane protein	CDO71081.1 hypothetical protein BN946_scf184844.g85 [Trametes cinnabarina]	Protein PIN-LIKES 2 OS=Arabidopsis thaliana OX=3702 GN=PILS2 PE=2 SV=1
A6324	GO:0055085(transmembrane transport),GO:0080162(intracellular auxin transport)	GO:0016021(integral component of membrane)	-	-	-	-	-	Uncharacterized transporter C5D6.04 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC5D6.04 PE=3 SV=1
A6325	-	-	GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	K18757 LARP1; la-related protein 1	-	KOG2591 7292338 c-Mpl binding protein, contains La domain	KAF7731724.1 La- protein 4 [Apophysomyces ossiformis]	La-related protein Larp4B OS=Drosophila melanogaster OX=7227 GN=Larp4B PE=1 SV=2
A6326	-	-	GO:0003824(catalytic activity)	K22966 HINT4; sulfate adenyltransferase (ADP) / adenylsulfatase [EC:2.7.7.5 3.6.2.1]	map01120 Microbial metabolism in diverse environments;map00920 Sulfur metabolism;map01100 Metabolic pathways	KOG4359 Hs21359982 Protein kinase C inhibitor-like protein	CDS01783.1 hypothetical protein [Sporisorium scitamineum]	Bifunctional adenosine 5'-phosphosulfate phosphorylase/adenylsulfatase HINT4 OS=Arabidopsis thaliana OX=3702 GN=HINT4 PE=1 SV=1

A6327	GO:0006813(potassium ion transport),GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0008076(voltage-gated potassium channel complex),GO:0016020(membrane)	GO:0005249(voltage-gated potassium channel activity),GO:0005515(protein binding),GO:0005216(ion channel activity),GO:0005509(calcium ion binding)	-	-	KOG3713 7295767 Voltage-gated K+ channel KCNB/KCNC	RCH86603.1 hypothetical protein CU097_007399 [Rhizopus azgyosporus]	Potassium voltage-gated channel subfamily V member 1 OS=Mesocricetus auratus OX=10036 GN=KCNV1 PE=2 SV=1
A6328	GO:0016567(protein ubiquitination),GO:000398(mRNA splicing via spliceosome),GO:0006281(DNA repair)	GO:0000974(Prp19 complex)	GO:0005515(protein binding),GO:0004842(ubiquitin-protein transferase activity),GO:0006163(ubiquitin protein ligase activity)	K10599 PRPF19, PRP19; pre-mRNA-processing factor 19 [EC:2.3.2.27]	map03040 Spliceosome;map04120 Ubiquitin mediated proteolysis	KOG0289 At1g04510 mRNA splicing factor	KAG0049338.1 hypothetical protein BGZ83_005877 [Gryganskiella cystojenkini]	Pre-mRNA-processing factor 19 homolog 1 OS=Arabidopsis thaliana OX=3702 GN=PRP19A PE=1 SV=1
A6329	-	-	-	-	-	-	-	cGMP-dependent 3',5'-cGMP phosphodiesterase A OS=Dictyostelium discoideum OX=44689 GN=pdeD PE=1 SV=1
A6330	-	-	-	-	-	-	-	Uncharacterized protein Rv1290c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv1290c PE=1 SV=1
A6331	-	-	GO:0005227(calcium activated cation channel activity)	-	-	-	-	-
A6332	-	-	-	-	-	-	-	Meiosis-specific nuclear structural protein 1 OS=Mus musculus
A6333	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K24512 VWA8; von Willebrand factor A domain-containing protein 8	-	KOG1808 Hs2053093 AAA ATPase containing von Willebrand factor type A (vWA) domain	KAG0209285.1 von Willebrand factor A domain-containing protein 8 [Mortierella sp. NVP41]	von Willebrand factor A domain-containing protein 8 OS=Danio rerio OX=7955 GN=sidkey-181.1 PE=3 SV=1
A6334	-	-	GO:0016787(hydrolase activity)	-	-	-	-	-
A6335	GO:0006468(protein phosphorylation)	-	GO:0005509(calcium ion binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At2g38910 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	CEP17314.1 hypothetical protein [Parasitella parasitica]	Calcium-dependent protein kinase 20 OS=Arabidopsis thaliana OX=3702 GN=CPK20 PE=3 SV=1
A6336	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A6337	-	-	GO:0016491(oxidoreductase activity)	K22745 AIFM2; apoptosis-inducing factor 2	map04115 p53 signaling pathway	KOG1336 Hs14318424 Monodehydroascorbate/ferredoxin reductase	KAF0485057.1 FAD/NADP-binding domain-containing protein [Gigaspora margarita]	Apoptosis-inducing factor homolog B OS=Dictyostelium discoideum OX=44689 GN=aifB PE=3 SV=1
A6338	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10405 KIFC1; kinesin family member C1	map04814 Motor proteins	KOG0239 At5g27550 Kinesin (KAR3 subfamily)	RKO98564.1 hypothetical protein CXG81DRAFT_6275, partial [Caulochytrium protostelioides]	Kinesin-like protein KIN-14R OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14R PE=2 SV=1

A6339	-	-	-	-	-	-	KAG1260773.1 hypothetical protein G6F65_015002 [Rhizopus oryzae]	-
A6340	GO:0060285(cilium-dependent cell motility),GO:0007018(microtubule-based movement)	GO:0005858(axonemal dynein complex),GO:0030286(dynein complex)	GO:0003777(microtubule motor activity),GO:0016887(ATP hydrolysis activity),GO:0005524(ATP binding),GO:0008569(minus-end-directed microtubule motor activity)	-	-	KOG3595 7293415 Dyneins, heavy chain	EPZ34616.1 Dynein heavy chain-2 domain-containing protein [Rozealla allomyces CSF55]	Dynein axonemal heavy chain 6 OS=Homo sapiens OX=9606 GN=DNAH6 PE=1 SV=3
A6341	-	-	-	-	-	-	PVU92037.1 hypothetical protein BB559_003864 [Furculomyces boomerangs]	Uncharacterized NAD(P)H oxidoreductase YcaK OS=Escherichia coli (strain K12) OX=83333 GN=ycaK PE=3 SV=2
A6342	-	-	-	-	-	-	-	-
A6343	GO:0042147(retrograde transport, endosome to Golgi)	GO:0000938(GARP complex)	-	K17600 VPS54; vacuolar protein sorting-associated protein 54	-	KOG2115 Hs7705397 Vacuolar sorting protein VPS45	XP_019025272.1 Vps54-domain-containing protein [Saitoella complicata NRRL Y-17804]	Vacuolar protein sorting-associated protein 54, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=VPS54 PE=1 SV=1
A6344	-	-	-	-	-	-	-	-
A6345	-	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	KOG0940 7293969 Ubiquitin protein ligase RSP5/NEDD4	KIJ34627.1 hypothetical protein M422DRAFT_34977 [Sphaerobolus stellatus SS14]	E3 ubiquitin-protein ligase Nedd-4 OS=Drosophila melanogaster OX=7227 GN=Nedd4 PE=1 SV=2
A6346	-	-	GO:0004518(nuclease activity)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518 YO R033c 5'-3' exonuclease	KAF8515840.1 PIN domain-like protein [Hysterangium stoloniferum]	Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EXO1 PE=1 SV=2
A6347	-	-	GO:0016746(acyltransferase activity),GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups)	K08764 SCP2, SCPX; sterol carrier protein 2 [EC:2.3.1.176]	map03320 PPAR signaling pathway;map04146 Peroxisome;map00120 Primary bile acid biosynthesis;map01040 Biosynthesis of unsaturated fatty acids;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG1406 Hs19923233_1 Peroxisomal 3-ketoacyl-CoA-thiolase P-44/SCP2	XP_016609586.1 hypothetical protein SPPG_03348 [Spizellomyces punctatus DAOM BR117]	Uncharacterized protein MTH_793 OS=Methanothermobacter thermautotrophicus (strain ATCC 29096 / DSM 1053 / JCM 10044 / NBRC 100330 / Delta H) OX=187420 GN=MTH_793 PE=4 SV=1

A6348	-	-	GO:0036402(proteasome-activating activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K03066 PSMC5, RPT6; 26S proteasome regulatory subunit T6	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG0728 At5g19990 26S proteasome regulatory complex, ATPase RPT6	RIA96918.1 26S proteasome regulatory complex [Glomus cerebriforme]	26S proteasome regulatory subunit 8 homolog A OS=Arabidopsis thaliana OX=3702 GN=RPT6A PE=1 SV=1
A6349	-	-	GO:0005515(protein binding)	-	-	KOG4351 CE26798 Uncharacterized conserved protein	-	-
A6350	-	-	GO:0005515(protein binding)	-	-	KOG0379 At1g51550 Kelch repeat-containing proteins	ORZ36182.1 hypothetical protein BCR44DRAFT_1432952 [Catenaria anguillulae PL171]	F-box/kelch-repeat protein At1g51550 OS=Arabidopsis thaliana OX=3702 GN=At1g51550 PE=2 SV=1
A6351	-	-	GO:0035091(phosphatidylinositol binding),GO:0008289(lipid binding)	-	-	-	-	-
A6352	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08867 WNK, PRKWNK; WNK lysine deficient protein kinase [EC:2.7.11.1]	-	KOG0584 Hs22055520 Serine/threonine protein kinase	RKP36208.1 kinase-like domain-containing protein, partial [Dimargaris cristalligena]	Probable serine/threonine-protein kinase WNK9 OS=Arabidopsis thaliana OX=3702 GN=WNK9 PE=2 SV=1
A6353	-	-	GO:0005515(protein binding),GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4502237 Sulfatase	KAF5718424.1 arylsulfatase A [Fusarium mundagurra]	N-acetyl/galactosamine-6-O-sulfatase OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / JCM 5827 / CCUG 10774 / NCTC 10582 / VPI-5482 / E50) OX=226186 GN=BT_3333 PE=1 SV=1
A6354	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4502237 Sulfatase	XP_018994174.1 hypothetical protein L202_03335 [Cryptococcus amyloletus CBS 6039]	N-acetyl/galactosamine-6-O-sulfatase OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / JCM 5827 / CCUG 10774 / NCTC 10582 / VPI-5482 / E50) OX=226186 GN=BT_3333 PE=1 SV=1
A6355	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0606 At5g62310 Microtubule-associated serine/threonine kinase and related proteins	ORX91060.1 serine/threonine protein kinase 15 [Basidiobolus meristosporus CBS 931.73]	Probable serine/threonine protein kinase IRE OS=Arabidopsis thaliana OX=3702 GN=IRE PE=2 SV=1
A6356	-	-	-	-	-	-	-	-

A6357	GO:0016226(iron-sulfur cluster assembly)	-	GO:0005524(ATP binding);GO:0051536(iron-sulfur cluster binding)	K03593 mrp, NUBPL; ATP-binding protein involved in chromosome partitioning	-	KOG3022 At3g24430 Predicted ATPase, nucleotide-binding	KAG1716369.1 hypothetical protein ID866_785 [Astraeus odoratus]	Fe-S cluster assembly factor HCF101, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=HCF101 PE=1 SV=1
A6358	GO:0006098(pentose-phosphate shunt);GO:0005975(carbohydrate metabolic process);GO:0006468(protein phosphorylation)	GO:0005737(cytoplasm)	GO:0004801(transaldolase activity);GO:0004672(protein kinase activity)	K00616 TALDO1, talB, talA; transaldolase [EC:2.2.1.2]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG2772 YLR354c Transaldolase	KAG0358521.1 Transaldolase [Gamsiella multivariata]	Transaldolase OS=Shewanella loihica (strain ATCC BAA-1088 / PV-4) OX=323850 GN=tal PE=3 SV=1
A6359	-	-	GO:0003676(nucleic acid binding);GO:0005524(ATP binding)	K14810 DDX56, DBP9; ATP-dependent RNA helicase DDX56/DBP9 [EC:3.6.4.13]	-	KOG0346 Hs9506931 RNA helicase	ORX85165.1 DEAD-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Probable ATP-dependent RNA helicase DDX56 OS=Mus musculus OX=10090 GN=Ddx56 PE=1 SV=1
A6360	GO:0006529(asparagine biosynthetic process)	-	GO:0004066(asparagine synthase (glutamine-hydrolyzing) activity)	-	-	KOG0571 CE04760 Asparagine synthase (glutamine-hydrolyzing)	ORX93894.1 adenine nucleotide alpha hydrolase-like protein [Basidiobolus meristosporus CBS 931.73]	-
A6361	-	-	GO:0005509(calcium ion binding)	-	-	KOG0043 Hs8922436 Uncharacterized conserved protein, contains DM10 domain	TPX38933.1 hypothetical protein SeLEV6574_g07509 [Synchytrium endobioticum]	EF-hand domain-containing protein 1 OS=Mus musculus OX=10090 GN=Efhc1 PE=1 SV=1
A6362	GO:0006596(polyamine biosynthetic process)	-	GO:0003824(catalytic activity)	K01581 E4.1.1.17, ODC1, speC, speF; ornithine decarboxylase [EC:4.1.1.17]	map01110 Biosynthesis of secondary metabolites;map00330 Arginine and proline metabolism;map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG0622 Hs4505489 Ornithine decarboxylase	OAJ42143.1 hypothetical protein BDEG_25642 [Batrachochytrium dendrobatidis JEL423]	Ornithine decarboxylase OS=Bos taurus OX=9913 GN=ODC1 PE=2 SV=1

A6363	GO:0006413(translational initiation)	-	GO:0003743(translation initiation factor activity),GO:0003723(RNA binding)	K15025 EIF1AD; probable RNA-binding protein EIF1AD	-	KOG2925 Hs1.4150102 Predicted translation initiation factor related to eIF-1A	KAG0226562.1 putative RNA-binding protein eif1ad [Mortierella sp. GBA43]	Probable RNA-binding protein EIF1AD OS=Danio rerio OX=7955 GN=eif1ad PE=2 SV=1
A6364	GO:0006904(vesicle docking involved in exocytosis),GO:0090522(vesicle tethering involved in exocytosis)	GO:0000145(exocyst)	-	K06111 EXOC4, SEC8; exocyst complex component 4	map05132 Salmonella infection	KOG3691 Hs1.4719408 Exocyst complex subunit Sec8	KAF1995102.1 hypothetical protein P154DRAFT_526585 [Amniculicola lignicola CBS 123094]	Exocyst complex component 4 OS=Homo sapiens OX=9606 GN=EXOC4 PE=1 SV=1
A6365	-	-	-	-	-	KOG1611 At4g20760 Predicted short chain-type dehydrogenase	ORX92445.1 cell-cell signaling protein csgA-like protein [Basidiobolus meristosporus CBS 931.73]	1-hydroxy-2-glutathionyl-2-methyl-3-butene dehydrogenase OS=Rhodococcus sp. (strain AD45) OX=103808 GN=isoH PE=1 SV=1
A6366	-	-	-	-	-	-	-	-
A6367	-	-	-	-	-	-	-	-
A6368	-	-	-	-	-	-	-	-
A6369	-	-	-	-	-	KOG2177 Hs1.0864061 Predicted E3 ubiquitin ligase	KAF9901032.1 RING finger and WD repeat domain-containing protein 2 [Linnemannia zychae]	E3 ubiquitin-protein ligase TRIM39 OS=Mus musculus OX=10090 GN=Trim39 PE=2 SV=1
A6370	-	-	-	-	-	-	-	-
A6371	GO:0006120(mitochondrial electron transport, NADH to ubiquinone)	-	-	K03965 NDUF89; NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 9	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG3466 At4g34700 NADH:ubiquinone oxidoreductase, NDUF89/B22 subunit	RIB05242.1 hypothetical protein C2G38_2253925 [Gigaspora rosea]	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Arabidopsis thaliana OX=3702 GN=CIB22 PE=1 SV=1
A6372	-	-	-	K14780 DHX37, DHR1; ATP-dependent RNA helicase DHX37/DHR1 [EC:3.6.4.13]	-	KOG0926 At1g33390 DEAH-box RNA helicase	ORX49992.1 P-loop containing nucleoside triphosphate hydrolase protein [Piromyces finnis]	Probable ATP-dependent RNA helicase DHX37 OS=Homo sapiens OX=9606 GN=DHX37 PE=1 SV=1

A6373	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	KZO94955.1 hypothetical protein CALVIDRAFT_565074 [Calocera viscosa TUFC12733]	-
A6374	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07943 ARL2; ADP-ribosylation factor-like protein 2	-	KOG0074 Hs4757774 GTP-binding ADP-ribosylation factor-like protein ARL3	KAG4096289.1 ADP-ribosylation factor-like 3-like protein [Neocallimastix sp. JGI-2020a]	ADP-ribosylation factor-like protein 3 OS=Taeniopygia guttata OX=59729 GN=ARL3 PE=2 SV=1
A6375	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K14780 DHX37, DHR1; ATP-dependent RNA helicase DHX37/DHR1 [EC:3.6.4.13]	-	KOG0926 YMR128w DEAH-box RNA helicase	KAF2710668.1 DEAH-box RNA helicase-like protein [Pleomassaria siparia CBS 279.74]	Probable ATP-dependent RNA helicase DHR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ECM16 PE=1 SV=1
A6376	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:0030126(COPI vesicle coat),GO:0030117(membrane coat)	GO:0005198(structural molecule activity)	K17267 COPG; coatamer subunit gamma	-	KOG1078 At4g34450 Vesicle coat complex COPI, gamma subunit	XP_016612960.1 hypothetical protein SPPG_00612 [Spizellomyces punctatus DAOM BR117]	Coatamer subunit gamma-2 OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0201100 PE=2 SV=1
A6377	-	-	-	-	-	-	-	-
A6378	-	-	-	-	-	-	KXS16165.1 NAD(P)-binding protein [Gonapodya prolifera JEL478]	Uncharacterized protein R665 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_R665 PE=4 SV=1
A6379	-	-	GO:0005515(protein binding)	-	-	KOG0504 At5g13530.3 FOG: Ankyrin repeat	KIH88116.1 hypothetical protein SPBR_06333 [Sporothrix brasiliensis 5110]	E3 ubiquitin-protein ligase KEG OS=Arabidopsis thaliana OX=3702 GN=KEG PE=1 SV=2
A6380	-	-	GO:0003824(catalytic activity)	K01115 PLD1_2; phospholipase D1/2 [EC:3.1.4.4]	map04024 cAMP signaling pathway;map04144 Endocytosis;map01110 Biosynthesis of secondary metabolites;map04071 Sphingolipid signaling pathway;map04072 Phospholipase D signaling pathway;map04912 GnRH signaling pathway;map04724 Glutamatergic synapse;map05212 Pancreatic cancer;map04666 Fc gamma R-mediated phagocytosis;map04014 Ras signaling	KOG1329 At4g11840 Phospholipase D1	RHZ82653.1 hypothetical protein Glove_106g15 [Diversispora epigaea]	Phospholipase D gamma 3 OS=Arabidopsis thaliana OX=3702 GN=PLDGAMMA3 PE=1 SV=1

A6381	GO:0000398(mRNA splicing, via spliceosome)	-	-	-	-	KOG2989 7302982 Uncharacterized conserved protein	RKP08954.1 CWC16 protein, partial [Thamnocephalis sphaerospora]	Splicing factor YJU2 OS=Mus musculus OX=10090 GN=Yju2 PE=1 SV=1
A6382	-	-	GO:0016746(acyltransferase activity)	K13509 AGPAT1_2; lysophosphatidate acyltransferase [EC:2.3.1.51]	map01110 Biosynthesis of secondary metabolites;map04072 Phospholipase D signaling pathway;map04975 Fat digestion and absorption;map00564 Glycerophospholipid metabolism;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	KOG2848 At4g30580 1-acyl-sn-glycerol-3-phosphate acyltransferase	KAG1445960.1 hypothetical protein G6F57_017445 [Rhizopus oryzae]	1-acyl-sn-glycerol-3-phosphate acyltransferase OS=Cocos nucifera OX=13894 PE=1 SV=1
A6383	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	-	KXS12596.1 Formate/nitrite transporter [Gonapodya prolifera JEL478]	Probable formate transporter OS=Methanothermobacter thermotrophicus OX=145262 GN=fdhC PE=3 SV=1
A6384	GO:0006470(protein dephosphorylation), GO:0046907(intracellular transport)	-	GO:0004722(protein serine/threonine phosphatase activity)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 At2g20050 Serine/threonine protein phosphatase	ORX39486.1 hypothetical protein BCR36DRAFT_588259 [Piromyces finnis]	Probable protein phosphatase 2C 35 OS=Arabidopsis thaliana OX=3702 GN=At3g06270 PE=2 SV=1
A6385	-	-	-	-	-	-	-	-
A6386	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0534 Hs19923907 NADH-cytochrome b-5 reductase	QDS71967.1 hypothetical protein FKW77_001211 [Venturia effusa]	Oxidoreductase NAD-binding domain-containing protein 1 OS=Danio rerio OX=7955 GN=oxnad1 PE=2 SV=1
A6387	-	-	GO:0005515(protein binding)	-	-	-	XP_031873546.1 Uncharacterized protein BP5553_00869 [Venustampulla echinocandica]	-
A6388	-	-	GO:0005509(calcium ion binding)	-	-	KOG2562 At5g28850 Protein phosphatase 2 regulatory subunit	EPZ31957.1 EF-Hand 1, calcium-binding site domain-containing protein [Rozella allomyces CSF55]	Serine/threonine protein phosphatase 2A regulatory subunit B''beta OS=Arabidopsis thaliana OX=3702 GN=B''BETA PE=1 SV=1
A6389	-	-	GO:0005515(protein binding)	K10752 RBBP4, HAT2, CAF1, MIS16; histone-binding protein RBBP4	map04218 Cellular senescence;map03082 ATP-dependent chromatin remodeling;map03083 Polycomb repressive complex	KOG0264 At2g19520 Nucleosome remodeling factor, subunit CAF1/NURF55/MSI1	PVF98607.1 WD40 repeat-like protein [Serendipita vermifera 'subsp. bescii']	WD-40 repeat-containing protein MSI4 OS=Arabidopsis thaliana OX=3702 GN=MSI4 PE=1 SV=3

A6390	-	-	-	-	-	-	-	-
A6391	-	-	-	-	-	-	-	-
A6392	-	-	-	-	-	-	-	Crystallin J1A OS=Tripedalia cystophora OX=6141 PE=1 SV=1
A6393	GO:0007010(cytoskeleton organization),GO:0046856(phosphatidylinositol dephosphorylation)	-	GO:0003779(acting binding),GO:0016791(phosphatase activity)	K20279 SYNJ; synaptojanin [EC:3.1.3.36]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0565[Hs4755142_1 Inositol polyphosphate 5-phosphatase and related proteins	XP_036665287.1 uncharacterized protein CPAR2_806640 [Candida parapsilosis]	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 OS=Xenopus laevis OX=8355 GN=inpp5d PE=2 SV=1
A6394	-	-	-	-	-	-	-	-
A6395	GO:0006352(DNA-templated transcription, initiation)	GO:0005669(transcription factor TFIIID complex),GO:0000124(SAGA complex),GO:0046695(SLIK (SAGA-like) complex)	GO:0046982(protein heterodimerization activity)	K03126 TAF12; transcription initiation factor TFIIID subunit 12	map03022 Basal transcription factors	KOG1142[Hs5032153 Transcription initiation factor TFIIID, subunit TAF12 (also component of histone acetyltransferase SAGA)	OZJ04287.1 hypothetical protein BZG36_02588 [Bifiguratus adelaidae]	Transcription initiation factor TFIIID subunit 12 OS=Homo sapiens OX=9606 GN=TAF12 PE=1 SV=1
A6396	GO:0006364(rRNA processing)	-	GO:0005515(protein binding)	K14553 UTP18; U3 small nucleolar RNA-associated protein 18	map03008 Ribosome biogenesis in eukaryotes	KOG2055[At5g14050 WD40 repeat protein	SAM09424.1 hypothetical protein [Absidia glauca]	U3 small nucleolar RNA-associated protein 18 homolog OS=Arabidopsis thaliana OX=3702 GN=At5g14050 PE=1 SV=1
A6397	-	-	-	-	-	KOG1420[7301192 Ca2+-activated K+ channel Slowpoke, alpha subunit	ORY38190.1 hypothetical protein BCR33DRAFT_720897 [Rhizoclostium globosum]	Calcium-activated potassium channel subunit alpha-1a OS=Danio rerio OX=7955 GN=kcnma1a PE=1 SV=1
A6398	-	-	-	K17279 REEP5_6; receptor expression-enhancing protein 5/6	-	KOG1725[CE24624 Protein involved in membrane traffic (YOP1/TB2/D P1/HVA22 family)	ORX75924.1 hypothetical protein BCR32DRAFT_224687 [Anaeromyces robustus]	Receptor expression-enhancing protein 6 OS=Danio rerio OX=7955 GN=reep6 PE=2 SV=1
A6399	-	-	-	-	-	KOG1208[At4g09750 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	ORX92807.1 dehydrogenase/reductase SDR family member 12 [Basidiobolus meristosporus CBS 931.73]	Dehydrogenase/reductase SDR family member 12 OS=Bos taurus OX=9913 GN=DHRS12 PE=2 SV=1
A6400	-	-	-	K10583 UBE2S, E2EPF; ubiquitin-conjugating enzyme E2 S [EC:2.3.2.23]	map04120 Ubiquitin mediated proteolysis	KOG0423[At5g05080 Ubiquitin-protein ligase	RKP35783.1 ubiquitin-conjugating enzyme E2s, partial [Dimargaris cristalligena]	Ubiquitin-conjugating enzyme E2 S OS=Drosophila ananassae OX=7217 GN=GF21161 PE=3 SV=1
A6401	-	-	GO:0005515(protein binding)	-	-	KOG1113[CE28749 cAMP-dependent protein kinase types I and II, regulatory subunit	-	-
A6402	-	-	-	-	-	-	-	Glycosyltransferase-like domain-containing protein 1-like OS=Drosophila melanogaster OX=7227 GN=CG15914 PE=2 SV=1

A6403	-	-	-	-	-	-	-	-
A6404	-	-	-	-	-	KOG0714[CE03412 Molecular chaperone (DnaJ superfamily)]	KIO34690.1 hypothetical protein M407DRAFT_63797 [Tulasnella calospora MUT 4182]	Chaperone protein DnaJ OS=Thermotoga petrophila (strain ATCC BAA-488 / DSM 13995 / JCM 10881 / RKU-1) OX=390874 GN=dnaJ PE=3 SV=1
A6405	-	-	-	-	-	KOG0769[At3g05290 Predicted mitochondrial carrier protein]	KAF1806412.1 mitochondrial carrier domain-containing protein [Mucor lusitanicus]	Peroxisomal adenine nucleotide carrier 1 OS=Glycine max OX=3847 GN=PNC1 PE=2 SV=1
A6406	-	-	GO:0003779(actin binding)	K05759 PFN; profilin	map05014 Amyotrophic lateral sclerosis;map05132 Salmonella infection;map05131 Shigellosis;map04810 Regulation of actin cytoskeleton;map04013 MAPK signaling pathway - fly;map04015 Rap1 signaling pathway	KOG1755[CE21418 Profilin]	KAF7732369.1 profilin, required for normal timing of actin polymerization in response to thermal stress [Apophysomyces ossiformis]	Profilin OS=Tetrahymena pyriformis OX=5908 PE=2 SV=1
A6407	-	-	GO:0005515(protein binding)	K20347 TMED2, EMP24; p24 family protein beta-1	-	KOG1692[CE14448 Putative cargo transport protein EMP24 (p24 protein family)]	XP_025381488.1 supernatant protein factor, C-terminal domain-containing protein [Acaromyces ingoldii]	Suppressor/enhancer of lin-12 protein 9 OS=Caenorhabditis elegans OX=6239 GN=scl-9 PE=1 SV=1
A6408	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6409	GO:0018216(peptidyl-arginine methylation)	-	GO:0016274(protein-arginine N-methyltransferase activity)	K05931 CARM1, PRMT4; type I protein arginine methyltransferase [EC:2.1.1.319]	map01522 Endocrine resistance	KOG1500[7299276 Protein arginine N-methyltransferase CARM1]	PJF19130.1 Protein arginine N-methyltransferase domain-containing protein [Paramicrosporidium saccamoebae]	Histone-arginine methyltransferase CARMER OS=Drosophila yakuba OX=7245 GN=Art4 PE=3 SV=1
A6410	-	-	GO:0016491(oxidoreductase activity),GO:0010181(FMN binding)	K00327 POR; NADPH-ferrihemoprotein reductase [EC:1.6.2.4]	-	KOG1158[At4g30210 NADP/FAD dependent oxidoreductase]	GBC06951.1 hypothetical protein RclHR1_0716009 [Rhizophagus clarus]	NADPH--cytochrome P450 reductase OS=Sorghum bicolor OX=4558 GN=CPR PE=1 SV=1
A6411	-	-	-	-	-	-	-	-
A6412	-	-	GO:0005509(calcium ion binding),GO:0016746(acyltransferase activity),GO:0008374(O-acyltransferase activity)	K03857 PIGA, GPI3; phosphatidylinositol N-acetylglucosaminyltransferase subunit A [EC:2.4.1.198]	map00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis;map01100 Metabolic pathways	KOG4666[Hs8923446 Predicted phosphate acyltransferase, contains PIsC domain]	ORY54440.1 hypothetical protein LY90DRAFT_702364 [Neocallimastix californiae]	Lysophospholipid acyltransferase LPEAT2 OS=Arabidopsis thaliana OX=3702 GN=LPEAT2 PE=1 SV=1

A6413	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A6414	GO:0009435(NAD biosynthetic process), GO:0006807(nitrogen compound metabolic process)	GO:0005737(cytoplasm)	GO:0003952(NAD+ synthase (glutamine-hydrolyzing) activity), GO:0004359(glutaminase activity), GO:0005524(ATP binding)	-	-	KOG2303 YHR074w Predicted NAD synthase, contains CN hydrolase domain	XP_003032688.1 uncharacterized protein SCHCODRAFT_67311 [Schizophyllum commune H4-8]	Glutamine-dependent NAD(+) synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QNS1 PE=1 SV=1
A6415	-	-	-	-	-	-	XP_016604420.1 hypothetical protein SPPG_08279 [Spizellomyces punctatus DAOM BR117]	-
A6416	-	-	-	-	-	-	-	-
A6417	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003723(RNA binding), GO:0003735(structural constituent of ribosome)	-	-	KOG1686 At4g30930.2 Mitochondrial/chloroplast ribosomal L21 protein	-	Large ribosomal subunit protein bL21m OS=Dictyostelium discoideum OX=44689 GN=mrpl21 PE=3 SV=1
A6418	-	-	-	-	-	-	-	-
A6419	-	-	GO:0005515(protein binding)	-	-	KOG4648 7291754 Uncharacterized conserved protein, contains LRR repeats	RHZ47464.1 hypothetical protein Glove_579g16 [Diversispora epigaea]	Sperm-associated antigen 1 OS=Mus musculus OX=10090 GN=Spag1 PE=1 SV=1
A6420	-	GO:0016021(integral component of membrane)	GO:0032977(membrane insertase activity)	K03217 yidC, spoIIJ, OXA1, ccfA; YidC/Oxa1 family membrane protein insertase	map03070 Bacterial secretion system; map03060 Protein export; map02024 Quorum sensing	KOG1239 At5g62050 Inner membrane protein translocase involved in respiratory chain assembly	KAG0378891.1 Mitochondrial inner membrane protein oxa1l [Mortierella sp. AD032]	Mitochondrial inner membrane protein OXA1 OS=Arabidopsis thaliana OX=3702 GN=OXA1 PE=2 SV=2
A6421	GO:0007018(microtubule-based movement)	GO:0005868(cytoplasmic dynein complex)	-	K10416 DYNC1LI1, DNCL1; dynein cytoplasmic 1 light intermediate chain	map04145 Phagosome; map05132 Salmonella infection; map04814 Motor proteins; map04962 Vasopressin-regulated water reabsorption	KOG3905 Hs14732533 Dynein light intermediate chain	KAF8838376.1 DLIC-domain-containing protein [Paxillus ammoniavirescens]	Cytoplasmic dynein 1 light intermediate chain 1 OS=Rattus norvegicus OX=10116 GN=Dync1li1 PE=1 SV=1
A6422	-	-	-	-	-	-	-	-
A6423	-	-	-	K14827 IPI1, TEX10; pre-rRNA-processing protein IPI1	map03083 Polycomb repressive complex	KOG2149 At5g06350 Uncharacterized conserved protein	OMJ07780.1 Testis-expressed sequence 10 protein-like protein [Smittium culicis]	Testis-expressed protein 10 OS=Homo sapiens OX=9606 GN=TEX10 PE=1 SV=2
A6424	-	GO:0016020(membrane)	-	-	-	-	-	Mycolic acid-containing lipids exporter MmpL11 OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=mmpL11 PE=3 SV=1
A6425	GO:0006887(exocytosis)	GO:0005737(cytoplasm)	-	-	-	-	-	-

A6426	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K07901 RAB8A, MEL; Ras-related protein Rab-8A	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map04140 Autophagy - animal;map04972 Pancreatic secretion;map04530 Tight junction;map05022 Pathways of neurodegeneration - multiple diseases;map04152 AMPK signaling pathway	KOG0078 At5g03520 GTP-binding protein SEC4, small G protein superfamily, and related Ras family GTP-binding proteins	KAG0265887.1 GTP-binding protein [Mortierella polycephala]	Ras-related protein RABE1d OS=Arabidopsis thaliana OX=3702 GN=RABE1D PE=1 SV=1
A6427	-	-	-	-	-	-	-	-
A6428	-	-	-	-	-	-	-	-
A6429	-	-	-	-	-	KOG1775 At5g48870 U6 snRNA-associated Sm-like protein	KAF8898844.1 Sm-like ribonucleoprotein [Infundibulicybe gibba]	Sm-like protein LSM5 OS=Arabidopsis thaliana OX=3702 GN=LSM5 PE=1 SV=1
A6430	-	-	-	-	-	KOG0048 Hs13641706_1 Transcription factor, Myb superfamily	KAF8940947.1 DNA binding transcription coactivator transcription factor [Dissophora ornata]	Transcriptional activator Myb OS=Xenopus laevis OX=8355 GN=myb PE=2 SV=1
A6431	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K15173 TTF2; transcription termination factor 2 [EC:5.6.2.-]	map04918 Thyroid hormone synthesis	-	ORX98845.1 hypothetical protein K493DRAFT_257864 [Basidiobolus meristosporus CBS 931.73]	Uncharacterized ATP-dependent helicase C582.10c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC582.10c PE=1 SV=1
A6432	-	-	-	-	-	-	-	-
A6433	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG4280 Hs4758646 Kinesin-like protein	RKO97108.1 kinesin-domain-containing protein, partial [Caulochytrium protostelioides]	Kinesin-like protein KIF3B OS=Homo sapiens OX=9606 GN=KIF3B PE=1 SV=1
A6434	-	-	-	-	-	-	-	-

A6435	GO:0002084(protein depalmitoylation)	-	GO:0008474(palmitoyl-(protein) hydrolase activity),GO:0098599(palmitoyl hydrolase activity)	K01074 PPT; palmitoyl-protein thioesterase [EC:3.1.2.22]	map04142 Lysosome;map00062 Fatty acid elongation;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG2541 At3g60340 Palmitoyl protein thioesterase	RHZ86097.1 hypothetical protein Glove_54g14 [Diversispora epigaea]	Palmitoyl-protein thioesterase 1 OS=Caenorhabditis elegans OX=6239 GN=ppt-1 PE=2 SV=2
A6436	-	-	GO:0005515(protein binding)	-	-	KOG1474 At1g73150 Transcription initiation factor TFIIID, subunit BDF1 and related bromodomai n proteins	KAG1505017.1 hypothetical protein G6F52_012127 [Rhizopus deleamar]	Transcription factor GTE3, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=GTE3 PE=1 SV=1
A6437	-	-	-	-	-	-	KAG1545916.1 hypothetical protein G6F50_013700 [Rhizopus deleamar]	Conjugated bile acid hydrolase OS=Clostridium perfringens (strain 13 / Type A) OX=195102 GN=cbh PE=1 SV=3
A6438	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K20872 NEK2; serine/threonine-protein kinase Nek2 [EC:2.7.11.1]	-	KOG0591 Hs19424132 NIMA (never in mitosis)-related G2-specific serine/threonine protein kinase	KXS16504.1 kinase-like protein [Gonapodya prolifera JEL478]	Serine/threonine-protein kinase Nek7 OS=Homo sapiens OX=9606 GN=NEK7 PE=1 SV=1
A6439	GO:0035556(intracellular signal transduction),GO:006629(lipid metabolic process),GO:0007165(signal transduction)	-	GO:0005509(calcium ion binding),GO:0004435(phosphatidylinositol phospholipase C activity),GO:0008081(phosphoric diester hydrolase activity)	K05857 PLCD; phosphatidylinositol phospholipase C, delta [EC:3.1.4.11]	map04020 Calcium signaling pathway;map05131 Shigellosis;map04933 AGE-RAGE signaling pathway in diabetic complications;map04070 Phosphatidylinositol signaling system;map04919 Thyroid hormone signaling pathway;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0169 Hs14249340 Phosphoinositide-specific phospholipase C	ORX89142.1 PLC-like phosphodiesterase [Basidiobolus meristosporus CBS 931.73]	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1 OS=Homo sapiens OX=9606 GN=PLCH1 PE=1 SV=1
A6440	GO:0030488(tRNA methylation)	GO:0031515(tRNA (m1A) methyltransferase complex)	-	K03256 TRM6, GCD10; tRNA (adenine58-N1)-methyltransferase non-catalytic subunit	-	KOG1416 Hs19923475 tRNA(1-methyladenosine) methyltransferase, subunit GCD10	KAF5323374.1 hypothetical protein D9611_005599 [Coprinellus angulatus]	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Bos taurus OX=9913 GN=TRMT6 PE=2 SV=1
A6441	-	-	-	K13989 DERL2_3; Derlin-2/3	map04141 Protein processing in endoplasmic reticulum	KOG0858 Hs13236516 Predicted membrane protein	KAF9927448.1 Derlin 1 [Linnemannia zychae]	Derlin-2.2 OS=Zea mays OX=4577 GN=DER2.2 PE=2 SV=1

A6442	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A6443	GO:0009443(pyridoxal 5'-phosphate salvage)	-	GO:0008478(pyridoxal kinase activity)	K00868 pdxK; pdxY; pyridoxine kinase [EC:2.7.1.35]	map01240 Biosynthesis of cofactors:map00750 Vitamin B6 metabolism:map01100 Metabolic pathways	KOG2599 At5g37850 Pyridoxal/pyridoxine/pyridoxamine kinase	RKP39688.1 Ribokinase-like protein [Dimargaris cristalligena]	Pyridoxal kinase OS=Arabidopsis thaliana OX=3702 GN=PK PE=1 SV=2
A6444	-	-	-	-	-	KOG1201 CE13054 Hydroxysteroid 17-beta dehydrogenase 11	KAE8225422.1 hypothetical protein CF319_g1828 [Tilletia indica]	Protein dhs-3 OS=Caenorhabditis elegans OX=6239 GN=dhs-3 PE=1 SV=1
A6445	-	-	-	-	-	KOG2316 Hs18087809 Predicted ATPase (PP-loop superfamily)	ORZ05425.1 protein E01A2.5 [Absidia repens]	Diphthine--ammonia ligase OS=Danio rerio OX=7955 GN=dph6 PE=2 SV=1
A6446	-	-	GO:0016791(phosphatase activity)	-	-	KOG1572 At1g05000 Predicted protein tyrosine phosphatase	XP_025172989.1 protein-tyrosine phosphatase [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Probable tyrosine-protein phosphatase DG1060 OS=Dictyostelium discoideum OX=44689 GN=DG1060 PE=3 SV=1
A6447	-	-	-	-	-	-	-	-
A6448	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0725 7296705 Reductases with broad range of substrate specificities	KAF9119850.1 hypothetical protein BGX30_003586 [Mortierella sp. GBA39]	3-oxoacyl-[acyl-carrier-protein] reductase FabG OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=fabG PE=3 SV=1
A6449	GO:0045892(negative regulation of transcription, DNA-templated),GO:0006281(DNA repair),GO:0006338(chromatin remodeling),GO:0043967(histone H4 acetylation),GO:0043968(histone H2A acetylation),GO:0006629(lipid metabolic process)	GO:0005634(nucleosome),GO:0035267(NuA4 histone acetyltransferase complex)	GO:0008081(phosphoric diester hydrolase activity)	-	-	KOG2656 At2g47210 DNA methyltransferase 1-associated protein-1	KAF9121439.1 hypothetical protein BGX30_002580 [Mortierella sp. GBA39]	Glycerophosphodiester phosphodiesterase OS=Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) OX=273068 GN=UgpQ PE=1 SV=1

A6450	GO:0009082(branch ed-chain amino acid biosynthetic process)	-	GO:0003824(catalytic activity),GO:000976(thiamine pyrophosphate binding),GO:000287(magnesium ion binding),GO:0003984(acetolactate synthase activity),GO:0050660(flavin adenine dinucleotide binding)	K01652 E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	map00770 Pantothenate and CoA biosynthesis;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00650 Butanoate metabolism;map00660 C5-Branched dibasic acid metabolism;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG4166[YM R108w Thiamine pyrophosphate-requiring enzyme	KAG2220672.1 hypothetical protein INT45_008215 [Mucor circinatus]	Acetolactate synthase, mitochondrial OS=Cryptococcus neoformans var. grubii serotype A (strain H99 / ATCC 208821 / CBS 10515 / FGSC 9487) OX=235443 GN=ILV2 PE=3 SV=1
A6451	-	GO:0016021(integral component of membrane)	GO:0005509(cal cium ion binding)	K03321 TC.SULP; sulfate permease, SulP family	-	-	OZJ05631.1 hypothetical protein BZG36_01522 [Bifiguratus adalaidae]	Uncharacterized protein C24H6.11c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC24H6.11c PE=4 SV=1
A6452	-	-	GO:0005515(protein binding)	-	-	-	KAG2737421.1 WD40 repeat-like protein [Suillus brevipes Sb2]	Mitochondrial division protein 1 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=MDV1 PE=3 SV=1
A6453	-	-	-	-	-	-	-	-
A6454	-	-	GO:0035091(phosphatidylinositol binding)	-	-	-	-	-
A6455	GO:0006289(nucleotide-excision repair),GO:0006367(transcription initiation from RNA polymerase II promoter)	-	GO:0003678(DNA helicase activity),GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0016787(hydrolase activity)	K10843 ERCC3, XPB; DNA excision repair protein ERCC-3 [EC:5.6.2.4]	map03420 Nucleotide excision repair;map03022 Basal transcription factors	-	CEG65485.1 Putative Rad3 protein [Rhizopus microsporus]	General transcription and DNA repair factor IIH helicase subunit XPB OS=Dictyostelium discoideum OX=44689 GN=repB PE=2 SV=1
A6456	-	-	-	-	-	-	-	-
A6457	GO:0019346(transsulfuration),GO:0007165(signal transduction)	-	GO:0030170(pyridoxal phosphate binding),GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity),GO:0003824(catalytic activity)	K01758 CTH; cystathionine gamma-lyase [EC:4.4.1.1]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map00450 Selenocompound metabolism;map00270 Cysteine and methionine metabolism	KOG0053[Hs2 1361334 Cystathionine beta-lyases/cystathionine gamma-synthases	ORY94162.1 Cys/Met metabolism PLP-dependent enzyme-domain-containing protein [Syncephalaster racemosum]	Cystathionine gamma-lyase OS=Dictyostelium discoideum OX=44689 GN=cysA PE=1 SV=1

A6458	-	-	GO:0016491(oxidoreductase activity)	K22745 AIFM2; apoptosis-inducing factor 2	map04115 p53 signaling pathway	KOG1336 Hs14318424 Monodehydroascorbate/ferredoxin reductase	XP_024685611.1 FAD/NAD(P)-binding domain-containing protein [Aspergillus novofumigatus IBT 16806]	Ferroptosis suppressor protein 1 OS=Bos taurus OX=9913 GN=AIFM2 PE=2 SV=1
A6459	-	-	GO:0016407(acyltransferase activity),GO:0010485(H4 histone acetyltransferase activity),GO:0043998(H2A histone acetyltransferase activity)	K20794 NAA40, NAT4; N-alpha-acetyltransferase 40 [EC:2.3.1.257]	-	KOG2488 Hs13376119 Acetyltransferase (GNAT) domain-containing protein	XP_019022226.1 acyl-CoA N-acyltransferase [Saitoella complicata NRRL Y-17804]	N-alpha-acetyltransferase 40 OS=Homo sapiens OX=9606 GN=NAA40 PE=1 SV=1
A6460	GO:0006779(porphyrin-containing compound biosynthetic process)	-	GO:0004853(uroporphyrinogen decarboxylase activity)	K01599 hemE, UROD; uroporphyrinogen decarboxylase [EC:4.1.1.37]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG2872 Hs14742907 Uroporphyrinogen decarboxylase	ORX99841.1 uroporphyrinogen decarboxylase [Basidiobolus meristosporus CBS 931.73]	Uroporphyrinogen decarboxylase OS=Danio rerio OX=7955 GN=urop PE=1 SV=1
A6461	GO:0006801(superoxide metabolic process)	-	GO:0046872(metal ion binding)	K04569 CCS; copper chaperone for superoxide dismutase	map05014 Amyotrophic lateral sclerosis;map05022 Pathways of neurodegeneration - multiple diseases	KOG4656 At1g12520 Copper chaperone for superoxide dismutase	XP_030996522.1 uncharacterized protein EOL32_005206 [Phialemonio psis curvata]	Copper chaperone for superoxide dismutase, chloroplastic/cytosolic OS=Arabidopsis thaliana OX=3702 GN=CCS PE=1 SV=1
A6462	-	-	-	-	-	-	-	-
A6463	-	-	GO:0005515(protein binding)	K16365 SGTA; small glutamine-rich tetratricopeptide repeat-containing protein alpha	-	KOG0553 CE04813 TPR repeat-containing protein	NP_983408.1 ACR005Wp [Eremothecium gossypii ATCC 10895]	Small glutamine-rich tetratricopeptide repeat-containing protein 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=sgt2 PE=3 SV=1
A6464	GO:0016579(protein deubiquitination),GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase),GO:0008168(methyltransferase activity)	K18162 NDUFAF5; NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 5 [EC:2.1.1.-]	map04714 Thermogenesis	KOG2940 7303243 Predicted methyltransferase	XP_016611491.1 hypothetical protein SPPG_00935 [Spizellomyces punctatus DAOM BR117]	Arginine-hydroxylase NDUFAF5, mitochondrial OS=Danio rerio OX=7955 GN=ndufaf5 PE=2 SV=1
A6465	-	-	-	-	-	KOG1763 Hs8923808 Uncharacterized conserved protein, contains CCCH-type Zn-finger	-	Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens OX=9606 GN=ZC3H15 PE=1 SV=1

A6466	-	-	-	-	-	KOG3142 At5g07110 Prenylated rab acceptor 1	-	PRA1 family protein B6 OS=Arabidopsis thaliana OX=3702 GN=PRA1B6 PE=1 SV=1
A6467	-	-	-	-	-	-	-	-
A6468	-	-	GO:0005509(calcium ion binding);GO:0017110(nucleoside-diphosphatase activity)	-	-	KOG4494 7299449 Cell surface ATP diphosphohydrolase Apyrase	-	Soluble calcium-activated nucleotidase 1 OS=Homo sapiens OX=9606 GN=CANT1 PE=1 SV=1
A6469	GO:0009435(NAD biosynthetic process)	-	GO:0004516(nicotinate phosphoribosyltransferase activity)	K00763 pncB; NAPRT1; nicotinate phosphoribosyltransferase [EC:6.3.4.21]	map01240 Biosynthesis of cofactors;map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	KOG2511 7295733 Nicotinic acid phosphoribosyltransferase	KAF9124264.1 hypothetical protein BGX30_001033 [Mortierella sp. GBA39]	Nicotinate phosphoribosyltransferase OS=Dictyostelium discoideum OX=44689 GN=naprt PE=2 SV=1
A6470	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG1330 CE05393 Sugar transporter/spinster transmembrane protein	EXA31557.1 hypothetical protein FOVG_17178 [Fusarium oxysporum f. sp. pisi HDV247]	Protein spinster homolog 1 OS=Homo sapiens OX=9606 GN=SPNS1 PE=1 SV=1
A6471	-	-	GO:0016787(hydrolase activity)	-	-	KOG1515 CE03271 Arylacetamide deacetylase	RKP15361.1 alpha/beta hydrolase fold-domain-containing protein [Piptocephalis cylindrospora]	Esterase OS=Acinetobacter venetianus (strain ATCC 31012 / DSM 23050 / BCRC 14357 / CCUG 45561 / CIP 110063 / KCTC 2702 / LMG 19082 / RAG-1) OX=1191460 GN=est PE=3 SV=2
A6472	-	GO:0005737(cytoplasm)	GO:0000287(magnesium ion binding);GO:0008253(5'-nucleotidase activity)	-	-	KOG3128 Hs7706031 Uncharacterized conserved protein	KAG4104688.1 5'-nucleotidase, cytosolic III [Neocallimastix sp. JGI-2020a]	Cytosolic 5'-nucleotidase 3 OS=Danio rerio OX=7955 GN=nt5c3 PE=2 SV=2
A6473	-	-	GO:0005515(protein binding)	K14558 PWP2, UTP1; periodic tryptophan protein 2	map03008 Ribosome biogenesis in eukaryotes	KOG3602 CE27437 WD40 repeat-containing protein	TPX72575.1 hypothetical protein CcCBS67573_g05748 [Chytridiomycetes confervae]	NACHT domain- and WD repeat-containing protein 1 OS=Mus musculus OX=10090 GN=Nwd1 PE=2 SV=2
A6474	-	-	-	K19327 ANO10, TMEM16K; anoctamin-10	-	-	KTB39508.1 hypothetical protein WG66_7903 [Moniliophthora roreri]	-
A6475	-	-	GO:0046961(proton-transporting ATPase activity, rotational mechanism)	-	-	KOG1647 Hs7706757 Vacuolar H+-ATPase V1 sector, subunit D	ORY56551.1 V-type H+-transporting ATPase subunit D [Leucosporidium creatinivorum]	V-type proton ATPase subunit D OS=Manduca sexta OX=7130 PE=2 SV=1

A6476	-	-	GO:0005509(cal cium ion binding)	-	-	KOG0027 At4 g26470 Calmodulin and related proteins (EF- Hand superfamily)	-	Probable calcium-binding protein CML21 OS=Arabidopsis thaliana OX=3702 GN=CML21 PE=2 SV=1
A6477	-	-	-	-	-	-	-	-
A6478	-	-	-	-	-	-	-	-
A6479	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	-	-	-	PKY39010.1 hypothetical protein RhiiirA4_4397 55 [Rhizophagus irregularis]	-
A6480	-	-	-	-	-	-	-	-
A6481	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	K08294 MKK1_2; mitogen- activated protein kinase kinase [EC:2.7.12.2]	map04139 Mitophagy - yeast;map04011 MAPK signaling pathway - yeast	KOG0589 At1 g54510 Serine/threon ine protein kinase	XP_00668146 7.1 uncharacteriz ed protein BATDEDRAFT _37325 [Batrachochyt rium dendrobatidi s JAM81]	Serine/threonine-protein kinase Nek3 OS=Oryza sativa subsp. japonica OX=39947 GN=NEK3 PE=1 SV=1
A6482	-	-	-	-	-	-	RHZ50113.1 hypothetical protein Glove_505g1 9 [Diversispora epigaea]	Putative transposase A625R OS=Paramecium bursaria Chlorella virus 1 OX=10506 GN=A625R PE=3 SV=1
A6483	GO:00550 85(transm embrane transport)	-	-	K15111 SLC25A26; solute carrier family 25 (mitochondri al S- adenosylmet hionine transporter), member 26	-	KOG0768 CE 03096 Mitochondria l carrier protein PET8	PIA16534.1 mitochondria l carrier [Coemansia reversa NRRL 1564]	Mitochondrial S-adenosylmethionine carrier protein OS=Mus musculus OX=10090 GN=Slc25a26 PE=1 SV=2
A6484	GO:00064 68(protein phosphor ylation)	-	GO:0005509(cal cium ion binding),GO:000 4672(protein kinase activity),GO:000 5524(ATP binding)	K08794 CAMK1; calcium/calm odulin- dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05 214 Glioma;map049 21 Oxytocin signaling pathway;map04 925 Aldosterone synthesis and secretion	KOG0032 At4 g21940 Ca2+/calmod ulin- dependent protein kinase, EF- Hand protein superfamily	ORY52947.1 Pkinase- domain- containing protein [Rhizoclosma tium globosum]	Calcium-dependent protein kinase 2 OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=CDPK2 PE=1 SV=4
A6485	-	-	-	-	-	KOG2458 730 0921 Endoplasmic reticulum protein EP58, contains filamin rod domain and KDEL motif	-	-
A6486	GO:00469 07(intrace llular transport)	-	-	K15304 RANBP3; Ran-binding protein 3	map05166 Human T-cell leukemia virus 1 infection	KOG0864 YIL 063c Ran- binding protein RANBP1 and related RanBD domain proteins	GAX71930.1 hypothetical protein SCKG_5031 [Saccharomy ces cerevisiae]	Ran-specific GTPase-activating protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRB2 PE=1 SV=1

A6487	GO:0042254(ribosome biogenesis)	GO:0005634(nucleus)	-	K14852 RRS1; regulator of ribosome biosynthesis	-	KOG1765 CE08186 Regulator of ribosome synthesis	RIB25247.1 ribosome biogenesis regulatory protein [Gigaspora rosea]	Ribosome biogenesis regulatory protein homolog OS=Mus musculus OX=10090 GN=Rrs1 PE=1 SV=1
A6488	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2156 Hs7661970 Tubulin-tyrosine ligase-related protein	ORY13327.1 TTL-domain-containing protein [Neocallimastix californiae]	Tubulin monoglutamylase TTL4 OS=Homo sapiens OX=9606 GN=TTLL4 PE=1 SV=2
A6489	-	-	GO:0005515(protein binding)	K11801 DCAF11; DDB1- and CUL4-associated factor 11	-	KOG2106 Hs18597790 Uncharacterized conserved protein, contains HELP and WD40 domains	RYO74164.1 hypothetical protein DL763_011008 [Monosporascus cannonballus]	WD repeat-containing protein 90 OS=Xenopus tropicalis OX=8364 GN=wdr90 PE=2 SV=1
A6490	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A6491	-	-	GO:0003677(DNA binding)	-	-	-	-	Sugar fermentation stimulation protein homolog OS=Phenylobacterium zucineum (strain HLK1) OX=450851 GN=sfsA PE=3 SV=1
A6492	GO:0006006(glucose metabolic process)	-	GO:0016614(oxidoreductase activity, acting on CH-OH group of donors),GO:0050661(NADP binding),GO:0004345(glucose-6-phosphate dehydrogenase activity)	K00036 G6PD, zwf; glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49 1.1.1.363]	map05415 Diabetic cardiomyopathy; map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00480 Glutathione metabolism;map00030 Pentose phosphate pathway;map05230 Central carbon metabolism in cancer;map01100 Metabolic pathways	KOG0563 At5g40760 Glucose-6-phosphate 1-dehydrogenase	XP_019006688.1 glucose-6-phosphate dehydrogenase [Kwoniella mangroviensis CBS 8507]	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform OS=Solanum tuberosum OX=4113 GN=G6PDH PE=1 SV=1
A6493	GO:0006357(regulation of transcription by RNA polymerase II)	-	GO:0016538(cyclin-dependent protein serine/threonine kinase regulator activity)	-	-	KOG2496 7296498 Cdk activating kinase (CAK)/RNA polymerase II transcription initiation/nucleotide excision repair factor TFIIH/TFIIK, cyclin H subunit	KAF9432065.1 hypothetical protein BGZ76_011308 [Entomortierella beljakovae]	Cyclin-H1-1 OS=Arabidopsis thaliana OX=3702 GN=CYCH1-1 PE=1 SV=1
A6494	-	-	-	K20176 SGSM3, MAP; small G protein signaling modulator 3	-	KOG2058 Hs8922167 Ypt/Rab GTPase activating protein	RKP13341.1 rab-GTPase-TBC domain-containing protein [Piptocephalis cylindrospora]	TBC1 domain family member 2A OS=Rattus norvegicus OX=10116 GN=Tbc1d2 PE=2 SV=1

A6495	GO:0019752(carboxylic acid metabolic process)	-	GO:0003824(catalytic activity),GO:0016830(carbon-carbon lyase activity),GO:0030170(pyridoxal phosphate binding)	K01634 SGPL1, DPL1; sphinganine-1-phosphate aldolase [EC:4.1.2.27]	map04071 Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG1383 At1g27980 Glutamate decarboxylase/sphingosine phosphate lyase	RIA95446.1 pyridoxal phosphate-dependent transferase [Gnomus cerebriforme]	Sphingosine-1-phosphate lyase OS=Dictyostelium discoideum OX=44689 GN=sglA PE=2 SV=1
A6496	-	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	KOG1426 Hs4557026 FOG:RCC1 domain	XP_0050551.2 YALI0805940p [Yarrowia lipolytica CLUB122]	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens OX=9606 GN=HERC1 PE=1 SV=2
A6497	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005216(ion channel activity)	-	-	KOG2301 Hs2058958 Voltage-gated Ca2+ channels, alpha1 subunits	-	Two pore channel protein 2 OS=Mus musculus OX=10090 GN=Tpcn2 PE=1 SV=1
A6498	-	-	-	-	-	KOG1305 Hs15723370 Amino acid transporter protein	XP_020056128.1 uncharacterized protein ASPACDRAFT_43420 [Aspergillus aculeatus ATCC 16872]	Sodium-coupled neutral amino acid symporter 2 OS=Gallus gallus OX=9031 GN=SLC38A2 PE=2 SV=2
A6499	-	-	-	K13205 AAR2, C20orf4; A1 cistron-splicing factor AAR2	-	KOG3937 At1g66510 mRNA splicing factor	XP_023465428.1 AAR2-domain-containing protein [Rhizopus microsporus ATCC 52813]	Protein AAR2 homolog OS=Bos taurus OX=9913 GN=AAR2 PE=2 SV=1
A6500	GO:0006367(transcription initiation from RNA polymerase II promoter),GO:0051123(RNA polymerase II preinitiation complex assembly)	GO:0005634(nucleus),GO:0005669(transcription factor TFIID complex)	GO:0046982(protein heterodimerization activity)	K03135 TAF11; transcription initiation factor TFIID subunit 11	map03022 Basal transcription factors	KOG3219 At1g20000 Transcription initiation factor TFIID, subunit TAF11	ORX64424.1 TAFII28-domain-containing protein [Anaeromyces robustus]	Transcription initiation factor TFIID subunit 11b OS=Arabidopsis thaliana OX=3702 GN=TAF11B PE=2 SV=1
A6501	GO:0046856(phosphatidylinositol dephosphorylation)	-	GO:0016791(phosphatase activity)	K20279 SYNJ2 synaptojanin [EC:3.1.3.36]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0566 YOR109w Inositol-1,4,5-triphosphate 5-phosphatase (synaptojanin), INP51/INP52/INP53 family	ORX91022.1 DNase I-like protein [Basidiobolus meristosporus CBS 931.73]	Polyphosphatidylinositol phosphatase INP53 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=INP53 PE=1 SV=1
A6502	-	-	-	K14784 CMS1; protein CMS1	-	KOG3089 Hs16158889 Predicted DEAD-box-containing helicase	KAG4084566.1 hypothetical protein H8356DRAFT_1063382 [Neocallimastix sp. JGI-2020a]	Protein CMSS1 OS=Rattus norvegicus OX=10116 GN=Cmss1 PE=1 SV=1

A6503	-	-	GO:0004499(N, N-dimethylaniline monooxygenase activity),GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding)	K00485 FMO; dimethylaniline monooxygenase (N-oxide forming) / hypotaurine monooxygenase [EC:1.14.13.8 1.8.1.-]	map00982 Drug metabolism - cytochrome P450;map00430 Taurine and hypotaurine metabolism;map01100 Metabolic pathways	KOG1399 Hs4503755 Flavin-containing monooxygenase	RUS18863.1 flavin monooxygenase-like protein [Endogone sp. FLAS-F59071]	Flavin-containing monooxygenase 5 OS=Rattus norvegicus OX=10116 GN=Fmo5 PE=1 SV=3
A6504	-	-	-	K04712 DEGS; sphingolipid 4-desaturase/C4-monooxygenase [EC:1.14.19.1 7 1.14.18.5]	map04071 Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map01100 Metabolic pathways	KOG2987 CE28791 Fatty acid desaturase	KXS12861.1 hypothetical protein M427DRAFT_59173 [Gonapodya prolifera JEL478]	Putative sphingolipid delta(4)-desaturase/C4-monooxygenase OS=Caenorhabditis elegans OX=6239 GN=ttm-5 PE=3 SV=1
A6505	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6506	-	-	-	K19525 VPS13A_C; vacuolar protein sorting-associated protein 13A/C	-	KOG1809 7304192 Vacuolar protein sorting-associated protein	KAF7985382.1 hypothetical protein HWV62_6631 [Athelia sp. TMB]	Intermembrane lipid transfer protein VPS13 OS=Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719) OX=759272 GN=VPS13 PE=1 SV=1
A6507	-	-	-	-	-	-	KAF9151997.1 Anaphase-promoting complex subunit 10 [Linnemannia schmuckeri]	-
A6508	-	-	-	K00940 ndk, NME; nucleoside-diphosphate kinase [EC:2.7.4.6]	map00983 Drug metabolism - other enzymes;map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map04016 MAPK signaling pathway - plant;map01100 Metabolic pathways	KOG0888 Hs7019465 Nucleoside diphosphate kinase	TPX60702.1 nucleoside-diphosphate kinase [Powellomyces hirtus]	Nucleoside diphosphate kinase 7 OS=Homo sapiens OX=9606 GN=NME7 PE=1 SV=1
A6509	GO:0006813(potassium ion transport)	GO:001620(membrane)	-	-	-	KOG1420 CE24409 Ca2+-activated K+ channel Slowpoke, alpha subunit	EPZ33661.1 hypothetical protein O9G_000436 [Rozella allomyces CSF55]	Potassium channel subfamily T member 2 OS=Homo sapiens OX=9606 GN=KCNT2 PE=1 SV=1

A6510	GO:0006402(mRNA catabolic process)	-	GO:0003723(RNA binding),GO:0004654(polyribonucleotide nucleotidyltransferase activity)	K11600 RRP41, EXOSC4, SKI6; exosome complex component RRP41	map03018 RNA degradation	KOG1067 At5g14580 Predicted RNA-binding polyribonucleotide nucleotidyltransferase	KAG1471815.1 hypothetical protein G6F57_01124.2 [Rhizopus oryzae]	Polyribonucleotide nucleotidyltransferase OS=Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / CCUG 37298 / CIP 103539 / LMG 7603 / PAI5) OX=272568 GN=pnp PE=3 SV=1
A6511	-	-	-	-	-	-	-	-
A6512	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2156 Hs7661970 Tubulin-tyrosine ligase-related protein	TPX56293.1 hypothetical protein CcCBS67573_g09370 [Chytriumyces confervae]	Tubulin polyglutamylase TTL5 OS=Homo sapiens OX=9606 GN=TLL5 PE=1 SV=3
A6513	GO:0072488(ammonium transmembrane transport)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 At3g24290 Ammonia permease	KAF9137593.1 hypothetical protein BGX30_010076 [Mortierella sp. GBA39]	Ammonium transporter 1 member 3 OS=Solanum lycopersicum OX=4081 GN=AMT1-3 PE=2 SV=1
A6514	GO:0072488(ammonium transmembrane transport)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 At3g24290 Ammonia permease	KAF9137593.1 hypothetical protein BGX30_010076 [Mortierella sp. GBA39]	Ammonium transporter 1 member 3 OS=Solanum lycopersicum OX=4081 GN=AMT1-3 PE=2 SV=1
A6515	-	-	GO:0005509(calcium ion binding)	K16466 CETN3, CDC31; centrin-3	-	KOG0032 At4g04710 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORY93070.1 calmodulin [Syncephalaster racemosum]	Troponin C, isoform 2A OS=Homarus americanus OX=6706 PE=1 SV=1
A6516	-	-	-	K15117 SLC25A34_35, OAC1; solute carrier family 25, member 34/35	-	KOG0753 At1g14140 Mitochondrial fatty acid anion carrier protein/Unco upling protein	XP_028478821.1 hypothetical protein EHS24_004236 [Apiotrichum porosum]	Kidney mitochondrial carrier protein 1 OS=Xenopus laevis OX=8355 GN=slc25a30 PE=2 SV=1
A6517	-	-	-	-	-	-	-	UPF0489 protein C5orf22 OS=Homo sapiens OX=9606 GN=C5orf22
A6518	-	-	-	-	-	-	-	-
A6519	GO:0001510(RNA methylation),GO:0009452(7-methylguanosine RNA capping)	-	GO:0008168(methyltransferase activity)	K14292 TGS1; trimethylguanosine synthase [EC:2.1.1.-]	-	KOG2730 At1g30550 Methylase	RKP09936.1 RNA cap guanine-N2 methyltransferase - domain-containing protein, partial [Thamnocephalus sphaerospora]	Trimethylguanosine synthase OS=Mus musculus OX=10090 GN=Tgs1 PE=1 SV=2
A6520	-	-	-	-	-	-	-	-
A6521	GO:000055(ribosomal large subunit export from nucleus), GO:0042273(ribosomal large subunit biogenesis)	-	-	K14856 SDA1, SDAD1; protein SDA1	-	KOG2229 7303942 Protein required for actin cytoskeleton organization and cell cycle progression	RKO88958.1 SDA1-domain-containing protein [Blyttomyces helicus]	Protein SDA1 homolog OS=Bos taurus OX=9913 GN=SDAD1 PE=2 SV=1

A6522	-	-	-	-	-	KOG3121 CE27022 Dynactin, subunit p25	KAF7746895.1 hypothetical protein DSO57_013513 [Entomophthora muscae]	Dynactin subunit 5 OS=Homo sapiens OX=9606 GN=DCTN5 PE=1 SV=1
A6523	-	-	-	-	-	-	-	-
A6524	-	-	-	-	-	-	-	-
A6525	-	-	GO:0005509(cal cium ion binding)	-	-	-	-	-
A6526	-	-	-	-	-	-	-	-
A6527	-	-	-	-	-	-	-	-
A6528	GO:0005975(carbohy drate metabolic process), GO:0030259(lipid glycosylati on)	-	GO:0008194(UD P- glycosyltransfer ase activity),GO:0016758(hexosyltra nsferase activity)	-	-	KOG1192 At3g07020 UDP- glucuronosyl and UDP- glucosyl transferase	PSK56060.1 Sterol 3- beta- glucosyltransf erase [Elsinoe australis]	Sterol 3- beta- glucosyltransferase UGT80A2 OS=Arabidopsis thaliana OX=3702 GN=UGT80A2 PE=1 SV=1
A6529	-	-	GO:0005515(pro tein binding)	K20523 SH3YL1; SH3 domain- containing YSC84- like protein 1	-	-	CDS09894.1 hypothetical protein LRAMOSA02571 [Lichtheimia ramosa]	LAS seventeen- binding protein 3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=LSB3 PE=3 SV=2
A6530	-	GO:0016020(membrane)	GO:0140359(AB C- type transporter activity),GO:0005524(ATP binding)	K08711 PDR, CDR1; ATP- binding cassette, subfamily G (WHITE), member 2, PDR	map02010 ABC transporters	KOG0065 At1g15520 Pleiotropic drug resistance proteins (PDR1-15), ABC superfamily	XP_021886648.1 ABC-2 type transporter- domain- containing protein [Lobosporan gium transversale]	ABC transporter G family member 40 OS=Arabidopsis thaliana OX=3702 GN=ABCG40 PE=1 SV=1
A6531	-	-	-	-	-	-	-	-
A6532	-	-	GO:0005515(pro tein binding)	-	-	-	-	-
A6533	-	GO:0016020(membrane)	-	K13199 SERBP1; plasminogen activator inhibitor 1 RNA- binding protein	-	KOG4267 At2g26240 Predicted membrane protein	XP_028478196.1 hypothetical protein EHS24_006272 [Apiotrichum porosum]	Protein FATTY ACID EXPORT 7 OS=Arabidopsis thaliana OX=3702 GN=FAX7 PE=3 SV=1
A6534	GO:0007165(signal transducti on),GO:007186(G protein- coupled receptor signaling pathway)	-	GO:0003924(GT Pase activity),GO:0019001(guanyl nucleotide binding),GO:0031683(G- protein beta/gamma- subunit complex binding)	K04630 GNAI; guanine nucleotide- binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP- PKG signaling pathway;map04730 Long- term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone- mediated oocyte maturation;map05170 Human immunodeficien cy virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082 Hs20330805 G- protein alpha subunit (small G protein superfamily)	KAG0165526.1 guanine nucleotide- binding protein subunit alpha [Apophysom yces sp. BC1015]	Guanine nucleotide- binding protein G(t) subunit alpha-2 OS=Mus musculus OX=10090 GN=Gnat2 PE=2 SV=2

A6535	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0003924(GTPase activity), GO:0019001(guanylnucleotide binding), GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance; map04024 cAMP signaling pathway; map04022 cGMP-PKG signaling pathway; map04730 Long-term depression; map05133 Pertussis; map04071 Sphingolipid signaling pathway; map04915 Estrogen signaling pathway; map04914 Progesterone-mediated oocyte maturation; map05170 Human immunodeficiency virus 1 infection; map04728 Dopaminergic synapse; map04724	KOG0082 CE08571 G-protein alpha subunit (small G protein superfamily)	KNE58083.1 hypothetical protein AMAG_04903 [Allomyces macrogynus ATCC 38327]	Guanine nucleotide-binding protein G(o) subunit alpha OS=Locusta migratoria OX=7004 PE=3 SV=1
A6536	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0003924(GTPase activity), GO:0019001(guanylnucleotide binding), GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance; map04024 cAMP signaling pathway; map04022 cGMP-PKG signaling pathway; map04730 Long-term depression; map05133 Pertussis; map04071 Sphingolipid signaling pathway; map04915 Estrogen signaling pathway; map04914 Progesterone-mediated oocyte maturation; map05170 Human immunodeficiency virus 1 infection; map04728 Dopaminergic synapse; map04724	KOG0082 7303740 G-protein alpha subunit (small G protein superfamily)	KIW67472.1 hypothetical protein PV04_06719 [Phialophora americana]	G protein alpha q subunit OS=Drosophila melanogaster OX=7227 GN=Galphaq PE=1 SV=2
A6537	GO:0006611(protein export from nucleus), GO:0051168(nuclear export)	-	GO:0005049(nuclear export signal receptor activity)	-	-	-	KAG0074703.1 hypothetical protein BGZ90_010551 [Linnemannia elongata]	Exportin-5 OS=Dictyostelium discoideum OX=44689 GN=xpo5 PE=3 SV=1
A6538	-	-	-	-	-	-	-	Tubby-related protein 2 OS=Mus musculus OX=10090 GN=Tulp2 PE=1
A6539	-	-	-	-	-	-	-	-
A6540	-	-	-	-	-	-	-	-
A6541	GO:0030833(regulation of actin filament polymerization)	-	GO:0031267(small GTPase binding)	-	-	KOG3951 Hs14741010 Uncharacterized conserved protein	RIB15963.1 hypothetical protein C2G38_2134702 [Gigaspora rosea]	CYFIP-related Rac1 interactor B OS=Bos taurus OX=9913 GN=CYRIB PE=2 SV=1
A6542	GO:0007165(signal transduction), GO:009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity), GO:0008081(phosphoric diester hydrolase activity)	K01120 cpdP; 3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]	map00230 Purine metabolism; map01100 Metabolic pathways	KOG3688 HsM4826892 Cyclic GMP phosphodiesterase	RKP16301.1 Pde9 in complex with lbmx [Rozella allomyces CSF55]	3',5'-cyclic-nucleotide phosphodiesterase regA OS=Dictyostelium discoideum OX=44689 GN=regA PE=1 SV=1
A6543	-	-	-	-	-	-	-	-

A6544	-	-	-	-	-	KOG1252 At3g59760 Cystathionine beta-synthase and related enzymes	ORY28396.1 cysteine synthase A [Rhizoclostium globosum]	O-ureido-L-serine synthase OS=Streptomyces lavendulae OX=1914 GN=dcsD PE=1 SV=1
A6545	-	-	-	-	-	-	-	-
A6546	GO:0006561(proline biosynthetic process)	-	GO:0004735(pyrroline-5-carboxylate reductase activity)	K00286 proC; pyrroline-5-carboxylate reductase [EC:1.5.1.2]	map01110 Biosynthesis of secondary metabolites;map00330 Arginine and proline metabolism;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways	KOG3124 At5g14800 Pyrroline-5-carboxylate reductase	KOS20407.1 Pyrroline-5-carboxylate reductase [Escovopsis weberi]	Pyrroline-5-carboxylate reductase OS=Arabidopsis thaliana OX=3702 GN=PROC1 PE=2 SV=1
A6547	GO:0009263(deoxyribonucleotide biosynthetic process)	-	GO:0016491(oxidoreductase activity)	-	-	KOG1567 At3g27060 Ribonucleotide reductase, beta subunit	EPB87510.1 ribonucleoside-diphosphate reductase subunit M2 [Mucor circinelloides 1006PhL]	Ribonucleoside-diphosphate reductase subunit M2 OS=Mus musculus OX=10090 GN=Rrm2 PE=1 SV=1
A6548	GO:0006468(protein phosphorylation)	-	GO:0005509(calcium ion binding);GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At4g23650 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORX54885.1 calcium/calmodulin-dependent protein kinase I delta short [Piromyces finnis]	Calcium-dependent protein kinase 2 OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=CDPK2 PE=1 SV=4
A6549	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	-	-
A6550	GO:0010265(SCF complex assembly)	-	-	K17263 CAND1, TIP120A; cullin-associated NEDD8-dissociated protein 1	-	KOG1824 At2g02560 TATA-binding protein-interacting protein	KAG0210629.1 Cullin-associated NEDD8-dissociated protein 1 [Mortierella sp. GBA30]	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus OX=10116 GN=Cand1 PE=1 SV=1
A6551	-	-	-	-	-	-	-	-
A6552	-	-	-	-	-	KOG4431 7293210 Uncharacterized protein, induced by hypoxia	KAE9366672.1 hypothetical protein N431DRAFT_487205 [Chalara longipes BDJ]	HIG1 domain family member 2A, mitochondrial OS=Homo sapiens OX=9606 GN=HIGD2A PE=1 SV=1
A6553	GO:0000413(protein peptidyl-prolyl isomerization)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K01802 E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8]	-	KOG0865 At2g21130 Cyclophilin type peptidyl-prolyl cis-trans isomerase	OMH81989.1 Peptidyl-prolyl cis-trans isomerase [Zancudomyces culisetae]	Peptidyl-prolyl cis-trans isomerase OS=Blattella germanica OX=6973 GN=CYP4 PE=2 SV=1
A6554	-	-	-	-	-	-	-	-

A6555	GO:0006508(proteolysis)	-	GO:0004190(serine-type endopeptidase activity)	K01381 PEP4; saccharopepsin [EC:3.4.23.25]	map04138 Autophagy - yeast	KOG1339 7304149 Aspartyl protease	KAG2173999.1 hypothetical protein INT44_000113 [Umbelopsis vinacea]	Cathepsin D OS=Clupea harengus OX=7950 GN=ctsd PE=1 SV=1
A6556	-	-	GO:0016791(phosphatase activity)	-	-	KOG3120 At4g29530 Predicted haloacid dehalogenase-like hydrolase	KAG2193319.1 hypothetical protein INT47_005632 [Mucor saturninus]	Thiamine phosphate phosphatase-like protein OS=Arabidopsis thaliana OX=3702 GN=At4g29530 PE=1 SV=1
A6557	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07905 RAB11B; Ras-related protein Rab-11B	map04144 Endocytosis;map04152 AMPK signaling pathway;map04962 Vasopressin-regulated water reabsorption;map05164 Influenza A	KOG0098 7302290 GTPase Rab2, small G protein superfamily	KAF9945421.1 Ras-protein Rab-11B [Modicella reniformis]	Ras-related protein Rab-2 OS=Drosophila melanogaster OX=7227 GN=Rab2 PE=1 SV=1
A6558	-	-	-	-	-	-	-	-
A6559	-	-	-	-	-	-	-	-
A6560	-	-	-	-	-	-	-	-
A6561	-	-	-	-	-	-	-	-
A6562	-	-	-	-	-	-	-	-
A6563	GO:0006631(fatty acid metabolic process)	-	GO:0016491(oxidoreductase activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor),GO:0003824(catalytic activity),GO:0070403(NAD+ binding)	K00022 HADH; 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]	map01110 Biosynthesis of secondary metabolites;map00907 Pinene, camphor and geraniol degradation;map01120 Microbial metabolism in diverse environments;map00930 Caprolactam degradation;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00062 Fatty acid elongation;map00310 Lysine degradation;map00380 Tryptophan metabolism;map	KOG1683 7297534 Hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase	KAG1715824.1 hypothetical protein ID866_1342 [Astraeus odoratus]	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=2
A6564	-	-	-	K01908 ACSS3, prpE; propionyl-CoA synthetase [EC:6.2.1.17]	map00640 Propanoate metabolism;map01100 Metabolic pathways	KOG1175 Hs13375727 Acyl-CoA synthetase	KZM27623.1 hypothetical protein ST47_g1340 [Ascochyta rabiei]	Uncharacterized protein PA3568 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA3568 PE=3 SV=2
A6565	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K11294 NCL, NSR1; nucleolin	map05130 Pathogenic Escherichia coli infection	KOG0118 At3g55340 FOG: RRM domain	KAF9166152.1 hypothetical protein DFQ26_008558 [Actinomyces rella ambigua]	Phragmoplastin interacting protein 1 OS=Arabidopsis thaliana OX=3702 GN=PHIP1 PE=1 SV=1
A6566	-	-	-	-	-	-	RKO89129.1 calmodulin-binding-domain-containing protein [Blyttomyces helicus]	Enkurin domain-containing protein 1 OS=Bos taurus OX=9913 GN=ENKD1 PE=2 SV=1

A6567	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02901 RP-L27e, RPL27; large subunit ribosomal protein L27e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3418 YDR471w 60S ribosomal protein L27	CDS12808.1 Putative 60S ribosomal protein L27 [Lichtheimia ramosa]	Large ribosomal subunit protein eL27 OS=Tetrahymena thermophila OX=5911 GN=RPL27 PE=1 SV=1
A6568	-	-	-	-	-	-	-	-
A6569	-	-	-	-	-	-	-	-
A6570	GO:0006086(acetyl-CoA biosynthetic process from pyruvate)	-	GO:0003824(catalytic activity),GO:0004739(pyruvate dehydrogenase (acetyl-transferring) activity)	K00162 PDHB, pdhB; pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]	map05415 Diabetic cardiomyopathy; map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00620 Pyruvate metabolism;map05230 Central carbon metabolism in cancer;map01100 Metabolic	KOG0524 At5g50850 Pyruvate dehydrogenase E1, beta subunit	KAG0301069.1 pyruvate dehydrogenase E1, beta subunit [Dissophora globulifera]	Pyruvate dehydrogenase E1 component subunit beta-1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=PDH2 PE=1 SV=2
A6571	GO:0006260(DNA replication)	-	GO:0003678(DNA helicase activity),GO:0005524(ATP binding),GO:0003697(single-stranded DNA binding),GO:0043139(5'-3' DNA helicase activity)	-	-	KOG2373 Hs1141909 Predicted mitochondrial DNA helicase twinkle	RIB10801.1 P-loop containing nucleoside triphosphate hydrolase protein [Gigaspora rosea]	Twinkle mtDNA helicase OS=Gallus gallus OX=9031 GN=TWNK PE=2 SV=1
A6572	-	-	-	-	-	-	-	-
A6573	-	-	-	-	-	-	-	-
A6574	-	-	-	-	-	-	-	-
A6575	-	-	GO:0016787(hydrolase activity),GO:0005509(calcium ion binding),GO:0005515(protein binding)	K04460 PPP5C; serine/threonine-protein phosphatase 5 [EC:3.1.3.16]	map04010 MAPK signaling pathway	KOG0377 Hs453944 Protein serine/threonine phosphatase RDGC/PPEF, contains STphosphatase and EF-hand domains	RIB23914.1 Metallo-dependent phosphatase -like protein, partial [Gigaspora rosea]	Serine/threonine-protein phosphatase with EF-hands 2 OS=Mus musculus OX=10090 GN=Ppef2 PE=2 SV=1
A6576	-	-	-	-	-	KOG4001 7299529 Axonemal dynein light chain	XP_006678959.1 uncharacterized protein BATDEDRAFT_24899 [Batrachochytrium dendrobatidis JAM81]	28 kDa inner dynein arm light chain, axonemal OS=Chlamydomonas reinhardtii OX=3055 GN=IDA4 PE=1 SV=1
A6577	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0006813(potassium ion transport)	GO:0016020(membrane)	GO:0005216(ion channel activity),GO:0005249(voltage-gated potassium channel activity)	-	-	KOG0501 Hs4504831 K+-channel KCNQ	TPX55371.1 hypothetical protein PhCBS80983.g05374 [Powellomyces hirtus]	Potassium voltage-gated channel subfamily H member 1 OS=Rattus norvegicus OX=10116 GN=Kcnh1 PE=1 SV=1

A6578	GO:000661(phosphatidylinositol biosynthetic process)	GO:0070772(PAS complex)	-	K15305 VAC14, TAX1BP2; vacuole morphology and inheritance protein 14	map05203 Viral carcinogenesis; map05166 Human T-cell leukemia virus 1 infection	KOG0212 At2g01690 Uncharacterized conserved protein	KHJ31763.1 putative vacuole-associated enzyme activator complex component [Erysiphe necator]	Protein VAC14 homolog OS=Arabidopsis thaliana OX=3702 GN=VAC14 PE=1 SV=2
A6579	-	-	-	-	-	-	-	-
A6580	-	-	-	-	-	-	SCV70749.1 BQ2448_3511 [Microbotryum intermedium]	Transmembrane protein 53-A OS=Xenopus laevis OX=8355 GN=tmem53-a PE=2 SV=1
A6581	-	-	-	K15634 gpmB; 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00680 Methane metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG0235 At3g50520 Phosphoglycerate mutase	KAG1603624.1 hypothetical protein G6F46_013820 [Rhizopus delemar]	Phosphoglycerate mutase-like protein 4 OS=Arabidopsis thaliana OX=3702 GN=At3g50520 PE=2 SV=1
A6582	-	-	-	-	-	-	-	-
A6583	GO:0009058(biosynthetic process), GO:0008610(lipid biosynthetic process)	-	GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups),GO:0004311(farnesyltransferase activity),GO:0004310(farnesyl-diphosphate farnesyltransferase activity)	-	-	KOG1459 Hs4758350 Squalene synthetase	XP_024731372.1 farnesyl-diphosphate farnesyltransferase [Hyaloscypha bicolor E]	Squalene synthase OS=Mus musculus OX=10090 GN=Fdft1 PE=1 SV=2
A6584	-	-	-	-	-	-	-	-
A6585	-	-	-	-	-	KOG2502 At2g47900 Tub family proteins	TPX63290.1 hypothetical protein SpCBS45565_g06711 [Spizellomyces sp. 'palustris']	Tubby-like F-box protein 3 OS=Arabidopsis thaliana OX=3702 GN=TULP3 PE=1 SV=1
A6586	-	GO:0042729(DASH complex), GO:0072686(mitotic spindle)	-	K11553 DAD1; DASH complex subunit DAD1	-	-	RKP38662.1 hypothetical protein BJ085DRAFT_36544 [Dimargaris cristalligena]	-

A6587	-	-	-	-	-	KOG1427 7297063 Uncharacterized conserved protein, contains RCC1 domain	ORZ23543.1 regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II [Absidia repens]	Protein RCC2 OS=Homo sapiens OX=9606 GN=RCC2 PE=1 SV=2
A6588	-	-	GO:0005515(protein binding)	K24155 DMXL, DMX, RAV1; rabconnectin-3a	map04142 Lysosome	KOG1064 7290688 RAVE (regulator of V-ATPase assembly) complex subunit RAV1/DMX protein, WD repeat superfamily	RKO89844.1 RAVE protein 1 C terminal-domain-containing protein [Blyttomyces helicus]	Dmx-like protein 1 OS=Homo sapiens OX=9606 GN=DMXL1 PE=1 SV=3
A6589	-	-	-	-	-	-	-	-
A6590	GO:0006511(ubiquitin-dependent protein catabolic process)	-	-	K14015 NPLOC4, NPL4; nuclear protein localization protein 4	map04141 Protein processing in endoplasmic reticulum	KOG2834 At2g47970 Nuclear pore complex, rNpl4 component (sc Npl4)	RIA96513.1 polyubiquitin-tagged protein recognition complex Npl4 component [Glomus cerebriforme]	NPL4-like protein OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0377700 PE=2 SV=1
A6591	-	-	GO:0005515(protein binding)	K20285 RABEPK; Rab9 effector protein with kelch motifs	-	KOG4152 Hs7019405 Host cell transcription factor HCFC1	RIA96737.1 hypothetical protein C1645_856866 [Glomus cerebriforme]	RING finger protein B OS=Dictyostelium discoideum OX=44689 GN=rngB PE=2 SV=2
A6592	-	-	-	-	-	-	-	-
A6593	GO:0048193(Golgi vesicle transport) GO:0016192(vesicle-mediated transport)	GO:0016020(membrane)	-	-	-	KOG3202 Hs4507285 SNARE protein TLG1/Syntaxin 6	KAF8937186.1 hypothetical protein BGZ58_003132 [Dissophora ornata]	Syntaxin-10 OS=Homo sapiens OX=9606 GN=STX10 PE=1 SV=1
A6594	GO:0000245(spliceosomal complex assembly)	-	GO:0003729(mRNA binding)	K12828 SF3B1, SAP155; splicing factor 3B subunit 1	map03040 Spliceosome	KOG0213 At5g64270 Splicing factor 3b, subunit 1	ORX75453.1 ARM repeat-containing protein [Basidiobolus meristosporus CBS 931.73]	Splicing factor 3B subunit 1 OS=Xenopus laevis OX=8355 GN=sf3b1 PE=2 SV=1
A6595	GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08851 TP53RK, PRPK, BUD32; TP53 regulating kinase and related kinases [EC:2.7.11.1]	-	KOG3087 Hs19923656 Serine/threonine protein kinase	KAG0223828.1 TP53 regulating kinase [Actinomotirella wolfii]	EKC/KEOPS complex subunit TP53RK OS=Homo sapiens OX=9606 GN=TP53RK PE=1 SV=2
A6596	-	-	-	-	-	-	-	-
A6597	GO:0000398(mRNA splicing, via spliceosome)	-	GO:0003723(RNA binding)	K12622 LSM3; U6 snRNA-associated Sm-like protein LSM3	map03040 Spliceosome;map03018 RNA degradation	KOG3460 At1g76860 Small nuclear ribonucleoprotein (snRNP) LSM3	KAF0552916.1 U6 snRNA-associated Sm-like protein LSM3 [Gigaspora margarita]	Sm-like protein LSM3B OS=Arabidopsis thaliana OX=3702 GN=LSM3B PE=1 SV=1

A6598	GO:0006520 (cellular amino acid metabolic process)	GO:0005737 (cytoplasm)	GO:0016787 (hydrolase activity), GO:0004046 (aminoacylase activity)	-	-	KOG2275 Hs4501901 Aminoacylase ACY1 and related metalloexopeptidases	KAF9190123.1 adenylate cyclase [Haplosporangium sp. Z767]	Aminoacylase-1 OS=Dictyostelium discoideum OX=44689 GN=acy1 PE=2 SV=1
A6599	GO:0006520 (cellular amino acid metabolic process)	GO:0005737 (cytoplasm)	GO:0016787 (hydrolase activity), GO:0004046 (aminoacylase activity)	-	-	KOG2275 Hs4501901 Aminoacylase ACY1 and related metalloexopeptidases	KAF9968508.1 adenylate cyclase [Mortierella alpina]	Aminoacylase-1 OS=Dictyostelium discoideum OX=44689 GN=acy1 PE=2 SV=1
A6600	-	-	-	-	-	KOG2353 Hs4757894 L-type voltage-dependent Ca2+ channel, alpha2/delta subunit	-	Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Mus musculus OX=10090 GN=Cacna2d1 PE=1 SV=1
A6601	-	-	-	-	-	KOG2353 Hs8923765 L-type voltage-dependent Ca2+ channel, alpha2/delta subunit	-	Voltage-dependent calcium channel subunit alpha-2/delta-3 OS=Homo sapiens OX=9606 GN=CACNA2D3 PE=1 SV=1
A6602	-	-	-	-	-	KOG2353 Hs8923765 L-type voltage-dependent Ca2+ channel, alpha2/delta subunit	-	Voltage-dependent calcium channel subunit alpha-2/delta-3 OS=Homo sapiens OX=9606 GN=CACNA2D3 PE=1 SV=1
A6603	GO:0009190 (cyclic nucleotide biosynthetic process), GO:0035556 (intracellular signal transduction)	-	-	-	-	KOG1023 7296844 Natriuretic peptide receptor, guanylate cyclase	TPX54390.1 hypothetical protein PhCBS80983.g05955 [Powellomyces hirtus]	Adenylate cyclase 1 OS=Rhizobium meliloti (strain 1021) OX=266834 GN=cya1 PE=3 SV=2
A6604	-	-	-	-	-	-	TPX76506.1 hypothetical protein CcCBS67573.g02223 [Chytridiomycota confervae]	Uncharacterized protein C1orf53 OS=Homo sapiens OX=9606 GN=C1orf53 PE=1 SV=1
A6605	-	-	-	K14821 BUD20; bud site selection protein 20	-	-	KXS13882.1 hypothetical protein M427DRAFT_359174 [Gonapodya prolifera JEL478]	Zinc finger protein bud20 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=bud20 PE=3 SV=1

A6606	GO:0009052(pentose-phosphate shunt, non-oxidative branch)	-	GO:0004751(ribose-5-phosphate isomerase activity)	K01807 rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00710 Carbon fixation in photosynthetic organisms;map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG3075[Hs21389337 Ribose 5-phosphate isomerase	XP_016605554.1 ribose 5-phosphate isomerase A [Spizellomyces punctatus DAOM BR117]	Ribose-5-phosphate isomerase (Fragment) OS=Bos taurus OX=9913 GN=RPIA PE=2 SV=2
A6607	-	-	-	-	-	-	-	-
A6608	-	-	GO:0003723(RNA binding);GO:0033897(ribonuclease T2 activity)	K01166 RNASET2; ribonuclease T2 [EC:4.6.1.19]	-	KOG1642[At2g02990 Ribonuclease, T2 family	SAM05124.1 hypothetical protein [Absidia glauca]	Intracellular ribonuclease LX OS=Solanum lycopersicum OX=4081 GN=RNALX PE=1 SV=2
A6609	-	-	GO:0071949(FAD binding);GO:0050660(flavin adenine dinucleotide binding);GO:0003824(catalytic activity)	K09828 DHCR24, DWF1; Delta24-sterol reductase [EC:1.3.1.72 1.3.1.-]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map011100 Metabolic pathways	KOG1262[Hs13375618 FAD-binding protein DIMINUTO	RKP38197.1 hypothetical protein BJ085DRAFT_37406 [Dimargaris cristalligena]	Delta(24)-sterol reductase OS=Rattus norvegicus OX=10116 GN=Dhcr24 PE=2 SV=2
A6610	-	-	-	K19525 VPS13A_C; vacuolar protein sorting-associated protein 13A/C	-	KOG1809[Hs8923545 Vacuolar protein sorting-associated protein	SAL99367.1 hypothetical protein [Absidia glauca]	Intermembrane lipid transfer protein VPS13B OS=Mus musculus OX=10090 GN=Vps13b PE=1 SV=3
A6611	-	-	-	-	-	-	-	-
A6612	-	-	-	-	-	-	-	-
A6613	-	-	GO:0016787(hydrolase activity)	K06269 PPP1C; serine/threonine-protein phosphatase PP1 catalytic subunit [EC:3.1.3.16]	map04390 Hippo signaling pathway;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05415 Diabetic cardiomyopathy;map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04218 Cellular senescence;map04910 Insulin signaling pathway;map04728 Dopaminergic synapse;map04720 Long-term potentiation;map05031 Amphetamine addiction;map04	KOG0374[Hs4506007 Serine/threonine specific protein phosphatase PP1, catalytic subunit	KAG0267509.1 Serine/threonine-protein phosphatase pp1 [Mortierella polycephala]	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit A OS=Xenopus laevis OX=8355 GN=ppp1cc-a PE=1 SV=2
A6614	GO:0008654(phospholipid biosynthetic process)	GO:0016020(membrane)	GO:0016780(phosphotransferase activity, for other substituted phosphate groups)	-	-	KOG2877[At1g13560 sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferases	KNE66799.1 hypothetical protein AMAG_11290 [Allomyces macrogynus ATCC 38327]	Uncharacterized CDP-alcohol phosphatidyltransferase class-I family protein 3 OS=Dictyostelium discoideum OX=44689 GN=captC PE=2 SV=1
A6615	-	-	-	-	-	-	-	-

A6616	GO:0055085(transmembrane transport),GO:0006811(ion transport)	GO:0016020(membrane),GO:0016021(integral component of membrane)	GO:0015377(cation:chloride symporter activity),GO:0022857(transmembrane transporter activity)	K14429 SLC12A9, CCC6; solute carrier family 12 (potassium/chloride transporters), member 9	-	KOG2083 Hs4557849 Na+/K+ symporter	XP_016612389.1 hypothetical protein, variant [Spizellomyces punctatus DAOM BR117]	Solute carrier family 12 member 1 OS=Homo sapiens OX=9606 GN=SLC12A1 PE=1 SV=2
A6617	GO:0007264(small GTPase mediated signal transduction)	-	GO:0005092(GDP-dissociation inhibitor activity)	K23460 CHM, CHML; Rab proteins geranylgeranyltransferase component A	-	KOG4405 7302459 GDP dissociation inhibitor	KAF7727692.1 hypothetical protein EC973_007248 [Apophysomyces ossiformis]	Rab proteins geranylgeranyltransferase component A OS=Drosophila melanogaster OX=7227 GN=Rep PE=1 SV=1
A6618	-	-	-	-	-	-	-	-
A6619	-	-	GO:0009055(electron transfer activity),GO:0020037(heme binding)	K08738 CYC; cytochrome c	map05014 Amyotrophic lateral sclerosis;map05417 Lipid and atherosclerosis;map05416 Viral myocarditis;map05134 Legionellosis;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map05222 Small cell lung cancer;map04214 Apoptosis - fly;map04215 Apoptosis - multiple species;map04210 Apoptosis;map01524 Platinum drug	KOG3453 Hs1128019 Cytochrome c	KAG2217787.1 hypothetical protein INT45_001112 [Mucor circinatus]	Cytochrome c OS=Macropus giganteus OX=9317 GN=CYCS PE=1 SV=2
A6620	-	-	GO:0004842(ubiquitin-protein transferase activity),GO:0005515(protein binding)	-	-	KOG0613 Hs19747267 Projectin/twitin and related proteins	ORY22745.1 hypothetical protein LY90DRAFT_675786 [Neocallimastix californiae]	Titin OS=Mus musculus OX=10090 GN=Ttn PE=1 SV=1
A6621	-	-	-	-	-	-	-	-
A6622	GO:0015689(molybdate ion transport)	-	GO:0015098(molybdate ion transmembrane transporter activity)	-	-	-	KKY13839.1 putative sulfate transporter [Diplodia seriata]	Molybdate transporter 2 OS=Arabidopsis thaliana OX=3702 GN=MOT2 PE=1 SV=2
A6623	-	-	GO:0016787(hydrolase activity),GO:0016831(carboxylase activity)	K03392 ACMSD; aminocarboxymuconate-semialdehyde decarboxylase [EC:4.1.1.45]	map00380 Tryptophan metabolism;map01100 Metabolic pathways	KOG4245 CE25548 Predicted metal-dependent hydrolase of the TIM-barrel fold	OON05981.1 hypothetical protein BSLG_04245 [Batrachochytrium salamandrivorans]	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase OS=Bos taurus OX=9913 GN=ACMSD PE=2 SV=1
A6624	-	-	-	-	-	-	-	-
A6625	-	-	GO:0005515(protein binding)	-	-	-	XP_007774171.1 hypothetical protein CONPUDRAFT_112021 [Coniophora puteana RWD-64-598 SS2]	NACHT, LRR and PYD domains-containing protein 13 OS=Homo sapiens OX=9606 GN=NLRP13 PE=2 SV=2

A6626	-	-	-	-	-	-	KAF9268645.1 hypothetical protein L218DRAFT_8-52693 [Marasmius fiardii PR-910]	-
A6627	-	-	-	-	-	-	-	-
A6628	GO:0006418(tRNA aminoacylation for protein translation),GO:0006429(leucyl-tRNA aminoacylation)	-	GO:0002161(aminoacyl-tRNA editing activity),GO:0000166(nucleotide binding),GO:0004823(leucine-tRNA ligase activity),GO:0005524(ATP binding),GO:0004812(aminoacyl-tRNA ligase activity)	K01869 LARS, leuS; leucyl-tRNA synthetase [EC:6.1.1.4]	map00970 Aminoacyl-tRNA biosynthesis	KOG0437 CE16317 Leucyl-tRNA synthetase	XP_031024436.1 leucine--tRNA ligase [Synchytrium microbalum]	Leucine--tRNA ligase, cytoplasmic OS=Pongo abelii OX=9601 GN=LARS1 PE=2 SV=1
A6629	-	-	-	-	-	-	KAG2181575.1 hypothetical protein INT44_008390 [Umbelopsis vinacea]	[Skp1-protein]-hydroxyproline N-acetylglucosaminyltransferase OS=Dictyostelium discoideum OX=44689 GN=gnt1 PE=1 SV=2
A6630	-	-	-	-	-	-	-	-
A6631	-	-	-	-	-	-	-	-
A6632	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0005886(plasma membrane),GO:0016020(membrane)	GO:0005509(calcium ion binding),GO:0005261(cation channel activity),GO:0005216(ion channel activity)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027 Hs4507617 Calmodulin and related proteins (EF-Hand superfamily)	XP_022499818.1 hypothetical protein AYO20_06001 [Fonsecaea nubica]	Troponin C, skeletal muscle OS=Sus scrofa OX=9823 GN=TNNC2 PE=1 SV=2
A6633	-	-	GO:0005515(protein binding),GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K11654 SMARCA5, SNF2H, ISWI; SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 [EC:5.6.2.-]	map03082 ATP-dependent chromatin remodeling	KOG0385 Hs21071058 Chromatin remodeling complex WSTF-ISWI, small subunit	XP_016605603.1 hypothetical protein SPPG_07036 [Spizellomyces punctatus DAOM BR117]	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens OX=9606 GN=SMARCA5 PE=1 SV=1

A6634	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG4280[Hs1641245 Kinesin-like protein	XP_016604117.1 hypothetical protein SPPG_08467 [Spizellomyces punctatus DAOM BR117]	Kinesin-like protein KIF6 OS=Homo sapiens OX=9606 GN=KIF6 PE=1 SV=3
A6635	-	-	-	-	-	-	-	-
A6636	-	-	GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027[Hs14150108 Calmodulin and related proteins (EF-Hand superfamily)	RKO90810.1 hypothetical protein BDK51DRAFT_12014, partial [Blyttiomycetes helicis]	Dynein regulatory complex protein 8 OS=Mus musculus OX=10090 GN=Efcab2 PE=1 SV=1
A6637	-	-	-	K09510 DNAJB4; DnaJ homolog subfamily B member 4	-	KOG0714[Hs4885495 Molecular chaperone (DnaJ superfamily)	KXS09380.1 DnaJ-domain-containing protein [Gonapodya prolifera JEL478]	DnaJ homolog subfamily B member 6 OS=Bos taurus OX=9913 GN=DNAJB6 PE=2 SV=1
A6638	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160[At4g28710 Myosin class V heavy chain	XP_002172206.2 myosin-51 [Schizosaccharomyces japonicus yFS275]	Myosin-5 OS=Arabidopsis thaliana OX=3702 GN=XI-1 PE=1 SV=1
A6639	GO:0006396(RNA processing)	-	GO:0008173(RNA methyltransferase activity)	K15331 TRMT2B, TRM2; tRNA (uracil-5-)-methyltransferase [EC:2.1.1.35]	-	KOG2187[HsM12232381 tRNA uracil-5-methyltransferase and related tRNA-modifying enzymes	KAG0170136.1 tRNA methyltransferase 2 [Apophysomyces sp. BC1015]	Uncharacterized RNA methyltransferase pc1998 OS=Protochlamydia amoebophila (strain UWE25) OX=264201 GN=pc1998 PE=3 SV=1
A6640	-	-	-	-	-	-	-	-
A6641	GO:0071705(nitrogen compound transport)	GO:0016020(membrane)	GO:0022857(transporter activity)	-	-	-	XP_006683473.1 uncharacterized protein BATDEDRAFT_28978, partial [Batrachochytrium dendrobatidis JAM81]	Trimethylamine transporter OS=Myroides profundus OX=480520 GN=tmaT PE=2 SV=1

A6642	GO:0071705(nitrogen compound transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	-	KAG1716752.1 hypothetical protein ID866_446 [Astraeus odoratus]	Trimethylamine transporter OS=Myroides profundus OX=480520 GN=tmaT PE=2 SV=1
A6643	GO:0071705(nitrogen compound transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	-	XP_006683473.1 uncharacterized protein BATDERAFT_28978, partial [Batrachochytrium dendrobatidis JAM81]	Trimethylamine transporter OS=Myroides profundus OX=480520 GN=tmaT PE=2 SV=1
A6644	-	-	-	-	-	-	-	-
A6645	GO:0000398(mRNA splicing, via spliceosome)	GO:0005681(spliceosomal complex)	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	K12848 SNU23; U4/U6.U5 tri-snRNP component SNU23	map03040 Spliceosome	KOG4727 Hs21389511 U1-like Zn-finger protein	CEH14769.1 zinc finger matrix-type protein [Ceraceosorus bombacis]	Zinc finger matrix-type protein 2 OS=Homo sapiens OX=9606 GN=ZMAT2 PE=1 SV=1
A6646	GO:0006351(transcription, DNA-templated)	-	GO:0003899(DNA-directed 5'-3' RNA polymerase activity),GO:0003677(DNA binding),GO:0002549(ribonucleoside binding)	K03021 RPC2, POLR3B; DNA-directed RNA polymerase III subunit RPC2 [EC:2.7.7.6]	map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway	-	ORX88413.1 DNA-directed RNA polymerase III subunit RPC2 [Basidiobolus meristosporus CBS 931.73]	DNA-directed RNA polymerase III subunit RPC2 OS=Homo sapiens OX=9606 GN=POLR3B PE=1 SV=2
A6647	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	K04536 GNB1; guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724 Glutamatergic synapse;map04725 Cholinergic synapse;map04726 Serotonergic synapse;map04727 GABAergic synapse;map04723 Retrograde endocannabinoid signaling;map05032 Morphine addiction;map05034 Alcoholism;map04713 Circadian entrainment;map04014 Ras signaling pathway;map05	KOG0286 Hs1321585 G-protein beta subunit	OQU94281.1 WD domain-containing protein isoform 1 [Cladophiala phora immunda]	Guanine nucleotide-binding protein subunit beta OS=Cryptosporidium parvum OX=5116 GN=GB-1 PE=3 SV=1
A6648	-	-	GO:0005515(protein binding)	-	-	KOG2502 Hs6715610 Tub family proteins	RUS21594.1 tubby C-terminal-like domain-containing protein [Jimgerdemonia flammicorona]	Tubby-related protein 1 OS=Homo sapiens OX=9606 GN=TULP1 PE=1 SV=3
A6649	-	-	GO:0005515(protein binding)	K10268 FBXL2_20; F-box and leucine-rich repeat protein 2/20	-	KOG1947 At5g51370 Leucine rich repeat proteins, some proteins contain F-box	KAG0368829.1 hypothetical protein BGZ54_001083 [Gamsiella multivaricata]	-
A6650	-	-	-	-	-	-	-	-
A6651	-	-	-	-	-	-	-	-

A6652	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003899(DNA-directed 5'-3' RNA polymerase activity),GO:0008270(zinc ion binding)	K02999 RPA1, POLR1A; DNA-directed RNA polymerase I subunit RPA1 [EC:2.7.7.6]	map03020 RNA polymerase	-	ORX89086.1 beta and beta-prime subunits of DNA dependent RNA-polymerase [Basidiobolus meristosporus CBS 931.73]	DNA-directed RNA polymerase I subunit rpa1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rpa1 PE=1 SV=2
A6653	-	-	-	-	-	-	-	-
A6654	GO:0006334(nucleosome assembly)	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:00030527(structural constituent of chromatin)	-	-	-	-	-
A6655	-	-	-	-	-	-	-	-
A6656	GO:0030001(metal ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG1113 Hs4506065 cAMP-dependent protein kinase types I and II, regulatory subunit	RCH82577.1 hypothetical protein CU098_007497, partial [Rhizopus stolonifer]	cAMP-dependent protein kinase regulatory subunit OS=Hypocrea atroviridis OX=63577 GN=pkari1 PE=3 SV=1
A6657	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity),GO:0003676(nucleic acid binding),GO:0004519(endonuclease activity)	K14440 SMARCAL1, HARP; SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1 [EC:5.6.2.-]	-	KOG1000 Hs21071060 Chromatin remodeling protein HARP/SMARCAL1, DEAD-box superfamily	PJF18907.1 SNF2-related domain-containing protein [Paramicrosporidium saccamoebae]	DNA annealing helicase and endonuclease ZRANB3 OS=Mus musculus OX=10090 GN=Zranb3 PE=1 SV=1
A6658	-	-	-	-	-	-	-	-
A6659	-	-	-	-	-	-	-	-
A6660	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K16196 EIF2AK4; eukaryotic translation initiation factor 2-alpha kinase 4 [EC:2.7.11.1]	map04140 Autophagy - animal;map04138 Autophagy - yeast;map05160 Hepatitis C;map05162 Measles;map05168 Herpes simplex virus 1 infection	-	XP_007723539.1 PEK protein kinase [Capronia coronata CBS 617.96]	Dual specificity testis-specific protein kinase 1 OS=Homo sapiens OX=9606 GN=TESK1 PE=1 SV=2
A6661	GO:0006281(DNA repair),GO:0006284(base-excision repair)	-	GO:0003824(catalytic activity)	K01247 alkA; DNA-3-methyladenine glycosylase II [EC:3.2.2.21]	map03410 Base excision repair	KOG1918 At3g50880 3-methyladenine DNA glycosidase	KAG2195857.1 hypothetical protein INT47_012398 [Mucor saturninus]	DNA-3-methyladenine glycosylase 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=mag1 PE=1 SV=1
A6662	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-

A6663	-	-	GO:0003677(DNA binding),GO:0008270(zinc ion binding),GO:0005515(protein binding),GO:0003678(DNA helicase activity),GO:0005524(ATP binding)	K10300 FBH1, FBXO18; F-box DNA helicase 1 [EC:5.6.2.4]	-	-	ORY30505.1 P-loop containing nucleoside triphosphate hydrolase protein [Rhizoclostium globosum]	F-box DNA helicase protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=fbh1 PE=1 SV=2
A6664	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003677(DNA binding)	-	-	KOG0773 YGL096w Transcription factor MEI1 and related HOX domain proteins	PKS08989.1 hypothetical protein jhhlp_003602 [Lomentospora prolificans]	Homeobox protein 4 OS=Dictyostelium discoideum OX=44689 GN=hbx4 PE=3 SV=1
A6665	-	-	-	-	-	KOG0051 At5g41020 RNA polymerase I termination factor, Myb superfamily	KAF8592177.1 hypothetical protein K439DRAFT_1325062 [Ramaria rubella]	Transcriptional activator Myb OS=Gallus gallus OX=9031 GN=MYB PE=1 SV=1
A6666	-	-	-	-	-	KOG3589 Hs4506519 G protein signaling regulators	-	Regulator of G-protein signaling 5 OS=Sus scrofa OX=9823 GN=RGS5 PE=2 SV=1
A6667	-	-	-	-	-	-	-	-
A6668	-	-	-	-	-	-	-	-
A6669	-	-	GO:0005096(GTPase activator activity)	K12493 ARFGAP2_3; ADP-ribosylation factor GTPase-activating protein 2/3	map04144 Endocytosis	KOG0706 At4g17890_1 Predicted GTPase-activating protein	OAA54831.1 Arf GTPase activating protein [Sporothrix insectorum RCEF 264]	Probable ADP-ribosylation factor GTPase-activating protein AGD8 OS=Arabidopsis thaliana OX=3702 GN=AGD8 PE=1 SV=1
A6670	-	-	-	-	-	-	PKY43015.1 alpha/beta-hydrolase [Rhizophagus irregularis]	-
A6671	-	-	-	-	-	-	-	-
A6672	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K12872 RBM22, SLT11; pre-mRNA-splicing factor RBM22/SLT11	map03040 Spliceosome	KOG0153 7296892 Predicted RNA-binding protein (RRM superfamily)	KAG0140306.1 hypothetical protein CROQUODRAFT_665361 [Cronartium quercuum f. sp. fusiforme G11]	Pre-mRNA-splicing factor RBM22 OS=Danio rerio OX=7955 GN=rmb22 PE=2 SV=1
A6673	-	-	GO:0004089(carbonate dehydratase activity),GO:0008270(zinc ion binding)	-	-	KOG0382 At4g20990 Carbonic anhydrase	RIA97225.1 alpha carbonic anhydrase [Glomus cerebriforme]	Carbonic anhydrase OS=Pectobacterium atrosepticum (strainSCRI 1043 / ATCC BAA-672) OX=218491 GN=cah PE=3 SV=1

A6674	GO:0006487(protein N-linked glycosylation),GO:0006488(dolichol-linked oligosaccharide biosynthetic process)	GO:0016021(integral component of membrane)	GO:0016780(phosphotransferase activity, for other substituted phosphate groups),GO:0003975(UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase activity)	K01001 ALG7; UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [EC:2.7.8.15]	map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG2788 At3g57220 Glycosyltransferase	ORY04917.1 hypothetical protein K493DRAFT_322823 [Basidiobolus meristosporus CBS 931.73]	UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase OS=Dictyostelium discoideum OX=44689 GN=alg7 PE=3 SV=1
A6675	-	-	-	-	-	-	-	-
A6676	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02877 RP-L15e, RPL15; large subunit ribosomal protein L15e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1678 At4g17390 60s ribosomal protein L15	KNE62354.1 60S ribosomal protein L15, variant [Allomyces macrogynus ATCC 38327]	Large ribosomal subunit protein eL15z OS=Picea mariana OX=3335 GN=SB61 PE=2 SV=1
A6677	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K11230 SSK2; mitogen-activated protein kinase kinase [EC:2.7.11.25]	map04011 MAPK signaling pathway - yeast;map02020 Two-component system	KOG4645 YNR031c MAPKKK (MAP kinase kinase kinase) SSK2 and related serine/threonine protein kinases	XP_003679299.1 hypothetical protein TDEL_OA07560 [Torulaspora delbrueckii]	MAP kinase kinase kinase SSK2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSK2 PE=1 SV=1
A6678	GO:0036211(protein modification process),GO:0030001(metal ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005509(calcium ion binding),GO:0046873(metal ion transmembrane transporter activity)	-	-	-	XP_016611238.1 magnesium and cobalt transporter CorA [Spizellomyces punctatus DAOM BR117]	Cobalt/magnesium transport protein CorA OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=corA PE=1 SV=1
A6679	-	-	-	-	-	-	XP_025173902.1 kinase-like domain-containing protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	-
A6680	-	-	-	-	-	-	-	-
A6681	-	GO:0016021(integral component of membrane)	-	K03321 TC.SULP; sulfate permease, SulP family	-	-	KAF7741142.1 hypothetical protein DSO57_022241 [Entomophthora muscae]	Uncharacterized protein C24H6.11c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC24H6.11c PE=4 SV=1
A6682	-	-	-	-	-	-	-	-

A6683	GO:0006561(proline biosynthetic process)	-	GO:0004735(pyrroline-5-carboxylate reductase activity)	K00286 proC; pyrroline-5-carboxylate reductase [EC:1.5.1.2]	map01110 Biosynthesis of secondary metabolites;map00330 Arginine and proline metabolism;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways	KOG3124 At5g14800 Pyrroline-5-carboxylate reductase	KAG1716876.1 hypothetical protein [D866_289 [Astraeus odoratus]	Pyrroline-5-carboxylate reductase OS=Arabidopsis thaliana OX=3702 GN=PROC1 PE=2 SV=1
A6684	GO:0007165(signal transduction)	GO:0000159(protein phosphatase type 2A complex)	GO:0019888(protein phosphatase regulator activity)	K11584 PPP2R5; serine/threonine-protein phosphatase 2A regulatory subunit B'	map04071 Sphingolipid signaling pathway;map04728 Dopaminergic synapse;map04660 T cell receptor signaling pathway;map04261 Adrenergic signaling in cardiomyocytes;map03015 mRNA surveillance pathway;map04152 AMPK signaling pathway;map04151 PI3K-Akt signaling pathway;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04110 Cell cycle;map05165	KOG2085 At3g09880 Serine/threonine protein phosphatase 2A, regulatory subunit	ORY97639.1 phosphatase 2A regulatory B subunit-domain-containing protein [Syncephalastrium racemosum]	Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' beta isoform OS=Arabidopsis thaliana OX=3702 GN=B'BETA PE=1 SV=1
A6685	-	-	GO:0005515(protein binding)	-	-	-	RKP25256.1 outer membrane protein lml2/Tetratricopeptide repeat protein 39 [Syncephalis pseudoplumigaleata]	-
A6686	-	-	-	-	-	-	-	-
A6687	-	GO:0005666(RNA polymerase III complex)	GO:0003697(single-stranded DNA binding)	K03023 RPC3, POLR3C; DNA-directed RNA polymerase III subunit RPC3	map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway	KOG2587 Hs21359969 RNA polymerase III (C) subunit	ORX92951.1 hypothetical protein K493DRAFT_262953 [Basidiobolus meristosporus CBS 931.73]	DNA-directed RNA polymerase III subunit rpc3 OS=Dictyostelium discoideum OX=44689 GN=polr3c PE=3 SV=1
A6688	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6689	-	-	-	K17279 REEP5_6; receptor expression-enhancing protein 5/6	-	KOG1725 CE29340 Protein involved in membrane traffic (YOP1/TB2/DPI1/HVA22 family)	ORY05602.1 hypothetical protein K493DRAFT_274828 [Basidiobolus meristosporus CBS 931.73]	Receptor expression-enhancing protein 5 OS=Bos taurus OX=9913 GN=REEP5 PE=2 SV=1

A6690	GO:0045292(mRNA cis splicing, via spliceosome)	-	GO:0005515(protein binding)	K12821 PRPF40, PRPF40; pre-mRNA-processing factor 40	map03040 Spliceosome	-	KXS20412.1 RhoGAP-domain-containing protein, partial [Gonapodya prolifera JEL478]	-
A6691	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0163 Hs4826846 Myosin class VI heavy chain	KAF2219669.1 P-loop containing nucleoside triphosphate hydrolase protein [Elsinoe ampelina]	Myosin-3 OS=Arabidopsis thaliana OX=3702 GN=VIII-A PE=2 SV=1
A6692	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6693	-	-	-	-	-	-	-	-
A6694	-	-	-	-	-	-	RIB06927.1 regulator of G protein signaling domain-containing protein [Gigaspora rosea]	-
A6695	-	-	-	-	-	-	KAF9021586.1 hypothetical protein BDZ89DRAFT_1137933 [Hymenopellis radicata]	-
A6696	-	-	-	-	-	-	-	-
A6697	-	-	GO:0003824(catalytic activity)	K07517 EC1.2; Delta3-Delta2-enoyl-CoA isomerase [EC:5.3.3.8]	map00071 Fatty acid degradation	-	KAG2172688.1 hypothetical protein INT43_000035 [Umbelopsis isabellina]	Enoyl-CoA delta isomerase 1, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=EC1 PE=1 SV=1
A6698	-	-	-	-	-	-	-	-
A6699	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07905 RAB11B; Ras-related protein Rab-11B	map04144 Endocytosis;map04152 AMPK signaling pathway;map04962 Vasopressin-regulated water reabsorption;map05164 Influenza A	KOG0091 7290828 GTPase Rab39, small G protein superfamily	KAF9764961.1 Ras-related protein RABA1b [Nosema granulosis]	Ras-related protein RIC2 OS=Oryza sativa subsp. japonica OX=39947 GN=RIC2 PE=2 SV=2
A6700	-	-	-	-	-	-	-	-
A6701	GO:0060962(regulation of ribosomal protein gene transcription by RNA polymerase II)	-	GO:0005515(protein binding)	-	-	KOG2294 At3g07220 Transcription factor of the Forkhead/HNF3 family	-	-

A6702	GO:0009058(biosynthetic process), GO:0006646(phosphatidylethanolamine biosynthetic process)	-	GO:0003824(catalytic activity), GO:0004306(ethanolamine-phosphate cytidylyltransferase activity)	K00993 EPT1: ethanolamine phosphotransferase [EC:2.7.8.1]	map01110 Biosynthesis of secondary metabolites;map00440 Phosphonate and phosphinate metabolism;map00564 Glycerophospholipid metabolism;map00565 Ether lipid metabolism;map01100 Metabolic pathways	KOG2804 Hs4826888 Phosphorylcholine transferase/c holinephosphate cytidylyltransferase	TBU06410.1 putative ethanolamine-phosphate cytidylyltransferase, partial [Hamiltosporidium tvaerminensis]	Choline-phosphate cytidylyltransferase A OS=Rattus norvegicus OX=10116 GN=Pcyt1a PE=1 SV=2
A6703	-	-	-	-	-	KOG0431 At1g21660 Auxilin-like protein and related proteins containing DnaJ domain	CAF9926463.1 hypothetical protein HETSPECPRD_006340 [Heterodermis speciosa]	Auxilin-related protein 2 OS=Arabidopsis thaliana OX=3702 GN=At4g12770 PE=1 SV=1
A6704	-	-	-	-	-	-	-	-
A6705	GO:0006812(cation transport), GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015299(solute:proton antiporter activity)	K13989 DERL2_3; Derlin-2/3	map04141 Protein processing in endoplasmic reticulum	KOG0858 At4g04860 Predicted membrane protein	XP_016611749.1 hypothetical protein, variant [Spizellomyces punctatus DAOM BR117]	Derlin-2.1 OS=Zea mays OX=4577 GN=DER2.1 PE=2 SV=2
A6706	-	-	-	-	-	-	-	-
A6707	GO:0006397(mRNA processing), GO:0016567(protein ubiquitination)	-	GO:0008270(zinc ion binding), GO:0061630(ubiquitin protein ligase activity)	K15541 MPE1; protein MPE1	map03015 mRNA surveillance pathway	KOG0314 7291741.1 Predicted E3 ubiquitin ligase	RKP18288.1 DWNN-domain-containing protein, partial [Rozella allomyces CSF55]	E3 ubiquitin ligase PARAQUAT TOLERANCE 3 OS=Arabidopsis thaliana OX=3702 GN=PQT3 PE=1 SV=1
A6708	GO:0006011(UDP-glucose metabolic process)	-	GO:0070569(uridylyltransferase activity), GO:0003983(UTP:glucose-1-phosphate uridylyltransferase activity)	K00963 UGP2, galU, galF; UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]	map01250 Biosynthesis of nucleotide sugars;map00040 Pentose and glucuronate interconversions; map01110 Biosynthesis of secondary metabolites;map00541 O-Antigen nucleotide sugar biosynthesis;map01240 Biosynthesis of cofactors;map00052 Galactose metabolism;map00500 Starch and sucrose metabolism;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG2638 Hs13027638 UDP-glucose pyrophosphorylase	CDH56095.1 utp-glucose-1-phosphate uridylyltransferase [Lichtheimia corymbifera JMRC:FSU:9682]	UTP--glucose-1-phosphate uridylyltransferase OS=Bos taurus OX=9913 GN=UGP2 PE=1 SV=2
A6709	-	-	GO:0005515(protein binding)	-	-	KOG0619 Hs4826876 FOG: Leucine rich repeat	KNG49385.1 hypothetical protein TW65_03555 [Stemphylium lycopersici]	Osteomodulin OS=Homo sapiens OX=9606 GN=OMD PE=1 SV=1
A6710	-	-	-	-	-	-	-	-

A6711	-	-	GO:0004601(peroxidase activity),GO:0020037(heme binding)	K07223 yfeX; porphyrinogen peroxidase [EC:1.11.1.-]	-	-	XP_009152798.1 iron-dependent peroxidase [Exophiala dermatitidis NIH/UT8656]	Dye-decolorizing peroxidase YfeX OS=Escherichia coli (strain K12) OX=83333 GN=yfeX PE=1 SV=2
A6712	GO:0008610(lipid biosynthetic process)	-	GO:0050660(flavin adenine dinucleotide binding),GO:0003824(catalytic activity),GO:0008609(alkylglycerone-phosphate synthase activity),GO:0071949(FAD binding)	K00102 LDHD, dld; D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG1233 7303115 Alkyl-dihydroxyacetonephosphate synthase	TAQ84945.1 hypothetical protein B7494_g6733 [Chlorociboria aeruginascens]	Alkyl-dihydroxyacetonephosphate synthase OS=Drosophila melanogaster OX=7227 GN=ADPS PE=2 SV=1
A6713	GO:0005975(carbohydrate metabolic process)	-	GO:0042132(fructose 1,6-bisphosphate 1-phosphatase activity),GO:0016791(phosphatase activity)	K03841 FBP, fbp; fructose-1,6-bisphosphatase I [EC:3.1.3.11]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map04910 Insulin signaling pathway;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00051 Fructose and mannose metabolism;map00680 Methane metabolism;map00710 Carbon fixation in photosynthetic organisms;map04152 AMPK signaling pathway;map00030 Pentose	KOG1458 At1g43670 Fructose-1,6-bisphosphatase	ORY58664.1 fructose-1,6-bisphosphatase [Leucosporidium creatinivorum]	Fructose-1,6-bisphosphatase, cytosolic OS=Brassica napus OX=3708 PE=2 SV=1
A6714	-	-	-	-	-	-	-	-
A6715	GO:0036211(protein modification process)	-	GO:0008641(ubiquitin-like modifier activating enzyme activity)	K03178 UBE1, UBA1; ubiquitin-activating enzyme E1 [EC:6.2.1.45]	map04120 Ubiquitin mediated proteolysis;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease	KOG2012 Hs4507763 Ubiquitin activating enzyme UBA1	XP_566574.1 ubiquitin activating enzyme, putative [Cryptococcus neoformans var. neoformans JEC21]	Ubiquitin-like modifier-activating enzyme 1 OS=Oryctolagus cuniculus OX=9986 GN=UBA1 PE=1 SV=1
A6716	-	-	-	-	-	-	-	-
A6717	-	-	-	-	-	-	-	-
A6718	-	-	-	K08515 VAMP7; vesicle-associated membrane protein 7	map04130 SNARE interactions in vesicular transport	KOG0859 At5g11150 Synaptobrevin/VAMP-like protein	KXN65010.1 vesicle-associated membrane protein [Conidiobolus coronatus NRRL 28638]	Vesicle-associated membrane protein 713 OS=Arabidopsis thaliana OX=3702 GN=VAMP713 PE=1 SV=1

A6719	GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0005839(proteasome core complex)	GO:0004298(threonine-type endopeptidase activity)	K02738 PSMB6; 20S proteasome subunit beta 1 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0174[Hs14774499 20S proteasome, regulatory subunit beta type PSMB6/PSMB9/PRE3	RIA90941.1 proteasome subunit beta type-6 [Glomus cerebriforme]	Proteasome subunit beta type-6 OS=Mus musculus OX=10090 GN=Psm6 PE=1 SV=3
A6720	-	-	-	-	-	-	-	-
A6721	GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0046872(metal ion binding);GO:0000166(nucleotide binding);GO:0005215(transporter activity);GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity);GO:0043169(cation binding);GO:0005507(copper ion binding);GO:0019829(ATPase-coupled cation transmembrane transporter activity)	K17686 copA; ctpA, ATP7; P-type Cu+ transporter [EC:7.2.2.8]	map01524 Platinum drug resistance;map04978 Mineral absorption;map04016 MAPK signaling pathway - plant	KOG0207[At1g63440 Cation transport ATPase	KAG0286457.1 hypothetical protein BGZ96_009442 [Linnemannia gamsii]	Probable copper-transporting ATPase HMA5 OS=Arabidopsis thaliana OX=3702 GN=HMA5 PE=1 SV=2
A6722	-	-	-	-	-	-	-	-
A6723	-	-	-	-	-	-	-	-
A6724	-	-	-	-	-	-	-	-
A6725	-	-	-	-	-	-	-	-
A6726	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867[Hs4557333 Sulfatase	XP_024663337.1 Arylsulfatase I [Wickerhamia sorbophila]	Arylsulfatase I OS=Rattus norvegicus OX=10116 GN=Arsi PE=2 SV=1
A6727	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6728	-	-	GO:0005515(protein binding)	-	-	KOG1113[7296360 cAMP-dependent protein kinase types I and II, regulatory subunit	KAG1148153.1 hypothetical protein G6F38_003702 [Rhizopus oryzae]	cAMP-dependent protein kinase regulatory subunit OS=Aplysia californica OX=6500 PE=2 SV=2
A6729	-	-	-	-	-	-	ORX97189.1 hypothetical protein K493DRAFT_314163 [Basidiobolus meristosporus CBS 931.73]	UPF0598 protein C8orf82 OS=Homo sapiens OX=9606 GN=C8orf82 PE=1 SV=2

A6730	GO:0046854(phosphatidylinositol phosphate biosynthetic process), GO:0048015(phosphatidylinositol-mediated signaling)	-	GO:0016301(kinase activity)	K00914 PIK3C3, VPS34; phosphatidylinositol 3-kinase [EC:2.7.1.137]	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map04140 Autophagy - animal;map05132 Salmonella infection;map05131 Shigellosis;map04070 Phosphatidylinositol signaling system;map04138 Autophagy - yeast;map04136 Autophagy - other;map05022 Pathways of neurodegeneration - multiple diseases;map04371 Apelin signaling pathway;map00562 Inositol phosphate	KOG0904[HsM4505803 Phosphatidylinositol 3-kinase catalytic subunit (p110)	RKP20799.1 kinase-like protein, partial [Rozella allomyces CSF55]	Phosphatidylinositol 3-kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pikB PE=2 SV=2
A6731	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0003995(acyl-CoA dehydrogenase activity),GO:0020037(heme binding),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG0141[Hs4501857 Isovaleryl-CoA dehydrogenase	RIA94589.1 putative acyl-CoA dehydrogenase [Glomus cerebiforme]	Acyl-CoA dehydrogenase AFT10-1 OS=Alternaria alternata OX=5599 GN=AFT10-1 PE=3 SV=1
A6732	GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0031625(ubiquitin protein ligase binding)	K03349 APC2, ANAPC2; anaphase-promoting complex subunit 2	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG2165[At2g04660 Anaphase-promoting complex (APC), subunit 2	ORY03191.1 hypothetical protein K493DRAFT_207320, partial [Basidiobolus meristosporus CBS 931.73]	Anaphase-promoting complex subunit 2 OS=Arabidopsis thaliana OX=3702 GN=APC2 PE=1 SV=1
A6733	-	-	-	-	-	-	-	-
A6734	-	-	GO:0004499(N,N-dimethylaniline monooxygenase activity),GO:0050660(flavin adenine dinucleotide binding),GO:0050661(NADP binding)	-	-	KOG1399[At1g48910 Flavin-containing monooxygenase	XP_016604134.1 hypothetical protein SPPG_08480 [Spizellomyces punctatus DAOM BR117]	Baeyer-Villiger monooxygenase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA1538 PE=1 SV=1
A6735	-	-	-	-	-	-	-	-

A6736	GO:0001522(pseudouridine synthesis), GO:0009451(RNA modification), GO:0016192(vesicle-mediated transport)	GO:0030008(TRAPP complex)	GO:0003723(RNA binding), GO:0009982(pseudouridine synthase activity)	K15454 PUS9; tRNA pseudouridine synthase [EC:5.4.99.28]	-	KOG1919 Hs17478211 RNA pseudouridylate synthases	KAG0175302.1 hypothetical protein DFO30_009574 [Apophysomycetes sp. BC1015]	Pseudouridylate synthase RPUSD2 OS=Homo sapiens OX=9606 GN=RPUSD2 PE=1 SV=2
A6737	-	-	-	-	-	-	-	-
A6738	GO:0006468(protein phosphorylation)	-	GO:0005509(calcium ion binding), GO:0005524(ATP binding), GO:0004672(protein kinase activity)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway; map05214 Glioma; map04921 Oxytocin signaling pathway; map04925 Aldosterone synthesis and secretion	KOG0032 At1g18890 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KIO19742.1 hypothetical protein M407DRAFT_16083 [Tulasnella calospora MUT 4182]	Calcium-dependent protein kinase 29 OS=Oryza sativa subsp. japonica OX=39947 GN=CPK29 PE=2 SV=1
A6739	-	-	-	-	-	KOG0769 Hs1453918 Predicted mitochondrial carrier protein	GBB83902.1 hypothetical protein RclHR1_10560012 [Rhizophagus clarus]	Peroxisomal membrane protein PMP34 OS=Mus musculus OX=10090 GN=Slc25a17 PE=1 SV=1
A6740	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG2816 Hs20533609 Predicted transporter ADD1 (major facilitator superfamily)	-	Hippocampus abundant transcript 1 protein OS=Homo sapiens OX=9606 GN=MFSD14A PE=1 SV=2
A6741	-	-	-	-	-	KOG2501 At1g60420 Thioredoxin, nucleoredoxin and related proteins	ORY48570.1 hypothetical protein BCR33DRAFT_714329 [Rhizoclostridium globosum]	Nucleoredoxin OS=Danio rerio OX=7955 GN=nxn PE=2 SV=1
A6742	-	-	-	-	-	-	-	-
A6743	-	-	GO:0005524(ATP binding), GO:0016887(ATP hydrolysis activity)	-	-	-	KNE55615.1 hypothetical protein AMAG_01504 [Allomyces macrogynus ATCC 38327]	Uncharacterized protein MJ0812 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ0812 PE=4 SV=1
A6744	-	-	GO:0005524(ATP binding), GO:0016887(ATP hydrolysis activity)	-	-	-	KNE55615.1 hypothetical protein AMAG_01504 [Allomyces macrogynus ATCC 38327]	Uncharacterized protein MJ0079 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ0079 PE=4 SV=1
A6745	GO:0006887(exocytosis)	GO:0000145(exocytosis)	-	-	-	-	-	-
A6746	-	-	GO:0042586(peptide deformylase activity)	-	-	KOG3137 At5g14660 Peptide deformylase	KAG0775491.1 hypothetical protein G6F22_013263 [Rhizopus oryzae]	Peptide deformylase 2 OS=Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) OX=103690 GN=def2 PE=3 SV=1

A6747	-	-	-	K13110 MFAP1; microfibrillar- associated protein 1	-	-	KAF7506229.1 hypothetical protein GJ744_01212 1 [Endocarpon pusillum]	-
A6748	-	-	-	K10276 FBXL10_11, KDM2; F-box and leucine- rich repeat protein 10/11 [EC:1.14.11.2 7]	map03083 Polycomb repressive complex	KOG1633 729 9136_1 F-box protein JEMMA and related proteins with JmjC, PHD, F- box and LRR domains	KAG1048728.1 hypothetical protein G6F43_00890 3 [Rhizopus delemar]	Lysine-specific demethylase 2A OS=Xenopus tropicalis OX=8364 GN=kdm2a PE=2 SV=1
A6749	-	-	-	K04097 HPGDS; prostaglandin -H2 D- isomerase / glutathione transferase [EC:5.3.99.2 2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00590 Arachidonic acid metabolism;map 00480 Glutathione metabolism;map 05204 Chemical carcinogenesis - DNA adducts;map011 00 Metabolic pathways	KOG1695 CE 22420 Glutathione S-transferase	TPX74949.1 hypothetical protein CcCBS67573_ g03788 [Chytriumyce s confervae]	Glutathione S-transferase 1 OS=Ascaris suum OX=6253 GN=GST1 PE=1 SV=3
A6750	-	-	-	K04097 HPGDS; prostaglandin -H2 D- isomerase / glutathione transferase [EC:5.3.99.2 2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00590 Arachidonic acid metabolism;map 00480 Glutathione metabolism;map 05204 Chemical carcinogenesis - DNA adducts;map011 00 Metabolic pathways	KOG1695 CE 22421 Glutathione S-transferase	ORY53224.1 thioredoxin- like protein [Rhizoclosma tium globosum]	Glutathione S-transferase 1 OS=Ascaris suum OX=6253 GN=GST1 PE=1 SV=3
A6751	-	-	-	-	-	KOG4170 Hs1 9923233_2 2- enoyl-CoA hydratase/3- hydroxyacyl- CoA dehydrogena se/Peroxisom al 3- ketoacyl- CoA-thiolase, sterol- binding domain and related enzymes	POS80285.1 oleate- induced peroxisomal protein [Diaporthe helianthi]	Sterol carrier protein 2 OS=Homo sapiens OX=9606 GN=SCP2 PE=1 SV=2

A6752	-	-	-	K04097 HPGDS; prostaglandin -H2 D- isomerase / glutathione transferase [EC:5.3.99.2 2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00590 Arachidonic acid metabolism;map 00480 Glutathione metabolism;map 05204 Chemical carcinogenesis - DNA adducts;map011 00 Metabolic pathways	KOG1695 CE 14870 Glutathione S-transferase	TPX74949.1 hypothetical protein CcCBS67573_ g03788 [Chytriomyc s confervae]	Glutathione S-transferase 1 OS=Ascaris suum OX=6253 GN=GST1 PE=1 SV=3
A6753	-	-	GO:0003824(cat alytic activity)	K12663 ECH1; Delta3,5- Delta2,4- dienoyl-CoA isomerase [EC:5.3.3.21]	map04146 Peroxisome	KOG1680 At4 g16210 Enoyl-CoA hydratase	XP_03102546 9.1 uncharacteriz ed protein SmJEL517_g0 2574 [Synchytrium microbalum]	Probable enoyl-CoA hydratase echA12 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=echA12 PE=3 SV=1
A6754	-	-	GO:0003824(cat alytic activity)	K12663 ECH1; Delta3,5- Delta2,4- dienoyl-CoA isomerase [EC:5.3.3.21]	map04146 Peroxisome	KOG1680 At4 g16210 Enoyl-CoA hydratase	XP_03102546 9.1 uncharacteriz ed protein SmJEL517_g0 2574 [Synchytrium microbalum]	Probable enoyl-CoA hydratase echA12 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=echA12 PE=3 SV=1
A6755	-	-	GO:0046872(met al ion binding);GO:000 5524(ATP binding);GO:014 0658(ATPase- dependent chromatin remodeler activity)	K15711 SMARCA3, HLTF; SWI/SNF- related matrix- associated actin- dependent regulator of chromatin subfamily A3 [EC:5.6.2. 2.3.2.27]	-	KOG1001 At5 g22750 Helicase-like transcription factor HLTF/DNA helicase RAD5, DEAD-box superfamily	KXS19842.1 hypothetical protein M427DRAFT_ 66950 [Gonapodya prolifera JEL478]	DNA repair protein RAD5A OS=Arabidopsis thaliana OX=3702 GN=RAD5A PE=1 SV=1
A6756	-	-	GO:0016616(oxi doreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor);GO:00 51287(NAD binding);GO:000 3979(UDP- glucose 6- dehydrogenase activity)	-	-	KOG2666 At3 g29360 UDP- glucose/GDP- mannose dehydrogena se	ORY95047.1 UDP- glucose/GDP- mannose dehydrogena se family, NAD binding domain- domain- containing protein [Syncephalast rum racemosum]	UDP-glucose 6-dehydrogenase 2 OS=Arabidopsis thaliana OX=3702 GN=UGD2 PE=1 SV=1

A6757	-	GO:0005737(cytoplasm),GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0005515(protein binding),GO:0003743(translation initiation factor activity)	K03246 EIF3; translation initiation factor 3 subunit I	-	KOG0643 At2g46290 Translation initiation factor 3, subunit i (eIF-3i)/TGF-beta receptor-interacting protein (TRIP-1)	ORX55906.1 WD40 repeat-like protein [Piromyces finnis]	Eukaryotic translation initiation factor 3 subunit I OS=Xenopus tropicalis OX=8364 GN=eif3i PE=2 SV=1
A6758	GO:0006801(superoxide metabolic process)	-	GO:0046872(metal ion binding)	K04565 SOD1; superoxide dismutase, Cu-Zn family [EC:1.15.1.1]	map05014 Amyotrophic lateral sclerosis;map04146 Peroxisome;map04213 Longevity regulating pathway - multiple species;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map05012 Parkinson disease;map05016 Huntington disease	KOG0441 At1g08830 Cu2+/Zn2+ superoxide dismutase SOD1	ORY04744.1 copper/zinc superoxide dismutase [Basidiobolus meristosporus CBS 931.73]	Superoxide dismutase [Cu-Zn] OS=Spinacia oleracea OX=3562 GN=SODCC PE=2 SV=1
A6759	GO:0006629(lipid metabolic process)	-	-	-	-	KOG2088 7292931 Predicted lipase/calmodulin-binding heat-shock protein	KAG2204711.1 hypothetical protein INT47_012007 [Mucor saturninus]	Diacylglycerol lipase-beta OS=Rattus norvegicus OX=10116 GN=Daglb PE=1 SV=1
A6760	-	-	-	K17065 DNM1L; dynamin 1-like protein [EC:3.6.5.5]	map04214 Apoptosis - fly;map04217 Necroptosis;map04139 Mitophagy - yeast;map04668 TNF signaling pathway;map04621 NOD-like receptor signaling pathway	-	TRX93943.1 hypothetical protein FHL15_005021 [Xylaria flabelliformis]	Dynamin-related protein dnm1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=dnm1 PE=3 SV=1
A6761	-	-	-	-	-	-	-	-
A6762	-	-	-	K15100 SLC25A1, CTP; solute carrier family 25 (mitochondrial citrate transporter), member 1	-	KOG0756 YBR291c Mitochondrial tricarboxylate/dicarboxylate carriers proteins	XP_001215573.1 conserved hypothetical protein [Aspergillus terreus NIH2624]	Mitochondrial citrate transporter B OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ctpB PE=3 SV=1

A6763	-	-	GO:0005524(ATP binding)	K06158 ABCF3; ATP-binding cassette, subfamily F, member 3	-	KOG0062 At1g64550 ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	XP_019040691.1 hypothetical protein WICANDRAFT_78110 [Wickerhamomyces anomalus NRRL Y-366-8]	ABC transporter F family member 3 OS=Arabidopsis thaliana OX=3702 GN=ABCF3 PE=1 SV=1
A6764	-	-	GO:0004462(lactoylglutathione lyase activity),GO:0046872(metal ion binding)	-	-	KOG2944 YML004c Glyoxalase	RPB08452.1 lactoylglutathione lyase [Morchella conica CCBA5932]	Glyoxalase I OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLO1 PE=1 SV=1
A6765	-	-	GO:0004462(lactoylglutathione lyase activity),GO:0046872(metal ion binding)	-	-	KOG2944 YML004c Glyoxalase	XP_019023684.1 glyoxalase I [Saitoella complicata NRRL Y-17804]	Glyoxalase I OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLO1 PE=1 SV=1
A6766	GO:0006096(glycolytic process)	-	GO:0004807(triose-phosphate isomerase activity)	K01803 TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00051 Fructose and mannose metabolism;map00710 Carbon fixation in photosynthetic organisms;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG1643 At3g55440 Triosephosphate isomerase	KAG0036754.1 triosephosphate isomerase [Podila clonocystis]	Triosephosphate isomerase, cytosolic OS=Secale cereale OX=4550 PE=2 SV=3
A6767	-	-	GO:0005515(protein binding)	K16794 PAFAH1B1, LIS1; platelet-activating factor acetylhydrolase IB subunit alpha	map00565 Ether lipid metabolism;map01100 Metabolic pathways	KOG4441 Hs17017982 Proteins containing BTB/POZ and Kelch domains, involved in regulatory/signal transduction processes	TKA34044.1 Nuclear distribution protein PAC1 [Hortaea thailandica]	Kelch-like protein 4 OS=Homo sapiens OX=9606 GN=KLHL4 PE=1 SV=2
A6768	-	-	-	K20523 SH3YL1; SH3 domain-containing YSC84-like protein 1	-	KOG1843 YHR016c Uncharacterized conserved protein	ANZ76542.1 BA75_03738T0 [Komagataella pastoris]	Protein YSC84 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YSC84 PE=1 SV=2
A6769	-	-	-	-	-	KOG1179 Hs4503653 Very long-chain acyl-CoA synthetase/fatty acid transporter	XP_016605871.1 hypothetical protein SPPG_06828 [Spizellomyces punctatus DAOM BR117]	Long-chain fatty acid transport protein 4 OS=Homo sapiens OX=9606 GN=SLC27A4 PE=1 SV=1
A6770	-	-	-	-	-	-	-	-

A6771	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0589 At1g54510 Serine/threonine protein kinase	KZV87993.1 kinase-like protein [Exidia glandulosa HHB12029]	Serine/threonine-protein kinase Nek1 OS=Arabidopsis thaliana OX=3702 GN=NEK1 PE=2 SV=2
A6772	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6773	-	-	GO:0005515(protein binding)	K19525 VPS13A_C; vacuolar protein sorting-associated protein 13A/C	-	KOG1809 YLL040c Vacuolar protein sorting-associated protein	ORY94972.1 hypothetical protein BCR43DRAFT_526091 [Syncephalastrum racemosum]	Intermembrane lipid transfer protein VPS13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VPS13 PE=1 SV=1
A6774	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A6775	GO:0006813(potassium ion transport),GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005249(voltage-gated potassium channel activity),GO:0005216(ion channel activity)	K10273 FBXL7; F-box and leucine-rich repeat protein 7	-	KOG0501 7293023 K+-channel KCNQ	KNE62879.1 hypothetical protein AMAG_18930 [Allomyces macrogynus ATCC 38327]	Cyclic nucleotide-gated channel cone photoreceptor subunit alpha OS=Gallus gallus OX=9031 PE=2 SV=1
A6776	-	-	-	-	-	KOG2947 Hs4557693 Carbohydrate kinase	PKC61520.1 Ribokinase-like protein, partial [Rhizophagus irregularis]	Ketohexokinase OS=Pongo abelii OX=9601 GN=KHK PE=3 SV=1
A6777	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A6778	-	-	-	-	-	-	-	Armadillo repeat-containing protein 1 OS=Gallus gallus OX=9031
A6779	-	-	GO:0003723(RNA binding)	-	-	-	XP_018293580.1 hypothetical protein PHYBLDRAFT_98829, partial [Phycomyces blakesleeana NRRL 1555(-)]	Pumilio domain-containing protein C6G9.14 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC6G9.14 PE=4 SV=1
A6780	-	-	-	-	-	-	-	-
A6781	GO:0045901(positive regulation of translational elongation),GO:0045905(positive regulation of translational termination)	-	GO:0003723(RNA binding),GO:0003746(translation elongation factor activity),GO:0043022(ribosome binding)	K03263 EIF5A; translation initiation factor 5A	-	KOG3271 YJR047c Translation initiation factor 5A (eIF-5A)	XP_024678149.1 eukaryotic translation initiation factor eIF-5A [Aspergillus novofumigatus IBT 16806]	Eukaryotic translation initiation factor 5A-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ANB1 PE=1 SV=3

A6782	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity);GO:0004965(G protein-coupled GABA receptor activity)	-	-	KOG1055 7300772 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	KAF9360258.1 Metabotropic GABA-B receptor subtype 2, isoform C [Mortierella sp. AD094]	Gamma-aminobutyric acid type B receptor subunit 2 OS=Rattus norvegicus OX=10116 GN=Gabbr2 PE=1 SV=2
A6783	GO:0006269(DNA replication, synthesis of RNA primer)	-	-	K02685 PRI2; DNA primase large subunit	map03030 DNA replication	KOG2267 Hs4506053 Eukaryotic-type DNA primase, large subunit	KAG2181188.1 hypothetical protein INT43_008770 [Umbelopsis isabellina]	Probable DNA primase large subunit OS=Arabidopsis thaliana OX=3702 GN=At1g67320 PE=2 SV=2
A6784	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6785	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6786	-	-	-	K12451 UER1; 3,5-epimerase/4-reductase [EC:5.1.3.-1.1.1.-]	map01250 Biosynthesis of nucleotide sugars;map01110 Biosynthesis of secondary metabolites;map00523 Polyketide sugar unit biosynthesis;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG0747 At1g63000 Putative NAD+-dependent epimerases	OTB17205.1 hypothetical protein K445DRAFT_315841 [Daldinia sp. EC12]	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana OX=3702 GN=NRS/ER PE=1 SV=1
A6787	GO:0006102(isocitrate metabolic process)	-	GO:0005509(calcium ion binding);GO:0004450(isocitrate dehydrogenase (NADP+) activity)	K00031 IDH1; IDH2, icd; isocitrate dehydrogenase [EC:1.1.1.42]	map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00480 Glutathione metabolism;map00720 Carbon fixation pathways in prokaryotes;map00020 Citrate cycle (TCA cycle);map05230 Central carbon metabolism in cancer;map01100 Metabolic pathways;map01100	-	OHW94457.1 isocitrate dehydrogenase [Colletotrichum incanum]	Isocitrate dehydrogenase [NAD(+)] 1, mitochondrial OS=Phaeodactylum tricornutum (strain CCAP 1055/1) OX=556484 GN=IDH1 PE=1 SV=2
A6788	GO:0006886(intracellular protein transport)	-	GO:0005515(protein binding);GO:0031267(small GTPase binding)	K18423 CSE1; CAS, XPO2; exportin-2 (importin alpha re-exporter)	map05132 Salmonella infection;map03013 Nucleocytoplasmic transport	KOG1992 Hs14786256 Nuclear export receptor CSE1/CAS (importin beta superfamily)	ORY01243.1 Cse1-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Exportin-2 OS=Oreochromis niloticus OX=8128 GN=cse1 PE=2 SV=1

A6789	GO:0046855(inositol phosphate dephosphorylation), GO:0046854(phosphatidylinositol phosphate biosynthetic process)	-	-	K01092 E3.1.3.25, IMPA, suhB; myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]	map01110 Biosynthesis of secondary metabolites;map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map00521 Streptomycin biosynthesis;map01100 Metabolic pathways	KOG3853 7292854 Inositol monophosphatase	KIH91816.1 myo-inositol-1(or 4)-monophosphatase [Sporothrix brasiliensis 5110]	3'(2'),5'-bisphosphate nucleotidase 1 OS=Dictyostelium discoideum OX=44689 GN=bpnt1 PE=3 SV=1
A6790	GO:0090305(nucleic acid phosphodiester bond hydrolysis)	-	GO:0004521(endoribonuclease activity)	-	-	-	-	-
A6791	-	-	-	-	-	-	-	-
A6792	-	-	-	-	-	-	-	-
A6793	-	-	-	-	-	-	-	-
A6794	-	-	GO:0005515(protein binding)	-	-	KOG1230 At5g50310 Protein containing repeated kelch motifs	XP_016609413.1 hypothetical protein SPPG_03186 [Spizellomyces punctatus DAOM BR117]	Kelch domain-containing protein 4 OS=Homo sapiens OX=9606 GN=KLHDC4 PE=1 SV=1
A6795	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0598 At3g08720 Ribosomal protein S6 kinase and related proteins	KNE67384.1 AGC/AKT protein kinase [Allomyces macrogynus ATCC 38327]	Ribosomal protein S6 kinase beta-2 OS=Mus musculus OX=10090 GN=Rps6kb2 PE=1 SV=1
A6796	GO:0006418(tRNA aminoacylation for protein translation)	GO:0005737(cytoplasm)	GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0016874(ligase activity),GO:0000166(nucleotide binding),GO:0003676(nucleic acid binding)	K01876 DARS2, aspS; aspartyl-tRNA synthetase [EC:6.1.1.12]	map00970 Aminoacyl-tRNA biosynthesis	KOG2411 7298349 Aspartyl-tRNA synthetase, mitochondrial	KAG0018553.1 hypothetical protein BGZ80_007027 [Entomortierella chlamydospora]	Aspartate--tRNA ligase OS=Thermus thermophilus (strain ATCC BAA-163 / DSM 7039 / HB27) OX=262724 GN=aspS PE=3 SV=1
A6797	-	-	GO:0016491(oxidoreductase activity)	K15303 AKR7; aflatoxin B1 aldehyde reductase	map00980 Metabolism of xenobiotics by cytochrome P450	-	KAG0346561.1 hypothetical protein BG005_000684 [Podila minutissima]	Aflatoxin B1 aldehyde reductase member 3 OS=Rattus norvegicus OX=10116 GN=Akr7a3 PE=1 SV=2
A6798	-	-	-	-	-	-	-	-
A6799	-	-	-	K09562 HSPBP1, FES1; hsp70-interacting protein	map04141 Protein processing in endoplasmic reticulum	KOG2160 At3g09350 Armadillo/beta-catenin-like repeat-containing protein	KZP33249.1 nucleotide exchange factors-like protein [Fibularhizoctonia sp. CBS 109695]	Nucleotide exchange factor SIL1 OS=Homo sapiens OX=9606 GN=SIL1 PE=1 SV=1

A6800	-	-	-	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ28687.1 LINE-1 retrotransposable element ORF2 protein, partial [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A6801	-	-	-	-	-	-	-	-
A6802	GO:0006508(proteolysis)	-	GO:0008270(zinc ion binding),GO:0008237(metalloproteinase activity)	-	-	KOG1046 At1g63770 Puromycin-sensitive aminopeptidase and related aminopeptidases	KAG0188465.1 hypothetical protein DFQ28_004805 [Apophysomyces sp. BC1034]	Puromycin-sensitive aminopeptidase OS=Arabidopsis thaliana OX=3702 GN=MPA1 PE=2 SV=1
A6803	-	-	-	-	-	-	-	-
A6804	-	-	GO:0005515(protein binding)	-	-	-	-	Probable serine/threonine-protein kinase roco6 OS=Dictyostelium discoideum OX=44689 GN=roco6 PE=3 SV=1
A6805	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005085(guanylnucleotide exchange factor activity)	K10352 MYH9s; myosin heavy chain 9/10/11/14	map05130 Pathogenic Escherichia coli infection;map04810 Regulation of actin cytoskeleton;map04814 Motor proteins;map04530 Tight junction;map04270 Vascular smooth muscle contraction	KOG0160 At4g28710 Myosin class V heavy chain	CAA62184.1 orf 06167, partial [Saccharomyces cerevisiae]	Myosin-3 OS=Arabidopsis thaliana OX=3702 GN=VIII-A PE=2 SV=1
A6806	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0059 At2g41700 Lipid exporter ABCA1 and related proteins, ABC superfamily	ORX93119.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	ABC transporter A family member 1 OS=Arabidopsis thaliana OX=3702 GN=ABCA1 PE=2 SV=2
A6807	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05643 ABCA3; ATP-binding cassette, subfamily A (ABC1), member 3	map02010 ABC transporters	KOG0059 At2g41700 Lipid exporter ABCA1 and related proteins, ABC superfamily	ORX93119.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	ABC transporter A family member 1 OS=Arabidopsis thaliana OX=3702 GN=ABCA1 PE=2 SV=2
A6808	-	-	GO:0016628(oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor)	-	-	KOG1196 At1g65560 Predicted NAD-dependent oxidoreductase	TRX92565.1 hypothetical protein FHL15_006492 [Xylaria flabelliformis]	Putative NADP-dependent oxidoreductase YfmJ OS=Bacillus subtilis (strain 168) OX=224308 GN=yfmJ PE=2 SV=1

A6809	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K23785 RCK2, CLK1; serine/threonine-protein kinase RCK2 [EC:2.7.11.1]	-	KOG0032[CE25046 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORY52947.1 Pkinase-domain-containing protein [Rhizoclostium globosum]	Calcium/calmodulin-dependent protein kinase type 1 OS=Caenorhabditis briggsae OX=6238 GN=cmk-1 PE=3 SV=4
A6810	-	-	GO:0003676(nucleic acid binding),GO:0005515(protein binding)	-	-	KOG2041[Hs22044174 WD40 repeat protein	TPX70337.1 hypothetical protein SpCBS45565.g01735 [Spizellomyces sp. 'palustris']	WD repeat-containing protein 35 OS=Rattus norvegicus OX=10116 GN=Wdr35 PE=1 SV=1
A6811	-	-	-	-	-	-	OON11209.1 hypothetical protein BSLG_00144 [Batrachochytrium salamandrivorans]	Cilia- and flagella-associated protein 65 (Fragment) OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP65 PE=1 SV=1
A6812	-	-	-	-	-	-	-	-
A6813	GO:0016559(peroxisome fission)	GO:0005779(integral component of peroxisomal membrane)	-	-	-	-	-	-
A6814	-	-	-	-	-	-	-	-
A6815	GO:0007166(cell surface receptor signaling pathway),GO:0006281(DNA repair)	GO:0016020(membrane),GO:0016021(integral component of membrane)	GO:0004519(endonuclease activity),GO:0004888(transmembrane signaling receptor activity)	K21813 ENDOV; endonuclease V [EC:3.1.26.-]	-	KOG4417[At4g31150 Predicted endonuclease	GES99960.1 endonuclease V [Rhizophagus clarus]	Endonuclease V OS=Mus musculus OX=10090 GN=Endov PE=1 SV=2
A6816	GO:0006284(base-excision repair),GO:0006281(DNA repair)	-	GO:0003824(catalytic activity)	K10773 NTHL1, nth; endonuclease III [EC:3.2.2.-4.2.99.18]	map03410 Base excision repair	KOG1921[Hs4505471 Endonuclease III	KAF8177586.1 DNA glycosylase [Pholiota molesta]	Endonuclease III-like protein 1 OS=Bos taurus OX=9913 GN=NTHL1 PE=2 SV=1
A6817	-	-	-	-	-	-	-	-
A6818	-	GO:0005634(nucleus)	GO:0003677(DNA binding),GO:0008270(zinc ion binding),GO:0003950(NAD+ ADP-ribosyltransferase activity),GO:0051287(NAD binding)	K10798 PARP2_3_4; poly [ADP-ribose] polymerase 2/3/4 [EC:2.4.2.30]	map04210 Apoptosis;map04212 Longevity regulating pathway - worm;map03410 Base excision repair	KOG1037[7289768 NAD+ ADP-ribosyltransferase Parp, required for poly-ADP ribosylation of nuclear proteins	XP_016611879.1 hypothetical protein SPPG_01296 [Spizellomyces punctatus DAOM BR117]	Poly [ADP-ribose] polymerase 1 OS=Gallus gallus OX=9031 GN=PARP1 PE=1 SV=2
A6819	-	-	-	-	-	KOG1296[7303347 Uncharacterized conserved protein	ORX70777.1 DUF866-domain-containing protein [Linderina pennisporea]	UPF0587 protein CG4646 OS=Drosophila melanogaster OX=7227 GN=CG4646 PE=2 SV=1
A6820	-	-	-	-	-	-	-	-
A6821	-	-	-	-	-	-	-	-
A6822	-	-	-	-	-	KOG4310[7300086 Synapse-associated protein	KAG0055881.1 Synapse-associated protein 1 [Gryganskiella cystojenkini]	Synapse-associated protein of 47 kDa OS=Drosophila melanogaster OX=7227 GN=Sap47 PE=1 SV=1

A6823	-	-	GO:0016836(hydro-lyase activity)	K17757 CARKD; ATP-dependent NAD(P)H-hydrate dehydratase [EC:4.2.1.93]	-	KOG3974[Hs8922654 Predicted sugar kinase	TPX62606.1 hypothetical protein PhCBS80983.g00346 [Powellomyces hirtus]	ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Pongo abelii OX=9601 GN=NAXD PE=2 SV=1
A6824	GO:0006508(proteolysis)	GO:0031012(extracellular matrix)	GO:0004222(metalloendopeptidase activity),GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity),GO:0008237(metalloproteinase activity)	-	-	KOG1012[At5g11100 Ca2+-dependent lipid-binding protein CLB1/vesicle protein vp115/Granophilin A, contains C2 domain	KAF9937275.1 hypothetical protein BGZ65_001612, partial [Modicella reniformis]	Matrilysin (Fragment) OS=Felis catus OX=9685 GN=MMP7 PE=2 SV=1
A6825	GO:0006406(mRNA export from nucleus)	-	GO:0005515(protein binding)	K14298 RAE1, GLE2; mRNA export factor	map05014 Amyotrophic lateral sclerosis;map03013 Nucleocytoplasmic transport;map05164 Influenza A	KOG0647[7291315 mRNA export protein (contains WD40 repeats)	CCA78052.1 probable SONA [Serendipita indica DSM 11827]	Protein Rae1 OS=Drosophila melanogaster OX=7227 GN=Rae1 PE=1 SV=1
A6826	-	-	GO:0005515(protein binding)	-	-	-	ORZ39705.1 WD40-repeat-containing domain protein [Catenaria anguillulae PL171]	-
A6827	-	-	-	-	-	-	-	-
A6828	-	-	-	-	-	-	-	-
A6829	-	-	-	-	-	-	-	-
A6830	GO:0009081(branch ed-chain amino acid metabolic process)	-	GO:0003824(catalytic activity),GO:0004084(branch ed-chain-amino acid transaminase activity)	K00826 E2.6.1.42, ilvE; branched-chain amino acid aminotransferase [EC:2.6.1.42]	map00770 Pantothenate and CoA biosynthesis;map01110 Biosynthesis of secondary metabolites;map00966 Glucosinolate biosynthesis;map01240 Biosynthesis of cofactors;map01230 Biosynthesis of amino acids;map00280 Valine, leucine and isoleucine degradation;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid	KOG0975[At5g65780 Branched chain aminotransferase BCAT1, pyridoxal phosphate enzymes type IV superfamily	ORX86787.1 branched-chain amino acid aminotransferase [Basisdiobolus meristosporus CBS 931.73]	Branched-chain-amino-acid aminotransferase OS=Helicobacter pylori (strain ATCC 700392 / 26695) OX=85962 GN=ilvE PE=3 SV=1
A6831	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	-
A6832	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	-	-	KOG0446[Hs6996005 Vacuolar sorting protein VPS1, dynamin, and related proteins	RHZ64153.1 hypothetical protein Glove_326g167 [Diversispora epigaea]	Dynamin-1-like protein OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=2
A6833	-	-	-	-	-	-	-	-

A6834	-	-	GO:0005509(cal cium ion binding)	-	-	-	KAF8123615. 1 hypothetical protein EV363DRAFT _1547333, partial [Boletus edulis]	-
A6835	GO:00065 69(trypto phan catabolic process), GO:00094 35(NAD biosynthe tic process)	GO:00057 37(cytopl asm)	GO:0030170(pyr idoxal phosphate binding),GO:003 0429(kynurenina se activity),GO:000 3824(catalytic activity)	K01556 KYNu, kynU; kynureninase [EC:3.7.1.3]	map01240 Biosynthesis of cofactors;map00 380 Tryptophan metabolism;map 01100 Metabolic pathways	KOG3846[Hs4 504937 L- kynurenine hydrolase	ORY05740.1 kynureninase -like protein [Basidiobolus meristosporu s CBS 931.73]	Kynureninase OS=Myxococcus xanthus (strain DK1622) OX=246197 GN=kynU PE=3 SV=1
A6836	GO:00068 86(intrace llular protein transport) GO:00161 92(vesicle - mediated transport)	GO:00160 20(membr ane)	-	K08493 VT11; vesicle transport through interaction with t- SNAREs 1	map04138 Autophagy - yeast;map04130 SNARE interactions in vesicular transport	KOG1666[At5 g39510 V- SNARE	KAF8558863. 1 V -snare- domain- containing protein [Xerocomus badius]	Vesicle transport v-SNARE 11 OS=Arabidopsis thaliana OX=3702 GN=VTI11 PE=1 SV=2
A6837	-	-	-	-	-	-	-	-
A6838	-	-	-	-	-	KOG0619[Hs2 0644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase roco5 OS=Dictyostelium discoideum OX=44689 GN=roco5 PE=3 SV=1
A6839	-	-	-	-	-	-	-	-
A6840	-	-	-	K01897 ACSL fadD; long- chain acyl- CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04 146 Peroxisome;map 04216 Ferroptosis;map 04714 Thermogenesis; map00061 Fatty acid biosynthesis;ma p02024 Quorum sensing;map011 00 Metabolic pathways;map01 212 Fatty acid metabolism;map 00071 Fatty acid degradation;ma p04920 Adipocytokine signaling pathway	KOG1256[Hs2 0070257 Long-chain acyl-CoA synthetases (AMP- forming)	EPZ36390.1 AMP-binding domain- containing protein [Rozella allomyces CSF55]	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Xenopus laevis OX=8355 GN=acsbg2 PE=2 SV=1
A6841	-	-	-	K01897 ACSL fadD; long- chain acyl- CoA synthetase [EC:6.2.1.3]	map03320 PPAR signaling pathway;map04 146 Peroxisome;map 04216 Ferroptosis;map 04714 Thermogenesis; map00061 Fatty acid biosynthesis;ma p02024 Quorum sensing;map011 00 Metabolic pathways;map01 212 Fatty acid metabolism;map 00071 Fatty acid degradation;ma p04920 Adipocytokine signaling pathway	KOG1256[Hs2 0070257 Long-chain acyl-CoA synthetases (AMP- forming)	PFH48184.1 hypothetical protein AMATHDRAF T_66061 [Amanita thiersii Skay4041]	Long-chain-fatty-acid--CoA ligase ACSBG2 OS=Gallus gallus OX=9031 GN=ACSBG2 PE=2 SV=2
A6842	-	-	-	-	-	-	-	-

A6843	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	-	-	KOG0160 At5g54280 Myosin class V heavy chain	KAF1798291.1 P-loop containing nucleoside triphosphate hydrolase protein [Mucor lusitanicus]	Myosin-I heavy chain OS=Dictyostelium discoideum OX=44689 GN=myol PE=1 SV=1
A6844	-	-	GO:0005254(chloride channel activity)	-	-	-	-	-
A6845	GO:0055085(transmembrane transport)	-	-	K15278 SLC35B4, YEA4; solute carrier family 35 (UDP-xylose/UDP-N-acetylglucosamine transporter), member B4	-	KOG1583 Hs14249528 UDP-N-acetylglucosamine transporter	GAN00720.1 UDP-xylose and UDP-N-acetylglucosamine transporter [Mucor ambiguus]	UDP-xylose and UDP-N-acetylglucosamine transporter OS=Danio rerio OX=7955 GN=slc35b4 PE=2 SV=1
A6846	GO:0006506(GPI anchor biosynthetic process)	-	GO:0051377(mannose-ethanolamine phosphotransferase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups)	K05288 PIGO, GPI ethanolamine phosphate transferase 3 subunit O [EC:2.7.-.-]	map00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis;map01100 Metabolic pathways	KOG2126 Hs12608 Glycosylphosphatidylinositol anchor synthesis protein	TPX66621.1 hypothetical protein SpCBS45565_g04325 [Spizellomyces sp. 'palustris']	GPI ethanolamine phosphate transferase 3 OS=Homo sapiens OX=9606 GN=PIGO PE=1 SV=3
A6847	GO:0000226(microtubule cytoskeleton organization)	-	GO:0008017(microtubule binding)	K16732 PRC1, ASE1, MAP65; Ase1/PRC1/MAP65 family protein	-	KOG4302 Hs4506039 Microtubule-associated protein essential for anaphase spindle elongation	OPB46706.1 hypothetical protein A0C28_0068300 [Trichoderma guizhouense]	Protein regulator of cytokinesis 1 OS=Mus musculus OX=10090 GN=Prc1 PE=1 SV=2
A6848	-	-	-	-	-	-	-	-
A6849	GO:0006401(RNA catabolic process)	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0003723(RNA binding),GO:0003724(RNA helicase activity)	K12598 MTR4, SKIV2L2; ATP-dependent RNA helicase DOB1 [EC:3.6.4.13]	map03018 RNA degradation	KOG0948 Hs14721269 Nuclear exosomal RNA helicase MTR4, DEAD-box superfamily	KAG2181792.1 hypothetical protein INT44_008607 [Umbelopsis vinacea]	Exosome RNA helicase MTR4 OS=Mus musculus OX=10090 GN=Mtrex PE=1 SV=1
A6850	-	-	-	-	-	-	-	-
A6851	-	-	-	-	-	-	-	-
A6852	-	-	-	-	-	-	-	-
A6853	-	-	-	-	-	KOG2557 7297242 Uncharacterized conserved protein, contains TLDc domain	KAF9917927.1 hypothetical protein BX616_010808, partial [Lobosporangium transversale]	MTOR-associated protein MEAK7 OS=Xenopus laevis OX=8355 GN=meak7 PE=2 SV=1
A6854	-	-	-	-	-	-	-	-
A6855	-	-	-	-	-	-	-	-

A6856	-	-	-	K05853 ATP2A; P- type Ca2+ transporter type 2A [EC:7.2.2.10]	map04024 cAMP signaling pathway;map04 022 cGMP-PKG signaling pathway;map04 020 Calcium signaling pathway;map05 415 Diabetic cardiomyopathy; map05414 Dilated cardiomyopathy; map05410 Hypertrophic cardiomyopathy; map05412 Arrhythmogenic right ventricular cardiomyopathy; map04919 Thyroid hormone signaling pathway;map04 380 Osteoclast differentiation;m ap04261 Adrenergic	KOG4383 Hs7 661986 Uncharacteriz ed conserved protein	OZJ02713.1 hypothetical protein BZG36_03847 [Bifiguratus adelaidae]	Transmembrane protein 94 OS=Mus musculus OX=10090 GN=Tmem94 PE=1 SV=1
A6857	-	GO:00164 59(myosin complex)	GO:0003774(mo tor activity);GO:000 3876(AMP binding)	K10356 MYO1; myosin I	map05130 Pathogenic Escherichia coli infection;map04 814 Motor proteins	KOG0162 Hs4 826844 Myosin class I heavy chain	RMV61385.1 hypothetical protein D0864_12947 [Gonapodya proliferans werneckii]	Myosin-K heavy chain OS=Dictyostelium discoideum OX=44689 GN=myoK PE=2 SV=1
A6858	-	-	-	-	-	-	-	-
A6859	GO:00091 68(purine ribonucle oside monopho sphate biosynthe tic process), GO:00322 64(IMP salvage)	-	GO:0019239(de aminase activity);GO:000 3876(AMP deaminase activity)	K01490 AMPD; AMP deaminase [EC:3.5.4.6]	map00230 Purine metabolism;map 01110 Biosynthesis of secondary metabolites;map 01232 Nucleotide metabolism;map 01100 Metabolic pathways	KOG1096 At2 g38280 Adenosine monophosph ate deaminase	KXS16152.1 AMP deaminase [Gonapodya proliferans JEL478]	Probable AMP deaminase OS=Oryza sativa subsp. japonica OX=39947 GN=AMPD PE=2 SV=1
A6860	-	-	GO:0016407(ace tyltransferase activity);GO:000 4596(peptide alpha-N- acetyltransferas e activity)	K20793 NAA50, NAT5; N- alpha- acetyltransfer ase 50 [EC:2.3.1.258 2.3.1.309]	-	KOG3138 CE 28316 Predicted N- acetyltransfer ase	CDS09010.1 hypothetical protein LRAMOS10 370 [Lichtheimia ramosa]	Histone acetyltransferase MCC1 OS=Arabidopsis thaliana OX=3702 GN=MCC1 PE=2 SV=1
A6861	-	-	-	-	-	-	-	-
A6862	GO:00193 46(transsu lfuration), GO:00065 20(cellular amino acid metabolic process)	-	GO:0003824(cat alytic activity);GO:003 0170(pyridoxal phosphate binding);GO:001 6765(transferase activity, transferring alkyl or aryl (other than methyl) groups)	K17069 MET17; O- acetylhomoserine/O- acetylserine sulfhydrylase [EC:2.5.1.49 2.5.1.47]	map01110 Biosynthesis of secondary metabolites;map 01200 Carbon metabolism;map 01120 Microbial metabolism in diverse environments;m ap01230 Biosynthesis of amino acids;map00920 Sulfur metabolism;map 01100 Metabolic pathways;map00 270 Cysteine and methionine metabolism	-	KXS99794.1 hypothetical protein AC578_8890 [Pseudocercos pora eumusae]	O-acetyl-L-homoserine sulphydrylase OS=Thermotoga maritima (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) OX=243274 GN=TM_0882 PE=1 SV=1
A6863	-	-	-	-	-	-	-	cGMP-dependent 3',5'-cGMP phosphodiesterase A OS=Dictyostelium discoideum OX=44689 GN=pdeD PE=1 SV=1

A6864	-	-	-	K08272 CAB39, MO25; calcium binding protein 39	map04152 AMPK signaling pathway;map04150 mTOR signaling pathway	KOG1566[Hs13569887 Conserved protein Mo25	TPX76410.1 hypothetical protein CcCBS67573_g02323 [Chytridiomycetes confervae]	Calcium-binding protein 39-like OS=Homo sapiens OX=9606 GN=CAB39L PE=1 SV=3
A6865	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A25; magnesium transporter	-	KOG2922[At3g26670 Uncharacterized conserved protein	XP_018741162.1 uncharacterized protein MSY001_2647 [Malassezia sympodialis ATCC 42132]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A6866	GO:0007031(peroxisome organization)	GO:0005779(integral component of peroxisomal membrane)	-	K13336 PEX3; peroxin-3	map04146 Peroxisome	KOG4444[Hs4505727 Peroxisomal assembly protein PEX3	ORX88320.1 Peroxin-3 [Basidiobolus meristosporus CBS 931.73]	Peroxisomal biogenesis factor 3 OS=Mus musculus OX=10090 GN=Pex3 PE=1 SV=1
A6867	-	-	-	-	-	-	XP_016606147.1 hypothetical protein SPPG_06516 [Spizellomyces punctatus DAOM BR117]	-
A6868	GO:0009165(nucleotide biosynthetic process)	-	GO:000287(magnesium ion binding);GO:0004749(ribose phosphate diphosphokinase activity)	-	-	KOG1448[At2g44530 Ribose-phosphate pyrophosphokinase	KGQ02247.1 Ribose-phosphate pyrophosphokinase [Beauveria bassiana D1-5]	Ribose-phosphate pyrophosphokinase OS=Wolinella succinogenes (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W) OX=273121 GN=prs PE=3 SV=1
A6869	-	-	-	K03953 NDUF9; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 9	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG2865[Hs6681764 NADH:ubiquinone oxidoreductase, NDUF9/39kDa subunit	PKY38175.1 putative NADH2 dehydrogenase 40K chain [Rhizophagus irregularis]	NADH-ubiquinone oxidoreductase 40 kDa subunit, mitochondrial OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=nuo40 PE=1 SV=2

A6870	GO:0006006(glucose metabolic process)	-	GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor);GO:0051287(NAD binding);GO:0050661(NADP binding)	K00134 GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]	map05415 Diabetic cardiomyopathy; map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00710 Carbon fixation in photosynthetic organisms;map0	-	KXN71502.1 glyceraldehyde-3-phosphate dehydrogenase [Conidiobolus coronatus NRRL 28638]	Glyceraldehyde-3-phosphate dehydrogenase OS=Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) OX=630626 GN=gapA PE=3 SV=1
A6871	GO:0045017(glycerolipid biosynthetic process)	-	GO:0004144(diacylglycerol O-acyltransferase activity);GO:0008374(O-acyltransferase activity)	-	-	-	ORX94049.1 hypothetical protein K493DRAFT_302292 [Basidiobolus meristosporus CBS 931.73]	Putative diacylglycerol O-acyltransferase MT1468 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=MT1468 PE=3 SV=1
A6872	-	-	GO:0016491(oxidoreductase activity)	-	-	-	KAF9122876.1 hypothetical protein BGX30_001738 [Mortierella sp. GBA39]	Uncharacterized oxidoreductase YtbE OS=Bacillus subtilis (strain 168) OX=224308 GN=ytbE PE=1 SV=1
A6873	-	GO:0016459(myosin complex)	GO:0005515(protein binding);GO:0003774(motor activity);GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160[CE26365 Myosin class V heavy chain	KDB12926.1 putative myosin MYO2 [Ustilaginoides virens]	Unconventional myosin-Vb OS=Rattus norvegicus OX=10116 GN=Myo5b PE=1 SV=1
A6874	-	-	-	-	-	-	TPX70211.1 hypothetical protein SpCBS45565_g01978 [Spizellomyces sp. 'palustris']	AIG2-like protein D OS=Arabidopsis thaliana OX=3702 GN=AIG2LD PE=2 SV=1
A6875	-	-	-	-	-	-	-	-
A6876	GO:0071805(potassium ion transmembrane transport)	GO:0016020(membrane)	GO:0005267(potassium channel activity);GO:0005509(calcium ion binding)	K05389 KCNKF; potassium channel subfamily K, other eukaryote	-	KOG1418[At5g46370 Tandem pore domain K+ channel	RMY23596.1 hypothetical protein D0867_01946 [Hortaea werneckii]	Two-pore potassium channel 2 OS=Arabidopsis thaliana OX=3702 GN=TPK2 PE=2 SV=1

A6877	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG4280 7295471 Kinesin-like protein	KAF5110022.1 hypothetical protein DV452_004594 [Geotrichum candidum]	Kinesin heavy chain OS=Strongylocentrotus purpuratus OX=7668 PE=2 SV=1
A6878	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG1287 At3g19553 Amino acid transporters	-	Probable polyamine transporter At3g19553 OS=Arabidopsis thaliana OX=3702 GN=At3g19553 PE=3 SV=1
A6879	-	-	-	K19951 TBC1D8_9; TBC1 domain family member 8/9	-	KOG2058 At3g07890 Ypt/Rab GTPase activating protein	TX10778.1 hypothetical protein VHUM_02283 [Vanrija humicola]	TBC1 domain family member 2B OS=Mus musculus OX=10090 GN=Tbc1d2b PE=1 SV=2
A6880	-	-	-	-	-	-	TPX66084.1 hypothetical protein SpCBS45565_g04730 [Spizellomyces sp. 'palustris']	-
A6881	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	TPX48083.1 hypothetical protein CcCBS67573_g10218 [Chytridiomycetes confervae]	Adenylate cyclase 1 OS=Rhizobium meliloti (strain 1021) OX=266834 GN=cya1 PE=3 SV=2
A6882	GO:0006566(threonine metabolic process)	-	GO:0004413(homoserine kinase activity),GO:0005524(ATP binding)	K00872 thrB; homoserine kinase [EC:2.7.1.39]	map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	-	CUA72373.1 homoserine kinase [Rhizoctonia solani]	Homoserine kinase OS=Carboxydotherrmus hydrogenoformans (strain ATCC BAA-161 / DSM 6008 / Z-2901) OX=246194 GN=thrB PE=3 SV=1

A6883	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	-	K13754 SLC24A6, NCKX6; solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	-	KOG1307[Hs9966787 K+ - dependent Ca2+/Na+ exchanger NCKX1 and related proteins	KAF8349075.1 Sodium/calcium exchanger protein-domain-containing protein [Amanita rubescens]	Sodium/potassium/calcium exchanger 5 OS=Homo sapiens OX=9606 GN=SLC24A5 PE=1 SV=1
A6884	-	-	-	-	-	-	-	-
A6885	-	-	-	-	-	-	-	-
A6886	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding),GO:0003899(DNA-directed 5'-3' RNA polymerase activity),GO:0008270(zinc ion binding)	K03009 RPABC4, RPB12, POLR2K; DNA-directed RNA polymerases I, II, and III subunit RPABC4	map03420 Nucleotide excision repair;map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway;map05016 Huntington disease	KOG3507[At5g41010 DNA-directed RNA polymerase, subunit RPB7.0	KAF2401443.1 polymerase II polypeptide K, 7.0kDa [Trichodelitschia bisporula]	DNA-directed RNA polymerases II, IV and V subunit 12 OS=Arabidopsis thaliana OX=3702 GN=NRPB12 PE=1 SV=1
A6887	-	-	-	-	-	KOG2972[YGR021w Uncharacterized conserved protein	KAG0190122.1 hypothetical protein DFQ28_002485 [Apophysomyces sp. BC1034]	Probable transcriptional regulatory protein PERMA_0079 OS=Persephonella marina (strain DSM 14350 / EX-H1) OX=123214 GN=PERMA_0079 PE=3 SV=1
A6888	-	-	GO:0005085(guanylate nucleotide exchange factor activity),GO:0005515(protein binding)	K20047 PAN1; actin cytoskeleton-regulatory complex protein PAN1	-	KOG3519[7295440 Invasion-inducing protein TIAM1/CDC24 and related RhoGEF GTPases	XP_016612686.1 hypothetical protein SPPG_00363 [Spizellomyces punctatus DAOM BR117]	Myosin-M heavy chain OS=Dictyostelium discoideum OX=44689 GN=myoM PE=1 SV=1
A6889	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02978 RPS27e, RPS27; small subunit ribosomal protein S27e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1779[Hs4506711 40s ribosomal protein S27	TPX60298.1 hypothetical protein PhCBS80983_g01869 [Powellomyces hirtus]	Small ribosomal subunit protein eS27 OS=Bos taurus OX=9913 GN=RPS27 PE=1 SV=3
A6890	-	-	-	-	-	-	-	-
A6891	GO:0006499(N-terminal protein myristoylation)	-	GO:0004379(glycylpeptide N-tetradecanoyltransferase activity)	K00671 NMT; glycylpeptide N-tetradecanoyltransferase [EC:2.3.1.97]	-	KOG2779[Hs4758816 N-myristoyl transferase	TPX62464.1 hypothetical protein SpCBS45565_g07025 [Spizellomyces sp. 'palustris']	Glycylpeptide N-tetradecanoyltransferase 1 OS=Arabidopsis thaliana OX=3702 GN=NMT1 PE=1 SV=2
A6892	-	-	-	-	-	-	-	-

A6893	-	-	GO:0005509(cal- cium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04 022 cGMP-PKG signaling pathway;map04 020 Calcium signaling pathway;map05 417 Lipid and atherosclerosis; map05133 Pertussis;map04 722 Neurotrophin signaling pathway;map04 218 Cellular senescence;map 04070 Phosphatidyli- nitro signaling system;map0491 5 Estrogen signaling pathway;map04 912 GnRH signaling pathway;map04 910 Insulin	-	XP_958218.3 effhand- domain- containing protein [Neurospora crassa OR74A]	-
A6894	-	-	GO:0005515(pro- tein binding)	-	-	-	-	-
A6895	GO:0055085(trans- membrane transport)	GO:0016021(integra- l compo- nent of membran- e)	GO:0005524(ATP- binding);GO:014 0359(ABC-type transporter activity)	K05657 ABCB10; ATP-binding cassette, subfamily B (MDR/TAP), member 10	map02010 ABC transporters	KOG0058 Hs9 961244 Peptide exporter, ABC superfamily	KXS13731.1 ATP-binding cassette sub- family B member 10, mitochondria I [Gonapodya proliferans JEL478]	ATP-binding cassette sub-family B member 10, mitochondrial OS=Homo sapiens OX=9606 GN=ABCB10 PE=1 SV=2
A6896	GO:0006979(respon- se to oxidative stress)	-	GO:0004096(cata- lase activity);GO:002 0037(heme binding)	K03781 katE, CAT, catB, srpA; catalase [EC:1.11.1.6]	map05014 Amyotrophic lateral sclerosis;map041 46 Peroxisome;map 01110 Biosynthesis of secondary metabolites;map 04211 Longevity regulating pathway;map04 212 Longevity regulating pathway - worm;map04213 Longevity regulating pathway - multiple species;map012 00 Carbon metabolism;map 05022 Pathways of neurodegenerati- on - multiple diseases;map052 08 Chemical	KOG0047 CE 22477 Catalase	ORX80958.1 catalase [Basidiobolus meristosporus CBS 931.73]	Catalase OS=Pseudomonas putida OX=303 GN=kata PE=3 SV=1
A6897	GO:0055085(trans- membrane transport)	GO:0016021(integra- l compo- nent of membran- e)	-	K13754 SLC24A6, NCKX6; solute carrier family 24 (sodium/pota- ssium/calciu- m exchanger), member 6	-	KOG1307 729 7547 K+- dependent Ca2+/Na+- exchanger NCKX1 and related proteins	PGH35090.1 solute carrier family 24 (sodium/pota- ssium/calciu- m exchanger), member 6 [Emmonsia crescens]	Sodium/potassium/calcium exchanger 2 OS=Gallus gallus OX=9031 GN=SLC24A2 PE=2 SV=1
A6898	GO:0016573(histon- e acetylation)	GO:0000123(histon- e acetyltran- sferase complex), GO:0005634(nucleu- s)	-	K08874 TRRAP; transformati- on domain- associated protein	map03082 ATP- dependent chromatin remodeling;map 05166 Human T-cell leukemia virus 1 infection	KOG0889 Hs4 507691 Histone acetyltransfer- ase SAGA, TRRAP/TRAP1 component, PI-3 kinase superfamily	RKP06666.1 hypothetical protein THASP1DRAFT_18177, partial [Thamnoceph- alus sphaerospora]	Transformation/transcription domain-associated protein OS=Danio rerio OX=7955 GN=trrap PE=3 SV=1

A6899	-	-	-	K08874 TRRAP; transformatio n/transcriptio n domain-associated protein	map03082 ATP-dependent chromatin remodeling;map05166 Human T-cell leukemia virus 1 infection	KOG0889 At2g17930 Histone acetyltransferase SAGA, TRRAP/TRAI1 component, PI-3 kinase superfamily	KAF9114444.1 hypothetical protein BGX27_01083.1, partial [Mortierella sp. AM989]	Probable transcription-associated protein 1 OS=Dictyostelium discoideum OX=44689 GN=tra1 PE=3 SV=2
A6900	-	-	-	-	-	-	-	-
A6901	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004707(MAP kinase activity)	K04371 ERK, MAPK1_3; mitogen-activated protein kinase 1/3 [EC:2.7.11.24]	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map04730 Long-term depression;map05135 Yersinia infection;map05132 Salmonella infection;map05133 Pertussis;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04350 TGF-beta signaling pathway;map04810 Regulation	KOG0660 At2g18170 Mitogen-activated protein kinase	PRQ76642.1 mitogen-activated protein kinase [Rhodotorula toruloides]	Extracellular signal-regulated kinase 2 OS=Dictyostelium discoideum OX=44689 GN=erkB PE=1 SV=1
A6902	-	-	GO:0008270(zinc ion binding)	-	-	KOG1940 At1g74760 Zn-finger protein	ORX65214.1 zf-CHY-domain-containing protein [Anaeromyces robustus]	Zinc finger protein BRUTUS-like At1g74770 OS=Arabidopsis thaliana OX=3702 GN=At1g74770 PE=2 SV=1
A6903	-	GO:0005634(nucleus)	GO:0003676(nucleic acid binding),GO:0005515(protein binding)	K10610 DDB1; DNA damage-binding protein 1	map03420 Nucleotide excision repair;map05170 Human immunodeficiency virus 1 infection;map04120 Ubiquitin mediated proteolysis;map05203 Viral carcinogenesis; map05161 Hepatitis B	KOG1897 At4g05420 Damage-specific DNA binding complex, subunit DDB1	ORX91440.1 DNA damage-binding protein 1-like protein [Basidiobolus meristosporus CBS 931.73]	DNA damage-binding protein 1 OS=Oryza sativa subsp. japonica OX=39947 GN=DDB1 PE=1 SV=1
A6904	-	-	GO:0005515(protein binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K12196 VPS4; vacuolar protein-sorting-associated protein 4	map04144 Endocytosis;map03250 Viral life cycle - HIV-1;map04217 Necroptosis	KOG0740 HsM13376038 AAA+ -type ATPase	TPX61180.1 hypothetical protein PhCBS80983_g01257 [Powellomyces hirtus]	Dynein regulatory complex protein 11 OS=Mus musculus OX=10090 GN=lqca1 PE=2 SV=2
A6905	-	-	GO:0005515(protein binding)	-	-	-	OQD66695.1 hypothetical protein PENPOL_c004G02475 [Penicillium polonicum]	-

A6906	-	-	GO:0016407(acyltransferase activity)	-	-	-	KAA8898432.1 hypothetical protein TRICL_006561 [Trichomonas ciferrii]	-
A6907	GO:0000398(mRNA splicing, via spliceosome),GO:0006396(RNA processing)	-	GO:0005515(protein binding)	K12855 PRPF6, PRPF6; pre-mRNA-processing factor 6	map03040 Spliceosome	KOG0495[CE28858 HAT repeat protein	KAF6757076.1 PRP1 splicing factor, N-terminal-domain-containing protein [Coprinellus angulatus]	Pre-mRNA-splicing factor prp1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=prp1 PE=1 SV=1
A6908	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	-	-	KOG0616[Hs4826948 cAMP-dependent protein kinase catalytic subunit (PKA)	ORX81550.1 camp-dependent protein kinase [Anaeromyxobacterium robustus]	cAMP-dependent protein kinase catalytic subunit PRKX OS=Homo sapiens OX=9606 GN=PRKX PE=1 SV=1
A6909	-	-	GO:0005515(protein binding)	K17970 MDV1, FIS2; mitochondrial division protein 1	-	KOG0646[Hs14765579 WD40 repeat protein	KAF7856559.1 hypothetical protein EAF03_009633 [Botryotinia squamosa]	WD repeat-containing protein 18 OS=Bos taurus OX=9913 GN=WDR18 PE=2 SV=1
A6910	GO:0006974(cellular response to DNA damage stimulus)	-	GO:0016301(kinase activity),GO:0004674(protein serine/threonine kinase activity),GO:0005515(protein binding)	K04728 ATM, TEL1; serine-protein kinase ATM [EC:2.7.11.1]	map05131 Shigellosis;map04214 Apoptosis - fly;map04210 Apoptosis;map04218 Cellular senescence;map01524 Platinum drug resistance;map05170 Human immunodeficiency virus 1 infection;map03440 Homologous recombination; map05202 Transcriptional misregulation in cancer;map05206 MicroRNAs in cancer;map04115 p53 signaling pathway;map04110 Cell cycle;map04064 NF-kappa B signaling pathway;map04	KOG0892[At3g48190 Protein kinase ATM/Tel1, involved in telomere length regulation and DNA repair	ORX90217.1 hypothetical protein K493DRAFT_288362 [Basidiobolus meristosporus CBS 931.73]	Serine/threonine-protein kinase ATM OS=Arabidopsis thaliana OX=3702 GN=ATM PE=1 SV=1
A6911	-	-	-	-	-	-	KAF8273130.1 NADP+-dependent D-mannitol dehydrogenase [Lactarius quietus]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces ribosidificus OX=80859 GN=rbcM PE=3 SV=1

A6912	GO:0120029(proton export across plasma membrane)	GO:0016021(integral component of membrane)	GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0000166(nucleotide binding),GO:0008553(P-type proton-exporting transporter activity)	K01535 PMA1, PMA2; H+ - transporting ATPase [EC:7.1.2.1]	map00190 Oxidative phosphorylation; map01100 Metabolic pathways	KOG0205 At5g62670 Plasma membrane H+ - transporting ATPase	KAG2217510.1 hypothetical protein INT45_001797 [Mucor circinatus]	ATPase 11, plasma membrane-type OS=Arabidopsis thaliana OX=3702 GN=AHA11 PE=1 SV=1
A6913	-	-	-	-	-	KOG2641 Hs8922707 Predicted seven transmembrane receptor - rhodopsin family	RKP01525.1 hypothetical protein CXG81DRAFT_11886, partial [Caulochytrium protostelioides]	Transmembrane protein 184C OS=Pongo abelii OX=9601 GN=TMEM184C PE=2 SV=1
A6914	-	-	GO:0016491(oxidoreductase activity)	K25881 LARA; L-arabinose reductase [EC:1.1.1.-]	map00040 Pentose and glucuronate interconversions; map01100 Metabolic pathways	KOG1577 Hs5174391 Aldo/keto reductase family proteins	RDW62391.1 alcohol dehydrogenase-4 [Coleophoma cylindrospora]	Aldo-keto reductase family 1 member A1 OS=Bos taurus OX=9913 GN=AKR1A1 PE=2 SV=1
A6915	-	-	-	-	-	KOG4754 At5g64460 Predicted phosphoglycerate mutase	XP_016610192.1 hypothetical protein SPPG_02645 [Spizellomyces punctatus DAOM BR117]	Phosphoglycerate mutase-like protein 1 OS=Arabidopsis thaliana OX=3702 GN=At5g64460 PE=2 SV=1
A6916	-	-	-	-	-	-	-	-
A6917	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG0140 7295201 Medium-chain acyl-CoA dehydrogenase	TPX78214.1 hypothetical protein CCBS67573_g00559 [Chytriumyces confervae]	Acyl-CoA dehydrogenase apdG OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=apdG PE=2 SV=1
A6918	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG0139 CE24778 Short-chain acyl-CoA dehydrogenase	ORY49046.1 acyl-CoA dehydrogenase NM domain-like protein [Rhizoclostium globosum]	Acyl-CoA dehydrogenase apdG OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=apdG PE=2 SV=1
A6919	-	-	-	-	-	-	-	-
A6920	-	GO:0005854(nascent polypeptide-associated complex)	-	K03626 EGD2, NACA; nascent polypeptide-associated complex subunit alpha	map04928 Parathyroid hormone synthesis, secretion and action	KOG2239 At3g49470 Transcription factor containing NAC and TS-N domains	OZJ05040.1 hypothetical protein BZG36_02136 [Bifiguratus adalaidae]	Nascent polypeptide-associated complex subunit alpha OS=Xenopus laevis OX=8355 GN=naca PE=2 SV=1

A6921	GO:0036211(protein modification process)	-	-	-	-	KOG2158 7301565 Tubulin-tyrosine ligase-related protein	RKP00531.1 hypothetical protein CXG81DRAFT_26760 [Caulochytrium protostelioides]	Tubulin polyglutamylase TTL6 OS=Mus musculus OX=10090 GN=Ttl6 PE=1 SV=1
A6922	GO:0007186(G protein-coupled receptor signaling pathway), GO:0019236(response to pheromone)	-	-	-	-	KOG4290 Hs20545671 Predicted membrane protein	-	Integral membrane protein GPR180 OS=Xenopus laevis OX=8355 GN=gpr180 PE=2 SV=1
A6923	-	-	-	-	-	-	-	-
A6924	-	-	-	-	-	-	-	-
A6925	-	-	GO:0005515(protein binding)	-	-	KOG1862 Hs12007656 GYF domain containing proteins	XP_021876380.1 hypothetical protein BCR41DRAFT_290221, partial [Lobosporangium transversale]	GRB10-interacting GYF protein 1 OS=Homo sapiens OX=9606 GN=GIGYF1 PE=1 SV=2
A6926	-	-	-	-	-	KOG2668 7303053 Flotillins	PKC51857.1 Flotillin-domain-containing protein, partial [Rhizophagus irregularis]	Flotillin-2 OS=Drosophila melanogaster OX=7227 GN=Flot2 PE=2 SV=3
A6927	-	-	-	-	-	-	-	-
A6928	-	-	-	K06630 YWHAE; 14-3-3 protein epsilon	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04722 Neurotrophin signaling pathway;map04621 NOD-like receptor signaling pathway;map05203 Viral carcinogenesis; map04151 PI3K-Akt signaling pathway;map04011 MAPK signaling pathway - yeast;map04114 Oocyte meiosis;map04110 Cell cycle;map05160 Hepatitis C	-	XP_025523002.1 putative 14-3-3 family protein ArtA [Aspergillus japonicus CBS 114.51]	14-3-3 protein zeta OS=Aedes aegypti OX=7159 GN=14-3-zeta PE=2 SV=1
A6929	GO:0019290(siderophore biosynthetic process)	-	-	-	-	-	KAF3173877.1 hypothetical protein TWF225_009671 [Orbilia oligospora]	Uncharacterized protein y4xN OS=Sinorhizobium fredii (strain NBRC 101917 / NGR234) OX=394 GN=NGR_a00750 PE=3 SV=1
A6930	-	-	GO:0005515(protein binding)	K12562 AMPH; amphiphysin	map04144 Endocytosis;map04666 Fc gamma R-mediated phagocytosis	KOG2856 Hs20555436 Adaptor protein PACSIN	XP_016607795.1 hypothetical protein SPPG_05133 [Spizellomyces punctatus DAOM BR117]	Protein DD3-3 OS=Dictyostelium discoideum OX=44689 GN=DD3-3 PE=2 SV=1

A6931	-	-	-	K19219 JMD7; peptidyl-lysine (3S)-dioxygenase / protease [EC:1.14.11.6 3 3.4.-.-]	-	KOG2132[Hs14741442 Uncharacterized conserved protein, contains JmjC domain	TIA93989.1 hypothetical protein E3P97_00484 [Wallemia ichthyophaga]	HSPB1-associated protein 1 OS=Rattus norvegicus OX=10116 GN=Hspbap1 PE=1 SV=1
A6932	-	-	-	-	-	KOG2845[At3g47610 Activating signal cointegrator 1	XP_031023348.1 uncharacterized protein SmJEL517_g04739 [Synchytrium microbalum]	Activating signal cointegrator 1 OS=Homo sapiens OX=9606 GN=TRIP4 PE=1 SV=4
A6933	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08876 SCYL1; SCY1-like protein 1	-	KOG1243[7301824 Protein kinase	KAG2186953.1 hypothetical protein INT44_003181 [Umbelopsis vinacea]	Probable inactive serine/threonine-protein kinase scy1 OS=Dictyostelium discoideum OX=44689 GN=scy1 PE=3 SV=1
A6934	-	-	-	-	-	KOG3472[CE20418 Predicted small membrane protein	XP_025380476.1 DUF423-domain-containing protein [Acaromyces ingoldii]	UPF0382 membrane protein SAB0533 OS=Staphylococcus aureus (strain bovine RF122 / ET3-1) OX=273036 GN=SAB0533 PE=3 SV=1
A6935	GO:0007165(signal transduction)	GO:0016020(membrane)	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07827 KRAS, KRAS2; GTPase KRas	map04360 Axon guidance;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map04730 Long-term depression;map04810 Regulation of actin cytoskeleton;map05223 Non-small cell lung cancer;map04722 Neurotrophin signaling pathway;map04320 Dorsal-ventral axis formation;map04933 AGE-RAGE signaling pathway in diabetic complications;map04214 Apoptosis - fly;map04210	KOG0395[YO R101w Ras-related GTPase	OON10391.1 hypothetical protein BSLG_00768 [Batrachochytrium salamandrivorans]	Ras-like protein 1 OS=Physarum polycephalum OX=5791 GN=RAS1 PE=2 SV=1
A6936	GO:0006457(protein folding)	-	GO:0005515(protein binding),GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding)	K09553 STIP1; stress-induced-phosphoprotein 1	map05020 Prion disease	KOG0548[YO R027w Molecular co-chaperone STI1	XP_001647395.1 hypothetical protein Kpol_1018p69 [Vanderwaltozyma polyspora DSM 70294]	Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STI1 PE=1 SV=1
A6937	-	-	-	-	-	-	-	-
A6938	-	-	-	-	-	-	-	-
A6939	-	-	-	K10573 UBE2A, UBC2, RAD6A; ubiquitin-conjugating enzyme E2 A [EC:2.3.2.23]	map04120 Ubiquitin mediated proteolysis	KOG0419[At1g14400 Ubiquitin-protein ligase	XP_021883424.1 ubiquitin-conjugating enzyme E2 2 [Lobosporangium transversale]	Ubiquitin-conjugating enzyme E2 2 OS=Medicago sativa OX=3879 GN=UBC2 PE=2 SV=1

A6940	-	GO:0016021(integral component of membrane)	GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0000166(nucleotide binding)	K05853 ATP2A; P-type Ca2+ transporter type 2A [EC:7.2.2.10]	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05415 Diabetic cardiomyopathy;map05414 Dilated cardiomyopathy;map05410 Hypertrophic cardiomyopathy;map05412 Arrhythmogenic right ventricular cardiomyopathy;map04919 Thyroid hormone signaling pathway;map04380 Osteoclast differentiation;map04261 Adrenergic	KOG0202[YG1167c Ca2+ transporting ATPase	KAG1716274.1 hypothetical protein ID866_932 [Astraeus odoratus]	Probable cation-transporting ATPase F OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=ctpF PE=3 SV=1
A6941	-	-	-	-	-	-	-	-
A6942	GO:0019243(methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione)	-	GO:0004416(hydroxyacylglutathione hydrolase activity)	K01069 gloB, gloC, HAGH; hydroxyacylglutathione hydrolase [EC:3.1.2.6]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG0813[At2g31350 Glyoxylase	KXN65673.1 hydroxyacylglutathione hydrolase [Conidiobolus coronatus NRRL 28638]	Hydroxyacylglutathione hydrolase OS=Hyphomona neptunium (strain ATCC 15444) OX=228405 GN=gloB PE=3 SV=1
A6943	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003723(RNA binding),GO:0003735(structural constituent of ribosome)	-	-	KOG0378[Hs4506725 40S ribosomal protein S4	RKP23168.1 40S ribosomal protein S4-A [Syncephalis pseudoplumigaleata]	Small ribosomal subunit protein eS4 OS=Bombyx mori OX=7091 GN=RpS4 PE=2 SV=1
A6944	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K03097 CSNK2A; casein kinase II subunit alpha [EC:2.7.11.1]	map04310 Wnt signaling pathway;map04139 Mitophagy - yeast;map04137 Mitophagy - animal;map04712 Circadian rhythm - plant;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05235 PD-L1 expression and PD-1 checkpoint pathway in cancer;map04520 Adherens junction;map03008 Ribosome biogenesis in eukaryotes;map04064 NF-kappa B signaling	KOG0668[At2g23080 Casein kinase II, alpha subunit	XP_031027427.1 uncharacterized protein SmJEL517_g00549 [Synchytrium microbalum]	Casein kinase II subunit alpha-2 OS=Oryza sativa subsp. indica OX=39946 GN=HD6 PE=2 SV=1
A6945	GO:0006508(proteolysis)	GO:0005886(plasma membrane)	GO:0008233(peptidase activity),GO:0004252(serine-type endopeptidase activity)	-	-	KOG0725[CE02490_1 Reductases with broad range of substrate specificities	RKP27783.1 short chain dehydrogenase [Syncephalis pseudoplumigaleata]	Hydroxysteroid dehydrogenase-like protein 2 OS=Pongo abelii OX=9601 GN=HSDL2 PE=2 SV=1

A6946	GO:0006069(ethanol oxidation)	-	GO:0008270(zinc ion binding),GO:0051903(S-(hydroxymethyl)glutathione dehydrogenase activity),GO:0016491(oxidoreductase activity)	K00121 frmA, ADH5, adhC; S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00830 Retinol metabolism;map00680 Methane metabolism;map01220 Degradation of aromatic compounds;map	KOG0022 At5g43940 Alcohol dehydrogenase, class III	XP_016605194.1 alcohol dehydrogenase class-3 [Spizellomyces punctatus DAOM BR117]	Alcohol dehydrogenase class-3 OS=Oryza sativa subsp. indica OX=39946 GN=ADHIII PE=3 SV=1
A6947	-	GO:0016021(integral component of membrane)	-	-	-	-	TPX77521.1 hypothetical protein CcCBS67573_g01204 [Chytridiomycetes confervae]	UPF0324 membrane protein RPA1770 OS=Rhodospseudomonas palustris (strain ATCC BAA-98 / CGA009) OX=258594 GN=RPA1770 PE=3 SV=1
A6948	-	-	-	-	-	-	TPX72183.1 hypothetical protein SpCBS45565_g00426 [Spizellomyces sp. 'palustris']	-
A6949	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015297(antipporter activity),GO:0042910(xenobiotic transmembrane transporter activity)	K03327 TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family	-	KOG1347 YDR338c Uncharacterized membrane protein, predicted efflux pump	QFR37244.1 MATE transporter [Cyberlindnera americana]	Uncharacterized transporter YDR338C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YDR338C PE=1 SV=1
A6950	GO:0006520(cellular amino acid metabolic process)	-	GO:0004067(asparaginase activity)	K13278 ASPG; 60kDa lysophospholipase [EC:3.1.1.5 3.1.1.47 3.5.1.1]	-	KOG0503 CE20527 Asparaginase	ORY48356.1 Asparaginase/glutaminase, partial [Neocallimastix californiae]	L-asparaginase 1 OS=Escherichia coli O157:H7 OX=83334 GN=ansA PE=3 SV=1
A6951	GO:0000209(protein polyubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity),GO:0061630(ubiquitin protein ligase activity)	K10589 UBE3C; ubiquitin-protein ligase E3 C [EC:2.3.2.26]	map04120 Ubiquitin mediated proteolysis	KOG0942 At3g17205 E3 ubiquitin protein ligase	TNY22063.1 hypothetical protein DMC30DRAFT_173988, partial [Rhodotorula diobovata]	Ubiquitin-protein ligase E3B OS=Xenopus tropicalis OX=8364 GN=ube3b PE=2 SV=1

A6952	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11254 H4; histone H4	map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG3467 At1g07660 Histone H4	XP_025187259.1 histone-fold-containing protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Histone H4 variant TH011 OS=Triticum aestivum OX=4565 PE=3 SV=2
A6953	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11253 H3; histone H3	map05131 Shigellosis;map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05202 Transcriptional misregulation in cancer	KOG1745 Hs17442169 Histones H3 and H4	KAF4920343.1 histone H3 [Colletotrichum fructicola]	Histone H3.2 OS=Bos taurus OX=9913 PE=1 SV=2
A6954	GO:0009073(aromatic amino acid family biosynthetic process)	-	GO:0004107(chorismate synthase activity)	K01736 aroC: chorismate synthase [EC:4.2.3.5]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map01100 Metabolic pathways	KOG4492 YGL148w Chorismate synthase	KAF8475062.1 5-enolpyruvylshikimate-3-phosphate phospholyase [Kalahariturber pfeilii]	Chorismate synthase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC1223.14 PE=3 SV=2
A6955	-	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups),GO:0016746(acyltransferase activity)	K00626 ACAT, atoB; acetyl-CoA C-acyltransferase [EC:2.3.1.9]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00900 Terpenoid backbone biosynthesis;map01120 Microbial metabolism in diverse environments;map00720 Carbon fixation pathways in prokaryotes;map04975 Fat digestion and absorption;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00620 Pyruvate metabolism;map	KOG1390 At5g48230 Acetyl-CoA acetyltransferase	TPX56044.1 hypothetical protein PhCBS80983_g04847 [Powellomyces hirtus]	Acetyl-CoA acetyltransferase 2 OS=Arabidopsis thaliana OX=3702 GN=ACCT2 PE=1 SV=1

A6956	-	-	-	-	-	-	KXS19190.1 hypothetical protein M427DRAFT_132214 [Gonapodya prolifera JEL478]	-
A6957	-	GO:0005634(nucleus),GO:0005737(cytoplasm)	-	K06691 RPN13; 26S proteasome regulatory subunit N13	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG3037 7303250 Cell membrane glycoprotein	ORZ39455.1 proteasome complex subunit Rpn13 ubiquitin receptor- domain- containing protein [Catenaria anguillulae PL171]	Proteasomal ubiquitin receptor ADRM1 OS=Danio rerio OX=7955 GN=adrm1b PE=1 SV=1
A6958	-	-	-	-	-	-	-	-
A6959	-	-	-	-	-	-	-	-
A6960	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	KOG1694 At1g18540 60s ribosomal protein L6	RKP14782.1 ribosomal protein L6e- domain- containing protein [Piptocephalis cylindrospora]	Large ribosomal subunit protein eL6z OS=Arabidopsis thaliana OX=3702 GN=RPL6A PE=2 SV=1
A6961	GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K07179 RIOK2; RIO kinase 2 [EC:2.7.11.1]	map03008 Ribosome biogenesis in eukaryotes	KOG2268 Hs8922905 Serine/threonine protein kinase	XP_023462254.1 RIO1- domain- containing protein [Rhizopus microsporus ATCC 52813]	Serine/threonine-protein kinase rio2 OS=Dictyostelium discoideum OX=44689 GN=rio2 PE=3 SV=1
A6962	-	-	-	-	-	-	-	-
A6963	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	K08592 SEN1; sentrin- specific protease 1 [EC:3.4.22.68]	-	KOG0778 Hs7657550 Protease, Ulp1 family	RKP39788.1 hypothetical protein BJ085DRAFT_43705 [Dimargaris cristalligena]	Sentrin-specific protease 1 OS=Mus musculus OX=10090 GN=Senp1 PE=1 SV=1

A6964	GO:00454, 54(cell redox homeostasis)	-	GO:0016491(oxidoreductase activity),GO:0050660(flavin adenine dinucleotide binding),GO:0016668(oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor),GO:0004791(thioredoxin-disulfide reductase activity)	K00383 GSR, gor; glutathione reductase (NADPH) [EC:1.8.1.7]	map05415 Diabetic cardiomyopathy; map04918 Thyroid hormone synthesis;map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG4716 Hs22035670 Thioredoxin reductase	KXS12547.1 thioredoxin reductase TR2 [Gonapodya prolifera JEL478]	Thioredoxin reductase SEP1 OS=Emiliania huxleyi OX=2903 GN=SEP1 PE=1 SV=1
A6965	-	-	-	-	-	-	-	-
A6966	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6967	GO:0006520(cellular amino acid metabolic process)	-	GO:0030170(pyridoxal phosphate binding)	K01754 E4.3.1.19, ilvA, tdcB; threonine dehydratase [EC:4.3.1.19]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways	KOG1251 At4g11640 Serine racemase	XP_016608699.1 hypothetical protein SPPG_03783 [Spizellomyces punctatus DAOM BR117]	Serine racemase OS=Oryza sativa subsp. indica OX=39946 GN=OsI_16936 PE=3 SV=1
A6968	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0660 At3g45640 Mitogen-activated protein kinase	ORX89848.1 putative MAK2 protein [Basidiobolus meristosporus CBS 931.73]	Mitogen-activated protein kinase 3 OS=Arabidopsis thaliana OX=3702 GN=MPK3 PE=1 SV=2
A6969	-	-	-	-	-	-	-	-
A6970	-	-	-	-	-	-	-	-
A6971	GO:0006520(cellular amino acid metabolic process)	-	GO:0016491(oxidoreductase activity),GO:0016639(oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor)	K00262 E1.4.1.4, gdhA; glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	map00910 Nitrogen metabolism;map01120 Microbial metabolism in diverse environments;map00250 Alanine, aspartate and glutamate metabolism;map00220 Arginine biosynthesis;map01100 Metabolic pathways	KOG2250 Hs4885281 Glutamate/leucine/phenylalanine/valine dehydrogenases	CEP09594.1 hypothetical protein [Parasitella parasitica]	Glutamate dehydrogenase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=gluD PE=1 SV=1

A6972	-	-	-	-	-	-	KAG2179176.1 hypothetical protein INT43_002026 [Umbelopsis isabellina]	-
A6973	-	-	GO:0003824(catalytic activity)	K07511 ECHS1; enoyl-CoA hydratase [EC:4.2.1.17]	map00410 beta-Alanine metabolism;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00930 Caprolactam degradation;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00062 Fatty acid elongation;map00627 Aminobenzoate	KOG1679[7303420 Enoyl-CoA hydratase	KXS18728.1 ClpP/crotonase [Gonapodya prolifera JEL478]	3-hydroxybutyryl-CoA dehydratase-like protein, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=DDB_G0271866 PE=3 SV=1
A6974	-	-	-	K22066 BOLA1; BolA-like protein 1	-	KOG2313[Hs705638 Stress-induced protein UVI31+	XP_01660941.7.1 hypothetical protein SPPG_03190 [Spizellomyces punctatus DAOM BR117]	BolA-like protein 1 OS=Bos taurus OX=9913 GN=BOLA1 PE=2 SV=1
A6975	-	GO:0005634(nucleus)	-	-	-	KOG2330[Hs803155 Splicing factor 3b, subunit 2	XP_03892000.7.1 uncharacterized protein EI90DRAFT_3279743 [Cantharellus anzutake]	Splicing factor 3B subunit 2 OS=Mus musculus OX=10090 GN=Sf3b2 PE=2 SV=1
A6976	-	-	-	-	-	-	-	-
A6977	GO:0009058(biosynthetic process), GO:0006189('de novo' IMP biosynthetic process)	-	GO:0004644(phosphoribosylglycinamide formyltransferase activity)	K00601 E2.1.2.2; phosphoribosylglycinamide formyltransferase [EC:2.1.2.2]	map00230 Purine metabolism;map00670 One carbon pool by folate;map01110 Biosynthesis of secondary metabolites;map01100 Metabolic pathways	KOG3076[7297208_3 5'-phosphoribosylglycinamide formyltransferase	KGQ13720.1 Polyphosphate kinase [Beauveria bassiana D1-5]	Phosphoribosylglycinamide formyltransferase OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=purN PE=3 SV=1
A6978	GO:0016192(vesicle-mediated transport)	-	-	K12479 VPS45; vacuolar protein sorting-associated protein 45	map04144 Endocytosis;map04138 Autophagy - yeast	KOG1299[Hs18105063 Vacuolar sorting protein VPS45/Stt10 (Sec1 family)	XP_02187958.3.1 Sec1-like protein [Lobosporangium transversale]	Vacuolar protein sorting-associated protein 45 OS=Dictyostelium discoideum OX=44689 GN=vps45 PE=1 SV=1
A6979	-	-	-	K23541 TMEM165, GDT1; Ca2+/H+ antiporter, TMEM165/GDT1 family	-	KOG2881[At1g68650 Predicted membrane protein	KAF9364546.1 hypothetical protein BGX34_001211 [Mortierella sp. NVP85]	GDT1-like protein 5 OS=Arabidopsis thaliana OX=3702 GN=At1g68650 PE=1 SV=1

A6980	-	-	GO:0005515(protein binding)	K03364 CDH1, FZR1; cell division cycle 20-like protein 1, cofactor of APC complex	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04111 Cell cycle yeast;map04110 Cell cycle	KOG1524 CE25876 WD40 repeat-containing protein CHE-2	TPX69276.1 hypothetical protein SpCBS45565_g02595 [Spizellomyces sp. 'palustris']	Intraflagellar transport protein 80 homolog OS=Homo sapiens OX=9606 GN=IFT80 PE=1 SV=3
A6981	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At5g50180 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9512944.1 hypothetical protein BS47DRAFT_1344890 [Hydnum rufescens UP504]	Probable serine/threonine-protein kinase PkwA OS=Thermomonospora curvata OX=2020 GN=pkwa PE=1 SV=1
A6982	GO:0006887(exocytosis)	GO:000145(exocyst)	GO:0046983(protein dimerization activity)	-	-	KOG2286 CE02613 Exocyst complex subunit SEC6	KAF7588075.1 SNARE-binding exocyst subunit S6 [Aspergillus hancockii]	-
A6983	-	-	-	-	-	-	-	-
A6984	GO:0007156(homophilic cell adhesion via plasma membrane adhesion molecules)	GO:0016020(membrane)	GO:0005509(calcium ion binding)	-	-	KOG1219 Hs4885229 Uncharacterized conserved protein, contains laminin, cadherin and EGF domains	-	Protocadherin Fat 1 OS=Homo sapiens OX=9606 GN=FAT1 PE=1 SV=2
A6985	-	-	-	-	-	-	RKP05011.1 hypothetical protein THASP1DRAFT_33163 [Thamnocephalus sphaerospora]	-
A6986	-	-	GO:0005515(protein binding)	-	-	-	-	-
A6987	-	-	GO:0005515(protein binding)	-	-	KOG3179 YLR126c Predicted glutamine synthetase	XP_016609029.1 hypothetical protein SPPG_04086 [Spizellomyces punctatus DAOM BR117]	Putative glutamine amidotransferase YLR126C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YLR126C PE=1 SV=1
A6988	-	-	-	-	-	-	-	-
A6989	GO:0006465(signal peptide processing)	GO:0005787(signal peptidase complex), GO:0016021(integral component of membrane)	-	-	-	-	-	Signal peptidase complex subunit 2 OS=Arabidopsis thaliana OX=3702 GN=At2g39960 PE=2 SV=1
A6990	-	-	-	K19525 VPS13A_C; vacuolar protein sorting-associated protein 13A/C	-	-	KAF3765567.1 vacuolar protein sorting-associated protein 13 [Cryphonectria parasitica EP155]	Intermembrane lipid transfer protein VPS13 OS=Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719) OX=759272 GN=VPS13 PE=1 SV=1

A6991	GO:000613(potassium ion transport)	GO:0016021(integral component of membrane)	GO:0005242(inward rectifier potassium channel activity)	-	-	KOG3827 Hs4504835 Inward rectifier K+ channel	-	Inward rectifier potassium channel 2 OS=Gallus gallus OX=9031 GN=KCNJ2 PE=2 SV=1
A6992	-	-	GO:0005524(ATP binding),GO:0016301(kinase activity)	K00876 udk, UCK; uridine kinase [EC:2.7.1.48]	map00983 Drug metabolism - other enzymes;map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG4203 At3g27190 Armadillo/beta-Catenin/plakoglobin	KGQ13982.1 Uridine kinase [Beauveria bassiana D1-5]	Uridine kinase OS=Chloroflexus aurantiacus (strain ATCC 29366 / DSM 635 / J-10-fl) OX=324602 GN=udk PE=3 SV=1
A6993	GO:0016567(protein ubiquitination),GO:0003341(cilium movement),GO:0036158(outer dynein arm assembly)	GO:0005929(cilium)	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	CEH12291.1 hypothetical protein CBOM_00290 [Ceraceosorus bombacis]	E3 ubiquitin-protein ligase ipaH9.8 OS=Shigella dysenteriae serotype 1 (strain Sd197) OX=300267 GN=ipaH9.8 PE=3 SV=2
A6994	-	-	-	K16578 CLASP1_2; CLIP-associating protein 1/2	-	KOG2956 Hs2041059 CLIP-associating protein	XP_001223831.1 hypothetical protein CHGG_04617 [Chaetomium globosum CBS 148.51]	CLIP-associating protein 1-B OS=Xenopus laevis OX=8355 GN=clasp1b PE=1 SV=1
A6995	-	-	-	-	-	-	-	-
A6996	-	-	-	-	-	-	-	-
A6997	-	-	GO:0005515(protein binding),GO:0004386(helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K18995 DHX29; ATP-dependent RNA helicase DHX29 [EC:3.6.4.13]	-	KOG0920 Hs18559453 ATP-dependent RNA helicase A	KAG0259018.1 hypothetical protein DFQ27_004344 [Actinomortierella ambigua]	ATP-dependent RNA helicase dhx29 OS=Xenopus laevis OX=8355 GN=dhx29 PE=2 SV=1
A6998	-	-	GO:0004062(aryl sulfotransferase activity)	-	-	-	KDQ05763.1 hypothetical protein BOTBODRAFT_182244, partial [Botryobasidium botryosum FD-172 SS1]	-
A6999	-	-	GO:0004386(helicase activity)	K10706 SETX, ALS4; senataxin [EC:5.6.2.-]	map05014 Amyotrophic lateral sclerosis	KOG1801 At2g19120 tRNA-splicing endonuclease positive effector (SEN1)	RKP26206.1 AAA domain-containing protein, partial [Syncephalis pseudoplumigaleata]	Probable helicase MAGATAMA 3 OS=Arabidopsis thaliana OX=3702 GN=MAA3 PE=2 SV=1
A7000	-	-	-	-	-	-	-	-
A7001	-	-	GO:0005509(calcium ion binding)	-	-	KOG4619 CE26908 Uncharacterized conserved protein	-	Transmembrane protein 65 OS=Mus musculus OX=10090 GN=Tmem65 PE=1 SV=1

A7002	GO:0006886(intracellular protein transport), GO:0016192(vesicle-mediated transport), GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	GO:0030117(membrane coat), GO:0030126(COP1 vesicle coat)	GO:0005515(protein binding), GO:0005198(structural molecule activity)	K05236 COPA, RET1; coatamer subunit alpha	-	KOG0292 At1g62020 Vesicle coat complex COP1, alpha subunit	KAF9365122.1 hypothetical protein BGX34_011322 [Mortierella sp. NVP85]	Coatamer subunit alpha-1 OS=Arabidopsis thaliana OX=3702 GN=At1g62020 PE=2 SV=2
A7003	-	-	-	K12471 EPN; epsin	map04144 Endocytosis	KOG2056 At2g43160 Equilibrative nucleoside transporter protein	CEG74299.1 Putative Epsin-3 [Rhizopus microsporus]	Clathrin interactor EPSIN 2 OS=Arabidopsis thaliana OX=3702 GN=EPSIN2 PE=1 SV=1
A7004	-	-	-	-	-	-	-	-
A7005	GO:0005975(carbohydrate metabolic process), GO:0030259(lipid glycosylation)	-	GO:0016758(hexosyltransferase activity)	K05841 E2.4.1.173; sterol 3beta-glucosyltransferase [EC:2.4.1.173]	-	KOG1192 YLR189c UDP-glucuronosyl and UDP-glucosyl transferase	XP_001646967.1 hypothetical protein Kpol_2000p77 [Vanderwaltozyma polyspora DSM 70294]	Sterol 3-beta-glucosyltransferase OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294 / BCRC 21397 / CBS 2163 / NBRC 10782 / NRRL Y-8283 / UCD 57-17) OX=436907 GN=ATG26 PE=3 SV=1
A7006	-	-	GO:0016787(hydrolase activity), GO:0005524(ATP binding), GO:0016887(ATP hydrolysis activity)	K13525 VCP, CDC48; transitional endoplasmic reticulum ATPase	map05014 Amyotrophic lateral sclerosis; map04141 Protein processing in endoplasmic reticulum; map05134 Legionellosis; map05022 Pathways of neurodegeneration - multiple diseases	KOG0730 At3g09840 AAA+-type ATPase	RIA87139.1 transitional endoplasmic reticulum ATPase [Glomus cerebriforme]	Cell division cycle protein 48 homolog OS=Glycine max OX=3847 GN=CDC48 PE=2 SV=1
A7007	-	-	-	-	-	-	-	-
A7008	-	-	-	-	-	-	-	-
A7009	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7010	-	-	GO:0003677(DNA binding)	-	-	KOG0724 At4g01280 Zuotin and related molecular chaperones (DnaJ superfamily), contains DNA-binding domains	GBC23587.1 cytochrome-b5 reductase [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Protein REVEILLE 5 OS=Arabidopsis thaliana OX=3702 GN=RVE5 PE=2 SV=1

A7011	GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0019829(ATPase-coupled cation transmembrane transporter activity),GO:0000166(nucleotide binding)	-	-	KOG0207 At4g30110 Cation transport ATPase	RYO73631.1 hypothetical protein DL763_011550 [Monosporascus cannonballus]	Silver exporting P-type ATPase OS=Salmonella typhimurium OX=90371 GN=silP PE=1 SV=1
A7012	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	TPX76941.1 hypothetical protein CcCBS67573_g01807 [Chytridiomycota confervae]	-
A7013	-	-	-	-	-	-	-	-
A7014	GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015299(solute:proton antiporter activity)	K12041 SLC9A6_7, NHE6_7; solute carrier family 9 (sodium/hydrogen exchanger), member 6/7	map04260 Cardiac muscle contraction	KOG1965 At2g01980 Sodium/hydrogen exchanger protein	RYO79157.1 hypothetical protein DL763_009381 [Monosporascus cannonballus]	Sodium/hydrogen exchanger 8 OS=Arabidopsis thaliana OX=3702 GN=NHX8 PE=2 SV=1
A7015	-	-	-	-	-	-	-	-
A7016	-	-	GO:0008270(zinc ion binding)	K10661 MARCH6, DOA10; E3 ubiquitin-protein ligase MARCH6 [EC:2.3.2.27]	map04141 Protein processing in endoplasmic reticulum	KOG1609 At4g34100 Protein involved in mRNA turnover and stability	OZJ02188.1 hypothetical protein BZG36_05494, partial [Bifurcatus adalaidae]	E3 ubiquitin-protein ligase MARCH6 OS=Mus musculus OX=10090 GN=Marchf6 PE=2 SV=2
A7017	-	-	-	-	-	KOG1721 Hs1055982 FOG: Zn-finger	XP_001730733.1 hypothetical protein MGL_2187 [Malassezia globosa CBS 7966]	Zinc finger Y-chromosomal protein OS=Bos taurus OX=9913 GN=ZFYP PE=2 SV=1
A7018	-	-	GO:0016491(oxidoreductase activity)	K00326 CYB5R; cytochrome-b5 reductase [EC:1.6.2.2]	map00520 Amino sugar and nucleotide sugar metabolism	KOG0534 Hs4503327 NADH-cytochrome b-5 reductase	ORY05600.1 molybdopterin binding oxidoreductase [Basidiobolus meristosporus CBS 931.73]	NADH-cytochrome b5 reductase 2 OS=Xenopus laevis OX=8355 GN=cyb5r2 PE=2 SV=1

A7019	-	-	GO:0016740(transferase activity)	K00645 fabD; MCAT, MCT1; [acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]	map01110 Biosynthesis of secondary metabolites;map00333 Prodigiosin biosynthesis;map00061 Fatty acid biosynthesis;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG2926 At2g30200 Malonyl-CoA:ACP transacylase	CDS10730.1 hypothetical protein LRAMOSA11216 [Lichtheimia ramosa]	Malonyl CoA-acyl carrier protein transacylase OS=Bacillus subtilis (strain 168) OX=224308 GN=fabD PE=3 SV=2
A7020	-	-	-	-	-	-	-	-
A7021	GO:1902600(proton transmembrane transport)	GO:0000221(vacuolar proton-transporting V-type ATPase, V1 domain)	GO:0046961(proton-transporting ATPase activity, rotational mechanism)	K02144 ATPeV1H; V-type H+-transporting ATPase subunit H	map04145 Phagosome;map04142 Lysosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation;map05110 Vibrio cholerae infection;map04150 mTOR signaling pathway;map05120 Epithelial cell signaling in Helicobacter pylori infection;map05152 Tuberculosis;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG2759 Hs7706262 Vacuolar H+-ATPase V1 sector, subunit H	ORX88831.1 ATPase V1 complex subunit H [Basidiobolus meristosporus CBS 931.73]	V-type proton ATPase subunit H OS=Manduca sexta OX=7130 PE=2 SV=1
A7022	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A7023	-	-	GO:0005085(guanylate nucleotide exchange factor activity)	-	-	KOG4424 7295262 Predicted Rho/Rac guanine nucleotide exchange factor/faciogenital dysplasia protein 3	ORX70034.1 Dbl homology domain-containing protein [Linderina pennisporea]	Rac guanine nucleotide exchange factor JJ OS=Dictyostelium discoideum OX=44689 GN=gxjJ PE=1 SV=1
A7024	-	-	-	-	-	-	-	-
A7025	-	-	GO:0005524(ATP binding);GO:0046872(metal ion binding)	-	-	-	-	Dapdiamide A synthase OS=Enterobacter agglomerans OX=549 GN=ddaF PE=1 SV=1
A7026	GO:0016126(sterol biosynthetic process)	GO:0016020(membrane)	GO:0016628(oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor)	K00213 DHCR7; 7-dehydrocholesterol reductase [EC:1.3.1.21]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG1435 At1g50430 Sterol reductase/lamin B receptor	RKP39211.1 7-dehydrosteroid-delta 7-reductase [Dimargaris cristalligena]	7-dehydrocholesterol reductase OS=Arabidopsis thaliana OX=3702 GN=DWF5 PE=1 SV=1

A7027	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding),GO:0003824(catalytic activity)	K12603 CNOT6, CCR4; CCR4-NOT transcription complex subunit 6 [EC:3.1.13.4]	map03018 RNA degradation	KOG2338[Hs]4784709 Transcriptional effector CCR4-related protein	ESK92029.1 ccr4-not complex subunit ccr4 [Moniliophthora roreri MCA 2997]	2',5'-phosphodiesterase 12 OS=Mus musculus OX=10090 GN=Pde12 PE=1 SV=2
A7028	GO:0097720(calciur-mediated signaling)	-	GO:0005509(calcium ion binding),GO:0016787(hydrolase activity),GO:0033192(calmodulin-dependent protein phosphatase activity)	K04348 PPP3C, CNA; serine/threonine-protein phosphatase 2B catalytic subunit [EC:3.1.3.16]	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	-	XP_024732307.1 serine/threonine-protein phosphatase 2B catalytic subunit [Hyaloscypha bicolor E]	Serine/threonine-protein phosphatase 2B catalytic subunit OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=cna-1 PE=2 SV=2
A7029	-	-	GO:0050220(prostaglandin-E synthase activity)	-	-	KOG3029[At]5g42150 Glutathione S-transferase-related protein	-	Prostaglandin E synthase 2 OS=Bos taurus OX=9913 GN=PTGES2 PE=1 SV=3
A7030	GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0031625(ubiquitin protein ligase binding)	K10609 CUL4; cullin 4	map03420 Nucleotide excision repair;map05170 Human immunodeficiency virus 1 infection;map04120 Ubiquitin mediated proteolysis	KOG2167[Hs]3270467 Cullins	ORX91617.1 ubiquitin-protein ligase, cullin 4 [Basidiobolus meristosporus CBS 931.73]	Cullin-4 OS=Arabidopsis thaliana OX=3702 GN=CUL4 PE=1 SV=1
A7031	-	-	-	-	-	-	-	Selenoprotein W OS=Danio rerio OX=7955 GN=selenow PE=3 SV=3
A7032	-	-	GO:0003756(protein disulfide isomerase activity)	K13996 EPS1; protein disulfide-isomerase [EC:5.3.4.1]	map04141 Protein processing in endoplasmic reticulum	KOG0191[At]5g32920 Thioredoxin/protein disulfide isomerase	KAG2195285.1 hypothetical protein INT47_005060 [Mucor saturninus]	Thioredoxin domain-containing protein OS=Theileria parva OX=5875 GN=TP02_0602 PE=1 SV=1
A7033	-	-	-	-	-	-	KXS12932.1 hypothetical protein M427DRAFT_156967 [Gonapodya prolifera JEL478]	-
A7034	-	-	-	-	-	-	-	-
A7035	GO:0006470(protein dephosphorylation),GO:0006450(regulation of translational fidelity)	-	GO:0004725(protein tyrosine phosphatase activity)	-	-	KOG0792[Hs]8375648 Protein tyrosine phosphatase PTPMEG, contains FERM domain	KAG1458332.1 hypothetical protein G6F56_006418 [Rhizopus delemar]	Tyrosine-protein phosphatase non-receptor type 20 OS=Mus musculus OX=10090 GN=Ptpn20 PE=1 SV=1
A7036	-	-	GO:0005515(protein binding)	-	-	-	-	-

A7037	GO:0007165(signal transduction)	-	-	-	-	KOG0619 7300644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A7038	-	-	-	-	-	-	-	-
A7039	-	-	-	-	-	-	-	-
A7040	-	-	-	-	-	-	-	-
A7041	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015297(antipporter activity),GO:0042910(xenobiotic transmembrane transporter activity)	K03327 TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family	-	KOG1347 Hs8922709 Uncharacterized membrane protein, predicted efflux pump	KAF7505572.1 hypothetical protein GJ744_000652 [Endocarpon pusillum]	Multidrug and toxin extrusion protein 1 OS=Danio rerio OX=7955 GN=slc47a1 PE=2 SV=1
A7042	-	-	-	-	-	-	-	-
A7043	GO:0030490(maturation of SSU-rRNA)	-	-	-	-	-	-	-
A7044	-	-	-	-	-	-	-	-
A7045	GO:0006269(DNA replication, synthesis of RNA primer)	-	GO:0003896(DNA primase activity)	K02684 PR1; DNA primase small subunit [EC:2.7.7.102]	map03030 DNA replication	KOG2851 Hs4506051 Eukaryotic-type DNA primase, catalytic (small) subunit	ORZ22608.1 hypothetical protein BCR42DRAFT_459147 [Absidia repens]	DNA primase small subunit OS=Mus musculus OX=10090 GN=Prim1 PE=1 SV=1
A7046	GO:0008299(isoprenoid biosynthetic process), GO:0019287(isopentenyl diphosphate biosynthetic process, mevalonate pathway)	GO:0005829(cytosol)	GO:0016831(carboxy-lyase activity),GO:0005524(ATP binding),GO:0004163(diphosphomevalonate decarboxylase activity)	K01597 MVD, mvaD; diphosphomevalonate decarboxylase [EC:4.1.1.33]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis;map01100 Metabolic pathways	KOG2833 Hs4505289 Mevalonate pyrophosphate decarboxylase	CEI99330.1 Putative Diphosphomevalonate decarboxylase [Rhizopus microsporus]	Diphosphomevalonate decarboxylase OS=Mus musculus OX=10090 GN=Mvd PE=1 SV=2
A7047	-	-	-	-	-	KOG0500 7291472 Cyclic nucleotide-gated cation channel CNGA1-3 and related proteins	TPX75276.1 hypothetical protein CcCBS67573_g03454 [Chytridiomycetes confervae]	Cyclic nucleotide-gated cation channel beta-3 OS=Canis lupus familiaris OX=9615 GN=CNGB3 PE=1 SV=1
A7048	-	-	-	-	-	-	-	-
A7049	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity)	-	-	-	-	-
A7050	-	-	GO:0016757(glycosyltransferase activity)	-	-	KOG1111 At5g01220 N-acetylglucosaminyltransferase complex, subunit PIG-A/SPT14, required for phosphatidylinositol biosynthesis/Sulfolipid synthase	KAG2207156.1 hypothetical protein INT47_012209 [Mucor saturninus]	Uncharacterized glycosyltransferase MJ1607 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ1607 PE=3 SV=1
A7051	-	-	-	-	-	KOG4652 At1g67370 HORMA domain	-	Meiosis-specific protein ASY1 OS=Arabidopsis thaliana OX=3702 GN=ASY1 PE=1 SV=1
A7052	-	-	-	-	-	-	-	-

A7053	GO:0006611(protein export from nucleus)	-	GO:0005049(nuclear export signal receptor activity)	K14290 XPO1, CRM1, exportin-1	map03250 Viral life cycle - HIV-1;map03013 Nucleocytoplasmic transport;map04013 MAPK signaling pathway - fly;map03008 Ribosome biogenesis in eukaryotes;map05164 Influenza A;map05166 Human T-cell leukemia virus 1 infection	KOG2020 Hs20562336 Nuclear transport receptor CRM1/MSN5 (importin beta superfamily)	ORY44249.1 ARM repeat-containing protein [Neocallimastix californiae]	Exportin-6-A OS=Xenopus laevis OX=8355 GN=xpo6-a PE=1 SV=1
A7054	GO:0006166(purine ribonucleoside salvage)	-	GO:0004422(hypoxanthine phosphoribosyltransferase activity)	-	-	KOG3367 At1g71750 Hypoxanthine-guanine phosphoribosyltransferase	KAF9134322.1 hypothetical protein BGX30_011962 [Mortierella sp. GBA39]	Hypoxanthine-guanine phosphoribosyltransferase OS=Enterococcus faecalis (strain ATCC 700802 / V583) OX=226185 GN=hpt PE=3 SV=1
A7055	-	-	-	-	-	-	-	-
A7056	-	GO:0016021(integral component of membrane)	-	-	-	-	KAG0362075.1 hypothetical protein BG005_006731 [Podila minutissima]	-
A7057	-	-	-	-	-	KOG2501 CE01848 Thioredoxin, nucleoredoxin and related proteins	ORY00680.1 thioredoxin-like protein [Basidiobolus meristosporus CBS 931.73]	-
A7058	-	-	GO:0005524(ATP binding)	-	-	-	RHZ50627.1 hypothetical protein Glove_494g15 [Diversispora epigaea]	UPF0014 membrane protein slr1647 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=slr1647 PE=3 SV=1
A7059	-	-	-	-	-	-	-	-
A7060	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7061	-	-	-	-	-	-	-	-
A7062	-	-	-	-	-	-	-	-
A7063	-	-	GO:0003723(RNA binding);GO:0003676(nucleic acid binding)	K14411 MSI; RNA-binding protein Musashi	map03015 mRNA surveillance pathway	KOG0118 Hs13654587 FOG: RRM domain	CEP07067.1 hypothetical protein [Parasitella parasitica]	Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens OX=9606 GN=HNRNPA1L2 PE=2 SV=2
A7064	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 At2g20050 Serine/threonine protein phosphatase	ORY70686.1 protein serine/threonine phosphatase 2C [Neocallimastix californiae]	Probable protein phosphatase 2C 35 OS=Arabidopsis thaliana OX=3702 GN=At3g06270 PE=2 SV=1

A7065	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	EXX77417.1 hypothetical protein RirG_023950 [Rhizophagus irregularis DAOM 197198w]	-
A7066	-	GO:0005737(cytoplasm)	GO:0008641(ubiquitin-like modifier activating enzyme activity)	K08337 ATG7; ubiquitin-like modifier-activating enzyme ATG7	map04140 Autophagy - animal;map04216 Ferroptosis;map04138 Autophagy - yeast;map04136 Autophagy - other;map04613 Neutrophil extracellular trap formation	KOG2337[Hs5453668 Ubiquitin activating E1 enzyme-like protein	KAG2188952.1 hypothetical protein INT44_004094 [Umbelopsis vinacea]	Ubiquitin-like modifier-activating enzyme atg7 OS=Arabidopsis thaliana OX=3702 GN=ATG7 PE=1 SV=1
A7067	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7068	-	-	-	-	-	-	-	-
A7069	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07937 ARF1_2; ADP-ribosylation factor 1/2	map04144 Endocytosis;map05134 Legionellosis;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04072 Phospholipase D signaling pathway;map05110 Vibrio cholerae infection	KOG0070[At2g47170 GTP-binding ADP-ribosylation factor Arf1	OMJ11283.1 ADP-ribosylation factor [Smittium culicis]	ADP-ribosylation factor 1 OS=Arabidopsis thaliana OX=3702 GN=ARF1 PE=1 SV=2
A7070	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07937 ARF1_2; ADP-ribosylation factor 1/2	map04144 Endocytosis;map05134 Legionellosis;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04072 Phospholipase D signaling pathway;map05110 Vibrio cholerae infection	KOG0070[7296589 GTP-binding ADP-ribosylation factor Arf1	TPX71788.1 hypothetical protein SpCBS45565_g00959 [Spizellomyces sp. 'palustris']	ADP-ribosylation factor OS=Dugesia japonica OX=6161 PE=2 SV=3
A7071	-	-	-	-	-	-	-	-

A7072	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07937 ARF1_2; ADP-ribosylation factor 1/2	map04144 Endocytosis;map05134 Legionellosis;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04072 Phospholipase D signaling pathway;map05110 Vibrio cholerae infection	KOG0070 At2g47170 GTP-binding ADP-ribosylation factor Arf1	KAG0229635.1 Arf GTPase arf1 [Mortierella sp. GBA43]	ADP-ribosylation factor OS=Dugesia japonica OX=6161 PE=2 SV=3
A7073	GO:0016567(protein ubiquitination)	-	GO:0005515(protein binding),GO:0004842(ubiquitin-protein transferase activity)	-	-	-	XP_018759359.1 hypothetical protein FVEG_17066 [Fusarium verticillioides 7600]	Ankyrin repeat domain-containing protein 61 OS=Homo sapiens OX=9606 GN=ANKRD61 PE=4 SV=2
A7074	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08838 STK24_25_MST4; serine/threonine-protein kinase 24/25/MST4 [EC:2.7.11.1]	-	KOG0574 Hs16178962 STE20-like serine/threonine kinase MST	TPX56277.1 hypothetical protein PhC8S80983_g04651 [Powellomyces hirtus]	Serine/threonine-protein kinase 3 OS=Mus musculus OX=10090 GN=Stk3 PE=1 SV=1
A7075	-	-	GO:0016787(hydrolase activity)	K15428 DUG1; Cys-Gly metalloprotease DUG1 [EC:3.4.13.-]	map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG2276 Hs922699 Metalloexopeptidases	KAG4092015.1 Zn-dependent exopeptidase [Neocallimastix sp. JGI-2020a]	Cysteinylglycine-S-conjugate dipeptidase OS=Corynebacterium striatum OX=43770 GN=tpdA PE=1 SV=1
A7076	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A7077	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	XP_031026095.1 uncharacterized protein SmJEL517_g01946 [Synchytrium microbalum]	-
A7078	-	-	GO:0008237(metallopeptidase activity)	-	-	-	-	-
A7079	-	-	GO:0005515(protein binding)	-	-	KOG2127 At1g49040 Calmodulin-binding protein CRAG, contains DENN domain	KAF1734362.1 F-box/WD repeat-containing protein 7 [Beauveria bassiana]	DENN domain and WD repeat-containing protein SCD1 OS=Arabidopsis thaliana OX=3702 GN=SCD1 PE=1 SV=1
A7080	-	-	-	-	-	-	-	-

A7081	-	-	GO:0016787(hydrolase activity)	K03574 mutT, NUDT15, MTH2; 8-oxo-dGTP diphosphatase [EC:3.6.1.55]	-	-	KXL45991.1 hypothetical protein FE78DRAFT_121881, partial [Acidomyces sp. 'richmondensis']	-
A7082	-	GO:0016021(integral component of membrane)	-	-	-	-	KXN70243.1 hypothetical protein CONCODRAFT_17786 [Conidiobolus coronatus NRRL 28638]	Uncharacterized protein HI_1586 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_1586 PE=4 SV=1
A7083	-	GO:0016021(integral component of membrane)	-	-	-	-	KXN70243.1 hypothetical protein CONCODRAFT_17786 [Conidiobolus coronatus NRRL 28638]	Uncharacterized protein HI_1586 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_1586 PE=4 SV=1
A7084	GO:0006188(IMP biosynthetic process), GO:0009152(purine ribonucleotide biosynthetic process)	-	GO:0003824(catalytic activity),GO:0004018(N6-(1,2-dicarboxyethyl) AMP AMP-lyase (fumarate-forming) activity)	K01756 purB, ADSL; adenylsuccinate lyase [EC:4.3.2.2]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG2700 At1g36280 Adenylsuccinate lyase	KAG1461425.1 hypothetical protein G6F57_014142 [Rhizopus oryzae]	Adenylsuccinate lyase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=purB PE=1 SV=1
A7085	-	-	GO:0005515(protein binding)	-	-	KOG1007 Hs4507703 WD repeat protein TSSC1, WD repeat superfamily	OON07159.1 hypothetical protein BSLG_03316 [Batrachochytrium salamandrivorans]	EARP-interacting protein homolog OS=Xenopus laevis OX=8355 GN=eipr1 PE=2 SV=1
A7086	-	-	GO:0003723(RNA binding),GO:0005515(protein binding)	K13100 CWC22; pre-mRNA-splicing factor CWC22	-	KOG2140 At1g80930 Uncharacterized conserved protein	XP_00954221.7.1 hypothetical protein HETIRDRAFT_311406, partial [Heterobasidion irregulare TC 32-1]	Pre-mRNA-splicing factor CWC22 OS=Cryptococcus neoformans var. neoformans serotype D (strain B-3501A) OX=283643 GN=CWC22 PE=3 SV=1
A7087	GO:0006412(translation)	GO:0015934(large ribosomal subunit)	GO:0003735(structural constituent of ribosome),GO:0003723(RNA binding)	K02898 RPL26e, RPL26; large subunit ribosomal protein L26e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3401 Hs4506621 60S ribosomal protein L26	EPZ31907.1 60S ribosomal protein L26-2 [Rozella allomycis CSF55]	Ribosomal protein uL24-like OS=Homo sapiens OX=9606 GN=RPL26L1 PE=1 SV=1
A7088	-	-	-	-	-	-	-	-

A7089	GO:0006481(C-terminal protein methylation)	GO:0016021(integral component of membrane),GO:0005783(endoplasmic reticulum)	GO:0004671(protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity)	K00587 ICMT, STE14; protein-S-isoprenylcysteine O-methyltransferase [EC:2.1.1.100]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis	KOG2628 Hs6912430 Farnesylcysteine-carboxyl methyltransferase	XP_008029191.1 uncharacterized protein SETTUDRAFT_164845 [Exserohilum turcica Et28A]	Protein-S-isoprenylcysteine O-methyltransferase OS=Xenopus laevis OX=8355 GN=icmt PE=1 SV=1
A7090	-	-	-	-	-	-	-	-
A7091	-	-	-	-	-	KOG3168 At4g20440 U1 snRNP component	TRM59132.1 hypothetical protein BD626DRAFT_509225 [Auriculariopsis ampla]	Small nuclear ribonucleoprotein-associated protein B' OS=Gallus gallus OX=9031 GN=SNRPB PE=2 SV=1
A7092	-	-	-	-	-	-	KNE64047.1 hypothetical protein AMAG_09105 [Allomyces macrogynus ATCC 38327]	TRPL translocation defect protein 14 OS=Drosophila melanogaster OX=7227 GN=Ttd14 PE=1 SV=1
A7093	GO:0019318(hexose metabolic process), GO:0005975(carbohydrate metabolic process)	-	GO:0030246(carbohydrate binding),GO:0016853(isomerase activity),GO:0003824(catalytic activity)	K01785 galM, GALM; aldose 1-epimerase [EC:5.1.3.3]	map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00052 Galactose metabolism;map01100 Metabolic pathways	KOG1604 At3g17940 Predicted mutarotase	KAG1716018.1 hypothetical protein ID866_1112 [Astraeus odoratus]	Aldose 1-epimerase OS=Acinetobacter calcoaceticus OX=471 GN=mro PE=1 SV=1
A7094	-	-	-	-	-	KOG1833 At5g40480 Nuclear pore complex, gp210 component	-	Nuclear pore complex protein GP210 OS=Arabidopsis thaliana OX=3702 GN=GB210 PE=1 SV=1
A7095	-	-	GO:0008146(sulfotransferase activity)	-	-	KOG1584 Hs5730071 Sulfotransferase	ORY00775.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	Amine sulfotransferase OS=Oryctolagus cuniculus OX=9986 GN=SULT3A1 PE=1 SV=1
A7096	-	-	-	-	-	-	-	-
A7097	-	-	GO:0030145(manganese ion binding),GO:0070006(metalloaminopeptidase activity)	K14213 PEPD; Xaa-Pro dipeptidase [EC:3.4.13.9]	-	KOG2737 Hs18590513 Putative metalloprotease	ORY44776.1 hypothetical protein BCR33DRAFT_716735 [Rhizoclostium globosum]	Xaa-Pro dipeptidase OS=Homo sapiens OX=9606 GN=PEPD PE=1 SV=3

A7098	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin---tyrosine ligase [EC:6.3.2.25]	-	KOG2157 7297165 Predicted tubulin-tyrosine ligase	XP_031023385.1 uncharacterized protein SmJEL517_g04708 [Synchytrium microbalum]	Protein polyglycolase TTL10 OS=Macaca fascicularis OX=9541 GN=TTLL10 PE=2 SV=1
A7099	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG0192 At2g17700 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9971665.1 hypothetical protein BGZ73_005296 [Actinomortierella ambigua]	Serine/threonine-protein kinase 24 OS=Rattus norvegicus OX=10116 GN=Stk24 PE=2 SV=1
A7100	-	-	-	K12849 PRPF38A; pre-mRNA-splicing factor 38A	map03040 Spliceosome	KOG2889 CE05532 Predicted PRP38-like splicing factor	RKP10117.1 Pre-mRNA-splicing factor 38, partial [Thamnocephalus sphaerospora]	Pre-mRNA-splicing factor 38A OS=Xenopus laevis OX=8355 GN=prpf38a PE=2 SV=1
A7101	GO:0045047(protein targeting to ER)	GO:0005783(endoplasmic reticulum)	GO:0005515(protein binding)	-	-	-	OLY77734.1 hypothetical protein AYI68_g8233 [Smittium mucronatum]	-
A7102	-	-	-	-	-	-	-	-
A7103	-	-	-	K06067 HDAC1_2; histone deacetylase 1/2 [EC:3.5.1.98]	map04350 TGF-beta signaling pathway;map04213 Longevity regulating pathway - multiple species;map04919 Thyroid hormone signaling pathway;map05031 Amphetamine addiction;map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map03082 ATP-dependent chromatin remodeling;map03083 Polycomb repressive complex;map05200 Pathways in cancer;map05202 Transcriptional	KOG1342 At5g63110 Histone deacetylase complex, catalytic component RPD3	ORX63722.1 histone deacetylase [Anaeromyces robustus]	Histone deacetylase 6 OS=Arabidopsis thaliana OX=3702 GN=HDA6 PE=1 SV=1
A7104	-	-	-	-	-	-	ORX88619.1 SET domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Ribosomal lysine N-methyltransferase set10 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=set10 PE=3 SV=1
A7105	-	-	GO:0005515(protein binding)	-	-	-	ODV89918.1 hypothetical protein CANCADRAFT_31017 [Tortispora caseinolytica NRRL Y-17796]	Leucine-zipper-like transcriptional regulator 1 OS=Pongo abelii OX=9601 GN=LZTR1 PE=2 SV=1

A7106	-	-	-	-	-	-	KXS12932.1 hypothetical protein M427DRAFT_156967 [Gonapodya prolifera JEL478]	-
A7107	-	-	GO:0050043(lactate racemase activity)	-	-	-	-	-
A7108	GO:0036211(protein modification process), GO:0009249(protein lipoylation)	-	GO:0033819(lipoyl(octanoyl) transferase activity)	K23735 LIP2, LIP2; lipoyl(octanoyl) transferase 2 [EC:2.3.1.181]	map00785 Lipoic acid metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG0325 7296849 Lipoyltransferase	KAF9116973.1 hypothetical protein BGX30_005793 [Mortierella sp. GBA39]	Octanoyltransferase OS=Gloeobacter violaceus (strain ATCC 29082 / PCC 7421) OX=251221 GN=lipB PE=3 SV=1
A7109	-	-	-	-	-	-	-	-
A7110	-	GO:0016020(membrane)	GO:0005227(calcium activated cation channel activity)	-	-	KOG1134 7304098 Uncharacterized conserved protein	KAG0222300.1 hypothetical protein BGW41_006075 [Actinomortella wolfii]	Calcium permeable stress-gated cation channel 1 OS=Mus musculus OX=10090 GN=Tmem63c PE=1 SV=1
A7111	GO:0006281(DNA repair)	-	GO:0003913(DNA photolyase activity)	K25656 cry, CRYD; cryptochrome	-	KOG0133 At5g24850 Deoxyribodipyrimidine photolyase/cryptochrome	TPX45083.1 hypothetical protein SeLEV6574_g04103 [Synchytrium endobioticum]	Cryptochrome DASH OS=Danio rerio OX=7955 GN=cry-dash PE=2 SV=2
A7112	-	-	-	-	-	-	TPX58854.1 hypothetical protein PhCBS80983_g02821 [Powellomyces hirtus]	-
A7113	-	-	-	-	-	-	-	Crt homolog 3 OS=Dictyostelium discoideum OX=44689 GN=crtp3
A7114	-	-	-	-	-	-	-	-
A7115	-	-	GO:0016491(oxidoreductase activity)	K22745 AIFM2; apoptosis-inducing factor 2	map04115 p53 signaling pathway	KOG1336 Hs14318424 Monodehydroascorbate/ferredoxin reductase	KAF8938210.1 hypothetical protein BGZ58_001388 [Dissophoromata]	Apoptosis-inducing factor homolog B OS=Dictyostelium discoideum OX=44689 GN=aifB PE=3 SV=1
A7116	-	-	-	-	-	KOG3450 7299834 Huntingtin interacting protein HYPK	XP_007863213.1 hypothetical protein GLOTRDRAFT_98692 [Gloeophyllum trabeum ATCC 11539]	-
A7117	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K03258 EIF4B; translation initiation factor 4B	map05205 Proteoglycans in cancer;map04151 PI3K-Akt signaling pathway;map04150 mTOR signaling pathway	KOG0118 Hs14702180 FOG: RRM domain	POY72229.1 hypothetical protein BMF94_4735 [Rhodotorula taiwanensis]	Eukaryotic translation initiation factor 4H OS=Pongo abelii OX=9601 GN=EIF4H PE=2 SV=1

A7118	-	-	-	-	-	-	TPX55688.1 hypothetical protein PhCBS80983. g05122 [Powellomyces hirtus]	Outer dynein arm protein 1 OS=Chlamydomonas reinhardtii OX=3055 GN=ODA1 PE=1 SV=1
A7119	GO:0048870(cell motility)	GO:0031514(motile cilium)	GO:0008017(mi crotubule binding),GO:0031267(small GTPase binding)	-	-	-	ORY36463.1 hypothetical protein BCR33DRAFT_855207 [Rhizoclostium globosum]	Dynein regulatory complex subunit 4 OS=Chlamydomonas reinhardtii OX=3055 GN=DRC4 PE=1 SV=1
A7120	-	-	-	-	-	-	-	-
A7121	GO:0006813(potassium ion transport), GO:0006811(ion transport), GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005249(voltage-gated potassium channel activity),GO:0005216(ion channel activity)	-	-	KOG0498 Hs4557729 K+- channel ERG and related proteins, contain PAS/PAC sensor domain	XP_016612440.1 hypothetical protein SPPG_00132 [Spizellomyces punctatus DAOM BR117]	Potassium voltage-gated channel subfamily H member 6 OS=Rattus norvegicus OX=10116 GN=Kcnh6 PE=1 SV=1
A7122	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7123	-	-	-	-	-	-	OQS54699.1 hypothetical protein EHP00_979 [Enterocytozoan hepatopenaei]	-
A7124	-	GO:0016020(membrane)	-	-	-	KOG3776 HsM5031629 Plasma membrane glycoprotein CD36 and related membrane receptors	-	Scavenger receptor class B member 1 OS=Rattus norvegicus OX=10116 GN=Scarb1 PE=1 SV=1
A7125	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At5g58950 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	THH31342.1 hypothetical protein EUX98_g2850 [Antrodiaella citrinella]	Cyclin-dependent kinase 4 OS=Mus musculus OX=10090 GN=Cdk4 PE=1 SV=1
A7126	GO:0000162(tryptophan biosynthetic process)	-	GO:0004048(anthranilate phosphoribosyltransferase activity),GO:0016757(glycosyltransferase activity)	K00766 trpD; anthranilate phosphoribosyltransferase [EC:2.4.2.18]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map01100 Metabolic pathways	KOG1438 At5g17990 Anthranilate phosphoribosyltransferase	KAG1468385.1 hypothetical protein G6F57_012624 [Rhizopus oryzae]	Anthranilate phosphoribosyltransferase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PAT1 PE=2 SV=1
A7127	-	-	-	-	-	-	-	-
A7128	-	-	-	-	-	-	-	-
A7129	-	-	-	-	-	-	-	-
A7130	-	-	-	-	-	-	-	-
A7131	-	-	-	-	-	-	-	-

A7132	-	-	-	-	-	-	KAG0195475.1 hypothetical protein BGX28_001302, partial [Mortierella sp. GBA30]	-
A7133	-	-	GO:0005515(protein binding)	-	-	-	KZO94955.1 hypothetical protein CALVIDRAFT_565074 [Calocera viscosa TUFC12733]	-
A7134	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0581 At5g40440 Mitogen-activated protein kinase kinase (MAP2K)	KAG4103406.1 kinase-like domain-containing protein [Neocallimastix sp. JGI-2020a]	Mitogen-activated protein kinase kinase 3 OS=Arabidopsis thaliana OX=3702 GN=MKK3 PE=1 SV=1
A7135	-	-	-	-	-	-	-	-
A7136	-	-	-	-	-	-	-	-
A7137	-	-	-	-	-	-	RDW46957.1 histidine phosphatase superfamily [Yarrowia lipolytica]	Phosphoglycerate mutase-like protein AT74H OS=Arabidopsis thaliana OX=3702 GN=At1g08940 PE=3 SV=2
A7138	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7139	-	-	-	-	-	-	-	-
A7140	-	-	-	-	-	-	-	-
A7141	-	-	-	-	-	-	-	-
A7142	GO:0006400(tRNA modification)	-	GO:0008176(tRNA (guanine-N7-)-methyltransferase activity)	K03439 trmB, METTL1, TRM8; tRNA (guanine-N7-)-methyltransferase [EC:2.1.1.33]	-	KOG3115 At5g17660 Methyltransferase-like protein	ORY23756.1 hypothetical protein BCR33DRAFT_860648 [Rhizoclostium globosum]	tRNA (guanine-N(7)-)-methyltransferase OS=Trichormus variabilis (strain ATCC 29413 / PCC 7937) OX=240292 GN=trmB PE=3 SV=1
A7143	-	-	-	-	-	-	-	-
A7144	GO:0005975(carbohydrate metabolic process)	GO:0009341(beta-galactosidase complex)	GO:0004565(beta-galactosidase activity),GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds),GO:0003824(catalytic activity),GO:0030246(carbohydrate binding)	K01190 lacZ; beta-galactosidase [EC:3.2.1.23]	map00511 Other glycan degradation;map00600 Sphingolipid metabolism;map00052 Galactose metabolism;map01100 Metabolic pathways	KOG2024 7302519 Beta-Glucuronidase GUSB (glycosylhydrolase superfamily 2)	RUS16356.1 glycosyl hydrolases family 2, TIM barrel domain-containing protein [Endogone sp. FLAS-F59071]	Beta-galactosidase OS=Vibrio cholerae serotype O1 (strain ATCC 39541 / Classical Ogawa 395 / O395) OX=345073 GN=lacZ PE=3 SV=2
A7145	-	-	-	-	-	-	-	-
A7146	-	-	-	-	-	-	-	-
A7147	-	-	GO:0005515(protein binding)	-	-	-	ORY05627.1 hypothetical protein K493DRAFT_274864 [Basidiobolus meristosporus CBS 931.73]	-

A7148	GO:0006260(DNA replication)	-	GO:0003677(DNA binding)	K02328 POLD2; DNA polymerase delta subunit 2	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03440 Homologous recombination; map03430 Mismatch repair	KOG2732 Hs5453924 DNA polymerase delta, regulatory subunit 55	KAG0260104.1 hypothetical protein BG011_002123 [Mortierella polycephala]	DNA polymerase delta subunit 2 OS=Homo sapiens OX=9606 GN=POLD2 PE=1 SV=1
A7149	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7150	-	-	-	-	-	-	-	-
A7151	-	-	GO:0016787(hydrolase activity),GO:0005524(ATP binding)	-	-	KOG0061 At1g71960 Transporter, ABC superfamily (Breast cancer resistance protein)	RKP36647.1 P-loop containing nucleoside triphosphate hydrolase protein [Dimargaris cristalligena]	ABC transporter G family member 25 OS=Arabidopsis thaliana OX=3702 GN=ABCG25 PE=1 SV=1
A7152	-	-	-	-	-	-	XP_035372257.1 GTP cyclohydrolase II RibA [Lasiodiplodia theobromae]	Uracil-regulated protein 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=urg1 PE=2 SV=1
A7153	-	-	-	-	-	-	-	-
A7154	-	-	GO:0005509(calcium ion binding)	-	-	KOG0027 CE27751 Calmodulin and related proteins (EF-Hand superfamily)	TPX58777.1 hypothetical protein CcCBS67573_g09137 [Chytrium confervae]	Probable calcium-binding protein CML11 OS=Oryza sativa subsp. japonica OX=39947 GN=CML11 PE=2 SV=1
A7155	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0032 Hs4826684_1 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	XP_007729105.1 CAMK/CAMK1 protein kinase [Capronia epimyces CBS 606.96]	Serine/threonine-protein kinase PKZ1 OS=Phytophthora infestans OX=4787 GN=PKZ1 PE=1 SV=1
A7156	-	-	-	-	-	-	-	-
A7157	-	-	-	-	-	-	-	-
A7158	-	-	GO:0005515(protein binding)	-	-	KOG4155 Hs13376840 FOG: WD40 repeat	RKO98619.1 hypothetical protein CXG81DRAFT_28571 [Caulochytrium protostelioides]	Superkiller complex protein 8 OS=Bos taurus OX=9913 GN=SKIC8 PE=2 SV=1
A7159	-	-	-	-	-	-	TPX64572.1 hypothetical protein CcCBS67573_g08379 [Chytrium confervae]	-
A7160	-	-	-	-	-	-	-	-

A7161	GO:0035556(intracellular signal transduction)	-	-	-	-	-	-	-
A7162	GO:0022904(respiratory electron transport chain)	-	-	-	-	-	XP_02007064.3.1 hypothetical protein CYBJADRAFT_167636 [Cyberlindnera jadinii NRRL Y-1542]	Electron transfer flavoprotein regulatory factor 1 OS=Salmo salar OX=8030 GN=etfrf1 PE=3 SV=1
A7163	-	-	-	-	-	-	-	-
A7164	-	-	-	-	-	-	-	-
A7165	-	-	-	-	-	-	-	-
A7166	-	-	GO:0005515(protein binding)	-	-	-	TPX71174.1 hypothetical protein SpCBS45565_g01378 [Spizellomyces sp. 'palustris']	Cilia- and flagella-associated protein 44 OS=Chlamydomonas reinhardtii OX=3055 GN=CFAP44 PE=1 SV=1
A7167	-	-	-	-	-	-	-	-
A7168	-	-	-	K09584 PDIA6, TXNDC7; protein disulfide-isomerase A6 [EC:5.3.4.1]	map04141 Protein processing in endoplasmic reticulum	KOG0190 CE00073 Protein disulfide isomerase (prolyl 4-hydroxylase beta subunit)	KAG0302540.1 hypothetical protein BGZ98_00742 [Dissophora globulifera]	Thioredoxin domain-containing protein 5 homolog OS=Drosophila melanogaster OX=7227 GN=prtp PE=1 SV=2
A7169	GO:0007017(microtubule-based process)	GO:0005874(microtubule)	GO:0005525(GTP binding)	K07375 TUBB; tubulin beta	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins;map04540 Gap junction;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG1375 Hs705915 Beta tubulin	XP_031022228.1 uncharacterized protein SmJEL517_g05892 [Synchytrium microbalum]	Tubulin epsilon chain OS=Mus musculus OX=10090 GN=Tube1 PE=1 SV=1
A7170	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7171	-	-	-	-	-	KOG0143 At3g46490 Iron/ascorbate family oxidoreductases	RAO64753.1 hypothetical protein BHQ10_000765 [Talaromyces amestolkiae]	2-oxoglutarate-dependent dioxygenase tropC OS=Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) OX=441959 GN=tropC PE=1 SV=1

A7172	GO:0006302(double-strand break repair)	GO:0005634(nucleus);GO:0030870(Mre11 complex)	GO:0004519(endonuclease activity);GO:0030145(manganese ion binding);GO:0004520(endonuclease activity);GO:0008296(3'-5'-exodeoxyribonuclease activity);GO:0016787(hydrolase activity)	K10865 MRE11; double-strand break repair protein MRE11	map04218 Cellular senescence;map03450 Non-homologous end-joining;map03440 Homologous recombination	KOG2310 7297844 DNA repair exonuclease MRE11	ORZ34906.1 Metallo-dependent phosphatase-like protein [Catenaria anguillulae PL171]	Double-strand break repair protein mus-23 OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=mus-23 PE=3 SV=3
A7173	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A7174	-	-	GO:0046982(protein heterodimerization activity)	-	-	-	-	-
A7175	-	-	GO:0005509(calcium ion binding)	-	-	-	KXX73933.1 Calmodulin [Madurella mycetomatis]	Glyoxylase I 4 OS=Arabidopsis thaliana OX=3702 GN=GLY4 PE=2 SV=1
A7176	GO:0015937(coenzyme A biosynthetic process)	-	GO:0004594(pantothenate kinase activity);GO:0005524(ATP binding)	K09680 PANK1_2_3, CAB1, coaW; type II pantothenate kinase [EC:2.7.1.33]	map00770 Pantothenate and CoA biosynthesis;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG2201 Hs13375789 Pantothenate kinase PanK and related proteins	ORY85507.1 type II pantothenate kinase [Protomyces lactucaedebilis]	Pantothenate kinase 3 OS=Mus musculus OX=10090 GN=Pank3 PE=1 SV=1
A7177	GO:0030026(cellular manganese ion homeostasis)	-	GO:0005384(manganese ion transmembrane transporter activity)	K22736 VIT; vacuolar iron transporter family protein	-	-	SAM02434.1 hypothetical protein [Absidia glauca]	Vacuolar iron transporter OS=Toxoplasma gondii (strain ATCC 50861 / VEG) OX=432359 GN=VIT PE=1 SV=1
A7178	-	-	-	-	-	-	-	-
A7179	-	-	-	-	-	KOG0143 At3g19010 Iron/ascorbate family oxidoreductases	XP_007913300.1 putative clavamin synthase-like protein [Phaeoacremonium minimum UCRPA7]	Protein LATERAL BRANCHING OXIDOREDUCTASE 1 OS=Arabidopsis thaliana OX=3702 GN=LBO1 PE=1 SV=1
A7180	GO:0031204(posttranslational protein targeting to membrane, translocation)	GO:0031207(Sec62/Sec63 complex)	-	-	-	-	-	-
A7181	GO:0007064(mitotic sister chromatid cohesion)	-	-	-	-	KOG1525 At5g10950 Sister chromatid cohesion complex Cohesin, subunit PDS5	-	DNA mismatch repair protein MSH6 OS=Arabidopsis thaliana OX=3702 GN=MSH6 PE=1 SV=2
A7182	-	-	-	-	-	-	-	-
A7183	-	-	-	-	-	KOG3827 CE07387 Inward rectifier K+ channel	KXS20929.1 E set domain-containing protein [Gonapodya prolifera JEL478]	Inward rectifier potassium channel Kirbac3.1 OS=Magnetospirillum magnetotacticum OX=188 PE=1 SV=2

A7184	-	-	GO:0005509(cal cium ion binding)	-	-	-	-	-
A7185	GO:0005975(carbohy drate metabolic process), GO:1904380(endopl asmic reticulum mannose trimming), GO:1904382(manno se trimming involved in glycoprot ein ERAD pathway)	GO:0016020(memb rane)	GO:0004571(ma nnosyl- oligosaccharide 1,2-alpha- mannosidase activity),GO:0005509(calcium ion binding)	K10084 EDEMI; ER degradation enhancer, mannosidase alpha-like 1	map04141 Protein processing in endoplasmic reticulum	KOG2429 Hs7662002 Glycosyl hydrolase, family 47	OON08241.1 hypothetical protein BSLG_02441, partial [Batrachochyt rium salamandrivo rans]	ER degradation-enhancing alpha-mannosidase-like protein 1 OS=Homo sapiens OX=9606 GN=EDEM1 PE=1 SV=1
A7186	-	-	-	-	-	-	-	-
A7187	GO:0016192(vesicle- mediated transport)	GO:0016020(memb rane)	-	K08490 STX5; syntaxin 5	map04130 SNARE interactions in vesicular transport	KOG0812 Hs4507293 SNARE protein SED5/Syntaxi n 5	XP_017990075.1 integral membrane protein sed5 [Malassezia pachydermati s]	Syntaxin-5 OS=Bos taurus OX=9913 GN=STX5 PE=2 SV=1
A7188	-	-	-	-	-	-	-	-
A7189	-	-	-	-	-	-	-	-
A7190	GO:0000079(regulat ion of cyclin- dependen t protein serine/thr eonine kinase activity)	-	GO:0019901(pro tein kinase binding)	-	-	KOG1674 At2g44740 Cyclin	-	Cyclin-U4-1 OS=Arabidopsis thaliana OX=3702 GN=CYCU4-1 PE=1 SV=1
A7191	-	-	-	-	-	-	-	-
A7192	-	-	-	-	-	-	-	-
A7193	-	-	GO:0005515(pro tein binding)	K24758 WDR89; WD repeat- containing protein 89	-	KOG1188 Hs18087841 WD40 repeat protein	QSL65093.1 hypothetical protein MERGE_002398 [Pneumocystis wakefieldiae]	WD repeat-containing protein 89 OS=Bos taurus OX=9913 GN=WDR89 PE=2 SV=1
A7194	-	-	-	-	-	-	SAL95062.1 hypothetical protein [Absidia glauca]	KICSTOR complex protein ITFG2 OS=Bos taurus OX=9913 GN=ITFG2 PE=2 SV=1
A7195	-	-	GO:0008113(pe ptide- methionine (S)- S-oxide reductase activity)	K07304 msrA; peptide- methionine (S)-S-oxide reductase [EC:1.8.4.11]	-	KOG1635 Hs6912516 Peptide methionine sulfoxide reductase	OMH80424.1 Peptide methionine sulfoxide reductase A2-1 [Zancudomyc es culisetae]	Peptide methionine sulfoxide reductase MsrA OS=Salinispora tropica (strain ATCC BAA-916 / DSM 44818 / JCM 13857 / NBRC 105044 / CNB-440) OX=369723 GN=msrA PE=3 SV=1
A7196	-	-	-	-	-	-	KAG0191963.1 hypothetical protein DFQ28_010489 [Apophysom yces sp. BC1034]	Uncharacterized protein PA3753 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA3753 PE=3 SV=2
A7197	-	-	-	K09425 K09425; Myb-like DNA-binding protein FlbD	-	KOG0048 At5g02320 Transcription factor, Myb superfamily	KAF9981062.1 Transcription factor myb3r-5 [Mortierella antarctica]	Transcription factor MYB3R-2 OS=Oryza sativa subsp. japonica OX=39947 GN=MYB3R-2 PE=2 SV=1

A7198	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding)	-	-	KOG0140 Hs7656849 Medium-chain acyl-CoA dehydrogenase	RKP26471.1 putative acyl-CoA dehydrogenase [Syncephalis pseudoplumigaleata]	Acyl-CoA dehydrogenase apdG OS=Emicella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=apdG PE=2 SV=1
A7199	-	-	-	-	-	-	-	-
A7200	-	GO:0016020(membrane)	GO:0140359(ABC-type transporter activity),GO:0005524(ATP binding)	K05681 ABCG2, CD338; ATP-binding cassette, subfamily G (WHITE), member 2	map01523 Antifolate resistance;map04976 Bile secretion;map02010 ABC transporters	KOG0061 Hs8051577 Transporter, ABC superfamily (Breast cancer resistance protein)	KAF8453177.1 P-loop containing nucleoside triphosphate hydrolase protein [Terfezia clavaryi]	Protein white OS=Ceratitis capitata OX=7213 GN=W PE=2 SV=1
A7201	-	-	-	-	-	-	-	-
A7202	-	-	-	K06685 MOB1, Mats; MOB kinase activator 1	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04392 Hippo signaling pathway - multiple species;map04111 Cell cycle - yeast	KOG0440 Hs8922671 Cell cycle-associated protein Mob1-1	KXS17134.1 mps one binder kinase activator-like 1 protein [Gonapodya prolifera JEL478]	MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B PE=1 SV=3
A7203	-	-	-	K06685 MOB1, Mats; MOB kinase activator 1	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04392 Hippo signaling pathway - multiple species;map04111 Cell cycle - yeast	KOG0440 Hs8922671 Cell cycle-associated protein Mob1-1	XP_01660668.2.1 mps one binder kinase activator-like 1A [Spizellomyces punctatus DAOM BR117]	MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B PE=1 SV=3
A7204	-	-	-	K06685 MOB1, Mats; MOB kinase activator 1	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04392 Hippo signaling pathway - multiple species;map04111 Cell cycle - yeast	KOG0440 Hs8922671 Cell cycle-associated protein Mob1-1	KXS17134.1 mps one binder kinase activator-like 1 protein [Gonapodya prolifera JEL478]	MOB kinase activator 1B OS=Homo sapiens OX=9606 GN=MOB1B PE=1 SV=3

A7205	-	-	-	K06685 MOB1, Mats; MOB kinase activator 1	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04 392 Hippo signaling pathway - multiple species;map041 11 Cell cycle - yeast	KOG0440 At5 g45550 Cell cycle- associated protein Mob1-1	XP_00667995 6.1 uncharacteriz ed protein BATDEDRAFT _30301 [Batrachochyt rium dendrobatidi s JAM81]	MOB kinase activator-like 1 homolog B OS=Dictyostelium discoideum OX=44689 GN=mobB PE=3 SV=1
A7206	-	-	GO:0003824(cat alytic activity)	-	-	KOG1562 At5 g19530 Spermidine synthase	CAE6532003. 1 unnamed protein product [Rhizoctonia solani]	Polyamine aminopropyltransferase OS=Aeropyrum pernix (strain ATCC 700893 / DSM 11879 / JCM 9820 / NBRC 100138 / K1) OX=272557 GN=speE PE=3 SV=2
A7207	-	-	GO:0004482(mR NA (guanine- N7-)- methyltransferas e activity);GO:000 4651(polynucleo tide 5'- phosphatase activity)	K00565 RNMT; mRNA (guanine- N7-)- methyltransfe rase [EC:2.1.1.56]	map03015 mRNA surveillance pathway	KOG1975 At3 g20650 mRNA cap methyltransfe rase	XP_00776429 4.1 guanine- N(7)- methyltransfe rase [Coniophora puteana RWD-64-598 SS2]	mRNA cap guanine-N7 methyltransferase 1 OS=Arabidopsis thaliana OX=3702 GN=At3g20650 PE=2 SV=1
A7208	-	GO:00057 37(cytopl asm)	GO:0002161(am inoacyl-tRNA editing activity);GO:005 1499(D- aminoacyl-tRNA deacylase activity)	K07560 dtd. DTD; D- aminoacyl- tRNA deacylase [EC:3.1.1.96]	-	KOG3323 Hs2 1361785_1 D-Tyr-tRNA (Tyr) deacylase	KAF5315970. 1 hypothetical protein D9611_00502 2 [Coprinellus angulatus]	D-aminoacyl-tRNA deacylase 1 OS=Bos taurus OX=9913 GN=DTD1 PE=2 SV=1
A7209	GO:00070 18(microt ubule- based movemen t)	-	GO:0003777(mi crotubule motor activity);GO:000 5524(ATP binding);GO:000 8017(microtubul e binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map041 44 Endocytosis;map 05132 Salmonella infection;map04 814 Motor proteins;map052 23 Non-small cell lung cancer;map0472 8 Dopaminergic synapse;map050 20 Prion disease;map050 22 Pathways of neurodegenerati on - multiple diseases;map050 10 Alzheimer disease;map050 12 Parkinson disease;map050 16 Huntington disease	KOG4280 CE 07978 Kinesin-like protein	OAC98528.1 hypothetical protein MUCCIDRAFT _44717, partial [Mucor lusitanicus CBS 277.49]	Kinesin-like protein KIN-14D OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14D PE=3 SV=2
A7210	-	-	GO:0005515(pro tein binding)	-	-	-	-	-
A7211	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity);GO:000 5524(ATP binding);GO:000 5515(protein binding)	K21157 SAK1; SNF1- activating kinase 1 [EC:2.7.11.1]	map04138 Autophagy - yeast	KOG0032 Hs2 1389439 Ca2+/calmod ulin- dependent protein kinase, EF- Hand protein superfamily	XP_00285103 8.1 serine/threon ine-protein kinase ssp1 [Microsporu m canis CBS 113480]	Serine/threonine-protein kinase Kist OS=Homo sapiens OX=9606 GN=UHMK1 PE=1 SV=2
A7212	-	-	-	-	-	-	-	-
A7213	-	-	-	-	-	-	-	-
A7214	-	-	GO:0005515(pro tein binding)	-	-	-	-	Regulator of microtubule dynamics protein 1 OS=Bos taurus OX=9913 GN=RMDN1 PE=2 SV=1

A7215	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K02358 tuf, TUFM; elongation factor Tu	map04626 Plant-pathogen interaction	KOG0461 Hs2041694 Selenocysteine-specific elongation factor	RUS27360.1 hypothetical protein BC938DRAFT_483354 [Jimgerdmania flammicorona]	Selenocysteine-specific elongation factor OS=Mus musculus OX=10090 GN=Eefsec PE=1 SV=2
A7216	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	KAF8223402.1 hypothetical protein L208DRAFT_1445431 [Tricholoma matsutake 945]	-
A7217	GO:0006536(glutamate metabolic process), GO:0019752(carboxylic acid metabolic process)	-	GO:0003824(catalytic activity),GO:0004351(glutamate decarboxylase activity),GO:0030170(pyridoxal phosphate binding),GO:0016830(carbon-carbon lyase activity)	K01580 E4.1.1.15, gadB, gadA, GAD; glutamate decarboxylase [EC:4.1.1.15]	map00410 beta-Alanine metabolism;map01110 Biosynthesis of secondary metabolites;map04940 Type I diabetes mellitus;map01120 Microbial metabolism in diverse environments;map04727 GABAergic synapse;map00250 Alanine, aspartate and glutamate metabolism;map00430 Taurine and hypotaurine metabolism;map00650 Butanoate metabolism;map02024 Quorum sensing;map01100 Metabolic	KOG1383 At3g17760 Glutamate decarboxylase/sphingosine phosphate lyase	ORY45621.1 glutamate decarboxylase [Rhizoclostium globosum]	Glutamate decarboxylase 5 OS=Arabidopsis thaliana OX=3702 GN=GAD5 PE=2 SV=1
A7218	-	-	-	K00323 NNT; proton-translocating NAD(P)+ transhydrogenase [EC:7.1.1.1]	map00760 Nicotinate and nicotinamide metabolism;map01100 Metabolic pathways	-	XP_031025687.1 uncharacterized protein SmJEL517_g02470 [Synchytrium microbalum]	NAD(P) transhydrogenase, mitochondrial OS=Bos taurus OX=9913 GN=NNT PE=1 SV=3
A7219	-	GO:0072546(EMC complex)	-	K23562 EMC1; ER membrane protein complex subunit 1	-	KOG2103 Hs20470446 Uncharacterized conserved protein	RKP08866.1 hypothetical protein THASP1DRAFT_29351 [Thamnocephalis sphaerospora]	ER membrane protein complex subunit 1 OS=Gallus gallus OX=9031 GN=EMC1 PE=2 SV=1
A7220	-	-	-	-	-	-	-	-
A7221	-	-	-	-	-	-	-	-
A7222	GO:0070475(rRNA base methylation)	-	GO:0070037(rRNA (pseudouridine) methyltransferase activity)	K14568 EMG1, NEP1; rRNA small subunit pseudouridine methyltransferase Nep1 [EC:2.1.1.260]	map03008 Ribosome biogenesis in eukaryotes	KOG3073 YLR186w Protein required for 18S rRNA maturation and 40S ribosome biogenesis	TPX56777.1 hypothetical protein PhCBS80983_g04307 [Powellomyces hirtus]	Ribosomal RNA small subunit methyltransferase NEP1 OS=Drosophila melanogaster OX=7227 GN=CG3527 PE=3 SV=2
A7223	-	-	GO:0005515(protein binding)	-	-	KOG2502 CE29091 Tub family proteins	ORX70984.1 Tub-domain-containing protein [Linderina pennisporea]	Tubby protein homolog 1 OS=Caenorhabditis briggsae OX=6238 GN=tub-1 PE=3 SV=1
A7224	-	-	-	-	-	-	-	-
A7225	-	-	-	-	-	-	-	-

A7226	-	-	GO:0005515(protein binding)	-	-	-	RUS17317.1 hypothetical protein BC937DRAFT_90138 [Endogone sp. FLAS-F59071]	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B OS=Arabidopsis thaliana OX=3702 GN=At3g62790 PE=1 SV=1
A7227	GO:0008654(phospholipid biosynthetic process)	-	GO:0004609(phosphatidylserine decarboxylase activity)	K01613 psd, PISD; phosphatidylserine decarboxylase [EC:4.1.1.65]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG2420[Hs13489112 Phosphatidylserine decarboxylase	KAF5312212.1 hypothetical protein D9619_003687 [Psilocybe cf. subviscida]	Phosphatidylserine decarboxylase proenzyme, mitochondrial OS=Mus musculus OX=10090 GN=Pisd PE=2 SV=1
A7228	-	-	-	-	-	-	-	Nucleolar protein 12 OS=Rattus norvegicus OX=10116 GN=Nol12 PE=2
A7229	GO:0007165(signal transduction)	GO:0005737(cytoplasm)	GO:0005515(protein binding)	K19844 BEM2; GTPase-activating protein BEM2	map04011 MAPK signaling pathway - yeast	KOG4270[Hs13775230 GTPase-activator protein	RPA79777.1 Rho GTPase activation protein [Ascobolus immersus RN42]	Rho GTPase-activating protein 24 OS=Mus musculus OX=10090 GN=Arhgap24 PE=1 SV=2
A7230	GO:0006614(SRP-dependent cotranslational protein targeting to membrane)	GO:0048500(signal recognition particle),GO:0005786(signal recognition particle, endoplasmic reticulum targeting)	GO:0008312(7S RNA binding),GO:0030942(endoplasmic reticulum signal peptide binding)	-	-	-	APA14146.1 hypothetical protein sscl_12g089160 [Sclerotinia sclerotiorum 1980 UF-70]	-
A7231	-	-	GO:0005515(protein binding)	-	-	KOG0128[At4g24270 RNA-binding protein SART3 (RRM superfamily)	KAF9571168.1 RNA-binding protein 4F [Mortierella alpina]	Squamous cell carcinoma antigen recognized by T-cells 3 OS=Mus musculus OX=10090 GN=Sart3 PE=1 SV=1
A7232	GO:0006508(proteolysis)	-	GO:0000049(tRNA binding),GO:0004181(metalloproteinase activity)	-	-	-	KAG0369698.1 hypothetical protein BGZ54_009124 [Gamsiella multivaricata]	Thermostable carboxypeptidase 1 OS=Thermus thermophilus (strain ATCC 27634 / DSM 579 / HB8) OX=300852 GN=TTHA0270 PE=1 SV=1
A7233	-	-	-	K19219 JMJD7; peptidyl-lysine (3S)-dioxygenase / protease [EC:1.14.11.63 3.4.-.-]	-	KOG2508[At3g45880 Predicted phospholipase	ORY91719.1 cupin-like domain-containing protein [Leucosporidium creatinivorum]	Bifunctional peptidase and (3S)-lysyl hydroxylase JMJD7 OS=Homo sapiens OX=9606 GN=JMJD7 PE=1 SV=1
A7234	GO:0006668(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	-	KAF7366335.1 Pkinase-domain-containing protein [Mycena sanguinolenta]	Calcium/calmodulin-dependent protein kinase cmkB OS=Emericella nidulans OX=162425 GN=cmkB PE=1 SV=1

A7235	GO:0006418(tRNA aminoacylation for protein translation),GO:0006421(asparaginyl-tRNA aminoacylation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004816(asparagine-tRNA ligase activity),GO:0003676(nucleic acid binding)	K01893 NARS, asnS; asparaginyl-tRNA synthetase [EC:6.1.1.22]	map00970 Aminoacyl-tRNA biosynthesis	KOG0554 At4g17300 Asparaginyl-tRNA synthetase (mitochondrial)	KAF9933497.1 hypothetical protein FBU30_005338 [Linnemannia zychae]	Asparagine--tRNA ligase OS=Protochlamydia amoebophila (strain UWE25) OX=264201 GN=asnS PE=3 SV=1
A7236	-	-	-	-	-	-	-	-
A7237	-	-	-	-	-	-	-	-
A7238	GO:0017183(peptidyl-diphthamide biosynthetic process from peptidyl-histidine)	-	GO:0046872(metal ion binding)	K15455 DPH3, KT111; diphthamide biosynthesis protein 3	-	-	KAG1439338.1 hypothetical protein G6F56_012326 [Rhizopus delemar]	Diphthamide biosynthesis protein 3 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=dph3 PE=3 SV=1
A7239	-	-	-	-	-	-	-	-
A7240	GO:0007165(signal transduction),GO:0000160(phosphorelay signal transduction system),GO:0016310(phosphorylation)	-	GO:0000155(phosphorelay sensor kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	KOG0519 At1g66340 Sensory transduction histidine kinase	RKP01258.1 hypothetical protein CXG81DRAFT_12249, partial [Caulochytrium protostelioides]	Hybrid signal transduction histidine kinase K OS=Dictyostelium discoideum OX=44689 GN=dhkk PE=1 SV=1
A7241	-	-	-	-	-	-	-	-
A7242	GO:0003341(cilium movement),GO:0036159(inner dynein arm assembly)	GO:0005930(axoneme)	-	-	-	-	TPX65201.1 hypothetical protein SpCBS45565_g05309 [Spizellomyces sp. 'palustris']	Coiled-coil domain-containing protein 39 OS=Xenopus tropicalis OX=8364 GN=ccdc39 PE=2 SV=1
A7243	GO:0055085(transmembrane transport)	-	-	K14684 SLC25A23S; solute carrier family 25 (mitochondrial phosphate transporter), member 23/24/25/41	-	KOG0752 At5g01500 Mitochondrial solute carrier protein	KAF0474119.1 mitochondrial carrier [Gigaspora margarita]	Thylakoid ADP,ATP carrier protein, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=TAAC PE=1 SV=1
A7244	-	-	-	-	-	-	ORY35169.1 hypothetical protein BCR33DRAFT_722516 [Rhizoclostium globosum]	G8 domain-containing protein DDB_G0286897 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0286897 PE=3 SV=1
A7245	GO:0006486(protein glycosylation)	-	GO:0008375(acylglucosaminyltransferase activity)	-	-	KOG1413 CE28401 N-acetylglucosaminyltransferase I	EPZ34122.1 Glycosyl transferase, family 13 domain-containing protein [Rozella allomyces CSF55]	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Arabidopsis thaliana OX=3702 GN=GNTI PE=1 SV=1

A7246	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At1g71900 Uncharacterized conserved protein	XP_025379230.1 DUF803-domain-containing protein [Acaromyces ingoldii]	Probable magnesium transporter NIPA6 OS=Arabidopsis thaliana OX=3702 GN=At2g21120 PE=2 SV=1
A7247	GO:0006355(regulation of transcription, DNA-templated),GO:0016573(histone acetylation)	-	GO:0005515(protein binding),GO:0004402(histone acetyltransferase activity)	K11684 BDF1; bromodomain-containing factor 1	-	KOG1778 Hs4557557 CREB binding protein/P300 and related TAZ Zn-finger proteins	OUM65932.1 hypothetical protein PIROE2DRAFT_41243, partial [Piromyces sp. E2]	Histone acetyltransferase p300 OS=Mus musculus OX=10090 GN=Ep300 PE=1 SV=2
A7248	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	-	-
A7249	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane),GO:0005886(plasma membrane)	GO:0005216(ion channel activity),GO:0005515(protein binding),GO:0005261(cation channel activity)	K21864 CCH1; voltage-dependent calcium channel	-	KOG2301 CE28820 Voltage-gated Ca2+ channels, alpha1 subunits	KAG0087922.1 calcium channel protein [Podila epicladia]	Sodium channel protein type 4 subunit alpha OS=Homo sapiens OX=9606 GN=SCN4A PE=1 SV=4
A7250	GO:0007528(neuromuscular junction development)	-	GO:0005515(protein binding)	-	-	KOG1899 7294457 LAR transmembrane tyrosine phosphatase-interacting protein liprin	-	Liprin-beta-1 OS=Mus musculus OX=10090 GN=Ppfbp1 PE=1 SV=3
A7251	-	-	-	-	-	KOG2470 Hs12597653 Similar to IMP-GMP specific 5'-nucleotidase	KAG2188259.1 hypothetical protein INT44_001012 [Umbelopsis vinacea]	5'-nucleotidase domain-containing protein 2 OS=Homo sapiens OX=9606 GN=NT5DC2 PE=1 SV=1
A7252	GO:0000724(double-strand break repair via homologous recombination),GO:1990426(mitotic recombination-dependent replication fork processing),GO:0006281(DNA repair),GO:0006259(DNA metabolic process)	-	GO:0003677(DNA binding),GO:0000150(DNA strand exchange activity),GO:0003690(double-stranded DNA binding),GO:0003697(single-stranded DNA binding),GO:0008094(ATPase, acting on DNA),GO:0000166(nucleotide binding),GO:0005524(ATP binding)	K04482 RAD51; DNA repair protein RAD51	map05212 Pancreatic cancer;map03440 Homologous recombination; map05200 Pathways in cancer;map03460 Fanconi anemia pathway	KOG1433 Hs19924133 DNA repair protein RAD51/RHP55	GBC04478.1 hypothetical protein RclHRL_00570034 [Rhizophagus clarus]	DNA repair protein RAD51 homolog A OS=Xenopus laevis OX=8355 GN=rad51-a PE=2 SV=1
A7253	-	-	-	-	-	-	-	-
A7254	-	-	-	K23538 ELMOD; ELMO domain-containing protein	-	KOG2998 Hs22042711 Uncharacterized conserved protein	ORX60103.1 hypothetical protein BCR36DRAFT_408464 [Piromyces finnis]	ELMO domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ELMOD2 PE=1 SV=1

A7255	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	GO:0016407(acyltransferase activity)	-	-	-	RKP21311.1 adenylyl cyclase, partial [Rozella allomyces CSF55]	Adenylate cyclase type 10 OS=Rattus norvegicus OX=10116 GN=Adcy10 PE=1 SV=1
A7256	-	-	-	K02896 RP-L24e, RPL24; large subunit ribosomal protein L24e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1723[Hs10047102 60s ribosomal protein L30 isolog	ORX55362.1 hypothetical protein BCR36DRAFT_402965 [Piromyces finnis]	Probable ribosome biogenesis protein RLP24 OS=Dictyostelium discoideum OX=44689 GN=rlp24 PE=2 SV=1
A7257	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7258	-	-	-	-	-	-	-	-
A7259	-	-	GO:0016746(acyltransferase activity)	-	-	-	XP_023630653.1 uncharacterized protein RCC_09644 [Ramularia collo-cygni]	-
A7260	GO:0055085(transmembrane transport)	-	-	-	-	KOG0770[At1g74240 Predicted mitochondrial carrier protein	QKK35458.1 mitochondria l Mme1 [Starmerella bombicola]	Mitochondrial substrate carrier family protein E OS=Dictyostelium discoideum OX=44689 GN=mcfE PE=3 SV=1
A7261	-	-	-	-	-	-	-	-
A7262	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K09569 FKBP2; FK506-binding protein 2 [EC:5.2.1.8]	-	KOG0544[YNL135c FKBP-type peptidyl-prolyl cis-trans isomerase	CDO92702.1 unnamed protein product [Kluyveromyces dobzhanskii CBS 2104]	FK506-binding protein 2 OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=FPR2 PE=3 SV=1
A7263	GO:0007186(G protein-coupled receptor signaling pathway)	-	-	-	-	-	-	-
A7264	GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0005515(protein binding)	K14016 UFD1; ubiquitin fusion degradation protein 1	map04141 Protein processing in endoplasmic reticulum	KOG1816[At4g15420.2 Ubiquitin fusion-degradation protein	TIA88902.1 hypothetical protein E3P99_02298 [Wallemia hederiae]	Ubiquitin recognition factor in ER-associated degradation protein 1 OS=Homo sapiens OX=9606 GN=UFD1 PE=1 SV=3
A7265	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG3298[7299973 DNA-directed RNA polymerase subunit E'	KAF9956807.1 hypothetical protein BGZ72_002447 [Mortierella alpina]	-
A7266	-	-	-	-	-	-	-	-
A7267	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K11853 USP34; ubiquitin carboxyl-terminal hydrolase 34 [EC:3.4.19.12]	-	KOG1866[7302097 Ubiquitin carboxyl-terminal hydrolase	RIB07257.1 hypothetical protein C2G38_2252726 [Gigaspora rosea]	Ubiquitin carboxyl-terminal hydrolase 9Y OS=Mus musculus OX=10090 GN=Usp9y PE=2 SV=1

A7268	GO:0007064(mitotic sister chromatid cohesion),GO:0000724(double-strand break repair via homologous recombination),GO:0006281(DNA repair)	GO:0031390(Ctf18 RFC-like complex),GO:0030915(Smc5-Smc6 complex)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K22803 SMC5; structural maintenance of chromosome protein 5	-	KOG0979 YOL034w Structural maintenance of chromosome protein SMC5/Spr18, SMC superfamily	KAF0492709.1 P-loop containing nucleoside triphosphate hydrolase protein [Gigaspora margarita]	Structural maintenance of chromosomes protein 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SMC5 PE=1 SV=1
A7269	-	-	-	-	-	-	-	-
A7270	-	-	-	-	-	-	-	-
A7271	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG3196 CE10972 NADH:ubiquinone oxidoreductase, E subunit, variant, NDUFV2/24 kD subunit	KNE57989.1 NADH-quinone oxidoreductase, E subunit, variant [Allomyces macrogynus ATCC 38327]	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=ndufv2 PE=3 SV=1
A7272	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7273	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At4g28710 Myosin class V heavy chain	KMU82960.1 myosin-2 [Coccidioides immitis H538.4]	Unconventional myosin-VI OS=Mus musculus OX=10090 GN=Myo6 PE=1 SV=2
A7274	-	-	GO:0016491(oxidoreductase activity)	K14729 FOX2; multifunctional beta-oxidation protein [EC:4.2.1.-1.1.1.-]	map00410 beta-Alanine metabolism;map01200 Carbon metabolism;map00640 Propanoate metabolism;map01100 Metabolic pathways	-	KAG1230895.1 hypothetical protein G6F35_001792 [Rhizopus oryzae]	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV=3
A7275	-	-	-	-	-	-	-	-
A7276	-	-	GO:0003824(catalytic activity)	K00797 speE, SRM, SPE3; spermidine synthase [EC:2.5.1.16]	map00330 Arginine and proline metabolism;map00480 Glutathione metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG1562 At5g19530 Spermidine synthase	CAE6532003.1 unnamed protein product [Rhizoctonia solani]	Polyamine aminopropyltransferase OS=Aeropyrum pernix (strain ATCC 700893 / DSM 11879 / JCM 9820 / NBRC 100138 / K1) OX=272557 GN=speE PE=3 SV=2
A7277	-	-	-	-	-	KOG3647 7295635 Predicted coiled-coil protein	TPX71732.1 hypothetical protein SpCBS45565_g00890 [Spizellomyces sp. 'palustris']	Clusterin-associated protein 1 homolog OS=Danio rerio OX=7955 GN=cluap1 PE=2 SV=2

A7278	-	-	-	K09562 HSPBP1, FES1; hsp70- interacting protein	map04141 Protein processing in endoplasmic reticulum	KOG2160 Hs1 1968009 Armadillo/bet a-catenin- like repeat- containing protein	ORY05420.1 hypothetical protein K493DRAFT_ 296471 [Basidiobolus meristosporu s CBS 931.73]	Nucleotide exchange factor SIL1 OS=Bos taurus OX=9913 GN=SIL1 PE=2 SV=1
A7279	-	-	-	K04648 DCTN1; dynactin 1	map05014 Amyotrophic lateral sclerosis;map051 32 Salmonella infection;map04 814 Motor proteins;map050 22 Pathways of neurodegenerati on - multiple diseases;map050 16 Huntington disease;map049 62 Vasopressin- regulated water reabsorption	KOG4568 Hs1 8496983 Cytoskeleton -associated protein and related proteins	KKY38169.1 putative dynactin [Diaporthe ampelina]	CAP-Gly domain-containing linker protein 3 OS=Homo sapiens OX=9606 GN=CLIP3 PE=1 SV=3
A7280	GO:00064 68(protein phosphor ylation)	GO:00164 59(myosin complex)	GO:0004674(pro tein serine/threonine kinase activity),GO:000 5524(ATP binding),GO:000 3774(motor activity),GO:000 4672(protein kinase activity)	K13303 SGK2, serum/glucoc orticoid- regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K- Akt signaling pathway;map04 068 FoxO signaling pathway	KOG0598 Hs5 032091 Ribosomal protein S6 kinase and related proteins	ORX80335.1 Pkinase- domain- containing protein [Anaeromyce s robustus]	Protein kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pkgB PE=1 SV=2
A7281	GO:00063 51(transcr iption, DNA- templated)GO:0030 001(metal ion transport), GO:00550 85(transm embrane transport)	GO:00160 20(membr ane)	GO:0003677(DN A binding),GO:000 3899(DNA- directed 5'-3' RNA polymerase activity),GO:004 6873(metal ion transmembrane transporter activity)	K10908 POLRMT, RPO41; DNA- directed RNA polymerase, mitochondria l [EC:2.7.7.6]	-	KOG1038 At2 g24120 Mitochondria l/chloroplast DNA- directed RNA polymerase RPO41, provides primers for DNA replication- initiation	KIN96613.1 hypothetical protein M404DRAFT_ 16854 [Pisolithus tinctorius Marx 270]	DNA-directed RNA polymerase 3, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=RPOT3 PE=2 SV=1
A7282	-	-	-	-	-	-	-	-
A7283	-	-	-	-	-	-	-	-
A7285	-	-	-	K15223 UAF30, SPP27; upstream activation factor subunit UAF30	-	KOG1946 At1 g49520 RNA polymerase I transcription factor UAF	RKO99804.1 hypothetical protein CXG81DRAFT_ 7190, partial [Caulochytrium protostelioides]	Upstream activation factor subunit spp27 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=spp27 PE=1 SV=1
A7286	GO:00161 92(vesicle- mediated transport)	GO:00160 21(integra l compone nt of membra ne)	-	-	-	KOG2887 729 6331 Membrane protein involved in ER to Golgi transport	XP_02187867 8.1 Got1/Sft2- like family- domain- containing protein [Lobosporan gium transversale]	Vesicle transport protein SFT2B OS=Mus musculus OX=10090 GN=Sft2d2 PE=1 SV=1
A7287	-	-	-	-	-	-	-	-
A7288	-	-	-	-	-	-	-	-

A7289	-	-	GO:0003950(NAD+ ADP-ribosyltransferase activity),GO:0005515(protein binding)	-	-	-	KAF8876772.1 hypothetical protein CPB84DRAFT_381179 [Gymnopilus junonius]	-
A7290	-	-	GO:0016491(oxidoreductase activity)	K25881 LARA; L-arabinose reductase [EC:1.1.1.-]	map00040 Pentose and glucuronate interconversions; map01100 Metabolic pathways	KOG1577 Hs5174391 Aldo/keto reductase family proteins	RDW62391.1 alcohol dehydrogenase-4 [Coleophoma cylindrospora]	Aldo-keto reductase family 1 member A1 OS=Bos taurus OX=9913 GN=AKR1A1 PE=2 SV=1
A7291	-	-	-	-	-	-	-	-
A7292	GO:0071108(protein K48-linked deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase), GO:1990380(Lys48-specific deubiquitinase activity)	-	-	KOG2871 At1g43690 Uncharacterized conserved protein	OON07431.1 hypothetical protein, variant [Batrachochytrium salamandrivorans]	Probable ubiquitin carboxyl-terminal hydrolase MINDY-4 OS=Xenopus tropicalis OX=8364 GN=mindy4 PE=2 SV=1
A7293	-	-	-	-	-	-	-	-
A7294	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K08287 E2.7.12.1; dual-specificity kinase [EC:2.7.12.1]	-	KOG0671 Hs10190706 LAMMER dual specificity kinases	ORY95619.1 hypothetical protein BCR43DRAFT_493292 [Syncephalastrium racemosum]	Dual specificity protein kinase CLK4 OS=Homo sapiens OX=9606 GN=CLK4 PE=1 SV=1
A7295	-	-	-	-	-	-	-	-
A7296	-	GO:0005634(nucleus)	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	-	-	-	-	-
A7297	-	-	-	-	-	KOG3085 Hs14743830.1 Predicted hydrolase (HAD superfamily)	KXS19973.1 alpha/beta-hydrolase [Gonapodya prolifera JEL478]	Bifunctional epoxide hydrolase 2 OS=Sus scrofa OX=9823 GN=EPHX2 PE=2 SV=1
A7298	GO:0006811(ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane),GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity),GO:0015377(cation:chloride symporter activity)	K14429 SLC12A9, CCC6; solute carrier family 12 (potassium/chloride transporters), member 9	-	KOG2082 Hs11968148 K+/Cl-cotransporter KCC1 and related transporters	RKO99271.1 hypothetical protein CXG81DRAFT_20617 [Caulochytrium protostelioides]	Solute carrier family 12 member 5 OS=Mus musculus OX=10090 GN=Slc12a5 PE=1 SV=2
A7299	GO:0006189('de novo' IMP biosynthetic process)	-	GO:0004641(phosphoribosylformylglycinamidine cyclo-ligase activity)	-	-	KOG0237 At3g55010 Glycinamide ribonucleotide synthetase (GARS)/Aminimidazole ribonucleotide synthetase (AIRS)	ORY47774.1 PurM C-terminal domain-like protein [Rhizoclosmatium globosum]	Phosphoribosylformylglycinamidine cyclo-ligase OS=Methanococcus vannielii (strain ATCC 35089 / DSM 1224 / JCM 13029 / OCM 148 / SB) OX=406327 GN=purM PE=3 SV=1
A7300	-	-	-	-	-	-	-	-

A7301	-	GO:0008180(COP9 signalosome)	GO:0004222(metalloendopeptidase activity),GO:0005515(protein binding),GO:0008233(peptidase activity),GO:0008237(metallopeptidase activity)	K09613 COP5, CSN5; COP9 signalosome complex subunit 5 [EC:3.4.-.-]	-	KOG1554 CE06722 COP9 signalosome, subunit CSN5	XP_013330652.1 COP9 signalosome subunit CsnE [Rasamsonia emersonii CBS 393.64]	COP9 signalosome complex subunit 5 OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=RR1 PE=3 SV=1
A7302	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0008569(minus-end-directed microtubule motor activity)	K10413 DYNC1H; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595 Hs17864092 Dyneins, heavy chain	TPX62534.1 hypothetical protein PhCBS80983_g00270 [Powellomyces hirtus]	Dynein axonemal heavy chain 7 OS=Homo sapiens OX=9606 GN=DNAH7 PE=1 SV=2
A7303	-	-	GO:0005509(calcium ion binding),GO:0008597(calcium-dependent protein serine/threonine phosphatase regulator activity)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	KOG0034 Hs4506025 Ca2+/calmodulin-dependent protein phosphatase (calcineurin subunit B), EF-Hand superfamily protein	ORX73838.1 calcineurin regulatory beta sub-unit [Linderina pennisporea]	Calcineurin subunit B type 1 OS=Bos taurus OX=9913 GN=PPP3R1 PE=1 SV=2
A7304	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07942 ARL1; ADP-ribosylation factor-like protein 1	-	KOG0072 Hs4502227 GTP-binding ADP-ribosylation factor-like protein ARL1	KAF9158566.1 Arf GTPase arl1 [Actinomyces rella ambigua]	ADP-ribosylation factor 1 OS=Brassica rapa subsp. pekinensis OX=51351 GN=ARF1 PE=2 SV=3
A7305	-	-	-	-	-	-	-	-
A7306	-	-	-	-	-	-	-	-
A7307	-	-	-	-	-	-	-	-
A7308	GO:0008272(sulfate transport),GO:0055085(transmembrane transport)	GO:0016020(membrane),GO:0016021(integral component of membrane)	GO:0008271(secondary active sulfate transmembrane transporter activity),GO:0015301(anion:anion antiporter activity)	K14708 SLC26A11; solute carrier family 26 (sodium-independent sulfate anion transporter), member 11	-	KOG0236 At5g13550 Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family)	XP_031022707.1 uncharacterized protein SmJEL517_g05362 [Synchytrium microbalum]	Sulfate transporter 4.1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=SULTR4;1 PE=1 SV=1
A7309	-	-	-	-	-	-	-	-

A7310	GO:0006631(fatty acid metabolic process)	GO:0005777(peroxisome)	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0003997(acyl-CoA oxidase activity),GO:0071949(FAD binding)	K00232 E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00410 beta-Alanine metabolism;map03320 PPAR signaling pathway;map04024 cAMP signaling pathway;map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00640 Propanoate metabolism;map01040 Biosynthesis of unsaturated fatty acids;map04936 Alcoholic liver disease;map00592 alpha-Linolenic acid metabolism;map	KOG0135 At5g65110 Pristanoyl-CoA oxidase	KAF7753722.1 hypothetical protein DSO57_01203 [Entomophthora muscae]	Acyl-coenzyme A oxidase 2, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=ACX2 PE=1 SV=2
A7311	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	-	-
A7312	-	GO:0016021(integral component of membrane)	-	-	-	KOG4243 7290797 Macrophage maturation-associated protein	KAG1257148.1 hypothetical protein G6F65_016024 [Rhizopus oryzae]	Hemolysin-3 OS=Bacillus cereus OX=1396 GN=hly-III PE=3 SV=1
A7313	-	-	-	-	-	-	-	-
A7314	GO:0007017(microtubule-based process)	GO:0030286(dynein complex)	-	K10418 DYNLL; dynein light chain LC8-type	map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3430 7290522 Dynein light chain type 1	KAG0148522.1 hypothetical protein CROQUUDRAFT_41311 [Cronartium quercuum f. sp. fusiforme G11]	Dynein light chain 1, cytoplasmic OS=Drosophila melanogaster OX=7227 GN=ctp PE=1 SV=1
A7315	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K14776 DDX10, DBP4; ATP-dependent RNA helicase DDX10/DBP4 [EC:3.6.4.13]	-	KOG0343 Hs13514831 RNA Helicase	ORX55887.1 DEAD-domain-containing protein [Piromyces finnis]	Probable ATP-dependent RNA helicase DDX10 OS=Homo sapiens OX=9606 GN=DDX10 PE=1 SV=2
A7316	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K07877 RAB2A; Ras-related protein Rab-2A	map04152 AMPK signaling pathway	KOG4423 Hs11641237 GTP-binding protein-like, RAS superfamily	KAF9582904.1 rab32, member RAS oncoprotein [Lunasporeangiospora selenospora]	Ras-related protein Rab-38 OS=Mus musculus OX=10090 GN=Rab38 PE=1 SV=1

A7317	-	-	GO:0004017(adenylate kinase activity);GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity)	K18532 AK6, FAP7; adenylate kinase [EC:2.7.4.3]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map01100 Metabolic pathways;map03008 Ribosome biogenesis in eukaryotes	KOG3347 Hs7706212 Predicted nucleotide kinase/nucleoside r protein involved oxidative stress response	RUS22762.1 AAA domain-containing protein [Endogone sp. FLAS-F59071]	Adenylate kinase isoenzyme 6 OS=Bos taurus OX=9913 GN=AK6 PE=2 SV=1
A7318	-	-	-	-	-	-	-	-
A7319	-	-	GO:0005515(protein binding)	-	-	-	-	Dynein axonemal light chain 1 OS=Chlamydomonas reinhardtii OX=3055 GN=LC1 PE=1 SV=1
A7320	GO:0006457(protein folding)	-	GO:0051082(unfolded protein binding)	K09510 DnaJB4; DnaJ homolog subfamily B member 4	-	KOG0714 At2g20560 Molecular chaperone (DnaJ superfamily)	TPX70546.1 hypothetical protein CcCBS67573_g06482 [Chytridiomycota confervae]	DnaJ homolog subfamily B member 1 OS=Mus musculus OX=10090 GN=DnaJb1 PE=1 SV=3
A7321	-	-	GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity)	K03695 clpB; ATP-dependent Clp protease ATP-binding subunit ClpB	map04213 Longevity regulating pathway - multiple species	KOG1051 At1g74310 Chaperone HSP104 and related ATP-dependent Clp proteases	XP_031026708.1 uncharacterized protein SmJEL517_g01312 [Synchytrium microbalum]	Chaperone protein ClpB1 OS=Arabidopsis thaliana OX=3702 GN=CLPB1 PE=1 SV=2
A7322	-	-	-	-	-	-	-	-
A7323	-	-	GO:0005515(protein binding)	K25058 CACTIN; cactin	-	KOG2370 7295594 Cactin	KAF9076467.1 mid region of cactin-domain-containing protein [Rhodocollybia butyracea]	Splicing factor Cactin OS=Drosophila melanogaster OX=7227 GN=cactin PE=1 SV=3
A7324	-	-	-	-	-	-	-	Testicular acid phosphatase OS=Mus musculus OX=10090 GN=Acp4
A7325	-	-	GO:0016790(thiolester hydrolase activity)	-	-	KOG2763 Hs18546373 Acyl-CoA thioesterase	CAE6445402.1 unnamed protein product, partial [Rhizoctonia solani]	Cytosolic acyl coenzyme A thioester hydrolase OS=Mus musculus OX=10090 GN=Acot7 PE=1 SV=2

A7326	-	-	GO:0016301(kinase activity),GO:0005515(protein binding)	K07203 MTOR, FRAP, TOR; serine/threonine-protein kinase mTOR [EC:2.7.11.1]	map04361 Axon regeneration;map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map04140 Autophagy - animal;map05131 Shigellosis;map04211 Longevity regulating pathway;map04212 Longevity regulating pathway - worm;map04213 Longevity regulating pathway - multiple species;map04218 Cellular senescence;map04072 Phospholipase D signaling	KOG0891 Hs14719394 DNA-dependent protein kinase	CEP17686.1 hypothetical protein [Parasitella parasitica]	Serine/threonine-protein kinase SMG1 OS=Danio rerio OX=7955 GN=smg1 PE=2 SV=1
A7327	-	-	-	-	-	-	-	-
A7328	-	GO:0016021(integral component of membrane)	-	-	-	-	-	-
A7329	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05665 ABCC1; ATP-binding cassette, subfamily C (CFTR/MRP), member 1 [EC:7.6.2.3]	map04071 Sphingolipid signaling pathway;map01523 Antifolate resistance;map04977 Vitamin digestion and absorption;map02010 ABC transporters;map05206 MicroRNAs in cancer	KOG0054 Hs955958 Multidrug resistance-associated protein/mitochondrion resistance protein, ABC superfamily	KAG1228529.1 hypothetical protein G6F35_00231.9 [Rhizopus oryzae]	Multidrug resistance-associated protein 1 OS=Gallus gallus OX=9031 GN=ABCC1 PE=2 SV=1
A7330	-	-	-	-	-	-	-	-
A7331	-	-	-	-	-	-	-	-
A7332	GO:0016310(phosphorylation),GO:0000160(phosphorelay signal transduction system)	-	GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	KOG0519 At1g66340 Sensory transduction histidine kinase	XP_007723789.1 hypothetical protein A1O1_04710 [Capronia coronata CBS 617.96]	Hybrid signal transduction histidine kinase A OS=Dictyostelium discoideum OX=44689 GN=dhka PE=1 SV=1
A7333	-	-	GO:0018024(histone-lysine N-methyltransferase activity)	-	-	KOG2155 7304151 Tubulin-tyrosine ligase-related protein	-	-
A7334	-	-	-	-	-	-	-	-
A7335	-	-	-	-	-	-	-	-
A7336	GO:0000160(phosphorelay signal transduction system),GO:0016310(phosphorylation)	-	GO:0016772(transferase activity, transferring phosphorus-containing groups)	K19692 TCSA; osomolarity two-component system, sensor histidine kinase TcsA [EC:2.7.13.3]	map02020 Two-component system	KOG0519 At1g66340 Sensory transduction histidine kinase	XP_016604759.1 hypothetical protein SPPG_07928 [Spizellomyces punctatus DAOM BR117]	Autoinducer 2 sensor kinase/phosphatase LuxQ OS=Vibrio vulnificus (strain CMCP6) OX=216895 GN=luxQ PE=3 SV=1

A7337	-	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups);GO:0016746(acyltransferase activity)	K07513 ACAA1; acetyl-CoA acyltransferase 1 [EC:2.3.1.16]	map03320 PPAR signaling pathway;map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map01040 Biosynthesis of unsaturated fatty acids;map00592 alpha-Linolenic acid metabolism;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG1389[Hs4501853 3-oxoacyl CoA thiolase	KAG0163642.1 3-ketoacyl-CoA thiolase with broad chain length specificity [Apophysomyces sp. BC1015]	3-ketoacyl-CoA thiolase A, peroxisomal OS=Rattus norvegicus OX=10116 GN=Acaa1a PE=1 SV=3
A7338	GO:0009152(purine ribonucleotide biosynthetic process)	-	GO:0003824(catalytic activity);GO:0004018(N6-(1,2-dicarboxyethyl) AMP AMP-lyase (fumarate-forming) activity)	K01756 purB, ADSL; adenylosuccinate lyase [EC:4.3.2.2]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG2700[Hs4557269 Adenylosuccinate lyase	RKP23565.1 adenylosuccinate lyase [Syncephalis pseudoplumigaleata]	Adenylosuccinate lyase OS=Mus musculus OX=10090 GN=Adsl PE=1 SV=2
A7339	-	-	GO:0005085(guanyl-nucleotide exchange factor activity)	-	-	KOG3569[Hs2047608 RAS signaling inhibitor ST5	-	DENN domain-containing protein 2A OS=Mus musculus OX=10090 GN=Dennd2a PE=1 SV=1
A7340	GO:0060271(cilium assembly)	GO:0036038(MKS complex)	-	-	-	KOG4611[Hs2048730 Uncharacterized conserved protein	TPX67518.1 hypothetical protein SpCBS45565_g03723 [Spizellomyces sp. 'palustris']	Meckelin OS=Rattus norvegicus OX=10116 GN=Tmem67 PE=1 SV=1
A7341	-	-	-	-	-	-	-	-
A7342	-	-	-	-	-	-	-	-
A7343	-	-	-	-	-	-	-	-
A7344	-	-	-	-	-	-	-	-
A7345	-	-	GO:0005515(protein binding)	-	-	KOG3602[CE27437 WD40 repeat-containing protein	TPX72575.1 hypothetical protein CcCBS67573_g05748 [Chytridiomycetes confervae]	NACHT domain- and WD repeat-containing protein 1 OS=Mus musculus OX=10090 GN=Nwd1 PE=2 SV=2
A7346	-	-	GO:0016407(acyltransferase activity)	-	-	-	-	-

A7347	-	-	-	K15015 SLC32A, VGAT; solute carrier family 32 (vesicular inhibitory amino acid transporter)	map04727 GABAergic synapse;map04721 Synaptic vesicle cycle;map04723 Retrograde endocannabinoid signaling;map05033 Nicotine addiction;map05032 Morphine addiction	KOG1303 CE26553 Amino acid transporters	KAF7741875.1 hypothetical protein DSO57_010159 [Entomophthora muscae]	-
A7348	-	-	-	-	-	KOG2132 At3g20810 Uncharacterized conserved protein, contains JmjC domain	KAF8195886.1 cupin-like domain-containing protein [Mycenogalopus ATCC 62051]	2-oxoglutarate and iron-dependent oxygenase JMJD4 OS=Danio rerio OX=7955 GN=jmjd4 PE=2 SV=1
A7349	-	-	-	-	-	-	ORY48340.1 hypothetical protein BCR33DRAFT_848344 [Rhizoclostium globosum]	-
A7350	-	-	-	-	-	-	-	-
A7351	-	-	-	K08679 GAE, cap1; UDP-glucuronate 4-epimerase [EC:5.1.3.6]	map01250 Biosynthesis of nucleotide sugars;map00541 O-Antigen nucleotide sugar biosynthesis;map01240 Biosynthesis of cofactors;map0053 Ascorbate and aldarate metabolism;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG1371 At2g45310 UDP-glucose 4-epimerase/UDP-sulfoquinovose synthase	XP_031024646.1 uncharacterized protein SmJEL517_g03406 [Synchytrium microbalum]	UDP-glucuronate 4-epimerase OS=Thermodesulfobacterium geofontis (strain OPF15) OX=795359 GN=TOPB45_0660 PE=1 SV=1
A7352	GO:0032508(DNA duplex unwinding),GO:0006270(DNA replication initiation),GO:0006260(DNA replication)	GO:0042555(MCM complex)	GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0003678(DNA helicase activity)	K02210 MCM7, CDC47; DNA replication licensing factor MCM7 [EC:5.6.2.3]	map03030 DNA replication;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0482 At4g02060 DNA replication licensing factor, MCM7 component	OCF40398.1 minichromosome maintenance protein 7 (cell division control protein 47) [Kwoniella heveanensis CBS 569]	DNA replication licensing factor MCM7 OS=Oryza sativa subsp. indica OX=39946 GN=MCM7 PE=3 SV=1
A7353	-	-	-	-	-	-	-	-
A7354	-	-	-	-	-	-	-	-
A7355	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	-	-	-	KXS12596.1 Formate/nitrite transporter [Gonapodya prolifera JEL478]	Probable formate transporter OS=Methanothermobacter thermautotrophicus OX=145262 GN=fdhC PE=3 SV=1
A7356	-	-	-	-	-	-	-	-

A7357	GO:0042256(mature ribosome assembly),GO:0042254(ribosome biogenesis)	-	-	K14574 SDO1, SBDS; ribosome maturation protein SDO1	map03008 Ribosome biogenesis in eukaryotes	KOG2917[Hs14746057 Predicted exosome subunit	KAG4096242.1 ribosome maturation protein SBDS-like protein [Neocallimastix sp. JGI-2020a]	Ribosome maturation protein SBDS OS=Gallus gallus OX=9031 GN=SBDS PE=2 SV=1
A7358	-	-	-	-	-	-	-	-
A7359	-	-	-	-	-	-	-	-
A7360	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	KOG1740[At1g49400 Predicted mitochondrial/chloroplast ribosomal protein S17	KAG0320804.1 hypothetical protein BGZ97_012768 [Linnemannia gamsii]	Small ribosomal subunit protein uS17 OS=Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) OX=243159 GN=rpsQ PE=3 SV=1
A7361	-	-	GO:0005509(calcium ion binding),GO:0005515(protein binding)	K14793 RRP9; ribosomal RNA-processing protein 9	-	KOG4155[Hs4502123_2 FOG: WD40 repeat	XP_001793916.1 hypothetical protein SNOG_03348 [Parastagonospora nodorum SN15]	Apoptotic protease-activating factor 1 OS=Homo sapiens OX=9606 GN=APAF1 PE=1 SV=2
A7362	-	-	-	-	-	-	OON08526.1 hypothetical protein BSLG_02230 [Batrachochytrium salamandrivorans]	Flagellar radial spoke protein 3 OS=Chlamydomonas reinhardtii OX=3055 GN=RSP3 PE=1 SV=1
A7363	GO:0006355(regulation of transcription, DNA-templated),GO:0009143(nucleoside triphosphate catabolic process)	-	GO:0000981(DNA-binding transcription factor activity, RNA polymerase II-specific),GO:0008270(zinc ion binding),GO:0047429(nucleoside-triphosphate diphosphatase activity)	K16904 DCTPP1; dCTP diphosphatase [EC:3.6.1.12]	map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	-	ORY47606.1 type II deoxyuridine triphosphatase [Rhizoclosmatium globosum]	dCTP pyrophosphatase 1 OS=Mus musculus OX=10090 GN=Dctpp1 PE=1 SV=1
A7364	-	-	-	-	-	-	-	-
A7365	-	-	GO:0005524(ATP binding)	K03235 EF3, TEF3; elongation factor 3	-	KOG0062[YPL226w_2 ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	XP_006680420.1 uncharacterized protein BATDEDRAFT_35572 [Batrachochytrium dendrobatidis JAM81]	Elongation factor 3 OS=Phytophthora infestans (strain T30-4) OX=403677 GN=TEF3 PE=1 SV=1
A7366	-	-	-	-	-	-	-	-
A7367	-	-	-	-	-	-	-	-
A7368	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	-	-	KOG0462[At2g31060 Elongation factor-type GTP-binding protein	ORX91615.1 small GTP-binding protein [Basidiobolus meristosporus CBS 931.73]	Large ribosomal subunit assembly factor BipA OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) OX=574521 GN=bipA PE=1 SV=1
A7369	-	-	-	-	-	-	-	-
A7370	GO:0006887(exocytosis)	GO:0000145(exocytosis)	-	-	-	-	-	-

A7371	-	-	-	-	-	-	KXS21736.1 hypothetical protein M427DRAFT_27319 [Gonapodya prolifera JEL478]	-
A7372	GO:0043039(tRNA aminoacylation),GO:0006432(phenylalanyl-tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0000049(tRNA binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0000166(nucleotide binding),GO:0004826(phenylalanine-tRNA ligase activity)	K01889 FARSA, pheS; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]	map00970 Aminoacyl-tRNA biosynthesis	KOG2784[Hs4 758340 Phenylalanyl-tRNA synthetase, beta subunit	ORX80740.1 hypothetical protein K493DRAFT_242506 [Basidiobolus meristosporus CBS 931.73]	Phenylalanine--tRNA ligase alpha subunit OS=Danio rerio OX=7955 GN=farsa PE=2 SV=2
A7373	GO:0006417(regulation of translation),GO:0033674(positive regulation of kinase activity)	-	GO:0019887(protein kinase regulator activity),GO:0019901(protein kinase binding),GO:0043022(ribosome binding),GO:0005515(protein binding)	-	-	KOG1242[At1 g64790 Protein containing adaptin N- terminal region	ORX96881.1 ARM repeat- containing protein [Basidiobolus meristosporus CBS 931.73]	Protein ILITYHIA OS=Arabidopsis thaliana OX=3702 GN=ILA PE=1 SV=1
A7374	-	-	GO:0046983(protein dimerization activity),GO:0016491(oxidoreductase activity),GO:0050660(flavin adenine dinucleotide binding)	K22747 AIFM3; apoptosis- inducing factor 3	-	KOG1346[Hs4 757732 Programmed cell death 8 (apoptosis- inducing factor)	EPZ31585.1 Pyridine nucleotide- disulfide oxidoreductase-like protein 4 [Rozella allomyces CSF55]	Apoptosis-inducing factor 1, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=aif PE=2 SV=1
A7375	GO:0006310(DNA recombination)	-	GO:0004386(helicase activity),GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	-	-	KOG0351[At1 g27880 ATP- dependent DNA helicase	RUS27251.1 P-loop containing nucleoside triphosphate hydrolase protein [Jimgerdemia flammicorona]	ATP-dependent DNA helicase Q-like 5 OS=Arabidopsis thaliana OX=3702 GN=RECQL5 PE=2 SV=2
A7376	-	-	GO:0046983(protein dimerization activity)	K03124 TFIIIB, GTF2B, SUA7, tfb; transcription initiation factor TFIIIB	map03022 Basal transcription factors;map05203 Viral carcinogenesis; map05017 Spinocerebellar ataxia	KOG1597[Hs4 504193 Transcription initiation factor TFIIIB	TXT09108.1 hypothetical protein VHUM_02582 [Vanrija humicola]	Transcription initiation factor IIB OS=Xenopus laevis OX=8355 GN=gtf2b PE=2 SV=1
A7377	-	-	-	-	-	-	-	-

A7378	-	-	GO:0003676(nucleic acid binding);GO:0005524(ATP binding)	K12823 DDX5, DBP2; ATP-dependent RNA helicase DDX5/DBP2 [EC:3.6.4.13]	map03040 Spliceosome;map05202 Transcriptional misregulation in cancer;map05205 Proteoglycans in cancer	KOG0331 7296646 ATP-dependent RNA helicase	XP_001383660.1 DEAD box RNA helicase [Scheffersomyces stipitis CBS 6054]	ATP-dependent RNA helicase DBP2 OS=Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) OX=322104 GN=DBP2 PE=3 SV=1
A7379	-	-	GO:0016407(acyltransferase activity)	-	-	-	KAG2180890.1 hypothetical protein INT43_008470 [Umbelopsis isabellina]	Putative acetyltransferase C18B11.09c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC18B11.09c PE=3 SV=2
A7380	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7381	-	-	GO:0005524(ATP binding)	K03235 EF3, TEF3; elongation factor 3	-	KOG0062 YPL226w_2 ATPase component of ABC transporters with duplicated ATPase domains/Translation elongation factor EF-3b	XP_006680420.1 uncharacterized protein BATDEDRAFT_35572 [Batrachochytrium dendrobatidis JAM81]	Elongation factor 3 OS=Phytophthora infestans (strain T30-4) OX=403677 GN=TEF3 PE=1 SV=1
A7382	-	-	GO:0022857(transmembrane transporter activity)	K15378 SLC45A1_2_4; solute carrier family 45, member 1/2/4	-	KOG0637 At2g02860 Sucrose transporter and related proteins	TPX47282.1 hypothetical protein SeMB42_g03384 [Synchytrium endobioticum]	Sucrose transport protein SUT1 OS=Oryza sativa subsp. indica OX=39946 GN=SUT1 PE=3 SV=1
A7383	GO:0016310(phosphorylation)	-	GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	-	XP_025359423.1 hypothetical protein BDZ90DRAFT_282132 [Jaminia rosea]	Autoinducer 2 sensor kinase/phosphatase LuxQ OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) OX=223926 GN=luxQ PE=3 SV=1
A7384	-	-	-	K02179 BUB2; cell cycle arrest protein BUB2	map04111 Cell cycle - yeast	-	KZV67774.1 bub2 protein [Peniophora sp. CONT]	Putative mitotic check point protein BUB2 OS=Dictyostelium discoideum OX=44689 GN=bub2 PE=3 SV=1
A7385	-	-	-	-	-	-	TPX59228.1 hypothetical protein PhCBS80983_g02615 [Powellomyces hirtus]	-
A7386	-	-	-	-	-	KOG0048 Hs13641706.1 Transcription factor, Myb superfamily	KAF9650187.1 hypothetical protein BDM02DRAFT_3185576 [Telephora ganbajun]	Transcriptional activator Myb OS=Xenopus laevis OX=8355 GN=myb PE=2 SV=1

A7387	-	-	GO:0005509(calcium ion binding)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	KOG0032 At4g04710 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	XP_008097588.1 hypothetical protein GLRG_08847 [Colletotrichum graminicola M1.001]	Calcium-dependent protein kinase 5 OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=CDPK5 PE=1 SV=1
A7388	-	-	-	-	-	-	-	-
A7389	GO:0006281(DNA repair),GO:0006310(DNA recombination)	-	GO:0003910(DNA ligase (ATP) activity),GO:0005524(ATP binding)	-	-	-	KAF8626423.1 hypothetical protein AX15_004885 [Amanita polypyraxis BW_CC]	DNA ligase OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=ligA PE=1 SV=2
A7390	-	-	-	-	-	-	-	-
A7391	GO:0044237(cellular metabolic process)	-	-	K03680 EIF2B4; translation initiation factor eIF-2B subunit delta	map05168 Herpes simplex virus 1 infection	KOG1467 At5g38640 Translation initiation factor 2B, delta subunit (eIF-2Bdelta/GCD2)	G8B97913.1 hypothetical protein RclHRI_00310041 [Rhizophagus clarus]	Translation initiation factor eIF2B subunit delta OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=tif224 PE=1 SV=1
A7392	GO:0001510(RNA methylation)	-	GO:0008168(methyltransferase activity),GO:0016428(tRNA (cytosine-5-)-methyltransferase activity),GO:0003723(RNA binding)	K15334 NCL1, TRM4; multisite-specific tRNA:(cytosine-C5)-methyltransferase [EC:2.1.1.202]	-	KOG2198 At2g22400 tRNA cytosine-5-methylases and related enzymes of the NOL1/NOP2/sun superfamily	RKP14861.1 S-adenosyl-L-methionine-dependent methyltransferase [Piptopezalis cylindrospora]	Multisite-specific tRNA:(cytosine-C(5))-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NCL1 PE=1 SV=1
A7393	-	-	-	-	-	-	-	-
A7394	-	-	-	-	-	-	-	-
A7395	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7396	-	-	-	-	-	-	-	-
A7397	GO:0009116(nucleoside metabolic process)	-	GO:0019239(deaminase activity),GO:0003824(catalytic activity),GO:0017061(S-methyl-5-thioadenosine phosphorylase activity),GO:0016810(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds),GO:0016787(hydrolase activity)	-	-	-	KAG1470284.1 hypothetical protein G6F57_011849 [Rhizopus oryzae]	5-methylthioadenosine/S-adenosylhomocysteine deaminase OS=Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024) OX=203122 GN=mtaD PE=3 SV=1

A7398	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7399	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7400	-	-	-	-	-	-	-	-
A7401	-	-	GO:0005515(protein binding)	-	-	-	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A7402	-	-	-	K18191 FMC1; ATP synthase assembly factor FMC1, mitochondria l	map04139 Mitophagy - yeast	-	KAF4619127.1 hypothetical protein D9613_005204 [Agroclybe pediades]	-
A7403	-	-	-	-	-	-	-	-
A7404	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	K10877 RAD54B; DNA repair and recombination protein RAD54B [EC:5.6.2.-]	map03440 Homologous recombination	KOG0390[Hs6912622_2 DNA repair protein, SNF2 family	KAF2461809.1 SNF2 family N-terminal domain-containing protein [Lineolata rhizophorae]	DNA repair and recombination protein RAD54B OS=Homo sapiens OX=9606 GN=RAD54B PE=1 SV=1
A7405	-	-	-	-	-	-	-	-
A7406	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0003995(acyl-CoA dehydrogenase activity),GO:0050660(flavin adenine dinucleotide binding)	K00249 ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map03320 PPAR signaling pathway;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map04936 Alcoholic liver disease;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG0140[Hs4557231 Medium-chain acyl-CoA dehydrogenase	KAF7727681.1 hypothetical protein EC973_007236 [Apophysom yces ossiformis]	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Bos taurus OX=9913 GN=ACADM PE=2 SV=1
A7407	-	-	-	-	-	-	-	-
A7408	GO:0006541(glutamine metabolic process)	-	GO:0005515(protein binding),GO:0004359(glutaminase activity)	-	-	KOG0506[Hs303415 Glutaminase (contains ankyrin repeat)	ORY47769.1 glutaminase-domain-containing protein [Rhizoclosmatium globosum]	Glutaminase liver isoform, mitochondrial OS=Homo sapiens OX=9606 GN=GLS2 PE=1 SV=2
A7409	-	-	GO:0005515(protein binding)	-	-	KOG4628[Hs21040269 Predicted E3 ubiquitin ligase	ORY07124.1 hypothetical protein K493DRAFT_332896 [Basidiobolus meristosporus CBS 931.73]	E3 ubiquitin-protein ligase RNF128 OS=Xenopus laevis OX=8355 GN=rnf128 PE=2 SV=2
A7410	GO:0007264(small GTPase mediated signal transduction)	-	GO:0005085(guanyl-nucleotide exchange factor activity)	K05727 DOCK3; dedicator of cytokinesis protein 3	-	KOG1998[Hs301710 Signaling protein DOCK180	TFY66230.1 hypothetical protein EVG20_g4859 [Dentipellis fragilis]	Dedicator of cytokinesis protein 4 OS=Homo sapiens OX=9606 GN=DOCK4 PE=1 SV=3
A7411	-	-	-	-	-	-	-	-

A7412	GO:0070286(axonemal dynein complex assembly)	GO:0005858(axonemal dynein complex)	-	-	-	-	XP_006680717.1 uncharacterized protein BATDEDRAFT_26624 [Batrachochytrium dendrobatidis JAM81]	Dynein regulatory complex protein 1 OS=Chlamydomonas reinhardtii OX=3055 GN=DRC1 PE=1 SV=1
A7413	-	-	-	-	-	-	-	-
A7414	-	GO:0031011(Ino80 complex), GO:0035267(NuA4 histone acetyltransferase complex), GO:0097255(R2TP complex)	GO:0005524(ATP binding),GO:0008094(ATPase, acting on DNA)	K04499 RUVBL1, RVB1, INO80H; RuvB-like protein 1 [EC:5.6.2.4]	map04310 Wnt signaling pathway;map03082 ATP-dependent chromatin remodeling	KOG1942 Hs4506753 DNA helicase, TBP-interacting protein	CDS04193.1 Putative RuvB-like 1 [Lichtheimia ramosa]	RuvB-like 1 OS=Xenopus laevis OX=8355 GN=ruvbl1 PE=2 SV=1
A7415	GO:0006367(transcription initiation from RNA polymerase II promoter)	GO:0005669(transcription factor TFIIID complex)	-	K03132 TAF7; transcription initiation factor TFIIID subunit 7	map03022 Basal transcription factors	KOG4011 At1g55300 Transcription initiation factor TFIIID, subunit TAF7	KXN68728.1 hypothetical protein CONCODRAFT_72043 [Conidiobolus coronatus NRRL 28638]	Transcription initiation factor TFIIID subunit 7 OS=Arabidopsis thaliana OX=3702 GN=TAF7 PE=1 SV=1
A7416	-	-	-	-	-	-	-	-
A7417	-	-	-	K15262 BCP1, BCCIP; protein BCP1	-	-	XP_016611949.1 hypothetical protein SPPG_01362 [Spizellomyces punctatus DAOM BR117]	Protein bcp1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=bcp1 PE=3 SV=2
A7418	GO:0009072(aromatic amino acid family metabolic process)	-	GO:0003868(4-hydroxyphenylpyruvate dioxygenase activity),GO:0016701(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen)	-	-	KOG0638 At1g06570 4-hydroxyphenylpyruvate dioxygenase	-	-
A7419	-	-	GO:0016491(oxidoreductase activity)	-	-	-	XP_025185322.1 DSBA oxidoreductase [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Uncharacterized protein YwbO OS=Bacillus subtilis (strain 168) OX=224308 GN=ywbO PE=4 SV=1
A7420	-	-	GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0016787(hydrolase activity)	K11592 DICER1, DCR1; endoribonuclease Dicer [EC:3.1.26.-]	map05206 MicroRNAs in cancer	KOG0701 At3g03300 dsRNA-specific nuclease Dicer and related ribonucleases	KAG0662219.1 Dicer-like protein 1 [Rhodotorula mucilaginosa]	Dicer-like protein 1 OS=Cryptosporidium parvum OX=5116 GN=DCL-1 PE=3 SV=1
A7421	-	-	-	-	-	-	-	-
A7422	GO:0006412(translation)	GO:0005840(ribosome),GO:0015934(large ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02900 RPL27Ae, RPL27A; large subunit ribosomal protein L27Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1742 At1g23290 60s ribosomal protein L15/L27	XP_012182572.1 predicted protein [Fibroporia radiculosa]	Large ribosomal subunit protein uL15y OS=Arabidopsis thaliana OX=3702 GN=RPL27AB PE=2 SV=1

A7423	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0598[Hs20070247_2 Ribosomal protein S6 kinase and related proteins	OBZ82593.1 Serine/threonine-protein kinase gad8, partial [Choanephora cucurbitarum]	Protein kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pkgB PE=1 SV=2
A7424	-	-	-	-	-	-	-	-
A7425	-	-	-	-	-	-	-	-
A7426	-	-	GO:0003824(catalytic activity)	-	-	KOG3275[At1g31160 Zinc-binding protein of the histidine triad (HIT) family	KAG1716110.1 hypothetical protein ID866_1014 [Astraeus odoratus]	Adenylylsulfatase HINT1 OS=Arabidopsis thaliana OX=3702 GN=HINT1 PE=1 SV=1
A7427	-	-	GO:0003824(catalytic activity)	-	-	-	EPB81807.1 hypothetical protein HMPREF1544_11463 [Mucor circinelloides 1006PhL]	Probable phosphatase C1687.21 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC1687.21 PE=3 SV=1
A7428	-	-	-	-	-	KOG4090[YM R002w Uncharacterized conserved protein	KAG0174244.1 hypothetical protein DFQ30_005286 [Apophysomyces sp. BC1015]	Mitochondrial intermembrane space cysteine motif-containing protein MIX17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIX17 PE=1 SV=1
A7429	-	-	-	-	-	-	-	-
A7430	-	-	-	-	-	-	-	-
A7431	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003723(RNA binding),GO:0003735(structural constituent of ribosome),GO:0003676(nucleic acid binding)	K02964 RP-S18e, RPS18; small subunit ribosomal protein S18e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3311[At1g22780 Ribosomal protein S18	RKP39103.1 40S ribosomal protein S18 [Dimargaris cristalligena]	Small ribosomal subunit protein uS13z/uS13y/uS13x OS=Arabidopsis thaliana OX=3702 GN=RPS18A PE=1 SV=1
A7432	GO:0006486(protein glycosylation)	-	GO:0016757(glycosyltransferase activity)	K05535 MNN2; alpha 1,2-mannosyltransferase [EC:2.4.1.-]	map00513 Various types of N-glycan biosynthesis;map01100 Metabolic pathways	-	CDH54574.1 alpha-glycosyltransferase family 71 protein [Lichtheimia corymbifera JMRC:FSU:9682]	-
A7433	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08294 MKK1_2; mitogen-activated protein kinase kinase [EC:2.7.12.2]	map04139 Mitophagy - yeast;map04011 MAPK signaling pathway - yeast	KOG0581[Hs21729899 Mitogen-activated protein kinase kinase (MAP2K)	RMZ11294.1 hypothetical protein D0864_01023 [Hortaea werneckii]	Mitogen-activated protein kinase mkk2 OS=Aspergillus fumigatus (strain CBS 144.89 / FGSC A1163 / CEA10) OX=451804 GN=mkk2 PE=3 SV=1
A7434	-	-	-	-	-	-	XP_031025008.1 uncharacterized protein SmJEL517_g03122 [Synchytrium microbalum]	-

A7435	-	-	GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding)	K07178 RIOK1; RIO kinase 1 [EC:2.7.11.1]	map03008 Ribosome biogenesis in eukaryotes	KOG2270 At5g37350.1 Serine/threonine protein kinase involved in cell cycle control	RKP06350.1 RIO1 family-domain-containing protein, partial [Thamnocephalis sphaerospora]	Serine/threonine-protein kinase RIO1 OS=Homo sapiens OX=9606 GN=RIOK1 PE=1 SV=2
A7436	-	-	GO:0016491(oxidoreductase activity)	-	-	-	SPO28005.1 uncharacterized protein UTRI_05148 [Ustilago trichophora]	Uncharacterized protein R188 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_R188 PE=1 SV=1
A7437	GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	KOG0597 At1g50230 Serine-threonine protein kinase FUSED	RKP36372.1 kinase-like domain-containing protein [Dimargaris cristalligena]	Serine/threonine-protein kinase TIO OS=Arabidopsis thaliana OX=3702 GN=TIO PE=1 SV=1
A7438	GO:0042732(D-xylose metabolic process)	-	GO:0048040(UDP-glucuronate decarboxylase activity),GO:0070403(NAD+ binding)	-	-	KOG1429 CE04302 dTDP-glucose 4-6-dehydratase/UDP-glucuronic acid decarboxylase	XP_006681589.1 uncharacterized protein BATDEDRAFT_13758 [Batrachochytrium dendrobatidis JAM81]	UDP-glucuronic acid decarboxylase 1 OS=Danio rerio OX=7955 GN=uxs1 PE=1 SV=2
A7439	-	-	-	-	-	-	-	-
A7440	-	-	GO:0005515(protein binding)	K11274 WDHD1, CTF4; chromosome transmission fidelity protein 4	-	KOG1274 Hs901892 WD40 repeat protein	TDL24165.1 hypothetical protein BD410DRAFT_111195 [Rickenella mellea]	WD repeat and HMG-box DNA-binding protein 1 OS=Homo sapiens OX=9606 GN=WDHD1 PE=1 SV=1
A7441	-	-	-	-	-	-	RPB01466.1 hypothetical protein L873DRAFT_659034 [Choiromyces venosus 120613-1]	-
A7442	-	-	-	-	-	-	EXX54053.1 Mkk2p [Rhizophagus irregularis DAOM 197198w]	-
A7443	-	-	-	-	-	-	-	-
A7444	-	-	-	-	-	-	-	-
A7445	-	-	-	-	-	-	-	Protein O-mannosyl-transferase TMEM260 OS=Homo sapiens
A7446	-	-	-	-	-	-	-	-
A7447	-	-	-	-	-	-	-	-
A7448	-	-	-	-	-	-	-	-
A7449	-	-	-	-	-	KOG0800 At5g17600 FOG: Predicted E3 ubiquitin ligase	XP_007868303.1 hypothetical protein GLOTRDRAFT_111805, partial [Gloeophyllum trabeum ATCC 11539]	E3 ubiquitin-protein ligase IE61 OS=Cercopithecine herpesvirus 9 (strain DHV) OX=36348 PE=1 SV=1

A7450	-	-	-	-	-	KOG1246 Hs2065716_2 DNA-binding protein jumonji/RBP2 /SMCY, contains JmjC domain	-	Lysine-specific demethylase 6B OS=Mus musculus OX=10090 GN=Kdm6b PE=1 SV=1
A7451	GO:0006508(proteolysis)	GO:0016021(integral component of membrane)	GO:0004252(serine-type endopeptidase activity)	-	-	KOG2289 At3g53780 Rhomboid family proteins	ORY00783.1 rhomboid-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	RHOMBOLD-like protein 4 OS=Arabidopsis thaliana OX=3702 GN=RBL4 PE=2 SV=1
A7452	GO:0006457(protein folding)	GO:0016272(prefoldin complex)	GO:0051082(unfolded protein binding)	K04797 pfdA, PFDN5; prefoldin alpha subunit	-	KOG3048 Hs4505743 Molecular chaperone Prefoldin, subunit 5	KAF3040942.1 subunit of tubulin prefoldin [Didymella heteroderae]	Prefoldin subunit 5 OS=Homo sapiens OX=9606 GN=PFDN5 PE=1 SV=2
A7453	-	-	-	-	-	-	RKO84696.1 hypothetical protein BDK51DRAFT_32565 [Blyttomyces helicus]	-
A7454	-	-	-	-	-	-	-	-
A7455	-	-	-	-	-	-	-	-
A7456	-	-	GO:0016491(oxidoreductase activity),GO:0010181(FMN binding)	-	-	-	RYO75879.1 hypothetical protein DL763_010936 [Monosporascus cannonballus]	2,4-dienoyl-CoA reductase [(2E)-enoyl-CoA-producing] OS=Escherichia coli (strain K12) OX=83333 GN=fadH PE=1 SV=3
A7457	-	-	GO:0016491(oxidoreductase activity)	K21421 NOX2, GP91, CYBB; NADPH oxidase 2 [EC:1.-.-.-]	map05415 Diabetic cardiomyopathy; map05417 Lipid and atherosclerosis; map04145 Phagosome;map04933 AGE-RAGE signaling pathway in diabetic complications;map04216 Ferroptosis;map04217 Necroptosis;map05171 Coronavirus disease - COVID-19;map04613 Neutrophil extracellular trap formation;map05140 Leishmaniasis;map04621 NOD-like receptor signaling	KOG0039 Hs20127624 Ferric reductase, NADH/NADPH oxidase and related proteins	TPX62687.1 hypothetical protein PhCBS80983_g00418 [Powellomyces hirtus]	Superoxide-generating NADPH oxidase heavy chain subunit A OS=Dictyostelium discoideum OX=44689 GN=noxA PE=2 SV=1
A7458	GO:0007017(microtubule-based process)	GO:0005869(dynactin complex)	-	-	-	-	-	-
A7459	-	-	-	-	-	-	-	-
A7460	-	-	-	-	-	-	-	-
A7461	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY44048.1 TPR-like protein [Rhizoclostium globosum]	-

A7462	-	-	-	-	-	-	KIM52504.1 hypothetical protein SCLCIDRAFT_1223705 [Scleroderma citrinum Foug A]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces ribosidificus OX=80859 GN=rbmC PE=3 SV=1
A7463	GO:0006508(proteolysis)	GO:0005576(extracellular region)	GO:0005515(protein binding)	-	-	-	TPX77043.1 hypothetical protein CcCBS67573_g01690 [Chytridiomycetes confervae]	G8 domain-containing protein DDB_G0286897 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0286897 PE=3 SV=1
A7464	-	-	-	-	-	KOG1454 7292204 Predicted hydrolase/acyltransferase (alpha/beta hydrolase superfamily)	TPX64693.1 hypothetical protein SpCBS45565_g05725 [Spizellomyces sp. 'palustris']	-
A7465	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K14811 DBP3; ATP-dependent RNA helicase DBP3 [EC:3.6.4.13]	-	-	XP_006957964.1 DEAD-domain-containing protein [Wallemia mellicola CBS 633.66]	ATP-dependent RNA helicase dbp3 OS=Aspergillus niger (strain ATCC MYA-4892 / CBS 513.88 / FGSC A1513) OX=425011 GN=dbp3 PE=3 SV=1
A7466	GO:0006508(proteolysis)	-	GO:0008236(serine-type peptidase activity)	-	-	KOG2183 Hs4826940 Prolylcarboxypeptidase (angiotensinase C)	TDZ38843.1 putative extracellular serine carboxypeptidase [Colletotrichum trifolii]	Lysosomal Pro-X carboxypeptidase OS=Pongo abelii OX=9601 GN=PRCP PE=2 SV=1
A7467	-	GO:000159(protein phosphatase type 2A complex)	GO:0005515(protein binding),GO:0019888(protein phosphatase regulator activity)	K04354 PPP2R2; serine/threonine-protein phosphatase 2A regulatory subunit B	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04071 Sphingolipid signaling pathway;map04728 Dopaminergic synapse;map04660 T cell receptor signaling pathway;map04261 Adrenergic signaling in cardiomyocytes; map05142 Chagas disease;map04530 Tight junction;map03015 mRNA surveillance pathway;map04152 AMPK signaling pathway;map04	KOG1354 At1g17720 Serine/threonine protein phosphatase 2A, regulatory subunit	KAG2205256.1 hypothetical protein INT47_009521, partial [Mucor saturninus]	Serine/threonine-protein phosphatase 2A regulatory subunit phr2AB OS=Dictyostelium discoideum OX=44689 GN=phr2aB PE=3 SV=1
A7468	-	-	-	-	-	-	-	-
A7469	-	-	-	-	-	-	-	-
A7470	-	-	GO:0005515(protein binding)	-	-	-	-	-

A7471	GO:0006829(zinc ion transport), GO:0006882(cellular zinc ion homeostasis), GO:0006812(cation transport), GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005385(zinc ion transmembrane transporter activity), GO:0008324(cation transmembrane transporter activity)	K14692 SLC30A5_7, ZNT5_7, MTP, MSC2; solute carrier family 30 (zinc transporter), member 5/7	-	KOG1484 At2g04620 Putative Zn2+ transporter MSC2 (cation diffusion facilitator superfamily)	OAD00393.1 hypothetical protein MUCCIDRAFT_15957, partial [Mucor lusitanicus CBS 277.49]	Probable zinc transporter protein DDB. G0291141 OS=Dictyostelium discoideum OX=44689 GN=DDb_G0291141 PE=3 SV=1
A7472	GO:0007010(cytoskeleton organization)	-	GO:0003779(action binding)	-	-	-	-	Villin-1 OS=Gallus gallus OX=9031 GN=VIL1 PE=1 SV=2
A7473	GO:0006744(ubiquinone biosynthetic process)	GO:0005743(mitochondrial inner membrane)	-	K18586 COQ4; ubiquinone biosynthesis protein COQ4	-	KOG3244 Hs7705807 Protein involved in ubiquinone biosynthesis	TPX63012.1 hypothetical protein PhCBS80983_g00064 [Powellomyces hirtus]	Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial OS=Xenopus tropicalis OX=8364 GN=coq4 PE=2 SV=1
A7474	-	-	-	-	-	-	KZT51674.1 TPR repeat-containing protein-like protein [Calocera cornea HHB12733]	-
A7475	GO:0006436(tryptophanyl-tRNA aminoacylation), GO:0006418(tRNA aminoacylation for protein translation)	-	GO:0000166(nucleotide binding), GO:0004830(tryptophan-tRNA ligase activity), GO:0005524(ATP binding), GO:0004812(aminoacyl-tRNA ligase activity)	K01867 WARS, trpS; tryptophanyl-tRNA synthetase [EC:6.1.1.2]	map00970 Aminoacyl-tRNA biosynthesis	KOG2145 Hs14754335 Cytoplasmic tryptophanyl-tRNA synthetase	XP_017992929.1 tryptophanyl-tRNA synthetase [Malassezia pachydermatis]	Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=WARS1 PE=1 SV=2
A7476	GO:0140647(P450-containing electron transport chain)	-	GO:0051537(2 iron, 2 sulfur cluster binding), GO:0051536(iron-sulfur cluster binding)	K22071 FDX2; ferredoxin-2, mitochondrial	-	KOG3309 At4g05450 Ferredoxin	PVU99301.1 hypothetical protein BB559_000838 [Furculomyces boomerangus]	Adrenodoxin-like protein 1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MFDX1 PE=1 SV=1
A7477	-	GO:0016459(myosin complex)	GO:0003774(motor activity), GO:0005524(ATP binding), GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection; map04814 Motor proteins	KOG0160 At3g19960 Myosin class V heavy chain	KAG4105538.1 hypothetical protein H8356DRAFT_1026682 [Neocallimastix sp. JGI-2020a]	Myosin-I heavy chain OS=Dictyostelium discoideum OX=44689 GN=myol PE=1 SV=1
A7478	-	GO:0016459(myosin complex)	GO:0005515(protein binding), GO:0003774(motor activity), GO:0005524(ATP binding)	K10356 MYO1; myosin I	map05130 Pathogenic Escherichia coli infection; map04814 Motor proteins	KOG0162 Hs4826844 Myosin class I heavy chain	XP_031025224.1 uncharacterized protein SmJEL517_g02861 [Synchytrium microbalum]	Unconventional myosin-Ie OS=Mus musculus OX=10090 GN=Myo1e PE=1 SV=1

A7479	-	-	-	K01527 EGD1, BTF3; nascent polypeptide- associated complex subunit beta	map04214 Apoptosis - fly	KOG2240 Hs1 6159637 RNA polymerase II general transcription factor BTF3 and related proteins	CDH54079.1 nascent polypeptide- associated complex subunitbeta [Lichtheimia corymbifera JMRC:FSU:96 82]	Transcription factor BTF3 homolog 4 OS=Danio rerio OX=7955 GN=btf3l4 PE=2 SV=1
A7480	-	-	-	-	-	-	-	-
A7481	-	-	-	-	-	-	-	-
A7482	-	-	GO:0016491(oxi doreductase activity)	-	-	KOG3851 Hs1 0864011 Sulfide:quino ne oxidoreducta se/flavo- binding protein	TPX58613.1 hypothetical protein PhCBS80983. g02999 [Powellomyce s hirtus]	Sulfide dehydrogenase [flavocytochrome c] flavoprotein chain OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) OX=572477 GN=fccB PE=1 SV=3
A7483	-	-	-	-	-	-	-	-
A7484	-	-	GO:0005515(pro tein binding)	-	-	-	ORY86492.1 hypothetical protein LY90DRAFT_9 9134 [Neocallimast ix californiae]	Centrosomal protein of 164 kDa OS=Homo sapiens OX=9606 GN=CEP164 PE=1 SV=3
A7485	-	-	-	-	-	-	-	-
A7486	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity);GO:000 5524(ATP binding)	K21157 SAK1; SNF1- activating kinase 1 [EC:2.7.11.1]	map04138 Autophagy - yeast	KOG0585 CE 01146 Ca2+/calmod ulin- dependent protein kinase kinase beta and related serine/threon ine protein kinases	PIA19277.1 kinase-like protein [Coemansia reversa NRRL 1564]	Calcium/calmodulin-dependent protein kinase kinase 2 OS=Mus musculus OX=10090 GN=Camkk2 PE=1 SV=2
A7487	-	-	-	-	-	-	-	-
A7488	-	-	-	-	-	-	XP_01661191 3.1 hypothetical protein SPPG_01326 [Spizellomyce s punctatus DAOM BR117]	Probable transporter PD_1892 OS=Xylella fastidiosa (strain Temecula1 / ATCC 700964) OX=183190 GN=PD_1892 PE=3 SV=1
A7489	-	-	-	-	-	-	-	-
A7490	-	-	-	-	-	-	-	-
A7491	GO:00465 13(cerami de biosynthe tic process)	GO:00160 21(integra l compone nt of membra ne)	GO:0050291(sp hingosine N- acyltransferase activity)	K04709 LAG1, LAC1; very-long- chain ceramide synthase [EC:2.3.1.297]	map00600 Sphingolipid metabolism;map 01100 Metabolic pathways	KOG1607 Hs2 0550645 Protein transporter of the TRAM (translocating chain- associating membrane) superfamily	ORX61270.1 LAG1- domain- containing protein, partial [Piromyces finnis]	Ceramide synthase 4 OS=Bos taurus OX=9913 GN=CERS4 PE=2 SV=1
A7492	GO:00362 11(protein modificati on process)	-	-	K06047 TTL; tubulin--- tyrosine ligase [EC:6.3.2.25]	-	KOG2157 YB R094w Predicted tubulin- tyrosine ligase	SCU93252.1 LAME_OF031 58g1_1 [Lachancea meyersii CBS 8951]	Protein polyglycylase TTL10 OS=Macaca fascicularis OX=9541 GN=TTL10 PE=2 SV=1
A7493	-	-	-	-	-	-	-	-
A7494	-	-	-	-	-	-	-	-
A7495	GO:00064 91(N- glycan processin g)	-	GO:0005515(pro tein binding)	-	-	KOG2397 At5 g56360 Protein kinase C substrate, 80 KD protein, heavy chain	XP_504443.1 YALIOE26895 p [Yarrowia lipolytica CLIB122]	Glucosidase 2 subunit beta OS=Oryza sativa subsp. indica OX=39946 GN=Osl_01383 PE=3 SV=1

A7496	-	-	GO:0003824(catalytic activity)	-	-	KOG1075[CE04575 FOG: Reverse transcriptase	OMJ28687.1 LINE-1 retrotransposable element ORF2 protein, partial [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A7497	-	-	GO:0003677(DNA binding),GO:0003824(catalytic activity),GO:0016788(hydrolase activity, acting on ester bonds),GO:0004518(nuclease activity)	K04799 FEN1 RAD2; flap endonuclease -1 [EC:3.1.-.-]	map03030 DNA replication;map03450 Non-homologous end-joining;map03410 Base excision repair	KOG2519[At5g26675 5'-3' exonuclease	RKP06385.1 flap endonuclease 1 [Thamnocephalis sphaerospora]	Flap endonuclease 1 OS=Phytophthora infestans (strain T30-4) OX=403677 GN=FEN1 PE=3 SV=1
A7498	-	-	-	-	-	-	-	-
A7499	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11251 H2A; histone H2A	map04217 Necroptosis;map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map03082 ATP-dependent chromatin remodeling	KOG1757[At2g38810 Histone 2A	XP_016607979.1 histone H2A [Spizellomyces punctatus DAOM BR117]	Probable histone H2A variant 2 OS=Oryza sativa subsp. japonica OX=39947 GN=Os10g0418000 PE=2 SV=1
A7500	GO:0006596(polyamine biosynthetic process)	-	GO:0003824(catalytic activity)	K01581 E4.1.1.17, ODC1, speC, speF; ornithine decarboxylase [EC:4.1.1.17]	map01110 Biosynthesis of secondary metabolites;map00330 Arginine and proline metabolism;map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG0622[YKL184w Ornithine decarboxylase	GFG12475.1 ornithine decarboxylase [Aspergillus udagawae]	Diaminopimelate decarboxylase OS=Helicobacter pylori (strain J99 / ATCC 700824) OX=85963 GN=lysA PE=3 SV=1
A7501	-	-	GO:0005515(protein binding)	-	-	-	XP_016612613.1 hypothetical protein SPPG_00295 [Spizellomyces punctatus DAOM BR117]	Cilia- and flagella-associated protein 57 OS=Homo sapiens OX=9606 GN=CFAP57 PE=1 SV=3
A7502	GO:0006812(cation transport),GO:0055085(transmembrane transport),GO:0006829(zinc ion transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	KOG2802[Hs22041450 Membrane protein HUEL (cation efflux superfamily)	KNE65762.1 cation diffusion facilitator family transporter, partial [Allomyces macrogynus ATCC 38327]	Proton-coupled zinc antiporter SLC30A9, mitochondrial OS=Homo sapiens OX=9606 GN=SLC30A9 PE=1 SV=1
A7503	-	-	-	-	-	-	-	-

A7504	GO:0006412(translation)	GO:0005840(ribosome),GO:0015934(large ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02880 RP-L17e, RPL17; large subunit ribosomal protein L17e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3353 At1g67430 60S ribosomal protein L22	RKP23856.1 50S ribosomal protein L22 [Syncephalis pseudoplumigaleata]	Large ribosomal subunit protein uL22z OS=Hordeum vulgare OX=4513 PE=2 SV=1
A7505	GO:1904263(positive regulation of TORC1 signaling)	-	GO:0005198(structural molecule activity),GO:0005515(protein binding)	-	-	KOG2445 Hs13654288 Nuclear pore complex component (sc Seh1)	RKP07427.1 WD40-repeat-containing domain protein [Thamnocephalis sphaerospora]	Nucleoporin SEH1-A OS=Xenopus laevis OX=8355 GN=seh1l-a PE=1 SV=1
A7506	GO:0006351(transcription, DNA-templated),GO:0006379(mRNA cleavage)	-	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	K03000 RPA12, POLR1H, ZNRD1; DNA-directed RNA polymerase I subunit RPA12	map03020 RNA polymerase	-	XP_017990499.1 dna-directed rna polymerase complex i subunit rpa12 [Malassezia pachydermatis]	DNA-directed RNA polymerase I subunit RPA12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rpa12 PE=1 SV=1
A7507	-	-	GO:0003743(translation initiation factor activity),GO:0003723(RNA binding),GO:0005515(protein binding)	K03260 EIF4G; translation initiation factor 4G	map05416 Viral myocarditis	KOG0401 At3g60240.1 Translation initiation factor 4F, ribosome/mRNA-bridging subunit (eIF-4G)	KWU41598.1 ARM repeat-containing protein, partial [Rhodotorula sp. JG-1b]	Eukaryotic translation initiation factor 4G OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0555200 PE=2 SV=2
A7508	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0006813(potassium ion transport)	GO:0016020(membrane)	GO:0005216(ion channel activity),GO:0005249(voltage-gated potassium channel activity)	-	-	KOG0501 Hs4504831 K+-channel KCNQ	TPX69675.1 hypothetical protein SpCBS45565_g02243 [Spizellomyces sp. 'palustris']	Potassium voltage-gated channel subfamily H member 1 OS=Rattus norvegicus OX=10116 GN=Kcnh1 PE=1 SV=1
A7509	-	-	-	-	-	-	KAF9925780.1 hypothetical protein FBU30_004486 [Linnemannia zychae]	-
A7510	-	-	-	-	-	-	-	-
A7511	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity)	K01110 PTEN; phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN [EC:3.1.3.16 3.1.3.48 3.1.3.67]	map04361 Axon regeneration;map05415 Diabetic cardiomyopathy; map04140 Autophagy - animal;map05222 Small cell lung cancer;map04510 Focal adhesion;map04212 Longevity regulating pathway - worm;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04071 Sphingolipid signaling pathway;map01521 EGFR tyrosine kinase inhibitor resistance;map05215 Prostate cancer;map0521	KOG2283 Hs4506249 Clathrin coat dissociation kinase GAK/PTEN/Auxilin and related tyrosine phosphatases	EPZ34584.1 Protein-tyrosine phosphatase domain-containing protein [Rozella allomycis CSF55]	Phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN OS=Canis lupus familiaris OX=9615 GN=PTEN PE=2 SV=1

A7512	GO:0006812(cation transport), GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	KOG1485 At2g47830 Mitochondrial Fe2+ transporter MMT1 and related transporters (cation diffusion facilitator superfamily)	KAG2186322.1 hypothetical protein INT43_002760 [Umbelopsis isabellina]	Metal tolerance protein 2 OS=Oryza sativa subsp. japonica OX=39947 GN=MTP2 PE=2 SV=1
A7513	-	-	GO:0106370(protein-L-histidine N-pros-methyltransferase activity)	-	-	KOG3987 Hs19923449 Uncharacterized conserved protein DREV/CGI-81	-	Protein-L-histidine N-pros-methyltransferase OS=Homo sapiens OX=9606 GN=METTL9 PE=1 SV=1
A7514	-	-	GO:0005507(copper ion binding)	K02258 COX11, ctaG; cytochrome c oxidase assembly protein subunit 11	map04714 Thermogenesis; map00190 Oxidative phosphorylation; map01100 Metabolic pathways	KOG2540 Hs4758034 Cytochrome oxidase assembly factor COX11	ORX89799.1 hypothetical protein K493DRAFT_288841 [Basidiobolus meristosporus CBS 931.73]	Cytochrome c oxidase assembly protein COX11, mitochondrial OS=Homo sapiens OX=9606 GN=COX11 PE=1 SV=3
A7515	GO:0016226(iron-sulfur cluster assembly)	-	GO:0051536(iron-sulfur cluster binding)	K22072 ISCA2; iron-sulfur cluster assembly 2	-	KOG1119 Hs20543669 Mitochondrial Fe-S cluster biosynthesis protein ISA2 (contains a HesB-like domain)	KAF0413861.1 iron-sulfur cluster assembly accessory protein isa2 [Gigaspora margarita]	Iron-sulfur cluster assembly 2 homolog, mitochondrial OS=Mus musculus OX=10090 GN=Isca2 PE=1 SV=2
A7516	GO:0015914(phospholipid transport)	GO:0016021(integral component of membrane)	GO:0000166(nucleotide binding),GO:0000287(magnesium ion binding),GO:0005524(ATP binding),GO:0140326(ATPase-coupled intramembrane lipid transporter activity),GO:0005215(transporter activity),GO:0016887(ATP hydrolysis activity)	K14802 DRS2, ATP8A; phospholipid-transporting ATPase [EC:7.6.2.1]	-	KOG0206 At3g25610 P-type ATPase	XP_03714074.4.1 uncharacterized protein HG536_0F03950 [Torulaspora globosa]	Phospholipid-transporting ATPase 10 OS=Arabidopsis thaliana OX=3702 GN=ALA10 PE=3 SV=1
A7517	GO:0006508(proteolysis)	-	GO:0004181(metalloprotease activity),GO:0008270(zinc ion binding)	K08783 ECM14; extracellular matrix protein 14 [EC:3.4.17.-]	-	KOG2650 Zn5238 Zinc carboxypeptidase	KAF7722160.1 hypothetical protein DSO57_005313 [Entomophthora muscae]	Putative carboxypeptidase suro-1 OS=Caenorhabditis elegans OX=6239 GN=suro-1 PE=1 SV=2
A7518	GO:0006508(proteolysis)	-	GO:0004181(metalloprotease activity),GO:0008270(zinc ion binding)	K08783 ECM14; extracellular matrix protein 14 [EC:3.4.17.-]	-	KOG2650 Zn5242 Zinc carboxypeptidase	KAF7755277.1 hypothetical protein DSO57_014277 [Entomophthora muscae]	Carboxypeptidase A4 OS=Mus musculus OX=10090 GN=Cpa4 PE=2 SV=2
A7519	-	-	-	-	-	-	-	-
A7520	-	-	GO:0005515(protein binding)	-	-	-	-	-

A7521	-	-	-	K20523 SH3YL1; SH3 domain- containing YSC84-like protein 1	-	KOG1843 YH R016c Uncharacteriz ed conserved protein	ORY81323.1 DUF500 and domain- containing protein [Protomyces lactucaedebili s]	Protein YSC84 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YSC84 PE=1 SV=2
A7522	-	-	-	-	-	-	-	-
A7523	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	-	-	KOG0671 Hs1 0190706 LAMMER dual specificity kinases	KAF9968121. 1 F-box only protein 42 [Mortierella alpina]	Dual specificity protein kinase CLK4 OS=Homo sapiens OX=9606 GN=CLK4 PE=1 SV=1
A7524	-	-	GO:0016746(acy ltransferase activity)	K08766 E2.3.1.21; carn itine O- palmitoyltran sferase 2 [EC:2.3.1.21]	map00071 Fatty acid degradation	KOG3719 Hs4 503023 Carnitine O- acyltransferas e CPT2/YAT1	KAF0446799. 1 acyltransferas e ChoActase/C OT/CPT [Gigaspora margarita]	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Danio rerio OX=7955 GN=cpt2 PE=2 SV=2
A7525	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	-	-	KOG0671 Hs1 0190706 LAMMER dual specificity kinases	XP_01902127 3.1 kinase- like protein [Saitoella complicata NRRL Y- 17804]	Serine/threonine-protein kinase ppk5 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ppk5 PE=1 SV=1
A7526	GO:00063 55(regulat ion of transcripti on, DNA- templated)	-	GO:0003713(tra nscription coactivator activity)	-	-	-	XP_01661054 2.1 hypothetical protein SPPG_02962 [Spizellomyce s punctatus DAOM BR117]	c-Myc-binding protein homolog OS=Dictyostelium discoideum OX=44689 GN=mycbp PE=3 SV=1
A7527	-	-	-	-	-	-	-	von Willebrand factor A domain-containing protein 5B1 OS=Homo sapiens OX=9606 GN=VWA5B1 PE=1 SV=2
A7528	-	-	-	-	-	-	-	-
A7529	GO:00165 59(peroxis ome fission)	GO:00057 79(integra l compone nt of peroxis omal membran e)	-	K13352 PEX11B; peroxin-11B	map04146 Peroxisome	KOG4186 At1 g01820 Peroxisomal biogenesis protein (peroxin)	XP_03353136 6.1 peroxisomal biogenesis factor 11 [Eremomyces bilateralis CBS 781.70]	Peroxisomal membrane protein 11C OS=Arabidopsis thaliana OX=3702 GN=PEX11C PE=1 SV=1
A7530	GO:19026 00(proton transmem brane transport)	GO:00331 79(proton- transporti ng V-type ATPase, V0 domain), GO:00002 20(vacuol ar proton- transporti ng V-type ATPase, V0 domain)	GO:0046961(pro ton- transporting ATPase activity, rotational mechanism)	K02154 ATPeV0A, ATP6N; V- type H+- transporting ATPase subunit a	map04145 Phagosome;map 04142 Lysosome;map0 4721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map001 90 Oxidative phosphorylation; map05110 Vibrio cholerae infection;map05 120 Epithelial cell signaling in Helicobacter pylori infection;map05 152 Tuberculosis;ma p04966 Collecting duct acid secretion;map01 100 Metabolic pathways;map05 165 Human papillomavirus infection	KOG2189 Hs1 9913418 Vacuolar H+- ATPase V0 sector, subunit a	RGB34378.1 H+-ATPase subunit [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Vacuolar proton translocating ATPase 100 kDa subunit OS=Dictyostelium discoideum OX=44689 GN=vatM PE=1 SV=2
A7531	-	-	-	-	-	-	-	-
A7532	-	GO:00057 83(endopl asmic reticulum)	-	-	-	-	-	Protein PHTF2 OS=Mus musculus OX=10090 GN=Phtf2 PE=1 SV=2

A7533	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K12893 SRSF4_5_6; SFRS4_5_6; serine/arginine-rich splicing factor 4/5/6	map03040 Spliceosome;map05168 Herpes simplex virus 1 infection	KOG0105[Hs4506903 Alternative splicing factor ASF/SF2 (RRM superfamily)	RKP25289.1 hypothetical protein SYNPS1DRAFT_1885, partial [Syncephalis pseudoplumigaleata]	Probable splicing factor, arginine/serine-rich 3 OS=Caenorhabditis elegans OX=6239 GN=rsp-3 PE=1 SV=2
A7534	-	GO:0016020(membrane)	-	K23544 SERINC1; serine incorporator 1	-	KOG2592[At1g16180 Tumor differentially expressed (TDE) protein	XP_006680018.1 uncharacterized protein BATDERAFT_37095 [Batrachochytrium dendrobatidis JAM81]	Serine incorporator 3 OS=Pongo abelii OX=9601 GN=SERINC3 PE=2 SV=1
A7535	-	-	-	K19951 TBC1D8_9; TBC1 domain family member 8/9	-	KOG4436[CE07531 Predicted GTPase activator NB4S/EVI5 (contains TBC domain)/Calmodulin-binding protein Pollux (contains PTB and TBC domains)	XP_018298541.1 hypothetical protein PHYBLDRAFT_91840, partial [Phycomyces blakesleeanus NRRL 1555(-)]	Rab GTPase-activating protein 1-like OS=Homo sapiens OX=9606 GN=RABGAP1L PE=1 SV=1
A7536	GO:0006508(proteolysis)	-	GO:0004190(aspartic-type endopeptidase activity)	-	-	KOG1339[At3g50050 Aspartyl protease	-	Aspartic proteinase CDR1 OS=Arabidopsis thaliana OX=3702 GN=CDR1 PE=1 SV=1
A7537	-	-	GO:0008641(ubiquitin-like modifier activating enzyme activity)	K22132 tcdA; tRNA threonylcarbamoyladenine dehydratase	-	KOG2018[At5g37530 Predicted dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis	RKO85210.1 hypothetical protein BDK51DRAFT_5224, partial [Blytiumyces helicus]	tRNA threonylcarbamoyladenine dehydratase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC1A6.10 PE=3 SV=1
A7538	GO:0006886(intracellular protein transport)	-	GO:0005515(protein binding)	-	-	KOG1585[Hs4505331 Protein required for fusion of vesicles in vesicular transport, gamma-SNAP	KAG0360164.1 hypothetical protein BGZ54_009661 [Gamsiella multidivariata]	Gamma-soluble NSF attachment protein OS=Dictyostelium discoideum OX=44689 GN=snpC PE=1 SV=1
A7539	-	-	-	-	-	-	KAE8246870.1 hypothetical protein A4X03_0g7195 [Tilletia caries]	-

A7540	GO:0045454(cell redox homeostasis)	-	GO:0016491(oxidoreductase activity),GO:0050660(flavin adenine dinucleotide binding),GO:0016668(oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor)	K00383 GSR, gor; glutathione reductase (NADPH) [EC:1.8.1.7]	map05415 Diabetic cardiomyopathy; map04918 Thyroid hormone synthesis;map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG4716 Hs2035670 Thioredoxin reductase	KXS12547.1 thioredoxin reductase TR2 [Gonapodya prolifera JEL478]	Thioredoxin reductase OS=Plasmodium falciparum (isolate FCH-5) OX=132416 GN=TRXR PE=1 SV=1
A7541	-	-	-	-	-	-	-	-
A7542	-	-	GO:0005515(protein binding),GO:0003779(actin binding)	-	-	-	-	-
A7543	-	-	-	-	-	-	-	-
A7544	GO:0006418(tRNA aminoacylation for protein translation),GO:0006423(cysteinylation),GO:0006423(cysteinylation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004817(cysteine-tRNA ligase activity)	K01883 CARS, cysS; cysteinyl-tRNA synthetase [EC:6.1.1.16]	map00970 Aminoacyl-tRNA biosynthesis	KOG2007 7302987 Cysteinylation synthetase	CEP13696.1 hypothetical protein [Parasitella parasitica]	Cysteine--tRNA ligase, cytoplasmic OS=Drosophila pseudoobscura pseudoobscura OX=46245 GN=Aats-cys PE=3 SV=1
A7545	GO:0008033(tRNA processing)	-	GO:0017150(tRNA dihydrouridine synthase activity),GO:0050660(flavin adenine dinucleotide binding)	K05543 DUS2; tRNA--dihydrouridine synthase 2 [EC:1.3.1.91]	-	KOG2334 At3g49640 tRNA--dihydrouridine synthase	KAG0235300.1 tRNA--dihydrouridine(20) synthase [NAD(P)+]-like [Actinomortierella wolfii]	tRNA--dihydrouridine(20) synthase [NAD(P)+]-like OS=Homo sapiens OX=9606 GN=DUS2 PE=1 SV=1
A7546	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K20872 NEK2; serine/threonine-protein kinase Nek2 [EC:2.7.11.1]	-	KOG0589 CE23001 Serine/threonine protein kinase	KAF9305038.1 G2-specific serine/threonine protein kinase [Mortierella antarctica]	Serine/threonine-protein kinase Nek8 OS=Mus musculus OX=10090 GN=Nek8 PE=1 SV=1
A7547	GO:0016051(carbohydrate biosynthetic process)	GO:0016021(integral component of membrane)	GO:0008146(sulfotransferase activity)	-	-	-	-	-
A7548	GO:0006189('de novo' IMP biosynthetic process)	-	GO:0016787(hydrolase activity)	K11808 ADE2; phosphoribosylaminoimidazole carboxylase [EC:4.1.1.21]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01100 Metabolic pathways	-	KAF9118842.1 hypothetical protein BGX30_004263, partial [Mortierella sp. GBA39]	Pyridinium-3,5-biscarboxylic acid mononucleotide synthase OS=Lactiplantibacillus plantarum (strain ATCC BAA-793 / NCIMB 8826 / WCFS1) OX=220668 GN=larB PE=1 SV=1
A7549	GO:0030047(actin modification)	-	GO:0018064(protein-L-histidine N-terminal methyltransferase activity)	K05302 SETD6; N-lysine methyltransferase SETD6 [EC:2.1.1.-]	-	KOG1337 Hs14149938 N-methyltransferase	KXN68770.1 SET domain-containing protein [Conidiobolus coronatus NRRL 28638]	Actin-histidine N-methyltransferase OS=Mus musculus OX=10090 GN=Setd3 PE=1 SV=1

A7550	GO:0009435(NAD biosynthetic process), GO:0009058(biosynthetic process)	-	GO:0016779(nucleotidyltransferase activity),GO:0003824(catalytic activity)	-	-	-	-	-
A7551	-	-	GO:0004764(shikimate 3-dehydrogenase (NADP+) activity)	K13830 ARO1; pentafunctional AROM polypeptide [EC.4.2.3.4 4.2.1.10 1.1.1.25 2.7.1.71 2.5.1.19]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map00999 Biosynthesis of various plant secondary metabolites;map01100 Metabolic pathways	-	TPX77798.1 hypothetical protein CcCBS67573.g00925 [Chytridiomycota confervae]	Pentafunctional AROM polypeptide OS=Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) OX=486041 GN=LACBIDRAFT_233717 PE=3 SV=1
A7552	GO:0006406(mRNA export from nucleus), GO:0045893(positive regulation of transcription, DNA-templated)	GO:0000124(SAGA complex), GO:0005643(nuclear pore)	GO:0003713(transcription coactivator activity)	K11368 ENY2, DC6, SUS1; enhancer of yellow 2 transcription factor	-	KOG4479[Hs910186 Transcription factor e(y)2	ORY33557.1 enhancer of yellow 2 transcription factor [Rhizoclostium globosum]	Transcription and mRNA export factor ENY2 OS=Bos taurus OX=9913 GN=ENY2 PE=3 SV=1
A7553	GO:0055085(transmembrane transport)	-	-	-	-	KOG0759[At5g19760 Mitochondrial oxoglutarate/malate carrier proteins	EPS33917.1 hypothetical protein PDE_08879 [Penicillium oxalicum 114-2]	Putative mitochondrial 2-oxoglutarate/malate carrier protein OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=mic-33 PE=3 SV=1
A7554	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02868 RP-L11e, RPL11; large subunit ribosomal protein L11e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0397[At3g58700 60S ribosomal protein L11	OLL23214.1 60S ribosomal protein L11 [Neoelecta irregularis DAH-3]	Large ribosomal subunit protein uL5 OS=Oryza sativa subsp. indica OX=39946 GN=RPL11 PE=2 SV=2
A7555	-	-	-	-	-	-	-	-
A7556	-	-	GO:0005515(protein binding)	-	-	-	KAF3184243.1 hypothetical protein TWF751_000225 [Orbilia oligospora]	-
A7557	GO:0017183(peptidyl-diphthamide biosynthetic process from peptidyl-histidine)	-	GO:0004164(diphthine synthase activity),GO:0008168(methyltransferase activity)	-	-	KOG3123[At4g31790 Diphthine synthase	TPX46989.1 hypothetical protein CcCBS67573.g10284 [Chytridiomycota confervae]	Probable diphthine methyl ester synthase OS=Arabidopsis thaliana OX=3702 GN=At4g31790 PE=2 SV=1

A7558	GO:0071805(potassium ion transmembrane transport)	GO:0016020(membrane)	GO:0005267(potassium channel activity)	K05389 KCNKF; potassium channel subfamily K, other eukaryote	-	KOG1418 At4g01840 Tandem pore domain K+ channel	GEQ66784.1 hypothetical protein JCM33374_g447 [Metschnikowia sp. JCM33374]	Two pore potassium channel a OS=Oryza sativa subsp. japonica OX=39947 GN=TPKA PE=1 SV=1
A7559	GO:0043631(RNA polyadenylation)	GO:0031499(TRANP complex)	GO:0016779(nucleotidyltransferase activity),GO:0004652(polynucleotide adenylyltransferase activity)	K03514 PAPD5_7, TRF4; non-canonical poly(A) RNA polymerase PAPD5/7 [EC:2.7.7.19]	map03018 RNA degradation	KOG1906 7290950 DNA polymerase sigma	XP_007000459.1 uncharacterized protein TREMEDRAFT_22292, partial [Tremella mesenterica DSM 1558]	Terminal nucleotidyltransferase 4B OS=Homo sapiens OX=9606 GN=TENT4B PE=1 SV=2
A7560	-	-	-	-	-	-	-	-
A7562	-	-	GO:0003677(DNA binding)	K06875 PDCD5, TFAR19; programmed cell death protein 5	-	KOG3431 At1g29850 Apoptosis-related protein/predicted DNA-binding protein	QIW98833.1 hypothetical protein AMS68_004351 [Peltaster fructicola]	DNA-binding protein DDB_G0278111 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0278111 PE=3 SV=2
A7563	-	-	GO:0008289(lipid binding)	-	-	-	-	-
A7564	-	-	-	-	-	-	-	-
A7565	GO:0006418(tRNA aminoacylation for protein translation),GO:0006438(valyl-tRNA aminoacylation)	-	GO:0002161(aminoacyl-tRNA editing activity),GO:000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0004832(valine-tRNA ligase activity)	K01873 VARS, valS; valyl-tRNA synthetase [EC:6.1.1.9]	map00970 Aminoacyl-tRNA biosynthesis	KOG0432 At1g14610 Valyl-tRNA synthetase	KAF9373455.1 hypothetical protein CPB97_000528 [Podila verticillata]	Valine--tRNA ligase, mitochondrial 1 OS=Arabidopsis thaliana OX=3702 GN=TNW2 PE=1 SV=2
A7566	-	-	-	-	-	-	-	-
A7567	-	-	-	-	-	-	-	-
A7568	-	-	-	-	-	-	-	-
A7569	-	-	-	K24205 TMBIM, LFG; protein lifeguard	-	KOG2322 7303389 N-methyl-D-aspartate receptor glutamate-binding subunit	KIM83316.1 hypothetical protein PILCRDRAFT_7258 [Piloderma croceum F1598]	Protein lifeguard 1 OS=Rattus norvegicus OX=10116 GN=Grina PE=2 SV=1
A7570	-	-	GO:0005515(protein binding)	-	-	-	GBB92606.1 hypothetical protein RclHR1_02030009 [Rhizophagus clarus]	Uncharacterized protein R883 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_R883 PE=4 SV=1

A7571	-	-	GO:0003677(DNA binding),GO:0003721(telomerase RNA reverse transcriptase activity)	K11126 TERT, EST2; telomerase reverse transcriptase [EC:2.7.7.49]	map05226 Gastric cancer;map05200 Pathways in cancer;map05225 Hepatocellular carcinoma;map05165 Human papillomavirus infection;map05166 Human T-cell leukemia virus 1 infection	KOG1005[Hs4507439 Telomerase catalytic subunit/reverse transcriptase TERT	TFY61469.1 hypothetical protein EVJ58_g4485 [Fomitopsis rosea]	Telomerase reverse transcriptase OS=Canis lupus familiaris OX=9615 GN=TERT PE=2 SV=1
A7572	GO:0051276(chromosome organization)	GO:0005694(chromosome)	GO:0005515(protein binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K06669 SMC3, CSPG6; structural maintenance of chromosome 3 (chondroitin sulfate proteoglycan 6)	map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0964[At2g27170 Structural maintenance of chromosome protein 3 (sister chromatid cohesion complex Cohesin, subunit SMC3)]	KAG0223701.1 Structural maintenance of chromosome protein 3 [Actinomorpha rella wolffii]	Structural maintenance of chromosomes protein 3 OS=Arabidopsis thaliana OX=3702 GN=SMC3 PE=2 SV=1
A7573	-	-	GO:0005509(calcium ion binding),GO:0005515(protein binding)	-	-	-	ORY42797.1 WD40 repeat-like protein [Rhizoclostium globosum]	-
A7574	-	-	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	-	-	-	-	-
A7575	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160[At4g28710 Myosin class V heavy chain	GAN04656.1 conserved hypothetical protein [Mucor ambiguus]	Myosin-14 OS=Arabidopsis thaliana OX=3702 GN=XI-H PE=3 SV=1
A7576	-	-	GO:0004471(malate dehydrogenase (decarboxylating) (NAD+) activity),GO:0004470(malic enzyme activity),GO:0051287(NAD binding)	K00029 E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]	map03320 PPAR signaling pathway;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00710 Carbon fixation in photosynthetic organisms;map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG1257[Hs5729920 NADP+-dependent malic enzyme	KAA8911667.1 hypothetical protein FN846DRAFT_773834 [Sphaerospora brunnea]	NADP-dependent malic enzyme OS=Columba livia OX=8932 GN=ME1 PE=1 SV=1

A7577	GO:0046488(phosphatidylinositol metabolic process)	-	GO:0035091(phosphatidylinositol binding);GO:0016307(phosphatidylinositol phosphate kinase activity)	K00889 PIP5K; 1-phosphatidylinositol-4-phosphate 5-kinase [EC:2.7.1.68]	map04144 Endocytosis;map05135 Yersinia infection;map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04070 Phosphatidylinositol signaling system;map04072 Phospholipase D signaling pathway;map04139 Mitophagy - yeast;map04666 Fc gamma R-mediated phagocytosis;map00562 Inositol phosphate metabolism;map04011 MAPK signaling pathway - yeast;map05231 Choline metabolism in	KOG0229 At3g07960 Phosphatidylinositol-4-phosphate 5-kinase	KAG1123350.1 hypothetical protein G6F42_010632 [Rhizopus oryzae]	Phosphatidylinositol 4-phosphate 5-kinase 6 OS=Arabidopsis thaliana OX=3702 GN=PIP5K6 PE=2 SV=1
A7578	-	-	-	-	-	KOG1305 Hs21361602 Amino acid transporter protein	KNE57500.1 hypothetical protein AMAG_03207 [Allomyces macrogynus ATCC 38327]	Sodium-coupled neutral amino acid symporter 2 OS=Mus musculus OX=10090 GN=Slc38a2 PE=1 SV=1
A7579	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A7580	-	-	-	-	-	-	-	-
A7581	-	-	-	-	-	-	-	-
A7582	-	-	GO:0016791(phosphatase activity)	K15731 CTDSP; carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase [EC:3.1.3.16]	-	KOG1605 At5g11860 TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	ORX94378.1 hypothetical protein K493DRAFT_30928 [Basidiobolus meristosporus CBS 931.73]	CTD small phosphatase-like protein 1 OS=Caenorhabditis elegans OX=6239 GN=scpl-1 PE=1 SV=2
A7583	GO:0017183(peptidyl-diphthamide biosynthetic process from peptidyl-histidine)	-	GO:0090560(2-(3-amino-3-carboxypropyl)histidine synthase activity)	K17866 DPH2; diphthamide biosynthesis protein 2	-	-	CAE6512824.1 unnamed protein product [Rhizoctonia solani]	2-(3-amino-3-carboxypropyl)histidine synthase subunit 2 OS=Danio rerio OX=7955 GN=dph2 PE=2 SV=1
A7584	-	-	-	K24127 MAGE; melanoma-associated antigen	-	-	PWW71662.1 MAGE-domain-containing protein [Tuber magnatum]	Non-structural maintenance of chromosomes element 3 homolog OS=Mus musculus OX=10090 GN=Nsmce3 PE=1 SV=1
A7585	-	-	GO:0035673(oligopeptide transmembrane transporter activity)	-	-	-	KAG1465768.1 hypothetical protein G6F57_013364 [Rhizopus oryzae]	Putative oligopeptide transporter HI_0561 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_0561 PE=3 SV=2

A7586	GO:0016579(protein deubiquitination).GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase)	K11839 USP8, UBP5; ubiquitin carboxyl-terminal hydrolase 8 [EC:3.4.19.12]	map04144 Endocytosis;map04137 Mitophagy - animal;map04934 Cushing syndrome	KOG1868[HsM19923759 Ubiquitin C-terminal hydrolase	RKP09098.1 hypothetical protein THASP1DRAFT_14708 [Thamnocephalis sphaerospora]	Ubiquitin carboxyl-terminal hydrolase 2 OS=Homo sapiens OX=9606 GN=USP2 PE=1 SV=2
A7587	GO:0035735(intraciliary transport involved in cilium assembly)	-	-	-	-	-	XP_031027182.1 uncharacterized protein SmJEL517_g00960 [Synchytrium microbalum]	Centrosomal protein of 131 kDa OS=Mus musculus OX=10090 GN=Cep131 PE=1 SV=2
A7588	-	-	-	-	-	-	KXS14873.1 hypothetical protein M427DRAFT_135548 [Gonapodya prolifera JEL478]	-
A7589	GO:0016192(vesicle-mediated transport)	-	-	K15292 STXBP1, MUNC18-1; syntaxin-binding protein 1	map04721 Synaptic vesicle cycle	KOG1300[At1g12360 Vesicle trafficking protein Sec1	KAG0328063.1 vacuolar sorting protein VPS33/slp1 [Podila horticola]	SNARE-interacting protein KEULE OS=Arabidopsis thaliana OX=3702 GN=KEU PE=1 SV=2
A7590	-	-	-	K14845 RAI1, DOM32; RAT1-interacting protein	-	KOG1982[Hs20631980 Nuclear 5'-3' exoribonuclease-interacting protein, Rai1p	ORX83401.1 RAI1-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Decapping and exoribonuclease protein OS=Mus musculus OX=10090 GN=Dxo PE=1 SV=2
A7591	-	-	-	-	-	-	-	-
A7592	GO:0032508(DNA duplex unwinding).GO:0006270(DNA replication initiation).GO:0006260(DNA replication)	GO:0005634(nucleus).GO:0042555(MCM complex)	GO:0003677(DNA binding).GO:0005524(ATP binding).GO:0003678(DNA helicase activity)	K02542 MCM6; DNA replication licensing factor MCM6 [EC:5.6.2.3]	map03030 DNA replication;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0480[YG1201c DNA replication licensing factor, MCM6 component	KJA29709.1 hypothetical protein HYP5UDRAFT_31691 [Hypholoma sublateritium FD-334 SS-4]	DNA replication licensing factor MCM6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MCM6 PE=1 SV=2
A7593	-	-	-	K06685 MOB1, Mats; MOB kinase activator 1	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04392 Hippo signaling pathway - multiple species;map04111 Cell cycle - yeast	KOG0440[Hs8922671 Cell cycle-associated protein Mob1-1	RUO96320.1 mps one binder kinase activator-like 1B-like protein [Jimgerdmania flammicorona]	MOB kinase activator-like 1 homolog B OS=Dictyostelium discoideum OX=44689 GN=mob8 PE=3 SV=1
A7594	-	-	GO:0004842(ubiquitin-protein transferase activity)	K12232 HECTD2; E3 ubiquitin-protein ligase HECTD2 [EC:2.3.2.26]	-	KOG0941[Hs19718762 E3 ubiquitin protein ligase	RUS18716.1 hypothetical protein BC937DRAFT_88420 [Endogone sp. FLAS-F59071]	Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens OX=9606 GN=HERC4 PE=1 SV=1

A7595	-	-	GO:0005515(protein binding)	-	-	KOG0504 Hs10835177_2 FOG: Ankyrin repeat	CVK87411.1 related to endocytosis ankyrin repeat protein Nuc-2 [Fusarium proliferatum]	Nuclear factor NF-kappa-B p105 subunit OS=Homo sapiens OX=9606 GN=NFKB1 PE=1 SV=2
A7596	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG0671 Hs4502885_2 LAMMER dual specificity kinases	PMD24199.1 kinase-like protein [Hyaloscypha hepaticicola]	Ribonuclease inhibitor OS=Sus scrofa OX=9823 GN=RNH1 PE=1 SV=1
A7597	-	-	GO:0047429(nucleoside-triphosphate diphosphatase activity)	K06287 yhdE; nucleoside triphosphate pyrophosphatase [EC:3.6.1.-]	map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG1509 At5g42770 Predicted nucleic acid-binding protein ASMTL	ORZ36075.1 inosine triphosphate pyrophosphatase-like protein [Catenaria anguillulae PL171]	7-methyl-GTP pyrophosphatase OS=Dictyostelium discoideum OX=44689 GN=DDB_G0281937 PE=3 SV=1
A7598	GO:0006435(threonyl-tRNA aminoacylation),GO:0043039(tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation)	GO:0005737(cytoplasm)	GO:0004829(threonine-tRNA ligase activity),GO:0005524(ATP binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0000166(nucleotide binding)	-	-	KOG1637 7297921 Threonyl-tRNA synthetase	KNE56469.1 threonine-tRNA ligase [Allomyces macrogynus ATCC 38327]	Threonine--tRNA ligase 1, cytoplasmic OS=Rattus norvegicus OX=10116 GN=Tars1 PE=1 SV=1
A7599	-	-	-	K22857 EEF1AKMT4; EEF1A lysine methyltransferase 4 [EC:2.1.1.-]	-	KOG2352 7298695 Predicted spermine/spermidine synthase	XP_007304464.1 S-adenosyl-L-methionine-dependent methyltransferase [Sterium hirsutum FP-91666 SS1]	eEF1A lysine and N-terminal methyltransferase OS=Homo sapiens OX=9606 GN=METTL13 PE=1 SV=1
A7600	-	-	-	-	-	-	-	-
A7601	-	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0008521(acytyl-CoA transmembrane transporter activity)	-	-	KOG3574 Hs4757708 Acetyl-CoA transporter	ODQ67829.1 hypothetical protein NADFUDRAFT_19430 [Nadsonia fulvescens var. elongata DSM 6958]	Acetyl-coenzyme A transporter 1 OS=Rattus norvegicus OX=10116 GN=Slc33a1 PE=2 SV=1
A7602	GO:0006413(translational initiation)	GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0003723(RNA binding),GO:0003743(translation initiation factor activity),GO:0001369(translation initiation factor binding)	K03252 EIF3C; translation initiation factor 3 subunit C	-	KOG1076 At3g56150 Translation initiation factor 3, subunit c (eIF-3c)	KAF0483193.1 eukaryotic translation initiation factor 3 subunit [Gigaspora margarita]	Eukaryotic translation initiation factor 3 subunit C OS=Medicago truncatula OX=3880 GN=TIF3C1 PE=2 SV=1

A7603	GO:0006544(glycine metabolic process), GO:0006546(glycine catabolic process)	-	GO:0003824(catalytic activity), GO:0004375(glycine dehydrogenase (decarboxylating) activity)	K00281 GLDC, gcvP; glycine cleavage system P protein (glycine dehydrogenase) [EC:1.4.4.2]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map00630 Glyoxylate and dicarboxylate metabolism	KOG2040 At2g26080 Glycine dehydrogenase (decarboxylating)	CDS12383.1 hypothetical protein LRAMOSA04578 [Lichtheimia ramosa]	Glycine dehydrogenase (decarboxylating) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gcvP PE=3 SV=1
A7604	-	-	-	K09425 K09425; Myb-like DNA-binding protein FlbD	-	KOG0048 Hs13641706.1 Transcription factor, Myb superfamily	KAF9100527.1 DNA binding transcription coactivator transcription factor, partial [Mortierella sp. GBA35]	Transcriptional activator Myb OS=Mus musculus OX=10090 GN=Myb PE=1 SV=2
A7605	GO:0006012(galactose metabolic process), GO:0046835(carbohydrate phosphorylation)	GO:0005737(cytoplasm)	GO:0005524(ATP binding), GO:0004335(galactokinase activity), GO:0016301(kinase activity), GO:0016773(phosphotransferase activity, alcohol group as acceptor)	K00849 galK; galactokinase [EC:2.7.1.6]	map01250 Biosynthesis of nucleotide sugars;map00052 Galactose metabolism;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG0631 Hs4503895 Galactokinase	AWI66857.1 Galactokinase, partial [Piromyces sp.]	Galactokinase OS=Homo sapiens OX=9606 GN=GALK1 PE=1 SV=1
A7606	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding), GO:0008569(minus-end-directed microtubule motor activity)	-	-	KOG3595 Hs17864092 Dyneins, heavy chain	TPX78177.1 hypothetical protein CcBS67573_g00561 [Chytridiomycota confervae]	Dynein axonemal heavy chain 1 OS=Homo sapiens OX=9606 GN=DNAH1 PE=1 SV=6
A7607	-	-	-	-	-	-	-	-
A7608	-	-	GO:0016787(hydrolase activity)	K01515 nudF; ADP-ribose diphosphatase [EC:3.6.1.13 3.6.1.-]	map00230 Purine metabolism;map00740 Riboflavin metabolism;map01100 Metabolic pathways	-	APA10903.1 hypothetical protein sscl_07g056730 [Sclerotinia sclerotiorum 1980 UF-70]	ADP-sugar pyrophosphatase OS=Homo sapiens OX=9606 GN=NUDT5 PE=1 SV=1
A7609	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	TPX54390.1 hypothetical protein PhCBS80983_g05955 [Powellomyces hirtus]	Adenylate cyclase OS=Anabaena cylindrica OX=1165 GN=cya PE=3 SV=1

A7610	-	-	GO:0003824(catalytic activity),GO:0051536(iron-sulfur cluster binding),GO:0016407(acetyltransferase activity)	K07739 ELP3, KAT9; elongator complex protein 3 (tRNA carboxymethyluridine synthase) [EC:2.3.1.311]	-	KOG2535 Hs21361689 RNA polymerase II elongator complex, subunit ELP3/histone acetyltransferase	OAG31077.1 elongator complex protein 3 [Nematocida dispodere]	tRNA uridine(34) acetyltransferase OS=Dehalococcoides mccartyi (strain CBDB1) OX=255470 GN=cdbdA595 PE=1 SV=2
A7611	-	-	-	-	-	-	-	-
A7612	-	-	-	-	-	-	-	-
A7613	-	-	-	-	-	-	-	-
A7614	GO:0006526(arginine biosynthetic process)	-	GO:0004358(glutamate N-acetyltransferase activity),GO:0003824(catalytic activity),GO:0008483(transaminase activity),GO:0030170(pyridoxal phosphate binding)	-	-	KOG1401 At1g80600 Acetylornithine aminotransferase	OZJ03536.1 hypothetical protein BZG36_04178 [Bifiguratus adalaidae]	Arginine biosynthesis bifunctional protein ArgJ, mitochondrial OS=Phytophthora infestans (strain T30-4) OX=403677 GN=PI TG_04698 PE=3 SV=1
A7615	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding)	K09478 ACADSB; short-chain 2-methylacyl-CoA dehydrogenase [EC:1.3.8.5]	map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG0139 Hs4501859 Short-chain acyl-CoA dehydrogenase	KAG0959303.1 hypothetical protein G6F31_01178 [Rhizopus oryzae]	3-methylmercaptopyruvate-CoA dehydrogenase OS=Roseovarius nubinhibens (strain ATCC BAA-591 / DSM 15170 / ISM) OX=89187 GN=dmdC PE=1 SV=1
A7616	GO:0006396(RNA processing)	GO:0005634(nucleus),GO:1990904(ribonucleoprotein complex)	GO:0003723(RNA binding)	K11090 LA, SSB; lupus La protein	map05322 Systemic lupus erythematosus	KOG4213 CE08718 RNA-binding protein La	TPX70844.1 hypothetical protein SpCBS45565_g01418 [Spizellomyces sp. 'palustris']	La-related protein 7 OS=Danio rerio OX=7955 GN=larp7 PE=2 SV=1
A7617	-	-	-	-	-	-	-	-
A7618	-	-	-	-	-	-	-	-
A7619	-	-	-	K23541 TMEM165, GDT1; Ca2+/H+ antiporter, TMEM165/GDT1 family	-	KOG2881 At5g36290 Predicted membrane protein	KAF9364546.1 hypothetical protein BGX34_00121 [Mortierella sp. NVP85]	GDT1-like protein 3 OS=Arabidopsis thaliana OX=3702 GN=At5g36290 PE=2 SV=1
A7620	-	-	GO:0003677(DNA binding)	-	-	KOG0724 At3g09600 Zuotin and related molecular chaperones (DnaJ superfamily), contains DNA-binding domains	ORX93100.1 hypothetical protein K493DRAFT_262785 [Basidiobolus meristosporus CBS 931.73]	Protein CCA1 OS=Arabidopsis thaliana OX=3702 GN=CCA1 PE=1 SV=1

A7621	-	-	-	-	-	KOG1725 At1g74520 Protein involved in membrane traffic (YOP1/TB2/D P1/HVA22 family)	RPA87084.1 hypothetical protein BJ508DRAFT_410648 [Ascobolus immersus RN42]	HVA22-like protein a OS=Arabidopsis thaliana OX=3702 GN=HVA22A PE=2 SV=1
A7622	-	-	-	-	-	-	-	-
A7623	-	-	-	-	-	-	-	-
A7624	-	-	-	-	-	-	-	-
A7625	-	-	-	-	-	-	-	-
A7626	-	-	GO:0016788(hydrolase activity, acting on ester bonds),GO:0016811(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides)	-	-	-	-	Probable aspartoacylase OS=Trichormus variabilis (strain ATCC 29413 / PCC 7937) OX=240292 GN=Ava_1785 PE=3 SV=1
A7627	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1543 At5g43060_1 Cysteine proteinase Cathepsin L	KFH62689.1 hypothetical protein MVEG_12081 [Podila verticillata NRRL 6337]	Probable cysteine protease RD21B OS=Arabidopsis thaliana OX=3702 GN=RD21B PE=1 SV=1
A7628	GO:000958(biosynthetic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0008483(transaminase activity),GO:0003824(catalytic activity)	K00814 GPT, ALT; alanine transaminase [EC:2.6.1.2]	map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map00710 Carbon fixation in photosynthetic organisms;map00220 Arginine biosynthesis;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	KOG0258 At1g72330 Alanine aminotransferase	KAG0231842.1 hypothetical protein BGW42_008591 [Actinomortierella wolfii]	Probable alanine aminotransferase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=gpt PE=3 SV=1
A7629	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11253 H3; histone H3	map05131 Shigellosis;map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05202 Transcriptional misregulation in cancer	KOG1745 Hs17442169 Histones H3 and H4	KAF4920343.1 histone H3 [Colletotrichum fructicola]	Histone H3.2 OS=Bos taurus OX=9913 PE=1 SV=2

A7630	-	-	GO:0070569(uridylyltransferase activity)	-	-	KOG2388 At5g52560 UDP-N-acetylglucosamine pyrophosphorylase	CDS12000.1 hypothetical protein LRAMOSA04196 [Lichtheimia ramosa]	UDP-sugar pyrophosphorylase OS=Pisum sativum OX=3888 GN=USP PE=1 SV=1
A7631	GO:0006260(DNA replication)	GO:0000811(GINS complex)	-	K10732 GINS1, PSF1; GINS complex subunit 1	-	KOG3303 Hs10800148 Predicted alpha-helical protein, potentially involved in replication/repair	ORX47537.1 GINS complex, Psf1 component [Piromyces finnis]	Probable DNA replication complex GINS protein PSF1 OS=Dictyostelium discoideum OX=44689 GN=gins1 PE=3 SV=1
A7632	-	-	GO:0016787(hydrolase activity)	-	-	-	KAG0188754.1 hypothetical protein DFQ28_004408 [Apophysomyces sp. BC1034]	Acyl-CoA thioester hydrolase YbgC OS=Escherichia coli O157:H7 OX=83334 GN=ybgC PE=3 SV=1
A7633	-	-	-	-	-	-	-	-
A7634	GO:0055085(transmembrane transport)	GO:0016020(membrane)	-	-	-	-	PIA18825.1 hypothetical protein COEREDRAFT_18611, partial [Coemansia reversa NRRL 1564]	Mechanosensitive ion channel protein Msy2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=msy2 PE=1 SV=1
A7635	GO:0055085(transmembrane transport)	GO:0016020(membrane)	-	-	-	KOG4629 At5g12080 Predicted mechanosensitive ion channel	PIA18825.1 hypothetical protein COEREDRAFT_18611, partial [Coemansia reversa NRRL 1564]	Mechanosensitive ion channel protein 10 OS=Arabidopsis thaliana OX=3702 GN=MSL10 PE=1 SV=1
A7636	GO:0055085(transmembrane transport)	GO:0016020(membrane)	-	-	-	-	ORX71645.1 hypothetical protein DL89DRAFT_205933, partial [Linderina pennisporea]	Mechanosensitive ion channel protein Msy2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=msy2 PE=1 SV=1
A7637	GO:0055085(transmembrane transport)	GO:0016020(membrane)	-	-	-	-	PVV04058.1 hypothetical protein BB560_001450 [Smittium megazygosporum]	Mechanosensitive ion channel protein Msy2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=msy2 PE=1 SV=1
A7638	-	-	GO:0005085(guananyl-nucleotide exchange factor activity)	-	-	KOG3519 Hs19882229_1 Invasion-inducing protein TIAM1/CDC24 and related RhoGEF GTPases	XP_011388833.1 cytokinesis protein Don1 [Ustilago maydis 521]	Pleckstrin homology domain-containing family G member 2 OS=Mus musculus OX=10090 GN=Plekhhg2 PE=2 SV=2
A7639	-	-	-	-	-	-	-	-
A7640	-	-	-	-	-	-	-	-
A7641	-	-	-	-	-	-	-	-
A7642	GO:0030705(cytoskeleton-dependent intracellular transport)	-	-	-	-	-	-	-

A7643	GO:0000724(double-strand break repair via homologous recombination)	GO:0030915(Smc5-Smc6 complex)	GO:0008270(zinc ion binding),GO:0019789(SUMO transferase activity)	K22756 NSMCE2, NSE2: E3 SUMO-protein ligase NSE2 [EC:2.3.2.-]	-	-	KNE57481.1 hypothetical protein AMAG_03190 [Allomyces macrogynus ATCC 38327]	-
A7644	-	-	GO:0008168(methyltransferase activity)	-	-	-	PWI68357.1 hypothetical protein PCL_02126 [Purpureocillium lilacinum]	Hercynine oxygenase OS=Mycolicibacterium thermoresistibile (strain ATCC 19527 / DSM 44167 / CIP 105390 / JCM 6362 / NCTC 10409 / 316) OX=1078020 GN=egtB PE=1 SV=1
A7645	GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K13303 SGK2; serum/glucocorticoid-regulated kinase 2 [EC:2.7.11.1]	map04151 PI3K-Akt signaling pathway;map04068 FoxO signaling pathway	-	RKP17416.1 Pkinase-domain-containing protein [Rozella allomyces CSF55]	Protein kinase 2 OS=Dictyostelium discoideum OX=44689 GN=pkgB PE=1 SV=2
A7646	-	-	GO:0016491(oxidoreductase activity),GO:0046872(metal ion binding)	K13954 yiaY; alcohol dehydrogenase [EC:1.1.1.1]	map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01220 Degradation of aromatic compounds;map00625 Chloroalkane and chloroalkene degradation;map00626 Naphthalene degradation;map00620 Pyruvate metabolism;map00350 Tyrosine metabolism;map01100 Metabolic pathways;map00	-	XP_00217153.3.1 alcohol dehydrogenase Adh4 [Schizosaccharomyces japonicus yFS275]	Probable alcohol dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=yiaY PE=3 SV=4
A7647	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04563 CDC28, CDC2; cyclin-dependent kinase [EC:2.7.11.22]	map04011 MAPK signaling pathway - yeast;map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0594 Hs4557439 Protein kinase PCTAIRE and related kinases	KAF9545099.1 cyclin-dependent serine/threonine protein kinase [Mortierella hygrophila]	Cyclin-dependent kinase 5 homolog OS=Dictyostelium discoideum OX=44689 GN=cdk5 PE=2 SV=2
A7648	GO:0018342(protein prenylation),GO:0018344(protein geranylgeranylation)	GO:0005968(Rab-protein geranylgeranyltransferase complex)	GO:0008318(protein prenyltransferase activity)	K14050 RABGGTA; geranylgeranyl transferase type-2 subunit alpha [EC:2.5.1.60]	-	KOG0529 Hs4759016 Protein geranylgeranyltransferase type II, alpha subunit	KAE827274.1 hypothetical protein CF319_g242 [Tilletia indica]	Geranylgeranyl transferase type-2 subunit alpha OS=Rattus norvegicus OX=10116 GN=RabggtA PE=1 SV=1

A7649	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination), GO:0043161(proteasome-mediated ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase), GO:0005515(protein binding)	K11843 USP14, UBP6; ubiquitin carboxyl-terminal hydrolase 14 [EC:3.4.19.12]	-	KOG1872[Hs4827050 Ubiquitin-specific protease	KAG0370354.1 Ubiquitin carboxyl-terminal hydrolase 14 [Gamsiella multidivariata]	Ubiquitin carboxyl-terminal hydrolase 6 OS=Arabidopsis thaliana OX=3702 GN=UBP6 PE=1 SV=1
A7650	-	-	-	-	-	KOG3589[Hs21361304 G protein signaling regulators	CDS06341.1 hypothetical protein LRAMOSA08869 [Lichtheimia ramosa]	Regulator of G-protein signaling 14 OS=Homo sapiens OX=9606 GN=RGS14 PE=1 SV=4
A7651	-	GO:0005739(mitochondrion)	GO:0004408(holocytochrome-c synthase activity)	K01764 HCCS; cytochrome c heme-lyase [EC:4.4.1.17]	map00860 Porphyrin metabolism; map01100 Metabolic pathways	KOG3996[Hs4885401 Holocytochrome c synthase/heme-lyase	KAG1139532.1 hypothetical protein G6F38_009767 [Rhizopus oryzae]	Holocytochrome c-type synthase OS=Bos taurus OX=9913 GN=HCCS PE=2 SV=1
A7652	GO:0006207('de novo' pyrimidine nucleobase biosynthetic process), GO:0006221(pyrimidine nucleotide biosynthetic process), GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0004127(cytidylate kinase activity), GO:0009041(uridylate kinase activity), GO:0016491(oxidoreductase activity), GO:0005524(ATP binding), GO:0019205(nucleobase-containing compound kinase activity)	K15303 AKR7; aflatoxin B1 aldehyde reductase	map00980 Metabolism of xenobiotics by cytochrome P450	-	XP_016606960.1 hypothetical protein SPPG_05883 [Spizellomyces punctatus DAOM BR117]	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus OX=10116 GN=Akr7a2 PE=1 SV=2
A7653	GO:0007165(signal transduction)	-	GO:0005096(GTPase activator activity)	-	-	KOG4270[At4g03100 GTPase-activator protein	-	Rho GTPase-activating protein 2 OS=Arabidopsis thaliana OX=3702 GN=ROPGAP2 PE=1 SV=1
A7654	-	-	-	K19525 VPS13A_C; vacuolar protein sorting-associated protein 13A/C	-	KOG1809[At1g48090 Vacuolar protein sorting-associated protein	RUP43863.1 vacuolar protein sorting-associated protein vps13, partial [Jimgerdmania flammicorona]	Intermembrane lipid transfer protein VPS13 OS=Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719) OX=759272 GN=VPS13 PE=1 SV=1

A7655	-	-	-	K06630 YWHAE; 14-3-3 protein epsilon	map04391 Hippo signaling pathway - fly;map04390 Hippo signaling pathway;map04722 Neurotrophin signaling pathway;map04621 NOD-like receptor signaling pathway;map05203 Viral carcinogenesis; map04151 PI3K-Akt signaling pathway;map04011 MAPK signaling pathway - yeast;map04114 Oocyte meiosis;map04110 Cell cycle;map05160 Hepatitis C	-	TID30830.1 hypothetical protein CANINC_000595 [[Candida] inconspicua]	14-3-3 protein homolog OS=Trichoderma harzianum OX=5544 PE=2 SV=1
A7656	-	-	GO:0005515(protein binding)	-	-	-	-	GRB10-interacting GYF protein 2 OS=Xenopus laevis OX=8355 GN=gigyf2 PE=2 SV=1
A7657	-	-	-	K23565 EMC4, TMEM85; ER membrane protein complex subunit 4	-	KOG3318 At5g10780 Predicted membrane protein	KAF8300474.1 DUF1077 - domain-containing protein [Clavulina sp. PML_390]	ER membrane protein complex subunit 4 OS=Danio rerio OX=7955 GN=emc4 PE=2 SV=1
A7658	-	-	-	-	-	-	-	-
A7659	-	-	-	-	-	-	-	-
A7660	GO:0030001(metal ion transport); GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	K14713 SLC39A7, KE4, ZIP7; solute carrier family 39 (zinc transporter), member 7	map05010 Alzheimer disease;map05012 Parkinson disease	KOG2693 Hs20473677 Putative zinc transporter	KAG1254073.1 hypothetical protein G6F68_011033 [Rhizopus microsporus]	Zinc transporter ZIP12 OS=Macaca fascicularis OX=9541 GN=SLC39A12 PE=2 SV=1
A7661	-	-	-	-	-	-	-	-
A7662	-	-	-	-	-	-	-	-
A7663	-	GO:0016459(myosin complex), GO:0005856(cytoskeleton)	GO:0005515(protein binding);GO:0003774(motor activity);GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At5g43900 Myosin class V heavy chain	KAF1798291.1 P-loop containing nucleoside triphosphate hydrolase protein [Mucor lusitanicus]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1
A7664	-	-	-	-	-	-	-	-
A7665	GO:0006508(proteolysis)	-	GO:0004190(aspatic-type endopeptidase activity);GO:0005515(protein binding)	K11885 DD11; DNA damage-inducible protein 1	-	-	XP_031023836.1 uncharacterized protein SmJEL517_g04186 [Synchytrium microbalum]	Protein DNA-DAMAGE INDUCIBLE 1 OS=Arabidopsis thaliana OX=3702 GN=DD11 PE=1 SV=1
A7666	GO:0006886(intracellular protein transport); GO:0016192(vesicle-mediated transport)	GO:0030117(membrane coat)	-	K12391 AP1G1; AP-1 complex subunit gamma-1	map04142 Lysosome;map05170 Human immunodeficiency virus 1 infection	KOG1062 At1g31730 Vesicle coat complex AP-1, gamma subunit	RIA93751.1 armadillo-type protein [Glomus cerebriforme]	AP-4 complex subunit epsilon OS=Arabidopsis thaliana OX=3702 GN=At1g31730 PE=1 SV=1
A7667	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 At4g34580 Phosphatidylinositol transfer protein SEC14 and related proteins	TPX43008.1 hypothetical protein SeLEV6574_g05288 [Synchytrium endobioticum]	SEC14-like protein 3 OS=Rattus norvegicus OX=10116 GN=Sec14I3 PE=1 SV=1

A7668	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7669	-	-	GO:0003723(RNA binding)	-	-	-	OCB86675.1 YTH-domain-containing protein [Sanguinaria officinalis]	-
A7670	GO:0042779(trRNA 3'-trailer cleavage)	-	GO:0016891(endoribonuclease activity, producing 5'-phosphomononucleotides)	-	-	KOG2121 Hs8922122 Predicted metal-dependent hydrolase (beta-lactamase superfamily)	KZV97310.1 Metallo-hydrolase/oxidoreductase [Exidia glandulosa HHB12029]	Zinc phosphodiesterase ELAC protein 1 OS=Bos taurus OX=9913 GN=ELAC1 PE=2 SV=1
A7671	GO:0006468(protein phosphorylation),GO:0006508(proteolysis)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004190(aspartic-type endopeptidase activity)	-	-	KOG4369 CE23926 RTK signaling protein MASK/UNC-44	KAF8592901.1 kinase-like protein [Ceratobasidium sp. AG-I]	Ankyrin repeat and KH domain-containing protein mask-1 OS=Caenorhabditis elegans OX=6239 GN=mask-1 PE=3 SV=3
A7672	GO:0006260(DNA replication),GO:0006281(DNA repair)	GO:0005634(nucleus),GO:0008622(epsilon DNA polymerase complex)	GO:0000166(nucleotide binding),GO:0003677(DNA binding),GO:0003887(DNA-directed DNA polymerase activity),GO:0008270(zinc ion binding),GO:0003676(nucleic acid binding)	K02324 POLE; DNA polymerase epsilon subunit 1 [EC:2.7.7.7]	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair	KOG1798 Hs5453926 DNA polymerase epsilon, catalytic subunit A	KAF9337178.1 DNA polymerase epsilon catalytic subunit [Linnemannia elongata]	DNA polymerase epsilon catalytic subunit A OS=Mus musculus OX=10090 GN=Pole PE=1 SV=3
A7673	-	-	-	-	-	-	-	-
A7674	-	-	-	-	-	-	-	-
A7675	-	-	-	-	-	KOG4446 Hs8923324 Uncharacterized conserved protein	ORY49870.1 hypothetical protein BCR33DRAFT_762970 [Rhizoclostium globosum]	Tectonic-like complex member MKS1 OS=Rattus norvegicus OX=10116 GN=Mks1 PE=2 SV=2
A7676	-	-	-	-	-	-	-	-
A7677	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity),GO:00030170(pyridoxal phosphate binding)	K00652 bioF; 8-amino-7-oxononanoate synthase [EC:2.3.1.47]	map00780 Biotin metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG1359 Hs7657118 Glycine C-acetyltransferase/2-amino-3-ketobutyrate-CoA ligase	KAF9971913.1 hypothetical protein BGZ73_005045 [Actinomyces rella ambigua]	8-amino-7-oxononanoate synthase OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=bioF PE=2 SV=1
A7678	-	-	-	K24781 BPH1; beige protein homolog 1	-	KOG1786 At4g02660.2 Lysosomal trafficking regulator LYST and related BEACH and WD40 repeat proteins	XP_031024890.1 uncharacterized protein SmJEL517_g03217 [Synchytrium microbalum]	Neurobeachin-like protein 2 OS=Danio rerio OX=7955 GN=nbeal2 PE=1 SV=1
A7679	-	-	-	-	-	-	-	-
A7680	-	-	-	-	-	-	-	AP-4 complex accessory subunit Tepsin OS=Rattus norvegicus
A7681	-	-	-	-	-	-	-	-

A7682	GO:0006779(porphyrin-containing compound biosynthetic process)	-	GO:0004109(coproporphyrinogen oxidase activity)	K00228 CPOX, hemF; coproporphyrinogen III oxidase [EC:1.3.3.3]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG1518 7297203 Coproporphyrinogen III oxidase CPO/HEM13	CCX32546.1 Similar to Coproporphyrinogen-III oxidase; acc. no. P11353 [Pyronema omphalodes CBS 100304]	Oxygen-dependent coproporphyrinogen-III oxidase OS=Drosophila melanogaster OX=7227 GN=CoproX PE=2 SV=1
A7683	GO:0006426(glycyl-tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0000166(nucleotide binding);GO:0004820(glycine-tRNA ligase activity);GO:0005524(ATP binding)	K01880 GARS, glyS1; glycyl-tRNA synthetase [EC:6.1.1.14]	map00970 Aminoacyl-tRNA biosynthesis	KOG2298 Hs6996010 Glycyl-tRNA synthetase and related class II tRNA synthetase	RKP22189.1 glycyl-tRNA synthetase 1 [Rozella allomyces CSF55]	Glycine--tRNA ligase OS=Mus musculus OX=10090 GN=Gars1 PE=1 SV=1
A7684	GO:0006886(intracellular protein transport);GO:0016192(vesicle-mediated transport)	-	-	K20181 VPS18, PEP3; vacuolar protein sorting-associated protein 18	map04140 Autophagy - animal;map05132 Salmonella infection;map04138 Autophagy - yeast	KOG2034 HsM17978485 Vacuolar sorting protein PEP3/VPS18	RHZ54569.1 hypothetical protein Glove_426g61 [Diversispora epigaea]	Vacuolar protein sorting-associated protein 18 homolog OS=Danio rerio OX=7955 GN=vps18 PE=2 SV=2
A7685	-	-	-	-	-	-	KLO16531.1 hypothetical protein SCHPADRAFT_887741 [Schizopora paradoxa]	-
A7686	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	-	KKA31098.1 hypothetical protein TD95_000589 [Thielaviopsis punctulata]	Serine/threonine-protein kinase cds1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=cds1 PE=1 SV=2
A7687	-	-	-	-	-	-	-	-
A7688	-	-	-	-	-	-	-	-
A7689	-	-	GO:0018024(histone-lysine N-methyltransferase activity)	K11427 DOT1L, DOT1; [histone H3]-lysine79 N-trimethyltransferase [EC:2.1.1.360]	map05202 Transcriptional misregulation in cancer;map00310 Lysine degradation;map01100 Metabolic pathways	KOG3924 YDR440w Putative protein methyltransferase involved in meiosis and transcriptional silencing (Dot1)	ORX88332.1 DOT1-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Emmericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=dot1 PE=3 SV=1
A7690	-	-	GO:0003824(catalytic activity);GO:0050660(flavin adenine dinucleotide binding);GO:0071949(FAD binding)	K00102 LDHD, dld; D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG1231 CE23698_3 Proteins containing the FAD binding domain	KAG0194173.1 hypothetical protein DFQ28_001310 [Apophysomycetes sp. BC1034]	Probable D-lactate dehydrogenase, mitochondrial OS=Danio rerio OX=7955 GN=ldhd PE=2 SV=1

A7691	-	-	-	K11407 HDAC6; histone deacetylase 6 [EC:3.5.1.98]	map05014 Amyotrophic lateral sclerosis;map046 13 Neutrophil extracellular trap formation;map0 5034 Alcoholism;map 05203 Viral carcinogenesis	KOG1343 Hs1 3128864 Histone deacetylase complex, catalytic component HDA1	PJF19637.1 hypothetical protein PSACC_0055 5 [Paramicrosp oridium saccamoebae]	Histone deacetylase 5 OS=Arabidopsis thaliana OX=3702 GN=HDA5 PE=1 SV=1
A7692	-	-	-	-	-	-	-	-
A7693	-	-	-	-	-	KOG1470 At4 g08690 Phosphatidyl inositol transfer protein PDR16 and related proteins	OJ165321.1 hypothetical protein ASPSYDRAFT _54615 [Aspergillus sydowii CBS 593.65]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH8 OS=Arabidopsis thaliana OX=3702 GN=SFH8 PE=2 SV=1
A7694	GO:00435 47(positiv e regulation of GTPase activity)	-	GO:0005096(GT Pase activator activity)	-	-	KOG2390 Hs2 0532873 Uncharacteriz ed conserved protein	GBC00001.1 hypothetical protein RclHRI_0370 0008 [Rhizophagus clarus]	Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens OX=9606 GN=RAB3GAP1 PE=1 SV=3
A7695	-	-	-	-	-	KOG3854 729 0212 SPRT- like metalloprote ase	TPX43010.1 hypothetical protein SeLEV6574_g 05286 [Synchytrium endobioticu m]	Germ cell nuclear acidic protein OS=Danio rerio OX=7955 GN=gcnA PE=3 SV=1
A7696	-	-	GO:0016491(oxi doreductase activity),GO:000 8270(zinc ion binding)	-	-	KOG1197 At5 g61510 Predicted quinone oxidoreducta se	PLN79193.1 NAD(P)- binding protein [Aspergillus taichungensis]	Quinone oxidoreductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=qor PE=3 SV=2
A7697	GO:00069 79(respon se to oxidative stress)	-	GO:0004602(glu tathione peroxidase activity)	K23856 GPX; peroxiredoxin [EC:1.11.1.24]	-	KOG1651 YB R244w Glutathione peroxidase	KLO08917.1 glutathione peroxidase [Schizopora paradoxa]	Glutathione peroxidase-like peroxiredoxin 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPX2 PE=1 SV=1
A7698	-	-	GO:0003824(cat alytic activity)	-	-	-	KAG1716034. 1 hypothetical protein ID866_1128 [Astraeus odoratus]	Cardiolipin synthase B OS=Salmonella typhi OX=90370 GN=clsB PE=3 SV=1
A7699	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	-	-	-	TPX53863.1 hypothetical protein PhCBS80983_ g06122 [Powellomyce s hirtus]	-
A7700	-	-	-	-	-	-	-	-

A7701	GO:0001522(pseudouridine synthesis), GO:0009451(RNA modification), GO:0031119(tRNA pseudouridine synthesis)	-	GO:0003723(RNA binding), GO:0009982(pseudouridine synthase activity)	K06173 truA, PUS1; tRNA pseudouridine synthase [EC:5.4.99.12]	-	KOG2553 At1g76120 Pseudouridylate synthase	ODV85661.1 hypothetical protein CANARDRAFT_27765 [[Candida] arabinoferrantans NRRL YB-2248]	tRNA pseudouridine synthase 1 OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=PUS1 PE=3 SV=1
A7702	-	-	-	-	-	-	-	-
A7703	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7704	-	-	-	-	-	-	-	-
A7705	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7706	-	-	-	-	-	-	-	-
A7707	-	-	GO:0016301(kinase activity)	-	-	-	-	Actin-fragmin kinase OS=Physarum polycephalum OX=5791 PE=1 SV=2
A7708	GO:0042254(ribosome biogenesis), GO:0006396(RNA processing)	GO:0005730(nucleolus)	GO:0003824(catalytic activity)	K11108 RCL1; RNA 3'-terminal phosphate cyclase-like protein	map03008 Ribosome biogenesis in eukaryotes	KOG3980 Hs21361285 RNA 3'-terminal phosphate cyclase	TPX58576.1 hypothetical protein PhCBS80983.g03050 [Powellomyces hirtus]	Probable RNA 3'-terminal phosphate cyclase-like protein OS=Dictyostelium discoideum OX=44689 GN=rd1 PE=1 SV=2
A7709	-	-	-	-	-	-	-	-
A7710	-	-	GO:0003756(protein disulfide isomerase activity)	K09584 PDIA6, TXNDC7; protein disulfide-isomerase A6 [EC:5.3.4.1]	map04141 Protein processing in endoplasmic reticulum	KOG0191 At2g47470 Thioredoxin/protein disulfide isomerase	XP_009216516.1 protein disulfide-isomerase erp38 [Gaeumannomyces tritici R3-111a-1]	Protein disulfide-isomerase-like protein EhSep2 OS=Emiliania huxleyi OX=2903 GN=SEP2 PE=1 SV=2
A7711	GO:005085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding), GO:0140359(ABC-type transporter activity)	K05662 ABCB7, ATM; ATP-binding cassette, subfamily B (MDR/TAP), member 7	map02010 ABC transporters	KOG0056 Hs9955963 Heavy metal exporter HMT1, ABC superfamily	ORX62569.1 hypothetical protein DM01DRAFT_318095 [Hesseltinella vesiculosa]	ATP-binding cassette sub-family B member 6 OS=Xenopus tropicalis OX=8364 GN=abcb6 PE=2 SV=1
A7712	-	-	-	-	-	-	-	-
A7713	-	GO:0016021(integral component of membrane)	-	K13348 MPV17; protein Mpv17	map04146 Peroxisome	KOG1944 YLR251w Peroxisomal membrane protein MPV17 and related proteins	XP_456102.1 uncharacterized protein KLLA0_F22924g [Kluyveromyces lactis]	Protein SYM1 OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=SYM1 PE=3 SV=1
A7714	GO:0006886(intracellular protein transport)	-	GO:0031267(small GTPase binding)	K20223 IPO7, RANBP7; importin-7	map03013 Nucleocytoplasmic transport; map04013 MAPK signaling pathway - fly	-	KJX92352.1 nonsense-mediated mRNA decay protein (Nmd5) [Zymoseptoria brevis]	Importin beta-like SAD2 OS=Arabidopsis thaliana OX=3702 GN=SAD2 PE=1 SV=1
A7715	GO:0006396(RNA processing)	-	GO:0003723(RNA binding), GO:0008173(RNA methyltransferase activity)	K15507 MRM1, PET56; 21S rRNA (GM2251-2'-O)-methyltransferase [EC:2.1.1.-]	-	KOG0838 At2g19870 RNA Methylase, SpoU family	CDH58143.1 rRNA methylase family protein [Lichtheimia corymbifera JMRC:FSU:9682]	rRNA methyltransferase 1, mitochondrial OS=Mus musculus OX=10090 GN=Mrm1 PE=2 SV=2
A7716	GO:0006486(protein glycosylation)	GO:0016020(membrane)	GO:0005254(chloride channel activity), GO:0008417(fucosyltransferase activity)	-	-	KOG2619 At1g71990 Fucosyltransferase	RIB11691.1 Glycosyltransferase Family 10 protein [Gigaspora rosea]	Alpha-(1,4)-fucosyltransferase OS=Arabidopsis thaliana OX=3702 GN=FUT13 PE=2 SV=2
A7717	-	-	-	-	-	-	-	-
A7718	-	-	-	-	-	-	-	-

A7719	GO:0032508(DNA duplex unwinding),GO:0006260(DNA replication),GO:0006270(DNA replication initiation)	GO:0042555(MCM complex)	GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0003678(DNA helicase activity)	K02212 MCM4, CDC54; DNA replication licensing factor MCM4 [EC:5.6.2.3]	map03030 DNA replication;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle	KOG0478 Hs14738665 DNA replication licensing factor, MCM4 component	KAG2221656.1 hypothetical protein INT45_00118.1 [Mucor circinatus]	DNA replication licensing factor mcm4-B OS=Xenopus laevis OX=8355 GN=mcm4-b PE=1 SV=3
A7720	-	-	-	-	-	-	KAF9277853.1 hypothetical protein BGZ88_00093.1 [Linnemannia elongata]	-
A7721	-	-	-	-	-	-	-	-
A7722	-	-	-	-	-	-	-	-
A7723	GO:0006094(gluconeogenesis),GO:0006096(glycolytic process),GO:1901135(carbohydrate derivative metabolic process)	-	GO:0004347(glucose-6-phosphate isomerase activity),GO:0097367(carbohydrate derivative binding)	K01810 GPI, pgi; glucose-6-phosphate isomerase [EC:5.3.1.9]	map01250 Biosynthesis of nucleotide sugars;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00500 Starch and sucrose metabolism;map00030 Pentose phosphate pathway;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG2446 At5g42740 Glucose-6-phosphate isomerase	XP_014559150.1 hypothetical protein COCVIDRAFT_92727 [Bipolaris victoriarum FI3]	Glucose-6-phosphate isomerase, cytosolic B OS=Oryza sativa subsp. japonica OX=39947 GN=Os06g0256500 PE=1 SV=2
A7724	-	-	GO:0005515(protein binding)	K14768 UTP7, WDR46; U3 small nucleolar RNA-associated protein 7	-	-	KAF0511296.1 BING4CT-domain-containing protein [Gigaspora margarita]	Probable U3 small nucleolar RNA-associated protein 7 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=utp7 PE=3 SV=1
A7725	-	-	GO:0005509(calcium ion binding)	-	-	-	-	Squidulin OS=Doryteuthis pealeii OX=1051067 PE=1 SV=1
A7726	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity),GO:0003677(DNA binding),GO:0008270(zinc ion binding)	K15083 RAD16; DNA repair protein RAD16	-	KOG1002 At1g05120 Nucleotide excision repair protein RAD16	OMH83638.1 DNA repair protein RAD16 [Zancudomyces culisetiae]	ATP-dependent helicase rhp16 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rhp16 PE=3 SV=2
A7727	GO:0009058(biosynthetic process)	-	GO:0016779(nucleotidyltransferase activity)	K03241 EIF2B3; translation initiation factor eIF-2B subunit gamma	map05168 Herpes simplex virus 1 infection	KOG1462 Hs9966779 Translation initiation factor 2B, gamma subunit (eIF-2Bgamma/GCD1)	ORX56896.1 nucleotide-diphosphosugar transferase [Hesseltinella vesiculosa]	Translation initiation factor eIF2B subunit gamma OS=Bos taurus OX=9913 GN=EIF2B3 PE=2 SV=1
A7728	GO:0006066(protein import into nucleus)	-	-	-	-	-	-	-

A7729	GO:0007131(reciprocal meiotic recombination)	-	-	-	-	-	CEL06672.1 hypothetical protein ASPCAL09844 [Aspergillus calidoustus]	Homologous-pairing protein 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=meu13 PE=1 SV=1
A7730	-	-	-	-	-	KOG1444 At5g19980 Nucleotide-sugar transporter VRG4/SQV-7	-	GDP-fucose transporter 1 OS=Arabidopsis thaliana OX=3702 GN=GFT1 PE=1 SV=1
A7731	GO:0007165(signal transduction)	-	-	-	-	-	-	-
A7732	-	-	-	K04739 PRKAR; cAMP-dependent protein kinase regulator	map04910 Insulin signaling pathway	KOG1113 YL033c cAMP-dependent protein kinase types I and II, regulatory subunit	KAF5092278.1 hypothetical protein D0Z03_002947 [Galactomyces reessii]	cAMP-dependent protein kinase regulatory subunit OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=PKAR PE=3 SV=1
A7733	GO:0006508(proteolysis)	-	GO:0004198(calcium-dependent cysteine-type endopeptidase activity)	-	-	KOG0045 Hs5032105_2 Cytosolic Ca2+-dependent cysteine protease (calpain), large subunit (EF-Hand protein superfamily)	KAG0340603.1 hypothetical protein BG000_011645 [Podila horticola]	Calpain-D OS=Drosophila melanogaster OX=7227 GN=sol PE=1 SV=2
A7734	GO:0006457(protein folding)	GO:0016021(integral component of membrane)	GO:0005515(protein binding),GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding)	K09553 STIP1; stress-induced-phosphoprotein 1	map05020 Prion disease	KOG0548 Hs5803181 Molecular co-chaperone STI1	KAF5355905.1 hypothetical protein D9756_004167 [Leucoagaricus leucothites]	Stress-induced-phosphoprotein 1 OS=Macaca fascicularis OX=9541 GN=STIP1 PE=2 SV=1
A7735	-	-	-	-	-	-	-	-
A7736	-	-	GO:0016491(oxidoreductase activity)	-	-	-	RYP58423.1 hypothetical protein DL771_011251 [Monosporascus sp. 5C6A]	Tuberculostearic acid methyltransferase UfaA1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=ufaA1 PE=1 SV=3
A7737	GO:0000160(phosphorelay signal transduction system),GO:0016310(phosphorylation)	-	GO:0016884(carbon-nitrogen ligase activity, with glutamine as amido-N-donor),GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	-	TPX44879.1 hypothetical protein SeLEV6574_g04231 [Synchytrium endobioticum]	(S)-coclaurine N-methyltransferase OS=Thalictrum flavum subsp. glaucum OX=150095 GN=fcNMT PE=1 SV=1

A7738	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005515(protein binding),GO:0008569(minus-end-directed microtubule motor activity),GO:0045505(dynein intermediate chain binding),GO:0051959(dynein light intermediate chain binding),GO:0005524(ATP binding)	K10413 DYNC1H1; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595[Hs13876382 Dyneins, heavy chain	KXS10801.1 hypothetical protein M427DRAFT_103173 [Gonapodya prolifera JEL478]	Dynein alpha chain, flagellar outer arm OS=Chlamydomonas reinhardtii OX=3055 GN=ODA11 PE=3 SV=2
A7739	-	-	-	-	-	-	SCO80718.1 related to thioesterase [Fusarium oxysporum]	Protein THEM6 OS=Danio rerio OX=7955 GN=them6 PE=2 SV=1
A7740	GO:0006629(lipid metabolic process)	-	-	K10256 FAD2; omega-6 fatty acid desaturase / acyl-lipid omega-6 desaturase (Delta-12 desaturase) [EC:1.14.19.6 1.14.19.22]	map01040 Biosynthesis of unsaturated fatty acids;map01100 Metabolic pathways;map01212 Fatty acid metabolism	-	RHZ75025.1 hypothetical protein Glove_218g3 [Diversispora epigaea]	Oleate hydroxylase FAH12 OS=Ricinus communis OX=3988 GN=FAH12 PE=1 SV=2
A7741	GO:0000398(mRNA splicing, via spliceosome)	-	-	K12625 LSM6; U6 snRNA-associated Sm-like protein LSM6	map03040 Spliceosome;map03018 RNA degradation	KOG1783[Hs5901998 Small nuclear ribonucleoprotein F	RIB04755.1 hypothetical protein C2G38_2119955 [Gigaspora rosea]	U6 snRNA-associated Sm-like protein LSM6 OS=Homo sapiens OX=9606 GN=LSM6 PE=1 SV=1
A7742	-	-	-	-	-	KOG1502[At5g19440 Flavonol reductase/cinnamoyl-CoA reductase	ORX90222.1 NAD(P)-binding protein [Basidiobolus meristosporus CBS 931.73]	Phenylacetaldehyde reductase OS=Rosa hybrid cultivar OX=128735 GN=PAR PE=1 SV=1
A7743	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2158[7301565 Tubulin-tyrosine ligase-related protein	XP_016608407.1 hypothetical protein SPPG_04692 [Spizellomyces punctatus DAOM BR117]	Tubulin polyglutamylase TTL13 OS=Mus musculus OX=10090 GN=Ttl13 PE=1 SV=1
A7744	-	-	-	-	-	-	-	-
A7745	-	-	GO:0005515(protein binding)	K11092 SNRPA1; U2 small nuclear ribonucleoprotein A'	map03040 Spliceosome	KOG1644[At1g09760 U2-associated snRNP A' protein	KEQ59661.1 L domain-like protein [Aureobasidium melanogenum CBS 110374]	Leucine-rich repeat-containing protein 72 OS=Bos taurus OX=9913 GN=LRRC72 PE=2 SV=1
A7746	-	-	-	-	-	-	-	-
A7747	-	-	-	-	-	-	-	-
A7748	-	-	GO:0016491(oxidoreductase activity)	-	-	-	ORZ21202.1 hypothetical protein BCR42DRAFT_488309 [Absidia repens]	Very-long-chain 3-oxoacyl-CoA reductase-like protein At1g24470 OS=Arabidopsis thaliana OX=3702 GN=KCR2 PE=2 SV=1

A7749	-	-	GO:0004842(ubiquitin-protein transferase activity),GO:0005515(protein binding)	K10592 HUWE1, MULE, ARF-BP1, TOM1; E3 ubiquitin-protein ligase HUWE1 [EC:2.3.2.26]	map04120 Ubiquitin mediated proteolysis	KOG0940[Hs20550102 Ubiquitin protein ligase RSP5/NEDD4	ORY22745.1 hypothetical protein LY90DRAFT_675786 [Neocallimastix californiae]	E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus OX=10090 GN=Nedd4 PE=1 SV=3
A7750	-	-	-	K03377 CASD1; N-acetylneuraminase 9-O-acetyltransferase [EC:2.3.1.45]	-	KOG1699[At3g06550 O-acetyltransferase	KJ168534.1 hypothetical protein HYDPIDRAFT_106735 [Hydnomerulis pinastri MD-312]	Protein REDUCED WALL ACETYLATION 2 OS=Arabidopsis thaliana OX=3702 GN=RWA2 PE=1 SV=1
A7751	-	GO:0005634(nucleus)	GO:0005515(protein binding)	K11684 BDF1; bromodomain-containing factor 1	-	KOG1245[Hs7304923 Chromatin remodeling complex WSTF-ISWI, large subunit (contains heterochromatin localization, PHD and BROMO domains)	XP_007877966.1 hypothetical protein PFL1_02262 [Anthracocystis flocculosa PF-1]	Bromodomain adjacent to zinc finger domain protein 2B OS=Homo sapiens OX=9606 GN=BAZ2B PE=1 SV=3
A7752	GO:0032012(regulation of ARF protein signal transduction)	-	GO:0005085(guanine-nucleotide exchange factor activity)	-	-	KOG0928[At1g13980 Pattern formation protein/guanine nucleotide exchange factor	KAF9569505.1 GDP/GTP exchange factor for ARF [Mortierella alpina]	ARF guanine-nucleotide exchange factor GNOM OS=Arabidopsis thaliana OX=3702 GN=GN PE=1 SV=1
A7753	-	-	-	K04554 UBE2J2, NCUBE2, UBC6; ubiquitin-conjugating enzyme E2 J2 [EC:2.3.2.23]	map04141 Protein processing in endoplasmic reticulum;map04120 Ubiquitin mediated proteolysis;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease	KOG0894[730265 Ubiquitin-protein ligase	TPX59252.1 hypothetical protein PhCBS80983_g02569 [Powellomyces hirtus]	Ubiquitin-conjugating enzyme E2 J2 OS=Bos taurus OX=9913 GN=UBE2J2 PE=2 SV=1
A7754	-	-	-	-	-	-	-	-
A7755	-	-	-	-	-	-	-	-
A7756	-	-	-	-	-	-	KAG0162894.1 hypothetical protein DFQ30_001101 [Apophysomyces sp. BC1015]	RutC family protein HI_1627 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_1627 PE=3 SV=1
A7757	-	-	-	-	-	-	-	-
A7758	-	-	-	-	-	-	-	-
A7759	-	-	-	-	-	-	-	-
A7760	-	-	-	-	-	-	-	-
A7761	GO:0006397(mRNA processing),GO:0006396(RNA processing)	-	GO:0005515(protein binding),GO:0003729(mRNA binding)	-	-	-	XP_016274818.1 antiviral protein SKI3 [Rhodotorula toruloides NP11]	-

A7762	-	-	-	-	-	-	-	-
A7763	GO:0005975(carbohydrate metabolic process), GO:0071704(organic substance metabolic process)	-	GO:0016868(intramolecular transferase activity, phosphotransferases), GO:0004614(phosphoglucosyltransferase activity)	K01835 pgm; phosphoglucosyltransferase [EC:5.4.2.2]	map01250 Biosynthesis of nucleotide sugars; map00230 Purine metabolism; map01110 Biosynthesis of secondary metabolites; map00010 Glycolysis / Gluconeogenesis; map01120 Microbial metabolism in diverse environments; map00052 Galactose metabolism; map00500 Starch and sucrose metabolism; map00030 Pentose phosphate pathway; map00520 Amino sugar and nucleotide sugar	KOG0625[At1g23190 Phosphoglucosyltransferase]	ORY03725.1 hypothetical protein K493DRAFT_311625 [Basidiobolus meristosporus CBS 931.73]	Probable phosphoglucosyltransferase, cytoplasmic 1 OS=Arabidopsis thaliana OX=3702 GN=At1g23190 PE=2 SV=2
A7764	-	-	GO:0046982(protein heterodimerization activity)	-	-	KOG1657[At5g43250 CCAAT-binding factor, subunit C (HAP5)]	EIE82245.1 hypothetical protein RO3G_06950 [Rhizopus delemar RA 99-880]	-
A7765	-	GO:0005643(nuclear pore)	-	-	-	-	-	-
A7766	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity), GO:0005524(ATP binding), GO:0008017(microtubule binding)	-	-	KOG0241[HsM19923582 Kinesin-like protein]	EOD50042.1 putative kinesin family protein [Neofusicoccum parvum UCRNP2]	Kinesin-like protein KIF13A OS=Homo sapiens OX=9606 GN=KIF13A PE=1 SV=2
A7767	GO:0007015(actin filament organization)	-	-	K23612 WASL; neural Wiskott-Aldrich syndrome protein	map04144 Endocytosis; map05135 Yersinia infection; map05132 Salmonella infection; map05130 Pathogenic Escherichia coli infection; map05131 Shigellosis; map04810 Regulation of actin cytoskeleton; map05100 Bacterial invasion of epithelial cells; map04520 Adherens junction	-	RKP11233.1 hypothetical protein BJ684DRAFT_23288 [Piptocephalis cylindrospora]	Actin-binding protein wsp1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=wsp1 PE=1 SV=3
A7768	-	-	-	K16639 LACTB2; endoribonuclease LACTB2 [EC:3.1.27.-]	-	KOG0813[Hs705793 Glyoxylase]	XP_01661252.1 hypothetical protein SPPG_00211 [Spizellomyces punctatus DAOM BR117]	Endoribonuclease LACTB2 OS=Xenopus laevis OX=8355 GN=lactb2 PE=2 SV=1

A7769	-	-	-	-	-	KOG0381 Hs4504425 HMG box-containing protein	CRK35341.1 hypothetical protein BN1708_006693, partial [Verticillium longisporum]	High mobility group protein B1 OS=Sus scrofa OX=9823 GN=HMGB1 PE=1 SV=3
A7770	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A7771	-	-	-	-	-	-	-	-
A7772	GO:0006811(ion transport), GO:0055085(transmembrane transport), GO:0006813(potassium ion transport)	GO:0016020(membrane)	GO:0005216(ion channel activity), GO:0005249(voltage-gated potassium channel activity)	-	-	KOG0501 Hs22024390 K+-channel KCNQ	KNE70337.1 hypothetical protein AMAG_14476 [Allomyces macrogynus ATCC 38327]	Potassium voltage-gated channel subfamily H member 5 OS=Homo sapiens OX=9606 GN=KCNH5 PE=1 SV=3
A7773	-	-	GO:0005515(protein binding)	-	-	KOG4389 CE07569 Acetylcholinesterase/Butyrylcholinesterase	KAF9577586.1 hypothetical protein BGW38_007112, partial [Lunasporea selenospora]	cAMP-regulated D2 protein OS=Dictyostelium discoideum OX=44689 GN=D2 PE=2 SV=3
A7774	GO:0006811(ion transport), GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005515(protein binding), GO:0005216(ion channel activity)	K01440 PNC1: nicotinamide [EC:3.5.1.19]	map04213 Longevity regulating pathway - multiple species; map01240 Biosynthesis of cofactors; map00760 Nicotinate and nicotinamide metabolism; map01100 Metabolic pathways	KOG2243 Hs10863871 Ca2+ release channel (ryanodine receptor)	KAF8839428.1 Isochorismatase hydrolase [Paxillus ammoniavirescens]	Ryanodine receptor 1 OS=Homo sapiens OX=9606 GN=RYR1 PE=1 SV=3
A7775	GO:0006418(tRNA aminoacylation for protein translation), GO:0006422(aspartyl-tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0000166(nucleotide binding), GO:0004812(aminoacyl-tRNA ligase activity), GO:0005524(ATP binding), GO:0004815(aspartate-tRNA ligase activity)	-	-	-	TPX73656.1 hypothetical protein CcBS67573_g05080 [Chytridiomycetes confervae]	Aspartate--tRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=DARS1 PE=2 SV=1
A7776	-	-	-	-	-	-	-	-
A7777	-	-	-	-	-	-	-	-
A7778	-	-	-	-	-	KOG1090 Hs22061701 Predicted dual-specificity phosphatase	KAF9205564.1 hypothetical protein BGZ49_003861, partial [Haplosporangium sp. Z27]	Myotubularin-related protein 13 OS=Xenopus laevis OX=8355 GN=sbf2 PE=2 SV=1

A7779	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0003724(RNA helicase activity)	K11594 DDX3X, bel; ATP-dependent RNA helicase DDX3X [EC:3.6.4.13]	map04622 RIG-I-like receptor signaling pathway;map05203 Viral carcinogenesis; map05161 Hepatitis B	KOG0331 At3g22330 ATP-dependent RNA helicase	ORY01863.1 DEAD-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	DEAD-box ATP-dependent RNA helicase 3A, chloroplastic OS=Zea mays OX=4577 GN=RH3A PE=3 SV=1
A7780	GO:0001522(pseudouridine synthesis), GO:0009451(RNA modification)	-	GO:0003723(RNA binding),GO:0009982(pseudouridine synthase activity)	K06176 truD, PUS7; tRNA pseudouridine synthase [EC:5.4.99.27]	-	KOG2339 YOR243c Uncharacterized conserved protein	EHN00086.1 Pus7p [Saccharomyces cerevisiae x Saccharomyces kudriavzevii VIN7]	Multisubstrate pseudouridine synthase 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUS7 PE=1 SV=1
A7781	-	-	-	-	-	-	-	-
A7782	GO:0036211(protein modification process), GO:0006364(rRNA processing)	GO:0090730(Las1 complex)	GO:0004519(endonuclease activity)	K16912 LAS1; ribosomal biogenesis protein LAS1	-	KOG2157 7292526 Predicted tubulin-tyrosine ligase	ORX76957.1 TTL-domain-containing protein [Anaeromyces robustus]	Tubulin polyglutamylase TTL5 OS=Mus musculus OX=10090 GN=Ttl5 PE=1 SV=3
A7783	-	-	GO:0005515(protein binding),GO:0003723(RNA binding)	-	-	-	-	-
A7784	-	-	-	-	-	KOG4754 At2g17280 Predicted phosphoglycerate mutase	KAF7526783.1 hypothetical protein PCG10_003850 [Penicillium crustosum]	Phosphoglycerate mutase-like protein OS=Arabidopsis thaliana OX=3702 GN=PGM PE=2 SV=1
A7785	-	-	-	-	-	-	-	-
A7786	-	-	-	-	-	-	-	-
A7787	-	-	-	-	-	-	-	-
A7788	GO:0010165(response to X-ray)	-	GO:0005515(protein binding)	-	-	-	-	-
A7789	GO:0006886(intracellular protein transport), GO:0016192(vesicle-mediated transport)	GO:0030117(membrane coat),GO:0030131(cathrin adaptor complex)	-	K12392 AP1B1; AP-1 complex subunit beta-1	map04142 Lysosome;map05170 Human immunodeficiency virus 1 infection	KOG1061 At5g11490 Vesicle coat complex AP-1/AP-2/AP-4, beta subunit	OZJ04597.1 AP-2 complex subunit beta [Bifiguratus adalaidae]	Beta-adaptin-like protein A OS=Arabidopsis thaliana OX=3702 GN=BETAA-AD PE=1 SV=1
A7790	-	-	GO:0005515(protein binding)	K23334 RANBP9_10, RANBPM; Ran-binding protein 9/10	-	-	ORX46066.1 SPRY-domain-containing protein [Hesseltinella vesiculosa]	Uncharacterized protein C1259.12c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC1259.12c PE=4 SV=2
A7791	-	-	GO:0050660(flavin adenine dinucleotide binding),GO:0071949(FAD binding)	-	-	-	-	-
A7792	-	-	-	-	-	-	-	-
A7793	-	-	-	-	-	-	-	-
A7794	-	-	-	K10579 UBE2M, UBC12; ubiquitin-conjugating enzyme E2 M [EC:2.3.2.34]	map04120 Ubiquitin mediated proteolysis	-	OCB86162.1 hypothetical protein A7U60_g6751 [Sanghuangporus baumii]	NEDD8-conjugating enzyme ubc12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=ubc12 PE=3 SV=1

A7795	-	-	GO:0008374(O-acyltransferase activity)	K14457 MOGAT2, MGAT2; 2-acylglycerol O-acyltransferase 2 [EC:2.3.1.22]	map04975 Fat digestion and absorption;map00561 Glycerolipid metabolism;map01100 Metabolic pathways	KOG0831 Hs14211871 Acyl-CoA:diacylglycerol acyltransferase (DGAT)	XP_003674621.1 hypothetical protein NCAS_0B01630 [Naumovozya castellii CBS 4309]	2-acylglycerol O-acyltransferase 2 OS=Mus musculus OX=10090 GN=Mogat2 PE=1 SV=1
A7796	-	-	-	-	-	-	-	-
A7797	GO:0018342(protein prenylation)	-	GO:0008318(protein prenyltransferase activity)	K05955 FNTA; protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha [EC:2.5.1.58 2.5.1.59]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis	KOG0530 Hs4503771 Protein farnesyltransferase, alpha subunit/protein geranylgeranyltransferase type I, alpha subunit	XP_020129023.1 farnesyltransferase alpha subunit [Diplodia corticola]	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens OX=9606 GN=FNTA PE=1 SV=1
A7798	-	-	-	-	-	-	-	-
A7799	-	-	GO:0046872(metal ion binding)	K15687 MKRN; E3 ubiquitin-protein ligase makorin [EC:2.3.2.27]	-	KOG1039 Hs13540509 Predicted E3 ubiquitin ligase	RIB18165.1 hypothetical protein C2G38_2037143 [Gigaspora rosea]	E3 ubiquitin-protein ligase makorin-1 OS=Notamacropus eugenii OX=9315 GN=MKRN1 PE=2 SV=1
A7800	-	-	GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity)	K18798 AFG1, LACE1; peroxisome-assembly ATPase [EC:3.6.4.7]	-	KOG2383 CE16882 Predicted ATPase	XP_025380020.1 AFG1-like ATPase [Acaromyces ingoldii]	AFG1-like ATPase OS=Rattus norvegicus OX=10116 GN=Afg1 PE=2 SV=1
A7801	GO:0006275(regulation of DNA replication)	-	GO:0003677(DNA binding);GO:0030337(DNA polymerase processivity factor activity)	K04802 PCNA; proliferating cell nuclear antigen	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map04530 Tight junction;map03430 Mismatch repair;map04110 Cell cycle;map05161 Hepatitis B	-	TPX57137.1 hypothetical protein PhCBS80983_g04027 [Powellomyces hirtus]	Proliferating cell nuclear antigen OS=Brassica napus OX=3708 PE=2 SV=1
A7802	-	-	GO:0003676(nucleic acid binding);GO:0005524(ATP binding);GO:0004386(helicase activity)	K13026 DHX57; ATP-dependent RNA helicase DHX57 [EC:3.6.4.13]	-	KOG0920 At2g35920 ATP-dependent RNA helicase A	RUP47114.1 hypothetical protein BC936DRAFT_146116 [Jimgerdennia flammicorona]	DExH-box ATP-dependent RNA helicase DExH1 OS=Arabidopsis thaliana OX=3702 GN=At2g35920 PE=2 SV=1
A7803	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1198 At1g23740 Zinc-binding oxidoreductase	KAF9348302.1 hypothetical protein BGX34_002559 [Mortierella sp. NVP85]	2-methylene-furan-3-one reductase OS=Solanum lycopersicum OX=4081 GN=EO PE=1 SV=1
A7804	-	-	GO:0016491(oxidoreductase activity)	-	-	-	KAF9348302.1 hypothetical protein BGX34_002559 [Mortierella sp. NVP85]	2-methylene-furan-3-one reductase OS=Solanum lycopersicum OX=4081 GN=EO PE=1 SV=1

A7805	GO:000079(regulation of cyclin-dependent protein serine/threonine kinase activity)	-	GO:0019901(protein kinase binding)	-	-	KOG1674 At2g44740 Cyclin	ORX89589.1 cyclin-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Cyclin-U4-1 OS=Arabidopsis thaliana OX=3702 GN=CYCU4-1 PE=1 SV=1
A7806	-	-	-	-	-	KOG0800 Hs8923522 FOG: Predicted E3 ubiquitin ligase	-	-
A7807	-	-	-	-	-	-	-	-
A7808	GO:0016579(protein deubiquitination),GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase)	K11855 USP36_42; ubiquitin carboxyl-terminal hydrolase 36/42 [EC:3.4.19.12]	-	KOG1873 At2g32780 Ubiquitin-specific protease	XP_019006065.1 hypothetical protein I203_01387 [Kwoniella mangroviensis CBS 8507]	Ubiquitin carboxyl-terminal hydrolase 1 OS=Arabidopsis thaliana OX=3702 GN=UBP1 PE=1 SV=2
A7809	GO:0006886(intracellular protein transport),GO:0016192(vesicle-mediated transport)	GO:003031(clathrin adaptor complex)	-	K12393 AP1M; AP-1 complex subunit mu	map04142 Lysosome;map05170 Human immunodeficiency virus 1 infection	KOG0937 Hs14210504 Adaptor complexes medium subunit family	PKC13024.1 clathrin adaptor, mu subunit [Rhizophagus irregularis]	AP-1 complex subunit mu-1 OS=Bos taurus OX=9913 GN=AP1M1 PE=1 SV=3
A7810	-	-	-	-	-	-	-	-
A7811	-	-	GO:0005524(ATP binding)	K09486 HYOU1; hypoxia up-regulated 1	map04141 Protein processing in endoplasmic reticulum	KOG0104 Hs22063141 Molecular chaperones GRP170/SIL1, HSP70 superfamily	CEP13674.1 hypothetical protein [Parasitella parasitica]	Hypoxia up-regulated protein 1 (Fragment) OS=Xenopus laevis OX=8355 GN=hyou1 PE=1 SV=2
A7812	GO:0006351(transcription, DNA-templated)	GO:0005634(nucleus),GO:0005665(RNA polymerase II, core complex)	GO:0003677(DNA binding),GO:0003899(DNA-directed 5'-3' RNA polymerase activity)	K03014 RPABC2, RPB6, POLR2F; DNA-directed RNA polymerases I, II, and III subunit RPABC2	map03420 Nucleotide excision repair;map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway;map05016 Huntington disease	KOG3405 Hs11527390 RNA polymerase subunit K	SAM03385.1 hypothetical protein [Absidia glauca]	DNA-directed RNA polymerases I, II, and III subunit rpabc2 OS=Dictyostelium discoideum OX=44689 GN=polr2f PE=3 SV=1
A7813	-	-	-	-	-	KOG2458 Hs13129086 Endoplasmic reticulum protein EP58, contains filamin rod domain and KDEL motif	CEJ83085.1 hypothetical protein VHEMI03115 [Torrubiella hemipterigena]	Protein O-glucosyltransferase 2 OS=Homo sapiens OX=9606 GN=POGLUT2 PE=1 SV=1
A7814	-	-	-	-	-	-	-	-
A7815	-	-	-	-	-	-	-	-
A7816	-	-	-	-	-	-	-	-
A7817	-	-	-	-	-	-	-	-
A7818	GO:0006508(proteolysis)	-	GO:0005515(protein binding),GO:0004198(calcium-dependent cysteine-type endopeptidase activity)	-	-	KOG2106 Hs6912356 Uncharacterized conserved protein, contains HELF and WD40 domains	XP_031023021.1 uncharacterized protein SmJEL517_g05070 [Synchytrium microbalum]	Echinoderm microtubule-associated protein-like 2 OS=Rattus norvegicus OX=10116 GN=Eml2 PE=1 SV=1
A7819	-	-	-	-	-	-	-	-
A7820	-	-	-	-	-	-	-	-
A7821	-	-	-	-	-	-	-	-

A7822	-	-	GO:0008270(zinc ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG1198 At1g23740 Zinc-binding oxidoreductase	RUS15973.1 alcohol dehydrogenase zinc-binding domain-containing protein [Endogone sp. FLAS-F59071]	2-methylene-furan-3-one reductase OS=Fragaria ananassa OX=3747 GN=EO PE=1 SV=2
A7823	-	-	GO:0004497(monoxygenase activity),GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0020037(heme binding)	-	-	KOG0158 CE01657 Cytochrome P450 CYP3/CYP5/CYP6/CYP9 subfamilies	KAF9582692.1 hypothetical protein BGW38_01086 [Lunasporea selenosporea]	Prostaglandin E2 omega-hydroxylase CYP4F21 OS=Ovis aries OX=9940 GN=CYP4F21 PE=1 SV=1
A7824	-	-	GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor),GO:0016491(oxidoreductase activity)	-	-	-	KAF9116111.1 hypothetical protein BGX30_006070, partial [Mortierella sp. GBA39]	Sulfoacetaldehyde dehydrogenase (acylating) OS=Cupriavidus necator (strain ATCC 17699 / DSM 428 / KCTC 22496 / NCIMB 10442 / H16 / Stanier 337) OX=381666 GN=sauS PE=1 SV=1
A7825	-	-	GO:0005515(protein binding)	-	-	-	KKY30221.1 putative tpr domain protein [Diaporthe ampelina]	-
A7826	-	-	-	K03676 grxC, GLRX, GLRX2; glutaredoxin 3	-	KOG1752 At5g40370 Glutaredoxin and related proteins	KAG0089646.1 hypothetical protein BGZ93_009763 [Podila epycladia]	Glutaredoxin OS=Ricinus communis OX=3988 PE=3 SV=1
A7827	-	-	GO:0005515(protein binding)	K14829 IPI3; pre-rRNA-processing protein IPI3	-	KOG0646 Hs14765579 WD40 repeat protein	GBC04692.1 hypothetical protein RclHRI_05810004 [Rhizophagus clarus]	WD repeat-containing protein 18 OS=Danio rerio OX=7955 GN=wdr18 PE=2 SV=1
A7828	-	-	GO:0005515(protein binding)	-	-	-	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A7829	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K02831 RAD53; ser/thr/tyr protein kinase RAD53 [EC:2.7.11.-]	map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0601 CE14884.1 Cyclin-dependent kinase WEE1	KAF9976048.1 hypothetical protein BGZ73_009207 [Actinomyces rella ambigua]	Cell division control protein 2 homolog 2 OS=Trypanosoma brucei OX=5702 GN=CRK2 PE=3 SV=1

A7830	GO:007248(ammonium transmembrane transport)	GO:0016020(membrane)	GO:0008519(ammonium transmembrane transporter activity)	K03320 amt, AMT, MEP; ammonium transporter, Amt family	-	KOG0682 CE06770 Ammonia permease	KAF9121223.1 hypothetical protein BGX30_002722 [Mortierella sp. GBA39]	Ammonium transporter 3 OS=Dictyostelium discoideum OX=44689 GN=amtC PE=2 SV=1
A7831	-	-	-	-	-	-	-	-
A7832	-	-	-	-	-	-	RVX72072.1 hypothetical protein B0A52_04670 [Exophiala mesophila]	-
A7833	-	-	GO:0005515(protein binding)	-	-	KOG4378 Hs22060896 Nuclear protein COP1	RKP26015.1 WD40-repeat-containing domain protein [Syncephalis pseudoplumigaleata]	Protein NEDD1 OS=Homo sapiens OX=9606 GN=NEDD1 PE=1 SV=1
A7834	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity),GO:0008236(serine-type peptidase activity)	K01336 PRB1; cerevisin [EC:3.4.21.48 3.4.21.-]	map04138 Autophagy - yeast	-	ORZ34811.1 peptidase S8 and S53 subtilisin kexin sedolisin [Catenaria anguillulae PL171]	Alkaline serine exoprotease A OS=Vibrio alginolyticus OX=663 GN=proA PE=3 SV=1
A7835	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7836	-	-	-	-	-	-	-	-
A7837	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K06944 DRG, RBG; developmentally-regulated GTP-binding protein [EC:3.6.5.-]	-	KOG1487 Hs4758796 GTP-binding protein DRG1 (ODN superfamily)	PJF17632.1 hypothetical protein PSACC_02577 [Paramicrosporidium saccamoebae]	Developmentally-regulated GTP-binding protein 1 OS=Bos taurus OX=9913 GN=DRG1 PE=2 SV=1
A7838	-	-	-	K00793 ribE, RIB5; riboflavin synthase [EC:2.5.1.9]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00740 Riboflavin metabolism;map01100 Metabolic pathways	KOG3310 At2g20690 Riboflavin synthase alpha chain	KAF9580502.1 Riboflavin synthase alpha chain [Lunasporengiospora selenospora]	Riboflavin synthase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rib5 PE=1 SV=1
A7839	-	-	-	-	-	-	-	-
A7840	GO:0006508(proteolysis)	-	GO:0046872(metal ion binding),GO:0004222(metalloendopeptidase activity)	K01412 PMPCA, MAS2; mitochondria l-processing peptidase subunit alpha [EC:3.4.24.64]	-	KOG2067 At1g51980 Mitochondrial processing peptidase, alpha subunit	XP_018293372.1 hypothetical protein PHYBLDRAFT_123845 [Phycomyces blakesleeanae NRRL 1555(-)]	Probable mitochondrial-processing peptidase subunit alpha-1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MPPalpha1 PE=1 SV=1

A7841	-	-	-	-	-	-	KXS16005.1 CRAL/TRIO domain- containing protein [Gonapodya prolifera JEL478]	-
A7842	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	K05643 ABCA3; ATP-binding cassette, subfamily A (ABC1), member 3	map02010 ABC transporters	KOG0059[HsM5915658 Lipid exporter ABCA1 and related proteins, ABC superfamily	ORX93119.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	Phospholipid-transporting ATPase ABCA1 OS=Homo sapiens OX=9606 GN=ABCA1 PE=1 SV=3
A7843	-	-	-	-	-	-	TPX65322.1 hypothetical protein SpCBS45565_g05265 [Spizellomyces sp. 'palustris']	Dynein axonemal intermediate chain 7 homolog OS=Ciona intestinalis OX=7719 GN=AXP83.9 PE=2 SV=1
A7844	GO:0051603(proteolysis involved in cellular protein catabolic process), GO:0006511(ubiquitin-dependent protein catabolic process)	GO:0019773(proteasome complex, alpha-subunit complex), GO:0005839(proteasome complex)	-	K02725 PSMA1; 20S proteasome subunit alpha 6 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0863[At1g47250 20S proteasome, regulatory subunit alpha type PSMA1/PRE5	ORZ18760.1 N-terminal nucleophile aminohydrolase [Absidia repens]	Proteasome subunit alpha type-1 OS=Dictyostelium discoideum OX=44689 GN=psmA1 PE=3 SV=1
A7845	GO:0055085(transmembrane transport)	-	-	K14684 SLC25A23S; solute carrier family 25 (mitochondrial phosphate transporter), member 23/24/25/41	-	KOG0752[At1g14560 Mitochondrial solute carrier protein	RKP06229.1 putative mitochondria l carrier protein [Thamnocephalus sphaerospora]	Mitochondrial substrate carrier family protein B OS=Dictyostelium discoideum OX=44689 GN=mcfB PE=3 SV=1

A7846	-	-	GO:0005515(protein binding)	K00605 gcvT, AMT; glycine cleavage system T protein (aminomethyltransferase) [EC:2.1.2.10]	map00670 One carbon pool by folate;map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map00630 Glyoxylate and dicarboxylate metabolism	KOG2770 At1g11860 Aminomethyltransferase	KXN67891.1 hypothetical protein CONCODRAFT_9956 [Conidiobolus coronatus NRRL 28638]	Aminomethyltransferase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=gcvT PE=3 SV=1
A7847	-	-	GO:0005515(protein binding)	K00605 gcvT, AMT; glycine cleavage system T protein (aminomethyltransferase) [EC:2.1.2.10]	map00670 One carbon pool by folate;map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways;map00630 Glyoxylate and dicarboxylate metabolism	KOG2770 Hs4502083 Aminomethyltransferase	KXN67891.1 hypothetical protein CONCODRAFT_9956 [Conidiobolus coronatus NRRL 28638]	Aminomethyltransferase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=gcvT PE=3 SV=1
A7848	GO:0006281(DNA repair)	-	GO:0003684(damaged DNA binding)	K03515 REV1; DNA repair protein REV1 [EC:2.7.7.-]	map03460 Fanconi anemia pathway	KOG2093 Hs7706681 Translesion DNA polymerase - REV1 deoxycytidyltransferase	KXS11055.1 DNA repair protein [Gonapodya prolifera JEL478]	DNA repair protein REV1 OS=Arabidopsis thaliana OX=3702 GN=REV1 PE=2 SV=1
A7849	GO:0006412(translation)	GO:0015935(small ribosomal subunit)	GO:0003723(RNA binding);GO:0003735(structural constituent of ribosome)	K02985 RP-S3e, RPS3; small subunit ribosomal protein S3e	map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3181 At2g31610 40S ribosomal protein S3	OON09013.1 40S ribosomal protein [Batrachochytrium salamandrivorans]	Small ribosomal subunit protein uS3z OS=Arabidopsis thaliana OX=3702 GN=RPS3A PE=1 SV=1
A7850	-	-	-	-	-	-	-	-
A7851	-	-	GO:0005085(guanyl-nucleotide exchange factor activity);GO:0005515(protein binding)	K20047 PAN1; actin cytoskeleton-regulatory complex protein PAN1	-	KOG3524 Z795184 Predicted guanine nucleotide exchange factor (PEBBLE)	GBC03133.1 hypothetical protein RclHR1_00050041 [Rhizophagus clarus]	RhoGEF domain-containing protein gxcJ OS=Dictyostelium discoideum OX=44689 GN=gxcJ PE=3 SV=1

A7852	-	-	-	-	-	-	TPX72615.1 hypothetical protein CcCBS67573_ g05713 [Chytriomyc s confervae]	-
A7853	-	-	-	-	-	-	-	-
A7854	GO:0071805(potassium ion transmembrane transport)	GO:0016020(membrane)	GO:0005267(potassium channel activity),GO:0042802(identical protein binding)	-	-	-	-	-
A7855	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7856	GO:0006357(regulation of transcription by RNA polymerase II),GO:0032784(regulation of DNA-templated transcription, elongation),GO:0006412(translation),GO:0006355(regulation of transcription, DNA-templated)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K15172 SPT5H, SPT5; transcription elongation factor SPT5	map03250 Viral life cycle - HIV-1	KOG1999 Hs20149524 RNA polymerase II transcription elongation factor DSIF/SPT5H/SPT5	ORX61614.1 transcription elongation factor Spt5 [Hesseltinella vesiculosa]	Transcription elongation factor SPT5 OS=Gallus gallus OX=9031 GN=SPT5H PE=2 SV=1
A7857	GO:0010506(regulation of autophagy)	GO:0035658(Mon1-Ccz1 complex)	-	-	-	KOG2377 At3g12010 Uncharacterized conserved protein	-	Regulator of MON1-CCZ1 complex homolog OS=Dictyostelium discoideum OX=44689 GN=DDB_G0286707 PE=3 SV=1
A7858	-	-	-	-	-	-	KAE8235634.1 hypothetical protein A4X03_0g9707, partial [Tilletia caries]	-
A7859	-	-	-	-	-	-	-	-
A7860	GO:0000398(mRNA splicing, via spliceosome)	GO:0005681(spliceosomal complex)	-	K11097 SNRPE, SME; small nuclear ribonucleoprotein E	map03040 Spliceosome	KOG1774 At4g30330 Small nuclear ribonucleoprotein E	ORX94691.1 hypothetical protein K493DRAFT_261230 [Basidiobolus meristodorus CBS 931.73]	Small nuclear ribonucleoprotein E OS=Bos taurus OX=9913 GN=SNRPE PE=3 SV=1
A7861	-	-	-	K12878 THOC1; THO complex subunit 1	map03040 Spliceosome;map03013 Nucleocytoplasmic transport	KOG2491 At5g09860 Nuclear matrix protein	TPX75007.1 hypothetical protein CcCBS67573_ g03715 [Chytriomyc s confervae]	THO complex subunit 1 OS=Arabidopsis thaliana OX=3702 GN=THO1 PE=1 SV=1
A7862	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs14766617 Sulfatase	XP_024663337.1 Arylsulfatase [Wickerhamia sorbophila]	N-acetylgalactosamine-6-sulfatase OS=Mus musculus OX=10090 GN=Gains PE=1 SV=2

A7863	GO:0010498(proteasomal protein catabolic process), GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0005839(proteasome core complex)	-	K02732 PSMB1; 20S proteasome subunit beta 6 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0179 At3g60820.20S proteasome, regulatory subunit beta type PSMB1/PRE7	KNE63078.1 hypothetical protein AMAG_08244 [Allomyces macrogynus ATCC 38327]	Proteasome subunit beta type-1-B OS=Carassius auratus OX=7957 GN=psmb1-B PE=2 SV=1
A7864	-	-	-	-	-	-	-	-
A7865	-	-	-	-	-	-	-	-
A7866	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	KAF7683146.1 putative magnesium transporter NIPA8 [Thelohanias contejeani]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A7867	GO:0045017(glycerolipid biosynthetic process)	-	GO:0008374(O-acyltransferase activity),GO:0004144(diacylglycerol O-acyltransferase activity)	-	-	-	XP_016604818.1 acyltransferase, WS/DGAT/MGAT [Spizellomyces punctatus DAOM BR117]	Putative diacylglycerol O-acyltransferase MT1468 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=MT1468 PE=3 SV=1
A7868	GO:0045017(glycerolipid biosynthetic process)	-	GO:0004144(diacylglycerol O-acyltransferase activity),GO:0008374(O-acyltransferase activity)	-	-	-	TPX69767.1 diacylglycerol O-acyltransferase [Spizellomyces sp. 'palustris']	Putative diacylglycerol O-acyltransferase MT1468 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=MT1468 PE=3 SV=1
A7869	GO:0045017(glycerolipid biosynthetic process)	-	GO:0004144(diacylglycerol O-acyltransferase activity),GO:0008374(O-acyltransferase activity)	-	-	-	TPX69767.1 diacylglycerol O-acyltransferase [Spizellomyces sp. 'palustris']	Wax ester synthase/diacylglycerol acyltransferase 2 OS=Arabidopsis thaliana OX=3702 GN=WSD2 PE=2 SV=1
A7870	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11253 H3; histone H3	map05131 Shigellosis;map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05202 Transcriptional misregulation in cancer	KOG1745 Hs17442169 Histones H3 and H4	KAF4920343.1 histone H3 [Colletotrichum fructicola]	Histone H3.2 OS=Bos taurus OX=9913 PE=1 SV=2

A7871	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0046982(protein heterodimerization activity),GO:0030527(structural constituent of chromatin)	K11254 H4; histone H4	map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG3467 At1g07660 Histone H4	OON10474.1 histone H4 [Batrachochytrium salamandrivorans]	Histone H4 variant TH011 OS=Triticum aestivum OX=4565 PE=3 SV=2
A7872	GO:0098869(cellular oxidant detoxification)	-	GO:0051920(peroxidoreductase activity),GO:0016209(antioxidant activity),GO:0016491(oxidoreductase activity)	K24137 PRX1; glutaredoxin/glutathione-dependent peroxidoreductase [EC:1.11.1.25 1.11.1.27]	map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG0854 7295884 Alkyl hydroperoxidase reductase, thiol specific antioxidant and related enzymes	CDH51300.1 cysteine peroxidoreductase [Lichtheimia corymbifera JMR:FSU:9682]	Peroxidoreductase-6 OS=Gallus gallus OX=9031 GN=PRDX6 PE=2 SV=3
A7873	GO:0000398(mRNA splicing, via spliceosome)	-	GO:0030620(U2 snRNA binding),GO:0005515(protein binding)	K11092 SNRPA1; U2 small nuclear ribonucleoprotein A'	map03040 Spliceosome	KOG1644 At1g09760 U2-associated snRNP A' protein	KAG0293546.1 U2 snRNP complex subunit [Dissophora globulifera]	U2 small nuclear ribonucleoprotein A' OS=Arabidopsis thaliana OX=3702 GN=At1g09760 PE=2 SV=2
A7874	GO:0055085(transmembrane transport)	GO:0016020(membrane),GO:0016021(integral component of membrane)	GO:0015301(anion:anion antiporter activity)	K14708 SLC26A11; solute carrier family 26 (sodium-independent sulfate anion transporter), member 11	-	KOG0236 At5g13550 Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family)	KAG0747478.1 hypothetical protein G6F23_002713 [Rhizopus oryzae]	Sulfate transporter 4.1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=SULTR4;1 PE=1 SV=1
A7875	-	-	-	-	-	-	-	-
A7876	GO:0009264(deoxyribonucleotide catabolic process)	-	GO:0008253(5'-nucleotidase activity)	-	-	-	TPX78453.1 hypothetical protein CcBS67573_g00332 [Chytridiomycota confervae]	-
A7877	GO:0006457(protein folding)	-	GO:0005515(protein binding),GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding)	-	-	-	-	-
A7878	-	-	-	-	-	KOG0691 At1g76700 Molecular chaperone (DnaJ superfamily)	TPX74967.1 hypothetical protein CcBS67573_g03776 [Chytridiomycota confervae]	Chaperone protein dnaJ 10 OS=Arabidopsis thaliana OX=3702 GN=ATJ10 PE=2 SV=2
A7879	GO:0016579(protein deubiquitination),GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase)	K11855 USP36_42; ubiquitin carboxyl-terminal hydrolase 36/42 [EC:3.4.19.12]	-	KOG1865 Hs13435157 Ubiquitin carboxyl-terminal hydrolase	RKP34582.1 hypothetical protein BJ085DRAFT_18031, partial [Dimargaris cristalligena]	Ubiquitin carboxyl-terminal hydrolase 36 OS=Mus musculus OX=10090 GN=Usp36 PE=1 SV=1

A7880	-	-	-	-	-	-	XP_01302541.9.1 NAD dependent epimerase/dehydratase [Schizosaccharomyces cryophilus OY26]	Uncharacterized protein C2A9.02 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC2A9.02 PE=3 SV=1
A7881	-	-	GO:0005509(cal cium ion binding)	-	-	KOG4099[Hs14781307 Predicted membrane protein	RUP49168.1 FUN14 family-domain-containing protein [Jimgerdennia flammicorona]	FUN14 domain-containing protein 1A OS=Xenopus laevis OX=8355 GN=fundc1-a PE=2 SV=1
A7882	GO:0008654(phospholipid biosynthetic process)	GO:0016020(membrane)	GO:0016780(phosphotransferase activity, for other substituted phosphate groups)	-	-	-	-	-
A7883	GO:0005975(carbohydrate metabolic process)	-	GO:0009045(xylose isomerase activity)	-	-	-	TPX77282.1 xylose isomerase [Chytriumyces confervae]	Xylose isomerase OS=Arabidopsis thaliana OX=3702 GN=XYLA PE=2 SV=2
A7884	-	-	-	-	-	-	-	-
A7885	-	-	-	-	-	-	-	-
A7886	-	-	-	-	-	-	-	-
A7887	-	-	GO:0005509(cal cium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027[At1g24620 Calmodulin and related proteins (EF-Hand superfamily)	KAG0656531.1 Calmodulin [Kazachstania unispora]	Putative calmodulin-like protein 6 OS=Oryza sativa subsp. japonica OX=39947 GN=CML6 PE=3 SV=1
A7888	-	-	-	-	-	-	-	-
A7889	-	-	-	-	-	-	-	-
A7890	-	-	GO:0003676(nucleic acid binding);GO:0005524(ATP binding)	K06877 K06877; DEAD/DEAH box helicase domain-containing protein	-	KOG4150[YDR291w Predicted ATP-dependent RNA helicase	TFY70534.1 hypothetical protein EVG20_g2477 [Dentipellis fragilis]	ATP-dependent helicase hrq1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=hrq1 PE=1 SV=4
A7891	-	-	-	-	-	-	-	-
A7892	-	-	-	-	-	-	-	-
A7893	GO:0006415(translational termination)	-	GO:0003747(translation release factor activity)	K15033 ICT1, MRPL58; peptidyl-tRNA hydrolase ICT1 [EC:3.1.1.29]	-	KOG3429[Hs4557657 Predicted peptidyl-tRNA hydrolase	KAG0210440.1 hypothetical protein BGX33_004913 [Mortierella sp. NVP41]	Large ribosomal subunit protein mL62 OS=Salmo salar OX=8030 GN=mrpl58 PE=2 SV=1

A7894	-	GO:0005743(mitochondrial inner membrane)	GO:0043022(ribosome binding)	K17800 LETM1, MDM38; LETM1 and EF-hand domain-containing protein 1, mitochondria l	map04139 Mitophagy - yeast	KOG1043 Hs6912482 Ca2+-binding transmembrane protein LETM1/MRS7	XP_025359144.1 LETM1-domain-containing protein, partial [Jaminaea rosea]	Mitochondrial proton/calcium exchanger protein OS=Homo sapiens OX=9606 GN=LETM1 PE=1 SV=1
A7895	-	-	-	-	-	-	-	-
A7896	GO:0036211(protein modification process)	-	-	-	-	KOG2157 7292526 Predicted tubulin-tyrosine ligase	TPX63010.1 hypothetical protein PhCBS80983.g00063 [Powellomyces hirtus]	Protein polyglycolase TTLL10 OS=Macaca fascicularis OX=9541 GN=TTLL10 PE=2 SV=1
A7897	-	-	GO:0005509(calcium ion binding)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	-	XP_003673220.1 hypothetical protein NCAS_0A02710 [Naumovozya ma castellii CBS 4309]	Calcineurin subunit B OS=Candida glabrata (strain ATCC 2001 / BCRC 20586 / JCM 3761 / NBRC 0622 / NRRL Y-65 / CBS 138) OX=284593 GN=CNB1 PE=3 SV=1
A7898	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	-	-	-
A7899	-	-	-	-	-	-	-	-
A7900	-	-	-	-	-	-	-	-
A7901	-	-	-	K15114 ORT1; mitochondria l ornithine carrier protein	-	KOG0763 Hs7657585 Mitochondria l ornithine transporter	KAF7725671.1 hypothetical protein DSO57_016407 [Entomophthora muscae]	Mitochondrial ornithine transporter 1 OS=Mus musculus OX=10090 GN=Slc25a15 PE=1 SV=1
A7902	-	-	-	-	-	-	-	-
A7903	-	-	-	-	-	-	-	-
A7904	-	-	-	-	-	-	-	-
A7905	-	-	-	-	-	-	-	-
A7906	-	-	-	-	-	-	-	-
A7907	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	RIB02250.1 hypothetical protein C2G38_2228360 [Gigaspora rosea]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1

A7908	GO:0006564(L-serine biosynthetic process)	-	GO:0036424(L-phosphoserine phosphatase activity)	K01079 serB, PSPH; phosphoserine phosphatase [EC:3.1.3.3]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00680 Methane metabolism;map00260 Glycine, serine and threonine metabolism;map01100 Metabolic pathways	KOG1615 At1g18640 Phosphoserine phosphatase	XP_024326145.1 hypothetical protein VC83_02382 [Pseudogymnoascus destructans]	Phosphoserine phosphatase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PSP PE=1 SV=2
A7909	GO:0006122(mitochondrial electron transport, ubiquinol to cytochrome c)	GO:0005750(mitochondrial respiratory chain complex III)	-	K00416 QCR6; ubiquinol-cytochrome c reductase subunit 6	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map04260 Cardiac muscle contraction;map04714 Thermogenesis;map00190 Oxidative phosphorylation;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map05010 Alzheimer disease;map05015	KOG4763 At1g15120 Ubiquinol-cytochrome c reductase hinge protein	CEG73544.1 Putative Ubiquinol-cytochrome c reductase subunit 6 [Rhizopus microsporus]	Cytochrome b-c1 complex subunit 6-1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=QCR6-1 PE=1 SV=1
A7910	GO:0032259(methylation)	-	GO:0003676(nucleic acid binding);GO:0008168(methyltransferase activity)	-	-	-	-	-
A7911	GO:0031167(rRNA methylation);GO:0032259(methylation);GO:0001510(rRNA methylation);GO:0006364(rRNA processing)	GO:0005634(nucleus)	GO:0008649(rRNA methyltransferase activity);GO:0008168(methyltransferase activity)	K14857 SPB1, FTSJ3; AdoMet-dependent rRNA methyltransferase SPB1 [EC:2.1.1.-]	-	-	ORX62262.1 FtsJ-domain-containing protein [Hesseltinella vesiculosa]	AdoMet-dependent rRNA methyltransferase spb1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=spb1 PE=1 SV=2
A7912	-	-	-	-	-	-	-	-
A7913	GO:0005975(carbohydrate metabolic process)	-	GO:0016773(phosphotransferase activity, alcohol group as acceptor)	K00854 xylB, XylB; xylulokinase [EC:2.7.1.17]	map00040 Pentose and glucuronate interconversions;map01100 Metabolic pathways	KOG2531 At5g49650 Sugar (pentulose and hexulose) kinases	KAF3290326.1 hypothetical protein TWF132_007115 [Orbilia oligospora]	Xylulose kinase 2 OS=Arabidopsis thaliana OX=3702 GN=XK2 PE=1 SV=1
A7914	-	-	-	-	-	-	-	-

A7915	-	-	GO:0008318(protein prenyltransferase activity),GO:0003824(catalytic activity)	K11713 PGTB1; geranylgeranyl transferase type-1 subunit beta [EC:2.5.1.59]	-	KOG0367 Hs4826900 Protein geranylgeranyltransferase Type I, beta subunit	KXS12656.1 geranylgeranyltransferase type I beta-subunit-like protein [Gonapodya prolifera JEL478]	Geranylgeranyl transferase type-1 subunit beta OS=Homo sapiens OX=9606 GN=PGGT1B PE=1 SV=2
A7916	-	-	-	-	-	-	PGH11010.1 hypothetical protein AJ79_05161 [Helicocarpus griseus UAMH5409]	-
A7917	-	-	GO:0016746(acyltransferase activity),GO:0005509(calcium ion binding),GO:0008374(O-acyltransferase activity)	K10769 ALKBH7; alkylated DNA repair protein alkB homolog 7 [EC:1.14.11.-]	-	KOG4666 Hs8923446 Predicted phosphate acyltransferase, contains PlsC domain	KNE86455.1 hypothetical protein PSTG_20184, partial [Puccinia striiformis f. sp. tritici PST-78]	Lysophosphatidylcholine acyltransferase 2 OS=Homo sapiens OX=9606 GN=LPCAT2 PE=1 SV=1
A7918	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	ORZ39244.1 magnesium transporter NIPA-domain-containing protein [Catenaria anguillulae PL171]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A7919	GO:0000077(DNA damage checkpoint signaling)	GO:0030896(checkpoint clamp complex)	-	K10994 RAD9A; cell cycle checkpoint control protein RAD9A [EC:3.1.11.2]	map04218 Cellular senescence	KOG2810 Hs4759022_1 Checkpoint 9-1-1 complex, RAD9 component	KAG4093156.1 hypothetical protein H8356DRAFT_1699806 [Neocallimastix sp. JGI-2020a]	Cell cycle checkpoint control protein RAD9A OS=Homo sapiens OX=9606 GN=RAD9A PE=1 SV=1
A7920	-	-	GO:0003824(catalytic activity)	K13239 ECI2, PECl; Delta3-Delta2-enoyl-CoA isomerase [EC:5.3.3.8]	map04146 Peroxisome;map00071 Fatty acid degradation	KOG0016 Hs5174625_2 Enoyl-CoA hydratase/isomerase	KAF9127377.1 Enoyl-CoA delta isomerase 2, mitochondrial [Mortierella sp. 14UC]	Enoyl-CoA delta isomerase 2 OS=Mus musculus OX=10090 GN=Eci2 PE=1 SV=2
A7921	-	-	-	-	-	-	XP_013266608.1 hypothetical protein Z518_11210 [Rhinoctadiella mackenziei CBS 650.93]	-
A7922	GO:0031146(SCF-dependent proteasomal ubiquitin-dependent protein catabolic process)	GO:0019005(SCF ubiquitin ligase complex)	GO:0005515(protein binding)	K10295 FBXO9; F-box protein 9	-	-	RPD64207.1 hypothetical protein L227DRAFT_583999 [Lentinus tigrinus ALCF2SS1-6]	F-box only protein 9 OS=Danio rerio OX=7955 GN=fbxo9 PE=2 SV=1

A7923	GO:0007165(signal transduction),GO:0043087(regulation of GTPase activity)	-	-	-	-	KOG1426 7295603 FOG: RCC1 domain	TPX68763.1 hypothetical protein SpCBS45565_g02894 [Spizellomyces sp. 'palustris']	RCC1 and BTB domain-containing protein 2 OS=Mus musculus OX=10090 GN=Rcbbt2 PE=1 SV=1
A7924	GO:0016192(vesicle-mediated transport)	GO:0016021(integral component of membrane)	-	-	-	KOG2887 At5g56020 Membrane protein involved in ER to Golgi transport	RKP10090.1 Got1/Sft2-like family-domain-containing protein [Thamnocephalus sphaerospora]	Protein transport protein SFT2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SFT2 PE=1 SV=1
A7925	GO:0009245(lipid A biosynthetic process)	-	GO:0016410(N-acyltransferase activity),GO:0016740(transferase activity)	-	-	-	XP_001590718.1 hypothetical protein SS1G_08458 [Sclerotinia sclerotiorum 1980 UF-70]	UDP-3-O-acylglucosamine N-acyltransferase OS=Methylobacterium extorquens (strain CM4 / NCIMB 13688) OX=440085 GN=lpd PE=3 SV=1
A7926	-	-	-	-	-	KOG0864 Hs7662062.2 Ran-binding protein RANBP1 and related RanBD domain proteins	-	-
A7927	GO:0006629(lipid metabolic process)	-	GO:0008374(O-acyltransferase activity)	K00679 E2.3.1.158; phospholipid:diacylglycerol acyltransferase [EC:2.3.1.158]	map00561 Glycerolipid metabolism;map01100 Metabolic pathways	-	KXS21833.1 hypothetical protein M427DRAFT_151099 [Gonapodya prolifera JEL478]	Phospholipid:diacylglycerol acyltransferase 1 OS=Arabidopsis thaliana OX=3702 GN=PDAT1 PE=2 SV=1
A7928	-	-	GO:0003824(catalytic activity)	-	-	KOG1075 CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A7929	GO:0006506(GPI anchor biosynthetic process)	-	-	-	-	-	-	-
A7930	-	-	-	-	-	-	-	-
A7931	GO:0007165(signal transduction),GO:0016072(rRNA metabolic process),GO:0034470(ncRNA processing)	-	GO:0016407(acyltransferase activity),GO:0005524(ATP binding),GO:0008080(N-acyltransferase activity)	K14521 NAT10, KRE33; N-acyltransferase 10 [EC:2.3.1.-]	map03008 Ribosome biogenesis in eukaryotes	KOG2036 Hs13399322 Predicted P-loop ATPase fused to an acetyltransferase	ORX99520.1 DUF699-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	RNA cytidine acetyltransferase OS=Mus musculus OX=10090 GN=Nat10 PE=1 SV=1

A7932	GO:0006535(cysteine biosynthetic process from serine),GO:0006520(cellular amino acid metabolic process)	-	GO:0030170(pyridoxal phosphate binding)	K01738 cysK; cysteine synthase [EC:2.5.1.47]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00920 Sulfur metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	-	KNE66204.1 hypothetical protein AMAG_10445 [Allomyces macrogynus ATCC 38327]	Cysteine synthase 1 OS=Emmericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=cysB PE=3 SV=2
A7933	-	-	GO:0004420(hydroxymethylglutaryl-CoA reductase (NADPH) activity),GO:0001666(nucleotide binding)	K18106 GAAA; D-galacturonate reductase [EC:1.1.1.-]	map00040 Pentose and glucuronate interconversions;map01100 Metabolic pathways	-	XP_006680823.1 uncharacterized protein BATDEDRAFT_37276 [Batrachochytrium dendrobatidis JAM81]	Uncharacterized oxidoreductase YdgJ OS=Escherichia coli (strain K12) OX=83333 GN=ydgJ PE=1 SV=2
A7934	-	-	-	-	-	-	-	-
A7935	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0004017(adenylate kinase activity),GO:0004127(cytidylate kinase activity),GO:0005524(ATP binding),GO:0019205(nucleobase-containing compound kinase activity)	-	-	KOG3078 Hs18582975 Adenylate kinase	XP_016608458.1 hypothetical protein SPPG_04741 [Spizellomyces punctatus DAOM BR117]	Adenylate kinase 7 OS=Homo sapiens OX=9606 GN=AK7 PE=1 SV=3
A7936	GO:0060271(cilium assembly),GO:0060294(cilium movement involved in cell motility)	GO:0001534(radial spoke)	-	-	-	-	KNE54499.1 hypothetical protein AMAG_00471 [Allomyces macrogynus ATCC 38327]	Radial spoke head protein 4 homolog A OS=Homo sapiens OX=9606 GN=RSPH4A PE=1 SV=1
A7937	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity)	-	-	KOG0384 Hs2047966 Chromodomain-helicase DNA-binding protein	ORZ34456.1 SNF2 family N-terminal domain-domain-containing protein, partial [Catenaria anguillulae PL171]	Chromodomain-helicase-DNA-binding protein 8 OS=Homo sapiens OX=9606 GN=CHD8 PE=1 SV=5
A7938	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	-	-	-	-	Tryptase beta-2 OS=Rattus norvegicus OX=10116 GN=Tpsb2 PE=2 SV=1
A7939	GO:0007031(peroxisome organization),GO:0006625(protein targeting to peroxisome)	GO:0005777(peroxisome),GO:0005778(peroxisomal membrane)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K13338 PEX1; peroxin-1	map04146 Peroxisome	KOG0735 At5g08470 AAA+-type ATPase	KAF0467795.1 AAA-domain-containing protein [Gigaspora margarita]	Peroxisomal ATPase PEX1 OS=Arthrobotrys oligospora (strain ATCC 24927 / CBS 115.81 / DSM 1491) OX=756982 GN=PEX1 PE=3 SV=1

A7940	GO:0006412(translation)	GO:0005840(ribosome),GO:0015934(large ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02872 RP-L13Ae, RPL13A; large subunit ribosomal protein L13Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	-	KAG0787079.1 hypothetical protein G6F21_008152 [Rhizopus oryzae]	Large ribosomal subunit protein uL13 OS=Cyanophora paradoxa OX=2762 PE=2 SV=1
A7941	-	-	-	-	-	-	-	-
A7942	-	-	GO:0005515(protein binding)	K03353 APC6, CDC16; anaphase-promoting complex subunit 6	map04914 Progesterone-mediated oocyte maturation;map04120 Ubiquitin mediated proteolysis;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG1173 At1g78770 Anaphase-promoting complex (APC), Cdc16 subunit	KUI71237.1 Anaphase-promoting complex subunit cut9 [Valsa mali]	Anaphase-promoting complex subunit 6 OS=Arabidopsis thaliana OX=3702 GN=APC6 PE=2 SV=1
A7943	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7944	-	-	-	-	-	-	-	Dynein axonemal heavy chain 1 OS=Mus musculus OX=10090
A7945	-	-	GO:0000062(fatty-acyl-CoA binding)	K08762 DBI, ACBP; diazepam-binding inhibitor (GABA receptor modulator, acyl-CoA-binding protein)	map03320 PPAR signaling pathway	KOG0817 7295521_2 Acyl-CoA-binding protein	KAF9938022.1 hypothetical protein BGZ65_000639 [Modicella reniformis]	Diazepam-binding inhibitor-like 5 OS=Bos taurus OX=9913 GN=DBIL5 PE=2 SV=1
A7946	GO:0008654(phospholipid biosynthetic process)	-	GO:0004609(phosphatidylserine decarboxylase activity)	K01613 psd, PSD; phosphatidylserine decarboxylase [EC:4.1.1.65]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG2420 7301094 Phosphatidylserine decarboxylase	ORY33260.1 phosphatidylserine decarboxylase, partial [Rhizoclosmatium globosum]	Phosphatidylserine decarboxylase proenzyme 1, mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=PSD1 PE=2 SV=1
A7947	-	-	-	-	-	-	-	-
A7948	-	-	GO:0016316(phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity)	-	-	KOG4428 Hs4755140 Inositol-polyphosphate 4-phosphatase	ORZ37676.1 hypothetical protein BCR44DRAFT_1429719 [Catenaria anguillulae PL171]	Inositol polyphosphate-4-phosphatase type I A OS=Rattus norvegicus OX=10116 GN=Inpp4a PE=1 SV=1
A7949	-	-	-	-	-	KOG1205 7301818 Predicted dehydrogenase	KXN71055.1 serine 3-dehydrogenase [Conidiobolus coronatus NRRL 28638]	Putative oxidoreductase SadH OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) OX=83331 GN=sadH PE=3 SV=1
A7950	-	-	-	-	-	-	-	-
A7951	-	-	-	-	-	-	-	-
A7952	-	-	-	-	-	-	-	-
A7953	-	-	-	-	-	-	-	-

A7954	GO:0043248(proteasome assembly)	-	-	-	-	-	RUP50483.1 proteasome maturation factor UMP1 [Jimgerdmania flammicorona]	Proteasome maturation protein homolog OS=Dictyostelium discoideum OX=44689 GN=pomp PE=3 SV=1
A7955	-	-	-	-	-	-	RIA87178.1 hypothetical protein C1645_72670.2 [Glomus cerebriforme]	Cyclic di-GMP phosphodiesterase PA2567 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA2567 PE=1 SV=1
A7956	GO:0000160(phosphorelay signal transduction system)	-	-	K19692 TCSA; osmolarity two-component system, sensor histidine kinase TcsA [EC:2.7.13.3]	map02020 Two-component system	-	TPX59583.1 hypothetical protein CcCBS67573_g09077 [Chytridiomycetes confervae]	Sensor histidine kinase RcsC OS=Escherichia coli (strain K12) OX=83333 GN=rcsC PE=1 SV=1
A7957	-	-	-	-	-	-	-	-
A7958	GO:0106035(protein maturation by [4Fe-4S] cluster transfer)	-	-	K26403 CIAO2, CIA2, FAM96; cytosolic iron-sulfur assembly component 2	-	KOG3381[Hs7706343 Uncharacterized conserved protein	OBZ83527.1 Mitotic spindle-associated MMXD complex subunit MIP18 [Choanephora cucurbitarum]	Cytosolic iron-sulfur assembly component 2B OS=Mus musculus OX=10090 GN=Ciao2b PE=1 SV=1
A7959	-	-	-	-	-	-	-	-
A7960	GO:0000493(box H/ACA snoRNP assembly)	-	-	K14764 SHQ1; protein SHQ1	-	-	GBB85679.1 hypothetical protein RclHR1_12160004 [Rhizophagus clarus]	Protein SHQ1 homolog OS=Xenopus tropicalis OX=8364 GN=shq1 PE=2 SV=1
A7961	-	-	-	-	-	-	-	-
A7962	-	-	-	-	-	-	OON08526.1 hypothetical protein BSLG_02230 [Batrachochytrium salamandrivorans]	Flagellar radial spoke protein 3 OS=Chlamydomonas reinhardtii OX=3055 GN=RSP3 PE=1 SV=1
A7963	-	-	-	K15015 SLC32A, VGAT; solute carrier family 32 (vesicular inhibitory amino acid transporter)	map04727 GABAergic synapse;map04721 Synaptic vesicle cycle;map04723 Retrograde endocannabinoid signaling;map05033 Nicotine addiction;map05032 Morphine addiction	KOG1303[At3g54830 Amino acid transporters	OBZ88152.1 Vacuolar amino acid transporter 1 [Choanephora cucurbitarum]	Amino acid transporter AVT1B OS=Arabidopsis thaliana OX=3702 GN=AVT1B PE=3 SV=2

A7964	GO:0006468 (protein phosphorylation)	-	GO:0004672 (protein kinase activity), GO:0005524 (ATP binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0606 Hs14249562 Microtubule-associated serine/threonine kinase and related proteins	PVF94739.1 kinase-like protein [Serendipita vermifera subsp. bescii]	Serine/threonine-protein kinase greatwall OS=Danio rerio OX=7955 GN=mastl PE=2 SV=1
A7965	-	GO:0016459 (myosin complex)	GO:0005515 (protein binding), GO:0003774 (motor activity), GO:0005524 (ATP binding)	K10356 MYO1; myosin I	map05130 Pathogenic Escherichia coli infection; map04814 Motor proteins	KOG0160 At5g43900 Myosin class V heavy chain	KAF8552197.1 glycosyltransferase family 2 protein [Xerocomus badius]	Unconventional myosin-VIIb OS=Homo sapiens OX=9606 GN=MYO7B PE=1 SV=2
A7966	-	-	GO:0005515 (protein binding)	-	-	-	-	-
A7967	-	-	-	-	-	-	ORX79061.1 MGC84796 protein-like protein [Anaeromyxos robustus]	ADP-ribosylation factor-like protein 2-binding protein OS=Gallus gallus OX=9031 GN=ARL2BP PE=2 SV=1
A7968	-	-	GO:0016491 (oxidoreductase activity)	-	-	KOG1800 Hs13435350 Ferredoxin/adenodoxin reductase	RCH84547.1 hypothetical protein CU097_006870 [Rhizopus azygosporus]	NADPH:adenodoxin oxidoreductase, mitochondrial OS=Salvelinus fontinalis OX=8038 GN=fdxr PE=2 SV=1
A7969	-	-	-	-	-	-	-	-
A7970	-	-	-	-	-	KOG1878 Hs5454138 Nuclear receptor coregulator SMRT/SMRTER, contains Myb-like domains	RKP20868.1 hypothetical protein ROZALSC1DRAFT_27681 [Rozella allomyces CSF55]	Nuclear receptor corepressor 1 OS=Mus musculus OX=10090 GN=Ncor1 PE=1 SV=1
A7971	-	-	GO:0016301 (kinase activity)	-	-	KOG1116 7292647 Sphingosine kinase, involved in sphingolipid metabolism	TPX65298.1 hypothetical protein SpCBS45565_g05257 [Spizellomyces sp. 'palustris']	Sphingosine kinase 1 OS=Arabidopsis thaliana OX=3702 GN=SPHK1 PE=1 SV=1
A7972	-	-	-	-	-	-	-	-
A7973	-	-	-	-	-	-	-	-
A7974	-	-	-	-	-	-	-	-
A7975	-	-	-	K15117 SLC25A34_35, OAC1; solute carrier family 25, member 34/35	-	KOG0755 7303225 Mitochondrial oxaloacetate carrier protein	RKP26709.1 mitochondria carrier domain-containing protein, partial [Syncephala pseudoplumigaleata]	Solute carrier family 25 member 35 OS=Bos taurus OX=9913 GN=SLC25A35 PE=2 SV=1
A7976	-	-	-	-	-	-	-	-
A7977	GO:0016311 (dephosphorylation)	-	GO:0016791 (phosphatase activity), GO:0004721 (phosphoprotein phosphatase activity)	-	-	-	KZL86761.1 tyrosine phosphatase [Colletotrichum incanum]	Triple specificity protein phosphatase PtpB OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=ptpB PE=1 SV=1
A7978	-	-	-	-	-	-	-	-
A7979	-	-	-	-	-	-	-	-
A7980	-	-	-	-	-	-	-	-

A7981	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity)	-	-	-	KAG0196171.1 hypothetical protein BGX28_010466 [Mortierella sp. GBA30]	-
A7982	-	-	GO:0005515(protein binding)	K11493 RCC1; regulator of chromosome condensation	-	KOG1426[Hs4758520 FOG:RCC1 domain	KAG0255362.1 hypothetical protein BGZ95_005782 [Linnemania exigua]	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens OX=9606 GN=HERC2 PE=1 SV=2
A7983	-	-	GO:0003723(RNA binding)	-	-	-	-	-
A7984	-	-	GO:0005515(protein binding)	-	-	KOG3616[Hs20535899 Selective LIM binding factor	TPX62114.1 hypothetical protein PhCBS80983_g00643 [Powellomyces hirtus]	Intraflagellar transport protein 172 homolog OS=Danio rerio OX=7955 GN=ift172 PE=2 SV=1
A7985	-	-	-	-	-	-	-	-
A7986	-	-	-	-	-	-	-	-
A7987	-	-	-	-	-	-	-	-
A7988	-	-	-	-	-	-	KAG0196171.1 hypothetical protein BGX28_010466 [Mortierella sp. GBA30]	-
A7989	-	-	-	-	-	-	-	-
A7990	-	-	GO:0005515(protein binding)	-	-	-	-	-
A7991	-	-	-	-	-	-	-	-
A7992	-	-	GO:0046982(protein heterodimerization activity)	K02326 POLE3; DNA polymerase epsilon subunit 3 [EC:2.7.7.7]	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03082 ATP-dependent chromatin remodeling	KOG0870[Hs8393120 DNA polymerase epsilon, subunit D	KAG4096148.1 histone-fold-containing protein [Neocallimastix sp. JGI-2020a]	DNA polymerase epsilon subunit 3 OS=Rattus norvegicus OX=10116 GN=Pole3 PE=1 SV=1
A7993	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015297(antipporter activity),GO:0042910(xenobiotic transmembrane transporter activity)	K03327 TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family	-	KOG1347[At1g51340 Uncharacterized membrane protein, predicted efflux pump	NP_588077.1 putative MatE family transporter [Schizosaccharomyces pombe]	Protein DETOXIFICATION 42 OS=Arabidopsis thaliana OX=3702 GN=DTX42 PE=2 SV=2
A7994	GO:0042981(regulation of apoptotic process)	-	-	-	-	-	-	-

A7995	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity);GO:0005524(ATP binding);GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG4280[Hs4758646 Kinesin-like protein	KXS10018.1 kinesin-domain-containing protein, partial [Gonapodya prolifera JEL478]	Kinesin-like protein KIF3B OS=Mus musculus OX=10090 GN=Kif3b PE=1 SV=1
A7996	-	-	GO:0010181(FMN binding);GO:0016491(oxidoreductase activity)	-	-	-	OJ165689.1 hypothetical protein ASPBRDRAFT_49584 [Aspergillus brasiliensis CBS 101740]	4,4'-dithiodibutanoate disulfide reductase OS=Rhodococcus erythropolis OX=1833 GN=nox PE=1 SV=1
A7997	-	-	-	-	-	-	KAF9579083.1 hypothetical protein BGW38_004815 [Lunasporengiospora selenospora]	Transmembrane protein 18 OS=Danio rerio OX=7955 GN=tmem18 PE=2 SV=1
A7998	-	-	GO:0005515(protein binding)	K17908 WIP1_2, ATG18; autophagy-related protein 18	map05014 Amyotrophic lateral sclerosis;map04140 Autophagy - animal;map05131 Shigellosis;map04138 Autophagy - yeast;map04136 Autophagy - other;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	-	XP_016609913.1 hypothetical protein SPPG_03663 [Spizellomyces punctatus DAOM BR117]	Autophagy-related protein 18 OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=ATG18 PE=3 SV=1
A7999	-	-	-	-	-	-	-	-
A8000	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity);GO:0005524(ATP binding);GO:0008017(microtubule binding)	-	-	-	OUM65952.1 hypothetical protein PIROE2DRAFT_41204 [Piromyces sp. E2]	Kinesin-like protein 6 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=klp6 PE=1 SV=1
A8001	-	-	-	-	-	-	-	-
A8002	-	-	-	-	-	-	-	-
A8003	-	-	-	-	-	-	-	-
A8004	-	-	-	-	-	-	-	-

A8005	GO:0006457(protein folding)	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0051082(unfolded protein binding)	K09493 CCT1, TCP1; T-complex protein 1 subunit alpha	-	KOG0360 At3g20050 Chaperonin complex component, TCP-1 alpha subunit (CCT1)	ORZ30578.1 T-complex protein 1 subunit alpha [Catenaria anguillulae PL171]	T-complex protein 1 subunit alpha OS=Arabidopsis thaliana OX=3702 GN=CCT1 PE=1 SV=1
A8006	-	-	GO:0008484(sulfuric ester hydrolase activity)	K01133 betC; choline-sulfatase [EC:3.1.6.6]	-	KOG3731 7292365 Sulfatases	GES59190.1 hypothetical protein ATETN484_0003041500 [Aspergillus terreus]	Iduronate 2-sulfatase OS=Mus musculus OX=10090 GN=Ids PE=2 SV=3
A8007	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	K13126 PABPC; polyadenylate-binding protein	map03018 RNA degradation;map03015 mRNA surveillance pathway	KOG0123 Hs4504715 Polyadenylate-binding protein (RRM superfamily)	OZJ03571.1 hypothetical protein BZG36_03098 [Bifiguratus adalaidae]	Polyadenylate-binding protein 1 OS=Mus musculus OX=10090 GN=Pabpc1 PE=1 SV=2
A8008	-	GO:0031428(box C/D RNP complex), GO:0032040(small-subunit processome)	GO:0030515(snRNA binding)	K14565 NOP58; nucleolar protein 58	map03008 Ribosome biogenesis in eukaryotes	KOG2572 Hs7706254 Ribosome biogenesis protein - Nop58p/Nop5p	KAG4091170.1 Nop domain-containing protein [Neocallimastix sp. JGI-2020a]	Nucleolar protein 58 OS=Mus musculus OX=10090 GN=Nop58 PE=1 SV=1
A8009	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02892 RP-L23, MRPL23, rplW; large subunit ribosomal protein L23	map03010 Ribosome	KOG4089 At4g39880 Predicted mitochondrial ribosomal protein L23	OZJ03721.1 hypothetical protein BZG36_04154 [Bifiguratus adalaidae]	Large ribosomal subunit protein uL23 OS=Alkaliphilus oremlandii (strain OhlAs) OX=350688 GN=rplW PE=3 SV=1
A8010	-	-	GO:0005515(protein binding)	-	-	KOG2386 Hs4506563 mRNA capping enzyme, guanylyltransferase (alpha) subunit	KAF2996188.1 hypothetical protein E8E13_000438 [Curvularia kusanoi]	mRNA-capping enzyme OS=Danio rerio OX=7955 GN=rngtt PE=2 SV=1
A8011	-	-	-	-	-	-	-	-
A8012	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2157 7297165 Predicted tubulin-tyrosine ligase	TPX59531.1 hypothetical protein PhCBS80983_g02429 [Powellomyces hirtus]	Protein polyglycolase TTL10 OS=Macaca fascicularis OX=9541 GN=TTL10 PE=2 SV=1
A8013	-	-	-	-	-	-	-	-
A8014	-	-	-	-	-	-	-	-
A8015	GO:0030163(protein catabolic process)	-	GO:0008914(leucyltransferase activity)	-	-	-	KAG1255543.1 hypothetical protein G6F68_010287 [Rhizopus microsporus]	Leucyl/phenylalanyl-tRNA--protein transferase OS=Pseudomonas syringae pv. syringae (strain B728a) OX=205918 GN=aat PE=3 SV=1
A8016	GO:0036211(protein modification process)	-	GO:0042802(identical protein binding),GO:0005515(protein binding)	-	-	KOG2156 Hs7661970 Tubulin-tyrosine ligase-related protein	XP_016612321.1 hypothetical protein SPPG_00019 [Spizellomyces punctatus DAOM BR117]	Tubulin polyglutamylase TTL6 OS=Mus musculus OX=10090 GN=Ttl6 PE=1 SV=1

A8017	GO:0006355(regulation of transcription, DNA-templated),GO:0032786(positive regulation of DNA-templated transcription, elongation)	GO:0005634(nucleus)	GO:0008270(zinc ion binding)	K15171 SUPT4H1, SPT4; transcription elongation factor SPT4	map03250 Viral life cycle - HIV-1	KOG3490 Hs4507311 Transcription elongation factor SPT4	OTB18941.1 hypothetical protein K445DRAFT_54570 [Daldinia sp. EC12]	Transcription elongation factor SPT4-A OS=Mus musculus OX=10090 GN=Supt4h1a PE=2 SV=1
A8018	-	-	-	-	-	KOG1269 CE12576 SAM-dependent methyltransferases	XP_031026613.1 uncharacterized protein SmJEL517_g01628 [Synchytrium microbalum]	S-adenosylmethionine-dependent methyltransferase Rv2258c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2258c PE=1 SV=1
A8019	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4557659 Sulfatase	PQE28381.1 choline-sulfatase protein [Rutstroemia sp. NJR-2017a BBW]	Iduronate 2-sulfatase OS=Mus musculus OX=10090 GN=Ids PE=2 SV=3
A8020	-	-	GO:0005509(calcium ion binding),GO:0005515(protein binding),GO:0005246(calcium channel regulator activity)	-	-	-	-	-
A8021	GO:0007018(microtubule-based movement),GO:1901673(regulation of mitotic spindle assembly)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10392 KIF1; kinesin family member 1	map04814 Motor proteins	KOG4280 Hs910266_1 Kinesin-like protein	KAG0229051.1 Kinesin-like protein kif15 [Actinomortella wolfii]	Kinesin-like protein KIF15 OS=Strongylocentrotus purpuratus OX=7668 GN=KIF15 PE=1 SV=1
A8022	GO:0006777(Molybdopterin cofactor biosynthetic process)	-	-	K15376 GPHN; gephyrin [EC:2.10.1.1 2.7.7.75]	map01240 Biosynthesis of cofactors;map04727 GABAergic synapse;map01100 Metabolic pathways;map00790 Folate biosynthesis	KOG2371 CE29358 Molybdopterin biosynthesis protein	KAG1716290.1 hypothetical protein ID866.852 [Astraeus odoratus]	Molybdopterin adenyllyltransferase OS=Escherichia coli O157:H7 OX=83334 GN=mog PE=3 SV=1
A8023	GO:0046855(inositol phosphate dephosphorylation)	-	-	-	-	KOG3099 Hs5174399 Bisphosphate 3'-nucleotidase BPNT1/Inositol polyphosphate 1-phosphatase	XP_016611889.1 hypothetical protein SPPG_01305 [Spizellomyces punctatus DAOM BR117]	3'(2'),5'-bisphosphate nucleotidase 1 OS=Dictyostelium discoideum OX=44689 GN=bpnt1 PE=3 SV=1
A8024	-	-	-	-	-	-	-	-
A8025	-	-	-	-	-	-	-	-
A8026	GO:0006629(lipid metabolic process)	-	-	-	-	-	-	-
A8027	-	-	GO:0005515(protein binding)	-	-	-	-	-

A8028	-	-	GO:0004488(methylenetetrahydrofolate dehydrogenase (NADP+) activity)	K00288 MTHFD; methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase [EC:1.5.1.5 3.5.4.9 6.3.4.3]	map00670 One carbon pool by folate;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG0089 At3g12290 Methylenetetrahydrofolate dehydrogenase/methylene tetrahydrofolate cyclohydrolase	KAG0186086.1 hypothetical protein DFQ28_008337 [Apophysomyces sp. BC1034]	Bifunctional protein Fold 2 OS=Mesorhizobium japonicum (strain LMG 29417 / CECT 9101 / MAFF 303099) OX=266835 GN=fold2 PE=3 SV=1
A8029	GO:0006413(translational initiation), GO:0001731(formation of translation preinitiation complex)	-	GO:0003743(translation initiation factor activity)	K15027 EIF2D; translation initiation factor 2D	-	KOG2522 At1g71350 Filamentous baseplate protein Ligatin, contains PUA domain	TPX61445.1 hypothetical protein PhCBS80983g01088 [Powellomyces hirtus]	Eukaryotic translation initiation factor 2D OS=Bos taurus OX=9913 GN=EIF2D PE=2 SV=1
A8030	-	-	-	-	-	KOG0266 At1g04140 WD40 repeat-containing protein	-	-
A8031	GO:0006419(alanyl-tRNA aminoacylation),GO:0043039(tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0000166(nucleotide binding),GO:0004813(alanine-tRNA ligase activity),GO:0005524(ATP binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0003676(nucleic acid binding)	K01872 AARS, alaS; alanyl-tRNA synthetase [EC:6.1.1.7]	map00970 Aminoacyl-tRNA biosynthesis	KOG0188 At1g50200 Alanyl-tRNA synthetase	XP_016607026.1 alanine-tRNA ligase [Spizellomyces punctatus DAOM BR117]	Alanine--tRNA ligase OS=Arabidopsis thaliana OX=3702 GN=ALATS PE=1 SV=3
A8032	-	-	-	-	-	KOG1611 7290912 Predicted short chain-type dehydrogenase	KDN71869.1 putative short chain dehydrogenase [Colletotrichum sublineola]	C-signal OS=Myxococcus xanthus OX=34 GN=csgA PE=1 SV=1
A8033	-	-	-	-	-	KOG2895 At5g35460 Uncharacterized conserved protein	ORX96182.1 hypothetical protein K493DRAFT_282158 [Basidiobolus meristiporus CBS 931.73]	Glycerophosphocholine acyltransferase 1 OS=Brassica napus OX=3708 GN=GPC1 PE=1 SV=1
A8034	GO:0007034(vacuolar transport)	-	-	K12194 CHMP4A_B, SNF7, VPS32A_B; charged multivesicular body protein 4A/B	map04144 Endocytosis;map03250 Viral life cycle - HIV-1;map04217 Necroptosis	KOG1656 At2g19830 Protein involved in glucose derepression and pre-vacuolar endosome protein sorting	KAF9165521.1 ESCRT-III subunit protein snf7 [Actinomyces rella ambigua]	Vacuolar protein sorting-associated protein 32 homolog 1 OS=Arabidopsis thaliana OX=3702 GN=VPS32.1 PE=1 SV=1

A8035	-	-	GO:0005515(protein binding)	-	-	KOG4070 Hs20542220 Putative signal transduction protein p25	XP_016604112.1 hypothetical protein SPPG_08463 [Spizellomyces punctatus DAOM BR117]	Tubulin polymerization-promoting protein family member 2 OS=Homo sapiens OX=9606 GN=TPPP2 PE=1 SV=2
A8036	-	-	GO:0008168(methyltransferase activity)	K06127 COQ5; 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase [EC:2.1.1.201]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map00130 Ubiquinone and other terpenoid-quinone biosynthesis;map01100 Metabolic pathways	KOG1540 At5g57300 Ubiquinone biosynthesis methyltransferase COQ5	ORY05444.1 ubiquinone/menaquinone [Basidiobolus meristosporus CBS 931.73]	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE OS=Bartonella tribocorum (strain CIP 105476 / IBS 506) OX=382640 GN=ubiE PE=3 SV=1
A8037	-	-	GO:0003824(catalytic activity)	-	-	-	-	-
A8038	GO:0009166(nucleotide catabolic process)	-	GO:0016787(hydrolase activity)	-	-	KOG4419 Hs4505467 5' nucleotidase	XP_033518254.1 5'-nucleotidase precursor [Dothidotthia symphoricarpi CBS 119687]	Snake venom 5'-nucleotidase OS=Gloydus brevicaudus OX=259325 PE=2 SV=1
A8039	-	-	-	-	-	-	ORX55336.1 hypothetical protein BCR36DRAFT_347072 [Piromyces finnis]	-
A8040	-	-	GO:0005509(calcium ion binding)	-	-	KOG0027 At2g41090 Calmodulin and related proteins (EF-Hand superfamily)	RCH96684.1 hypothetical protein CU098_002856, partial [Rhizopus stolonifer]	Parvalbumin alpha OS=Cyprinus carpio OX=7962 PE=1 SV=2
A8041	GO:0006351(transcription, DNA-templated)	GO:0005634(nucleus)	GO:0003677(DNA binding);GO:0003899(DNA-directed 5'-3' RNA polymerase activity);GO:0032549(ribonucleoside binding)	K03002 RPA2, POLR1B; DNA-directed RNA polymerase I subunit RPA2 [EC:2.7.7.6]	map03020 RNA polymerase	-	KAF9975962.1 DNA-directed RNA polymerase I subunit rpa2 [Actinomyces rella ambigua]	Probable DNA-directed RNA polymerase I subunit RPA2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=rpa2 PE=1 SV=2
A8042	GO:0032958(inositol phosphate biosynthetic process)	-	GO:0016301(kinase activity)	K07756 IP6K, IHPK; inositol-hexakisphosphate 5-kinase [EC:2.7.4.21]	map04070 Phosphatidylinositol signaling system;map04138 Autophagy - yeast	KOG1620 7291313 Inositol polyphosphate multikinase, component of the ARGR transcription regulatory complex	KAF3049810.1 hypothetical protein E8E11_002280 [Didymella keratinophila]	Inositol hexakisphosphate kinase 1 OS=Homo sapiens OX=9606 GN=IP6K1 PE=1 SV=3
A8043	-	-	-	-	-	-	-	-

A8044	-	-	-	-	-	-	XP_006681370.1 uncharacterized protein BATDEDRAFT_27078 [Batrachochytrium dendrobatidis JAM81]	Centrosomal protein of 76 kDa OS=Pongo abelii OX=9601 GN=CEP76 PE=2 SV=1
A8045	-	-	GO:0005525(GTP binding)	K06943 NOG1; nucleolar GTP-binding protein	map03008 Ribosome biogenesis in eukaryotes	KOG1490[Hs14737772 GTP-binding protein CRFG/NOG1 (ODN superfamily)]	OBZ87612.1 putative nucleolar GTP-binding protein 1 [Choanephora cucurbitarum]	GTP-binding protein 4 OS=Mus musculus OX=10090 GN=Gtpbp4 PE=1 SV=3
A8046	GO:0006413(translational initiation)	-	GO:0003743(translation initiation factor activity),GO:0005515(protein binding)	K15026 EIF2A; translation initiation factor 2A	-	KOG2315[At1g73180 Predicted translation initiation factor related to eIF-3a]	TPX63014.1 hypothetical protein PhCBS80983_g00066 [Powellomyces hirtus]	Eukaryotic translation initiation factor 2A OS=Dictyostelium discoideum OX=44689 GN=eif2a PE=3 SV=1
A8047	GO:0006021(inositol biosynthetic process), GO:0008654(phospholipid biosynthetic process)	-	GO:0004512(inositol-3-phosphate synthase activity)	K01858 INO1; ISYNA1; myo-inositol-1-phosphate synthase [EC:5.5.1.4]	map01110 Biosynthesis of secondary metabolites;map00562 Inositol phosphate metabolism;map00521 Streptomycin biosynthesis;map01100 Metabolic pathways	KOG0693[At2g22240 Myo-inositol-1-phosphate synthase]	RKP09819.1 hypothetical protein THASP1DRAFT_13758 [Thamnocephalus sphaerosporus]	Inositol-3-phosphate synthase OS=Dictyostelium discoideum OX=44689 GN=ino1 PE=3 SV=1
A8048	GO:0006568(tryptophan metabolic process), GO:0000162(tryptophan biosynthetic process)	-	GO:0004834(tryptophan synthase activity)	K01694 TRP; tryptophan synthase [EC:4.2.1.20]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map01100 Metabolic pathways	KOG1395[YL026c_2 Tryptophan synthase beta chain]	KAF9363710.1 tryptophan synthetase [Mortierella sp. NVP85]	Tryptophan synthase beta chain 1 OS=Aquifex aeolicus (strain VF5) OX=224324 GN=trpB1 PE=3 SV=1
A8049	-	-	-	-	-	-	-	cGMP-dependent 3',5'-cGMP phosphodiesterase A OS=Dictyostelium discoideum OX=44689 GN=pdeD PE=1 SV=1
A8050	-	-	-	-	-	-	-	-
A8051	-	-	-	-	-	-	-	-
A8052	GO:0006813(potassium ion transport)	GO:0016021(integral component of membrane)	GO:0005242(inward rectifier potassium channel activity)	-	-	KOG3827[Hs10337591 Inward rectifier K+ channel]	-	ATP-sensitive inward rectifier potassium channel 12 OS=Rattus norvegicus OX=10116 GN=Kcnj12 PE=1 SV=1

A8053	-	-	GO:0005085(guanyl-nucleotide exchange factor activity),GO:0005515(protein binding)	K11236 CDC24; cell division control protein 24	map04011 MAPK signaling pathway - yeast	KOG4424 7295262 Predicted Rho/Rac guanine nucleotide exchange factor/faciotenital dysplasia protein 3	OA145309.1 hypothetical protein BDEG_28459 [Batrachochytrium dendrobatidis JEL423]	Pleckstrin homology domain-containing family G member 2 OS=Mus musculus OX=10090 GN=Plekhhg2 PE=2 SV=2
A8054	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07901 RAB8A, MEL; Ras-related protein Rab-8A	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map04140 Autophagy - animal;map04972 Pancreatic secretion;map04530 Tight junction;map05022 Pathways of neurodegeneration - multiple diseases;map04152 AMPK signaling pathway	KOG0078 At5g03520 GTP-binding protein SEC4, small G protein superfamily, and related Ras family GTP-binding proteins	OQO26517.1 GTP-binding protein ypt2, partial [Rachicladospirium sp. CCREE 5018]	Ras-related protein RAB1d OS=Arabidopsis thaliana OX=3702 GN=RAB1D PE=1 SV=1
A8055	-	-	-	-	-	-	-	-
A8056	-	-	-	K19219 JMD7; peptidyl-lysine (3S)-dioxygenase / protease [EC:1.14.11.6 3 3.4.-.-]	-	KOG2131 Hs22068464 Uncharacterized conserved protein, contains JmjC domain	GAT59428.1 clavamine synthase-like protein [Mycena chlorophos]	JmjC domain-containing protein C OS=Dictyostelium discoideum OX=44689 GN=jcdC PE=4 SV=2
A8057	-	-	-	-	-	-	-	-
A8058	-	-	-	-	-	-	-	-
A8059	-	-	GO:0005509(calcium ion binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027 CE27325 Calmodulin and related proteins (EF-Hand superfamily)	KAG1469155.1 hypothetical protein G6F56_003422 [Rhizopus delemar]	Calmodulin OS=Macrocystis pyrifera OX=35122 PE=2 SV=3
A8060	-	-	GO:0030246(carbohydrate binding)	-	-	-	CDS03574.1 hypothetical protein LRAMOSA00976 [Lichtheimia ramosa]	Probable inactive L-type lectin-domain containing receptor kinase III.1 OS=Arabidopsis thaliana OX=3702 GN=LECRK31 PE=3 SV=1

A8061	GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0005839(proteasome core complex)	GO:0004298(threonine-type endopeptidase activity)	K02739 PSMB7; 20S proteasome subunit beta 2 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease	KOG0173 At5g40580 20S proteasome, regulatory subunit beta type PSMB7/PSMB10/PUP1	KAG2209641.1 hypothetical protein INT46_007333 [Mucor plumbeus]	Proteasome subunit beta type-7-B OS=Arabidopsis thaliana OX=3702 GN=PBB2 PE=1 SV=2
A8062	GO:0006400(tRNA modification),GO:0101030(tRNA-guanine transglycosylation)	-	GO:0016763(pentosyltransferase activity),GO:0008479(queueine tRNA-ribosyltransferase activity)	K00777 QTRT1; queueine tRNA-ribosyltransferase catalytic subunit [EC:2.4.2.64]	-	KOG3908 7296102 Queueine-tRNA ribosyltransferase	GU82555.1 hypothetical protein Asppvi_001064 [Aspergillus pseudoviridutans]	Queueine tRNA-ribosyltransferase catalytic subunit 1 OS=Danio rerio OX=7955 GN=qtrt1 PE=2 SV=1
A8063	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity),GO:0005515(protein binding)	K09568 FKBP1; FK506-binding protein 1 [EC:5.2.1.8]	-	KOG0543 7297564 FKBP-type peptidyl-prolyl cis-trans isomerase	KAF9104732.1 cytochrome P450 monooxygenase 9 [Mortierella sp. AM989]	FK506-binding protein 59 OS=Drosophila melanogaster OX=7227 GN=Fkbp59 PE=1 SV=1
A8064	GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0046872(metal ion binding),GO:0019829(ATPase-coupled cation transmembrane transporter activity),GO:0001666(nucleotide binding),GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K17686 copA ctpA, ATP7; P-type Cu+ transporter [EC:7.2.2.8]	map01524 Platinum drug resistance;map04978 Mineral absorption;map04016 MAPK signaling pathway - plant	KOG0207 At5g44790 Cation transport ATPase	CAE7138344.1 unnamed protein product [Rhizoctonia solani]	Copper-transporting ATPase RAN1 OS=Arabidopsis thaliana OX=3702 GN=RAN1 PE=1 SV=1
A8065	GO:0034755(iron ion transmembrane transport)	GO:0016020(membrane),GO:0033573(high-affinity iron permease complex)	GO:0005381(iron ion transmembrane transporter activity)	K07243 FTR, FTH1, efeU; high-affinity iron transporter	-	-	RIA89852.1 ferric iron permease FTR1-like protein [Glomus cerebriforme]	High affinity iron permease 1 OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) OX=246409 GN=ftr1 PE=1 SV=1
A8066	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0058 CE07240 Peptide exporter, ABC superfamily	XP_024662502.1 ATP-dependent permease MDL1, mitochondria [Wickerhamia sorbophila]	ATP-binding cassette sub-family B member 10, mitochondrial OS=Mus musculus OX=10090 GN=Abcb10 PE=1 SV=1

A8067	GO:0015031(protein transport)	GO:0005743(mitochondrial inner membrane),GO:0005744(TIM23 mitochondrial import inner membrane translocase complex)	-	K17496 TIM50; mitochondrial import inner membrane translocase subunit TIM50	-	KOG2832 At1g55900 TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	KAG0280801.1 mitochondria inner membrane protein required for protein import [Linnemannia exigua]	Mitochondrial import inner membrane translocase subunit tim50 OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=tim50 PE=3 SV=1
A8068	-	-	-	-	-	-	-	-
A8069	-	-	-	-	-	-	-	-
A8070	-	-	-	-	-	-	-	-
A8071	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding)	K00472 P4HA; prolyl 4-hydroxylase [EC:1.14.11.2]	map00330 Arginine and proline metabolism;map01100 Metabolic pathways	KOG1591 At1g20270 Prolyl 4-hydroxylase alpha subunit	KAF2740756.1 hypothetical protein EJ04DRAFT_507772 [Polyposphaeria fusca]	Probable prolyl 4-hydroxylase 3 OS=Arabidopsis thaliana OX=3702 GN=P4H3 PE=2 SV=1
A8072	-	-	GO:0051287(NAD binding),GO:0008863(formate dehydrogenase (NAD+) activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)	-	-	KOG0069 At5g14780 Glyoxylate/hydroxypyruvate reductase (D-isomer-specific 2-hydroxy acid dehydrogenase superfamily)	KAG0163267.1 hypothetical protein DFQ30_000420 [Apophysomyces sp. BC1015]	Formate dehydrogenase OS=Pseudomonas sp. (strain 101) OX=33067 PE=1 SV=3
A8073	-	-	-	-	-	-	-	-
A8074	-	-	-	K00559 SMT1, ERG6; sterol 24-C-methyltransferase [EC:2.1.1.41]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	-	PSR85774.1 sterol 24-C-methyltransferase [Coniella lustricola]	Uncharacterized protein HI_0095 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_0095 PE=4 SV=1
A8075	-	-	-	-	-	-	-	-
A8076	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08850 AURKX; aurora kinase, other [EC:2.7.11.1]	-	KOG4236 Hs19923468 Serine/threonine protein kinase PKC mu/PKD and related proteins	TPX76225.1 hypothetical protein CcCBS67573_g02503 [Chytridiomycetes confervae]	Intraflagellar transport protein 57 homolog OS=Xenopus laevis OX=8355 GN=ift57 PE=2 SV=2

A8077	-	-	GO:0005524(ATP binding)	K09489 HSPA4; heat shock 70kDa protein 4	map05417 Lipid and atherosclerosis; map04612 Antigen processing and presentation;map04530 Tight junction	KOG0103 At1g79930 Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily	XP_013242845.1 putative heat shock protein Hsp88 [Tilletiaria anomala UBC951]	Heat shock 70 kDa protein 14 OS=Arabidopsis thaliana OX=3702 GN=HSP70-14 PE=1 SV=1
A8078	-	-	-	-	-	KOG1305 At3g30390 Amino acid transporter protein	KAG1461218.1 hypothetical protein G6F55_003689 [Rhizopus delemar]	Amino acid transporter AVT6A OS=Arabidopsis thaliana OX=3702 GN=AVT6A PE=2 SV=1
A8079	-	-	-	-	-	-	-	-
A8080	-	-	-	-	-	-	-	-
A8081	-	-	-	-	-	-	-	-
A8082	-	-	-	-	-	-	-	-
A8083	GO:0000387(spliceosomal snRNP assembly),GO:0006396(RNA processing)	-	-	K11087 SNRPD1, SMD1; small nuclear ribonucleoprotein D1	map03040 Spliceosome;map05322 Systemic lupus erythematosus	KOG3428 At3g07590 Small nuclear ribonucleoprotein SMD1 and related snRNPs	RIB11883.1 hypothetical protein C2G38_68757 [Gigaspora rosea]	Small nuclear ribonucleoprotein SmD1a OS=Arabidopsis thaliana OX=3702 GN=SMD1A PE=3 SV=1
A8084	-	-	-	K25162 GUP1_2; membrane-bound O-acyltransferase GUP1_2	-	-	ORY45174.1 acetyl-CoA synthetase-like protein [Rhizoclostium globosum]	Long-chain-fatty-acid--AMP ligase FadD32 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=fadD32 PE=1 SV=1
A8085	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0578 Hs4505599 p21-activated serine/threonine protein kinase	ORX90623.1 Pkinase-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Serine/threonine-protein kinase paka OS=Dictyostelium discoideum OX=44689 GN=paka PE=1 SV=1
A8086	GO:0046855(inositol phosphate dephosphorylation),GO:0046854(phosphatidylinositol phosphate biosynthetic process)	-	-	-	-	KOG3099 CE05079 Bisphosphate 3'-nucleotidase BPNT1/Inositol polyphosphate 1-phosphatase	KAG1462938.1 hypothetical protein G6F57_013844 [Rhizopus oryzae]	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1
A8088	GO:0006013(mannose metabolic process),GO:0005975(carbohydrate metabolic process)	-	GO:0004559(alpha-mannosidase activity),GO:0003824(catalytic activity),GO:0030246(carbohydrate binding)	K01191 MAN2C1; alpha-mannosidase [EC:3.2.1.24]	map00511 Other glycan degradation	KOG1959 At3g26720 Glycosyl hydrolase, family 38 - alpha-mannosidase	ORX67622.1 hypothetical protein DL89DRAFT_47974 [Linderina pennisporea]	Lysosomal alpha-mannosidase OS=Bos taurus OX=9913 GN=MAN2B1 PE=1 SV=4
A8089	-	-	-	-	-	-	-	Surfeit locus protein 2 OS=Takifugu rubripes OX=31033 GN=surf2 PE=3
A8090	-	GO:0016021(integral component of membrane)	-	-	-	KOG1623 At2g39060 Multitransmembrane protein	TPX39259.1 hypothetical protein SeLEV6574_g07350 [Synchytrium endobioticum]	Bidirectional sugar transporter SWEET15 OS=Oryza sativa subsp. indica OX=39946 GN=SWEET15 PE=3 SV=1

A8091	GO:0006508(proteolysis)	-	GO:0004198(cal cium-dependent cysteine-type endopeptidase activity)	-	-	-	-	-
A8092	GO:0016192(vesicle-mediated transport)	GO:0005794(Golgi apparatus)	GO:0031267(sm all GTPase binding)	K22940 YIPF1.2; protein YIPF1/2	-	KOG3114 At5g27490 Uncharacterized conserved protein	GBC15030.1 rab GTPase binding [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Protein YIPF1 OS=Mus musculus OX=10090 GN=Yipf1 PE=2 SV=1
A8093	-	-	-	K15100 SLC25A1, CTP; solute carrier family 25 (mitochondrial citrate transporter), member 1	-	KOG0756 At5g01340 Mitochondrial tricarboxylate/dicarboxylate carrier proteins	CCE33727.1 probable succinate-fumarate transporter [Claviceps purpurea 20.1]	Mitochondrial succinate-fumarate transporter 1 OS=Arabidopsis thaliana OX=3702 GN=SFC1 PE=2 SV=1
A8094	-	-	-	-	-	-	-	-
A8095	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4557333 Sulfatase	TQV91287.1 sulfatase [Cordyceps javanica]	Arylsulfatase B OS=Mus musculus OX=10090 GN=Arse PE=1 SV=3
A8096	-	-	-	-	-	-	-	-
A8097	GO:0001510(RNA methylation)	-	GO:0008168(methyltransferase activity)	K15334 NCL1, TRM4; multisite-specific tRNA:(cytosine-C5)-methyltransferase [EC:2.1.1.202]	-	KOG2198 At2g22400 tRNA cytosine-5-methylases and related enzymes of the NOL1/NOP2/sun superfamily	OZJ03575.1 hypothetical protein BZG36_03041 [Bifiguratus adelaidae]	RNA cytosine-C(5)-methyltransferase NSUN2 OS=Xenopus tropicalis OX=8364 GN=nsun2 PE=2 SV=1
A8098	-	-	-	K12185 VPS37; ESCRT-I complex subunit VPS37	map04144 Endocytosis	KOG3270 Hs17449277 Uncharacterized conserved protein	RHZ85445.1 hypothetical protein Glove_65g68 [Diversispora epigaea]	Vacuolar protein sorting-associated protein 37A OS=Homo sapiens OX=9606 GN=VPS37A PE=1 SV=1
A8099	GO:0060285(cilium-dependent cell motility)	GO:0005858(axonemal dynein complex)	GO:0003777(microtubule motor activity),GO:0016887(ATP hydrolysis activity),GO:0005524(ATP binding)	-	-	KOG3595 Hs17864092 Dyneins, heavy chain	EPZ34616.1 Dynein heavy chain-2 domain-containing protein [Rozella allomyces CSF55]	Dynein axonemal heavy chain 6 OS=Homo sapiens OX=9606 GN=DNAH6 PE=1 SV=3
A8100	GO:0005975(carbohydrate metabolic process)	-	GO:0003824(catalytic activity),GO:0030246(carbohydrate binding),GO:0004553(hydrolase activity, hydrolyzing O-glycosyl compounds)	-	-	KOG1065 At3g45940 Maltase glucoamylase and related hydrolases, glycosyl hydrolase family 31	KAG2176274.1 hypothetical protein INT43_005508 [Umbelopsis isabellina]	Sulfoquinovosidase OS=Agrobacterium fabrum (strain C58 / ATCC 33970) OX=176299 GN=smol PE=1 SV=1

A8101	GO:0009058(biosynthetic process)	-	GO:0003824(catalytic activity)	-	-	KOG2803 CE26830 Choline phosphate cytidyltransferase/Predicted CDP-ethanolamine synthase	OJJ35810.1 hypothetical protein ASPWEDRAFT_41052 [Aspergillus wentii DTO 134E9]	Bifunctional protein HldE OS=Pelobacter propionicus (strain DSM 2379 / NBRC 103807 / OttBd1) OX=338966 GN=hldE PE=3 SV=1
A8102	-	-	-	K08997 SELENOO, selO; protein adenyltransferase [EC:2.7.7.108]	-	KOG2542 Hs14779836 Uncharacterized conserved protein (YdiU family)	KAG1212689.1 hypothetical protein G6F35_010353 [Rhizopus oryzae]	Protein adenyltransferase SelO OS=Moritella marina OX=90736 GN=selO PE=3 SV=1
A8103	GO:0006979(response to oxidative stress)	-	GO:0004602(glutathione peroxidase activity)	K23856 GPX; peroxiredoxin [EC:1.11.1.24]	-	KOG1651 Hs4504103 Glutathione peroxidase	ELQ75285.1 Glutathione peroxidase [Trachipleistophora hominis]	Glutathione peroxidase 1 OS=Mus musculus OX=10090 GN=Gpx1 PE=1 SV=2
A8104	-	-	-	-	-	-	-	-
A8105	-	GO:0016021(integral component of membrane)	-	-	-	KOG2489 At5g08500 Transmembrane protein	KXS13023.1 cleft lip and palate transmembrane 1 [Gonapodya prolifera JEL478]	Lipid scramblase CLPTM1L OS=Mus musculus OX=10090 GN=Clptm1l PE=1 SV=1
A8106	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8107	-	GO:0005737(cytoplasm),GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0003743(translation initiation factor activity)	K03251 EIF3D; translation initiation factor 3 subunit D	-	KOG2479 At4g20980 Translation initiation factor 3, subunit d (eIF-3d)	XP_009543813.1 hypothetical protein HETIRDRAFT_472549 [Heterobasidion irregularare TC 32-1]	Eukaryotic translation initiation factor 3 subunit D OS=Arabidopsis thaliana OX=3702 GN=TIF3D1 PE=1 SV=1
A8108	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8109	-	-	-	-	-	-	-	-
A8110	GO:0006629(lipid metabolic process)	-	-	-	-	-	ORX88755.1 patatin-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Patatin-like phospholipase domain-containing protein AFUA_1G04970 OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=AFUA_1G04970 PE=3 SV=1
A8111	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	KOG1840 At4g10840 Kinesin light chain	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A8112	-	-	-	K09423 BAS1; Myb-like DNA-binding protein BAS1	-	KOG0048 Hs13641706_1 Transcription factor, Myb superfamily	KAF8950372.1 hypothetical protein BGZ52_002759 [Haplosporangium bisporale]	Transforming protein Myb OS=Avian myeloblastosis virus OX=11866 GN=V-MYB PE=1 SV=2

A8113	GO:0006260(DNA replication),GO:0006281(DNA repair),GO:0006310(DNA recombination)	GO:0005634(nucleus)	GO:0003676(nucleic acid binding),GO:0003677(DNA binding)	K07466 RPA1, rpa; replication factor A1	map03420 Nucleotide excision repair;map03030 DNA replication;map03440 Homologous recombination;map03430 Mismatch repair;map03460 Fanconi anemia pathway	KOG0851 Hs4506583 Single-stranded DNA-binding replication protein A (RPA), large (70 kD) subunit and related ssDNA-binding proteins	PWN54342.1 replication factor-a protein [Violaceomyces palustris]	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RPA1 PE=1 SV=2
A8114	-	-	-	-	-	KOG3131 Hs18593894 Uncharacterized conserved protein	KTB32801.1 hypothetical protein WG66_14604 [Moniliophthora roreri]	SRR1-like protein OS=Mus musculus OX=10090 GN=Srrd PE=2 SV=4
A8115	-	-	-	K15424 PPP4R1; serine/threonine-protein phosphatase 4 regulatory subunit 1	-	KOG0211 Hs4826934 Protein phosphatase 2A regulatory subunit A and related proteins	KAG0192959.1 hypothetical protein DFQ28_006991 [Apophysomyces sp. BC1034]	Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Homo sapiens OX=9606 GN=PPP4R1 PE=1 SV=1
A8116	-	-	-	-	-	KOG1073 At1g26110 Uncharacterized mRNA-associated protein RAP55	OZJ01992.1 hypothetical protein BZG36_04692, partial [Bifiguratus adalaidae]	Protein decapping 5 OS=Arabidopsis thaliana OX=3702 GN=DCP5 PE=1 SV=1
A8117	GO:0032511(late endosome to vacuole transport via multivesicular body sorting pathway)	-	-	-	-	KOG0917 At4g26750 Uncharacterized conserved protein	KJA28668.1 hypothetical protein HYP5UDRAFT_129629, partial [Hypholoma sublateritium FD-334 SS-4]	Protein HOMOLOG OF MAMMALIAN LYST-INTERACTING PROTEIN 5 OS=Arabidopsis thaliana OX=3702 GN=LIP5 PE=1 SV=1
A8118	GO:0006468(protein phosphorylation),GO:0006470(protein dephosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004722(protein serine/threonine phosphatase activity)	K05743 LIMK1; LIM domain kinase 1 [EC:2.7.11.1]	map04360 Axon guidance;map05135 Yersinia infection;map04810 Regulation of actin cytoskeleton;map05170 Human immunodeficiency virus 1 infection;map04666 Fc gamma R-mediated phagocytosis	KOG0192 At4g31170 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9648290.1 kinase-like protein [Thelephora ganbajun]	Protein kinase and PP2C-like domain-containing protein OS=Arabidopsis thaliana OX=3702 GN=At2g40860/At2g40870 PE=2 SV=1
A8119	-	-	-	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698 At2g40860.2 Serine/threonine protein phosphatase	SCU80412.1 LAME_0803026g1_1 [Lachancea meyersii CBS 8951]	Protein kinase and PP2C-like domain-containing protein OS=Arabidopsis thaliana OX=3702 GN=At2g40860/At2g40870 PE=2 SV=1

A8120	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K19584 PRKX; protein kinase X [EC:2.7.11.11]	-	KOG0616 CE15473 cAMP-dependent protein kinase catalytic subunit (PKA)	KAF0493789.1 Pkinase-domain-containing protein [Gigaspora margarita]	cAMP-dependent protein kinase catalytic subunit 3 OS=Drosophila melanogaster OX=7227 GN=Pka-C3 PE=2 SV=2
A8121	-	-	-	-	-	KOG3940 CE04871 Uncharacterized conserved protein	-	Zinc finger C2HC domain-containing protein 1B OS=Mus musculus OX=10090 GN=Zc2hc1b PE=2 SV=1
A8122	GO:0055085(transmembrane transport),GO:0006811(ion transport)	GO:0016020(membrane),GO:0016021(integral component of membrane)	GO:0015377(cation:chloride symporter activity)	K14429 SLC12A9, CCC6; solute carrier family 12 (potassium/chloride transporters), member 9	-	KOG1288 Hs910386 Amino acid transporters	KAG0362066.1 hypothetical protein BGZ54_00871 [Gamsiella multidivariata]	Solute carrier family 12 member 9 OS=Homo sapiens OX=9606 GN=SLC12A9 PE=1 SV=1
A8123	-	-	-	-	-	-	-	-
A8124	GO:0006486(protein glycosylation)	GO:0016020(membrane)	GO:0008417(fucosyltransferase activity)	-	-	KOG2619 Hs19923648 Fucosyltransferase	KAG4097226.1 hypothetical protein H8356DRAFT_1041689 [Neocallimastix sp. JGI-2020a]	Alpha-(1,3)-fucosyltransferase 10 OS=Xenopus laevis OX=8355 GN=fut10 PE=2 SV=2
A8125	GO:0006302(double-strand break repair),GO:0006310(DNA recombination)	GO:0005634(nucleus)	GO:0003677(DNA binding)	-	-	-	-	-
A8126	-	-	-	K15445 TRMT10, TRM10, RG9MTD; tRNA (guanine9-N1)-methyltransferase [EC:2.1.1.221]	-	KOG2967 Hs14724179 Uncharacterized conserved protein	XP_031027224.1 uncharacterized protein SmJEL517_g01051 [Synchytrium microbalum]	tRNA methyltransferase 10 homolog A OS=Rattus norvegicus OX=10116 GN=Trmt10a PE=1 SV=1
A8127	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8128	-	-	GO:0005515(protein binding)	-	-	KOG0619 7300644.2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A8129	-	-	-	K20523 SH3YL1; SH3 domain-containing YSC84-like protein 1	-	-	ORY43969.1 DUF500-domain-containing protein [Rhizoclostium globosum]	SH3 domain-containing protein PJ696.02 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAPJ696.02 PE=1 SV=1
A8130	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	CEH12291.1 hypothetical protein CBOM_00290 [Ceraceosorus bombacis]	-
A8131	-	-	-	-	-	-	-	-

A8132	-	-	-	-	-	KOG0048 Hs13641706.1 Transcription factor, Myb superfamily	RGB38897.1 Homeodomain-like protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Myb-related protein A OS=Mus musculus OX=10090 GN=Mybl1 PE=1 SV=2
A8133	GO:0008033(tRNA processing)	-	GO:0003723(RNA binding),GO:0004809(tRNA (guanine-N2-)-methyltransferase activity)	K00555 TRMT1, trm1; tRNA (guanine26-N2/guanine27-N2)-dimethyltransferase [EC:2.1.1.215 2.1.1.216]	-	KOG1253 At3g02320 tRNA methyltransferase	ORZ10876.1 N2,N2-dimethylguanosine tRNA methyltransferase [Absidia repens]	tRNA (guanine(26)-N(2))-dimethyltransferase 2 OS=Arabidopsis thaliana OX=3702 GN=At3g02320 PE=1 SV=3
A8134	-	GO:0032040(small-subunit processosome)	-	K14766 NOP14, UTP2; nucleolar protein 14	-	-	ORY07457.1 Nop14-like protein [Basidiobolus meristosporus CBS 931.73]	Probable nucleolar complex protein 14 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=nop14 PE=1 SV=1
A8135	-	GO:0016021(integral component of membrane)	-	K17086 TM9SF2_4; transmembrane 9 superfamily member 2/4	-	KOG1278 At2g24170 Endosomal membrane proteins, EMP70	KAG0340642.1 hypothetical protein BG004_006339 [Podila humilis]	Transmembrane 9 superfamily member 10 OS=Arabidopsis thaliana OX=3702 GN=TMN10 PE=2 SV=1
A8136	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG0029 At3g59050 Amine oxidase	ORY07814.1 amine oxidase [Basidiobolus meristosporus CBS 931.73]	Lysine-specific histone demethylase 1 homolog 3 OS=Oryza sativa subsp. indica OX=39946 GN=B0103C08-B0602B01.13 PE=3 SV=1
A8137	GO:1905515(non-motile cilium assembly)	GO:0034464(BBSome)	-	-	-	-	KAG4101694.1 hypothetical protein H8356DRAFT_985190 [Neocallimastix sp. JGI-2020a]	Bardet-Biedl syndrome 2 protein homolog OS=Danio rerio OX=7955 GN=bbs2 PE=2 SV=1
A8138	GO:0006413(translational initiation)	GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0003743(translation initiation factor activity),GO:0031369(translation initiation factor binding),GO:0005515(protein binding),GO:0003676(nucleic acid binding)	K03253 EIF3B; translation initiation factor 3 subunit B	-	KOG2314 Hs4503527 Translation initiation factor 3, subunit b (eIF-3b)	RHZ54201.1 hypothetical protein Glove_429g14 [Diversispora epigaea]	Eukaryotic translation initiation factor 3 subunit B OS=Rattus norvegicus OX=10116 GN=EIF3b PE=1 SV=1
A8139	-	-	-	-	-	-	-	-

A8140	GO:0006914 (autophagy)	-	-	K08334 BECN, VPS30, ATG6; beclin	map05014 Amyotrophic lateral sclerosis;map04140 Autophagy - animal;map05131 Shigellosis;map04215 Apoptosis - multiple species;map04138 Autophagy - yeast;map04137 Mitophagy - animal;map04136 Autophagy - other;map05022 Pathways of neurodegeneration - multiple diseases;map04371 Apelin signaling pathway;map05010 Alzheimer disease;map05017 Spinocerebellar ataxia;map05016 Huntington	KOG2751 7301093 Beclin-like protein	KAF8971997.1 autophagy protein 6 [Entomortierella lignicola]	Beclin-1-like protein B OS=Dictyostelium discoideum OX=44689 GN=atg6B PE=3 SV=1
A8141	-	-	-	-	-	-	-	-
A8142	-	-	-	-	-	-	-	-
A8143	-	-	GO:0005515 (protein binding)	-	-	-	-	-
A8144	-	-	GO:0005515 (protein binding)	-	-	-	-	-
A8145	GO:0016070 (RNA metabolic process), GO:0006406 (mRNA export from nucleus)	GO:0005846 (nuclear cap binding complex)	GO:0000339 (RNA cap binding)	-	-	KOG1104 7290517 Nuclear cap-binding complex, subunit NCBP1/CBP80	KAF8075867.1 armadillo-type protein [Lyophyllum atratum]	Nuclear cap-binding protein subunit 1 OS=Drosophila mojavensis OX=7230 GN=Cbp80 PE=3 SV=1
A8146	-	-	-	-	-	-	-	-
A8147	GO:0022900 (electron transport chain)	GO:0005747 (mitochondrial respiratory chain complex I)	-	K03937 NDUFS4; NADH dehydrogenase (ubiquinone) Fe-S protein 4	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy;map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis;map00190 Oxidative phosphorylation;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG3389 Hs4505369 NADH:ubiquinone oxidoreductase, NDUFS4/18 kDa subunit	KAG1170681.1 hypothetical protein G6F71_007499 [Rhizopus microsporus]	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Drosophila melanogaster OX=7227 GN=ND-18 PE=1 SV=2
A8148	-	-	GO:0051087 (chaperone binding), GO:0005515 (protein binding)	K12795 SUGT1, SGT1; suppressor of G2 allele of SKP1	map04621 NOD-like receptor signaling pathway;map04626 Plant-pathogen interaction	KOG1309 At4g23570.2 Suppressor of G2 allele of skp1	KAF9924250.1 Protein SGT1 A [Linnemannia zychae]	Protein SGT1 homolog OS=Zea mays OX=4577 GN=SGT1 PE=1 SV=1
A8149	GO:0006412 (translation)	GO:0005840 (ribosome), GO:0015934 (large ribosomal subunit)	GO:0003735 (structural constituent of ribosome)	-	-	KOG1711 At1g52370 Mitochondrial/chloroplast ribosomal protein L22	XP_004179304.1 hypothetical protein TBLA_0B09690 [Tetrapispora blattae CBS 6284]	Large ribosomal subunit protein uL22 OS=Methylocella silvestris (strain DSM 15510 / CIP 108128 / LMG 27833 / NCIMB 13906 / BL2) OX=395965 GN=rplV PE=3 SV=1

A8150	GO:0006357(regulation of transcription by RNA polymerase II)	-	GO:0016538(cyclin-dependent protein serine/threonine kinase regulator activity)	K23326 CCNK; cyclin K	-	KOG0834 Hs18583591 CDK9 kinase-activating protein cyclin T	ORX99123.1 cyclin-like protein [Basidiobolus meristosporus CBS 931.73]	Cyclin-K OS=Mus musculus OX=10090 GN=Ccnk PE=1 SV=3
A8151	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity),GO:0004674(protein serine/threonine kinase activity)	K22008 PSK1; serine/threonine-protein kinase Psk1 [EC:2.7.11.1]	-	KOG0986 Hs4501971 G protein-coupled receptor kinase	RKP09853.1 kinase-like domain-containing protein, partial [Thamnocephalis sphaerospora]	G protein-coupled receptor kinase 4 OS=Mus musculus OX=10090 GN=Grk4 PE=2 SV=2
A8152	-	-	-	-	-	KOG0769 At3g05290 Predicted mitochondrial carrier protein	TPX69576.1 hypothetical protein SpCBS45565.g02297 [Spizellomyces sp. 'palustris']	Peroxisomal adenine nucleotide carrier 1 OS=Arabidopsis thaliana OX=3702 GN=PNC1 PE=1 SV=1
A8153	-	-	-	-	-	-	-	Calcium-regulated actin-bundling protein OS=Dictyostelium
A8154	-	-	-	-	-	-	-	-
A8155	-	-	-	K24971 NEMF, RQC2; nuclear export mediator factor NEMF	-	KOG2030 At5g49930 Predicted RNA-binding protein	KAG0171134.1 hypothetical protein DFQ30_001406 [Apophysomyces sp. BC1015]	Ribosome quality control complex subunit NEMF OS=Mus musculus OX=10090 GN=Nemf PE=1 SV=2
A8156	-	-	-	-	-	-	-	-
A8157	-	GO:0016020(membrane)	-	-	-	KOG2952 At3g12740 Cell cycle control protein	KNE65341.1 hypothetical protein AMAG_10983 [Allomyces macrogynus ATCC 38327]	ALA-interacting subunit 1 OS=Arabidopsis thaliana OX=3702 GN=ALIS1 PE=1 SV=1
A8158	-	-	-	-	-	-	XP_016608351.1 hypothetical protein SPPG_09212 [Spizellomyces punctatus DAOM BR117]	Uncharacterized protein MJ1628 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ1628 PE=4 SV=1
A8159	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	-	-	-	CEH12291.1 hypothetical protein CBOM_00290 [Ceraceosorus bombacis]	E3 ubiquitin-protein ligase IpaH2.5 OS=Shigella flexneri OX=623 GN=ipaH2.5 PE=1 SV=1
A8160	-	-	-	-	-	-	-	-
A8161	GO:0006364(rRNA processing)	-	GO:0008173(RNA methyltransferase activity),GO:0003824(catalytic activity),GO:0051536(iron-sulfur cluster binding)	-	-	-	XP_006674904.1 uncharacterized protein BATDEDRAFT_3639, partial [Batrachochytrium dendrobatidis JAM81]	Probable dual-specificity RNA methyltransferase RlmN 2 OS=Protochlamydia amoebophila (strain UWE25) OX=264201 GN=rlmN2 PE=3 SV=2

A8162	GO:0006303(double-strand break repair via nonhomologous end joining),GO:0000723(telomere maintenance)	GO:0005634(nucleus),GO:0043564(Ku70:Ku80 complex)	GO:0003677(DNA binding),GO:0003684(damaged DNA binding),GO:0042162(telomeric DNA binding),GO:0003678(DNA helicase activity)	K10884 XRCC6, KU70, G22P1; ATP-dependent DNA helicase 2 subunit 1	map03450 Non-homologous end-joining	KOG2327 Hs4503841 DNA-binding subunit of a DNA-dependent protein kinase (Ku70 autoantigen)	OZJ01818.1 hypothetical protein BZG36_04811 [Bifiguratus adelaidae]	X-ray repair cross-complementing protein 5 OS=Gallus gallus OX=9031 GN=XRCC6 PE=2 SV=1
A8163	-	-	-	-	-	-	-	-
A8164	GO:0015031(protein transport)	GO:0030176(integral component of endoplasmic reticulum membrane)	-	K12275 SEC62; translocation protein SEC62	map04141 Protein processing in endoplasmic reticulum;map03060 Protein export	-	EPZ31029.1 Translocation protein Sec62 domain-containing protein [Rozella allomycis CSF55]	Translocation protein SEC62 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SEC62 PE=3 SV=1
A8165	-	-	-	K16575 ACTR1, ARP1, centractin	map05014 Amyotrophic lateral sclerosis;map05132 Salmonella infection;map04814 Motor proteins;map05022 Pathways of neurodegeneration - multiple diseases;map05016 Huntington disease	KOG0676 Hs5031569 Actin and related proteins	KAF8591845.1 actin-related protein [Ramaria rubella]	Alpha-centractin OS=Canis lupus familiaris OX=9615 GN=ACTR1A PE=2 SV=1
A8166	GO:0008033(tRNA processing)	-	GO:0016783(sulfurtransferase activity),GO:0016740(transferase activity)	K21027 TRMU, SLM3; tRNA-5-taurinomethyluridine 2-sulfurtransferase [EC:2.8.1.14]	-	KOG2805 7290113 tRNA (5-methylamino methyl-2-thiouridylate) - methyltransferase	XP_016612097.1 tRNA (5-methylamino methyl-2-thiouridylate) - methyltransferase [Spizellomyces punctatus DAOM BR117]	tRNA-specific 2-thiouridylase MnmA OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) OX=272620 GN=mnmA PE=3 SV=2
A8167	-	-	-	K10428 DCTN6; dynactin 6	map05014 Amyotrophic lateral sclerosis;map05132 Salmonella infection;map04814 Motor proteins;map05022 Pathways of neurodegeneration - multiple diseases;map05016 Huntington disease;map04962 Vasopressin-regulated water reabsorption	KOG4042 Hs5730116 Dynactin subunit p27/WS-3, involved in transport of organelles along microtubules	OJ02655.1 hypothetical protein ASPVEDRAFT_42157 [Aspergillus versicolor CBS 583.65]	Dynactin subunit 6 OS=Nematostella vectensis OX=45351 GN=dctn6 PE=3 SV=1
A8168	-	-	-	-	-	-	-	-

A8169	GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	-	GO:0005515(protein binding)	K14005 SEC31; protein transport protein SEC31	map04141 Protein processing in endoplasmic reticulum	KOG0307 At3g63460 Vesicle coat complex COPII, subunit SEC31	ORX71094.1 WD40 repeat-like protein [Linderina pennisporea]	Protein transport protein SEC31 OS=Dictyostelium discoideum OX=44689 GN=sec31 PE=3 SV=1
A8170	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors);GO:0050660(flavin adenine dinucleotide binding)	K00249 ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map03320 PPAR signaling pathway;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map04936 Alcoholic liver disease;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG1469 HsM14149851 Predicted acyl-CoA dehydrogenase	ORX92576.1 acyl-CoA dehydrogenase domain protein [Basidiobolus meristosporus CBS 931.73]	Probable acyl-CoA dehydrogenase FadE2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=fadE2 PE=1 SV=4
A8171	-	-	-	-	-	-	-	-
A8172	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding);GO:0003899(DNA-directed 5'-3' RNA polymerase activity)	K03013 RPABC1, RPB5, POLR2E; DNA-directed RNA polymerases I, II, and III subunit RPABC1	map03420 Nucleotide excision repair;map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway;map05016 Huntington disease	KOG3218 CE23831 RNA polymerase, 25-kDa subunit (common to polymerases I, II and III)	PVU96375.1 hypothetical protein BB561_001223 [Smittium simulii]	DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Caenorhabditis briggsae OX=6238 GN=rpb-5 PE=3 SV=1
A8173	-	-	GO:0003723(RNA binding);GO:0003676(nucleic acid binding);GO:0003743(translation initiation factor activity)	K03237 EIF2S1; translation initiation factor 2 subunit 1	map05014 Amyotrophic lateral sclerosis;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map04141 Protein processing in endoplasmic reticulum;map04210 Apoptosis;map04138 Autophagy - yeast;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map04932 Non-alcoholic fatty liver disease;map05010 Alzheimer disease;map05011	-	TPX53767.1 hypothetical protein PhCBS80983_g06170 [Powellomyces hirtus]	Eukaryotic translation initiation factor 2 subunit alpha OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=tif211 PE=1 SV=1
A8174	-	-	-	-	-	-	-	-
A8175	GO:0035434(copper ion transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005375(copper ion transmembrane transporter activity)	-	-	-	KAG0053597.1 hypothetical protein BGZ83_000807 [Gryganskiella cystojenkini]	Protein P80 OS=Dictyostelium discoideum OX=44689 GN=p80 PE=2 SV=1

A8176	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05658 ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:7.6.2.2]	map04976 Bile secretion;map02010 ABC transporters;map05226 Gastric cancer;map05206 MicroRNAs in cancer	KOG0055 At1g02520 Multidrug/phoromone exporter, ABC superfamily	KAF0430296.1 P-loop containing nucleoside triphosphate hydrolase protein [Gigaspora margarita]	ABC transporter B family member 2 OS=Dictyostelium discoideum OX=44689 GN=abcB2 PE=3 SV=1
A8177	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs14776113 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KXS21686.1 Pkinase-domain-containing protein [Gonapodya prolifera JEL478]	Probable serine/threonine-protein kinase pXi OS=Dictyostelium discoideum OX=44689 GN=pXi PE=2 SV=1
A8178	-	-	-	-	-	-	-	-
A8179	-	-	-	K09423 BAS1; Myb-like DNA-binding protein BAS1	-	KOG0048 Hs13641706.1 Transcription factor, Myb superfamily	RCH79461.1 Myb-like DNA-binding domain protein [Rhizopus stolonifer]	Transcriptional activator Myb OS=Gallus gallus OX=9031 GN=MYB PE=1 SV=1
A8180	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY44048.1 TPR-like protein [Rhizoclosmatium globosum]	-
A8181	-	-	-	-	-	-	-	-
A8182	GO:0006807(nitrogen compound metabolic process)	-	GO:0016811(hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides)	K11206 NIT1, ybeM; deaminated glutathione amidase [EC:3.5.1.128]	-	KOG0807 At4g08790 Carbon-nitrogen hydrolase	KAF9080553.1 Nitrilase [Mortierella sp. AD031]	Deaminated glutathione amidase, chloroplastic/cytosolic OS=Arabidopsis thaliana OX=3702 GN=NLP2 PE=1 SV=1
A8183	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	-	-	KOG0192 At1g62400 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAF9130990.1 hypothetical protein BGW39_002402 [Mortierella sp. 14UC]	Probable serine/threonine-protein kinase drkA OS=Dictyostelium discoideum OX=44689 GN=drkA PE=3 SV=1
A8184	GO:0006355(regulation of transcription, DNA-templated),GO:0016573(histone acetylation)	-	GO:0005515(protein binding),GO:0004402(histone acetyltransferase activity),GO:0008270(zinc ion binding)	K11684 BDF1; bromodomain-containing factor 1	-	KOG1778 Hs4758056 CREB binding protein/P300 and related TAZ Zn-finger proteins	OMH83849.1 SWR1 complex bromodomain subunit bdf1 [Zancudomyces culisetae]	Probable histone acetyltransferase HAC-like 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0137500 PE=3 SV=2
A8185	-	-	-	K02896 RP-L24e, RPL24; large subunit ribosomal protein L24e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1722 At3g53020 60s ribosomal protein L24	KNE63417.1 hypothetical protein AMAG_08547 [Allomyces macrogynus ATCC 38327]	Large ribosomal subunit protein eL24y OS=Arabidopsis thaliana OX=3702 GN=RPL24B PE=1 SV=2

A8186	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04371 ERK, MAPK1.3; mitogen-activated protein kinase 1/3 [EC:2.7.11.24]	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map04730 Long-term depression;map05135 Yersinia infection;map05132 Salmonella infection;map05133 Pertussis;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04350 TGF-beta signaling pathway;map04810 Regulation of	KOG0660 At4g01370 Mitogen-activated protein kinase	KAF1797781.1 hypothetical protein FB192DRAFT_1396083 [Mucor lusitanicus]	Extracellular signal-regulated kinase 1 OS=Dictyostelium discoideum OX=44689 GN=erkA PE=2 SV=2
A8187	-	-	-	-	-	-	-	-
A8188	GO:0006629(lipid metabolic process)	-	-	K13806 DAGL; sn1-specific diacylglycerol lipase [EC:3.1.1.116]	map04723 Retrograde endocannabinoid signaling;map04745 Phototransduction - fly;map04925 Aldosterone synthesis and secretion	KOG2088 CE01305 Predicted lipase/calmodulin-binding heat-shock protein	PIA16895.1 alpha/beta-hydrolase [Coemansia reversa NRRL 1564]	Diacylglycerol lipase-beta OS=Rattus norvegicus OX=10116 GN=Daglb PE=1 SV=1
A8189	-	-	-	-	-	-	-	-
A8190	GO:0006486(protein glycosylation)	-	GO:0003980(UDP-glucose:glycoprotein glucosyltransferase activity)	-	-	-	CEI95189.1 Putative UDP-glucose:glycoprotein glucosyltransferase [Rhizopus microsporus]	Probable UDP-glucose:glycoprotein glucosyltransferase A OS=Dictyostelium discoideum OX=44689 GN=ggTA PE=1 SV=2
A8191	-	-	-	-	-	-	-	-
A8192	-	-	-	-	-	-	-	-
A8193	-	-	GO:0003824(catalytic activity)	-	-	-	XP_035334629.1 uncharacterized protein HER10_EVM0001246 [Colletotrichum scovillei]	2-keto-4-pentenoate hydratase OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) OX=322710 GN=mhpD PE=3 SV=1
A8194	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	K20520 DBNL, ABP1; drebrin-like protein	-	KOG1453 Hs7706107 Chimaerin and related Rho GTPase activating proteins	XP_025547595.1 hypothetical protein BO97DRAFT_428399 [Aspergillus homomorphus CBS 101889]	Protein app1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=app1 PE=2 SV=1
A8195	-	-	GO:0016407(acetyltransferase activity)	-	-	KOG3234 Hs7705823 Acetyltransferase, (GNAT) family	TPX50333.1 hypothetical protein SeLEV6574_g00952 [Synchytrium endobioticum]	N-alpha-acetyltransferase 20 OS=Xenopus tropicalis OX=8364 GN=naa20 PE=2 SV=1

A8196	GO:0006352(DNA-templated transcription, initiation)	-	GO:0003677(DNA binding)	K03120 TBP, tbp; transcription initiation factor TFIID TATA-box-binding protein	map03022 Basal transcription factors;map05203 Viral carcinogenesis;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05165 Human papillomavirus infection;map05166 Human T-cell leukemia virus 1 infection	KOG3302 YER148w TATA-box binding protein (TBP), component of TFIID and TFIIB	KAE8209596.1 hypothetical protein CF327_g6441 [Tilletia walkeri]	TATA-box-binding protein OS=Solanium tuberosum OX=4113 GN=TBP PE=2 SV=1
A8197	GO:0006482(protein demethylation)	-	GO:0051723(protein methyltransferase activity)	-	-	KOG2564 CE26705 Predicted acetyltransferases and hydrolases with the alpha/beta hydrolase fold	TKA56716.1 hypothetical protein B0A53_01911 [Rhodotorula sp. CCFEE 5036]	Protein phosphatase methyltransferase 1 OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=PPE1 PE=3 SV=1
A8198	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K20872 NEK2; serine/threonine-protein kinase Nek2 [EC:2.7.11.1]	-	KOG0591 Hs19424132 NIMA (never in mitosis)-related G2-specific serine/threonine protein kinase	XP_006676402.1 uncharacterized protein BATDEDRAFT_85310 [Batrachochytrium dendrobatidis JAM81]	Serine/threonine-protein kinase Nek7 OS=Homo sapiens OX=9606 GN=NEK7 PE=1 SV=1
A8199	-	-	-	-	-	-	-	-
A8200	-	-	-	-	-	KOG4244 CE22138 Failed axon connections (fax) protein/glutathione S-transferase-like protein	XP_031022330.1 uncharacterized protein SmJEL517_g05757 [Synchytrium microbalum]	Failed axon connections homolog OS=Rattus norvegicus OX=10116 GN=Faxc PE=3 SV=1
A8201	-	-	GO:0003824(catalytic activity)	-	-	KOG1535 Hs13637384 Predicted fumarylacetoacetate hydrolase	KAF8935238.1 hypothetical protein BGZ58_005156 [Dissophoromata]	Fumarylacetoacetate hydrolase domain-containing protein 2A OS=Homo sapiens OX=9606 GN=FAHD2A PE=1 SV=1
A8202	GO:0006811(ion transport);GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005216(ion channel activity)	-	-	KOG2301 Hs7657542 Voltage-gated Ca2+ channels, alpha1 subunits	ORZ30665.1 ion transport protein-domain-containing protein [Catenaria anguillulae PL171]	Cation channel sperm-associated protein 3 OS=Mus musculus OX=10090 GN=Catsper3 PE=1 SV=2
A8203	-	-	-	-	-	-	-	Monoacylglycerol lipase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv0183 PE=1 SV=2
A8204	-	-	-	-	-	-	-	-

A8205	GO:0006511(ubiquitin-dependent protein catabolic process)	GO:0008540(proteasome regulatory particle, base subcomplex)	-	K03029 PSMD4, RPN10; 26S proteasome regulatory subunit N10	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG2884 At4g38630 26S proteasome regulatory complex, subunit RPN10/PSMD4	PKY42499.1 vWA-like protein [Rhizophagus irregularis]	26S proteasome non-ATPase regulatory subunit 4 homolog OS=Arabidopsis thaliana OX=3702 GN=RPN10 PE=1 SV=1
A8206	-	-	-	-	-	-	-	-
A8207	GO:0032509(endosome transport via multivesicular body sorting pathway)	GO:0000813(ESCRT-I complex)	-	K12184 VPS28; ESCRT-I complex subunit VPS28	map04144 Endocytosis	KOG3284 At4g21560 Vacuolar sorting protein VPS28	OON09291.1 hypothetical protein BSLG_01638 [Batrachochytrium salamandrivorans]	Vacuolar protein sorting-associated protein 28 homolog 1 OS=Arabidopsis thaliana OX=3702 GN=VPS28-1 PE=1 SV=1
A8208	-	-	-	K01054 MGLL; acylglycerol lipase [EC:3.1.1.23]	map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis;map00561 Glycerolipid metabolism;map01100 Metabolic pathways;map04923 Regulation of lipolysis in adipocytes	KOG1455 At1g18360 Lysophospholipase	XP_016612372.1 hypothetical protein SPPG_00063 [Spizellomyces punctatus DAOM BR117]	Monoacylglycerol lipase OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=MSMEG_0220 PE=1 SV=1
A8209	GO:0042325(regulation of phosphorylation)	GO:0005737(cytoplasm)	-	-	-	-	-	-
A8210	-	-	-	K13984 TXNDC5, ERP46; thioredoxin domain-containing protein 5 [EC:5.3.4.1]	map04141 Protein processing in endoplasmic reticulum	KOG4277 Hs20558506 Uncharacterized conserved protein, contains thioredoxin domain	KXS10568.1 thioredoxin-domain-containing protein [Gonapodya prolifera JEL478]	Protein disulfide-isomerase TMX3 OS=Homo sapiens OX=9606 GN=TMX3 PE=1 SV=2

A8211	GO:0006424(glutamyl-tRNA aminoacylation),GO:0043039(tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation)	-	GO:0000166(nucleotide binding),GO:0004818(glutamate-tRNA ligase activity),GO:0005524(ATP binding),GO:0000049(tRNA binding),GO:0008270(zinc ion binding),GO:0004812(aminoacyl-tRNA ligase activity)	K01885 EARS gltX; glutamyl-tRNA synthetase [EC:6.1.1.17]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map00970 Aminoacyl-tRNA biosynthesis;map01100 Metabolic pathways	KOG1149 YOL033w Glutamyl-tRNA synthetase (mitochondrial)	KAG0042092.1 Glutamyl-tRNA synthetase [Gryganskiella cystojenkinii]	Glutamate--tRNA ligase OS=Alkaliphilus oremlandii (strain OhILAs) OX=350688 GN=gltX PE=3 SV=1
A8212	-	-	GO:0016209(antioxidant activity),GO:0016491(oxidoreductase activity)	-	-	-	-	-
A8213	GO:0042176(regulation of protein catabolic process)	GO:0000502(proteasome complex)	GO:0030234(enzyme regulator activity)	K03033 PSMD3, RPN3; 26S proteasome regulatory subunit N3	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG2581 Hs4506229 26S proteasome regulatory complex, subunit RPN3/PSMD3	RIB23000.1 proteasome regulatory subunit C-terminal-domain-containing protein [Gigaspora rosea]	26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PSMD3 PE=1 SV=2
A8214	GO:0005975(carbohydrate metabolic process)	-	GO:0016773(phosphotransferase activity, alcohol group as acceptor)	-	-	KOG4184 CE08892_1 Predicted sugar kinase	-	ADP-dependent glucokinase OS=Bos taurus OX=9913 GN=ADPGK PE=2 SV=1
A8215	-	-	-	-	-	-	RIB04444.1 Fcf2 pre-rRNA processing-domain-containing protein [Gigaspora rosea]	Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Bos taurus OX=9913 GN=DNTTIP2 PE=2 SV=1
A8216	-	-	GO:0043169(cation binding),GO:0005509(calcium ion binding)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 At5g24940 Serine/threonine protein phosphatase	CEG71564.1 Putative Protein phosphatase [Rhizopus microsporus]	Probable protein phosphatase 2C 52 OS=Oryza sativa subsp. japonica OX=39947 GN=Os05g0587100 PE=2 SV=1

A8217	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007166(cell surface receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity), GO:0004888(transmembrane signaling receptor activity)	-	-	-	KLU91637.1 G-protein coupled receptor [Magnaporthe oryzae ATCC 64411]	G-protein coupled receptor 1 OS=Arabidopsis thaliana OX=3702 GN=GCR1 PE=1 SV=1
A8218	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K05610 UCHL5, UCH37; ubiquitin carboxyl-terminal hydrolase L5 [EC:3.4.19.12]	map03082 ATP-dependent chromatin remodeling	KOG2778 At1g65650 Ubiquitin C-terminal hydrolase	KAG0169664.1 ubiquitin carboxyl-terminal hydrolase [Apophysomycetes sp. BC1015]	Ubiquitin carboxyl-terminal hydrolase 2 OS=Arabidopsis thaliana OX=3702 GN=UCH2 PE=1 SV=1
A8219	-	-	-	-	-	-	-	-
A8220	-	-	GO:0005524(ATP binding)	K00938 E2.7.4.2, mvaK2; phosphomevalonate kinase [EC:2.7.4.2]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis;map01100 Metabolic pathways	KOG4519 At1g31910 Phosphomevalonate kinase	CDH52938.1 phosphomevalonate kinase [Lichtheimia corymbifera JMRc:FSU:9682]	Phosphomevalonate kinase, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=PMK PE=1 SV=1
A8221	-	-	-	-	-	-	-	-
A8222	-	-	-	-	-	-	GES90691.1 alpha/beta hydrolase [Rhizophagus clarus]	Probable carboxylic ester hydrolase LipM OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=lipM PE=1 SV=1
A8223	-	-	-	-	-	-	-	-
A8224	-	-	GO:0005515(protein binding)	K14830 MAK11, PAK1IP1; protein MAK11	-	KOG0294 YKL021c WD40 repeat-containing protein	KAF9200457.1 p21-activated protein kinase-interacting protein 1-like protein [Haplosporangium sp. Z27]	p21-activated protein kinase-interacting protein 1-like OS=Xenopus laevis OX=8355 GN=pak1ip1 PE=2 SV=1
A8225	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG1362 Hs14249468 Choline transporter-like protein	XP_006674882.1 uncharacterized protein BATDEDRAFT_1420, partial [Batrachochytrium dendrobatidis JAM81]	Choline transporter-like protein 4 OS=Sus scrofa OX=9823 GN=SLC44A4 PE=3 SV=1
A8226	-	-	-	K01083 E3.1.3.8; 3-phytase [EC:3.1.3.8]	map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	-	-	-

A8227	GO:0007017(microtubule-based process)	GO:0005874(microtubule)	GO:0005200(structural constituent of cytoskeleton),GO:0005525(GTP binding)	K07374 TUBA; tubulin alpha	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins;map04210 Apoptosis;map04540 Gap junction;map04530 Tight junction;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map050	KOG1376 At1g04820 Alpha tubulin	RKO92378.1 tubulin, alpha, ubiquitous, partial [Blyttiomycetes helicus]	Tubulin alpha chain OS=Neospora caninum OX=29176 GN=TUBA PE=2 SV=1
A8228	GO:0007017(microtubule-based process)	GO:0005874(microtubule)	GO:0005200(structural constituent of cytoskeleton),GO:0005525(GTP binding)	K07374 TUBA; tubulin alpha	map05014 Amyotrophic lateral sclerosis;map04145 Phagosome;map05132 Salmonella infection;map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins;map04210 Apoptosis;map04540 Gap junction;map04530 Tight junction;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map050	KOG1376 At1g04820 Alpha tubulin	RKO92378.1 tubulin, alpha, ubiquitous, partial [Blyttiomycetes helicus]	Tubulin alpha chain OS=Neospora caninum OX=29176 GN=TUBA PE=2 SV=1
A8229	GO:0071108(protein K48-linked deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase),GO:1990380(Lys48-specific deubiquitinase activity)	-	-	KOG2871 At1g43690 Uncharacterized conserved protein	TPX60269.1 hypothetical protein SpCBS45565_g07564 [Spizellomyces sp. 'palustris']	Probable ubiquitin carboxyl-terminal hydrolase MINDY-4 OS=Bos taurus OX=9913 GN=MINDY4 PE=2 SV=1
A8230	-	-	GO:0008270(zinc ion binding)	-	-	KOG4351 Hs13236514.1 Uncharacterized conserved protein	KAF8899092.1 hypothetical protein BD779DRAFT_1486970 [Infundibulicybe gibba]	Protein JOKA2 OS=Solanum tuberosum OX=4113 GN=JOKA2 PE=1 SV=1

A8231	GO:0019346(transsulfuration), GO:0006520(cellular amino acid metabolic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0003824(catalytic activity),GO:0016765(transferase activity, transferring alkyl or aryl (other than methyl) groups)	K17069 MET17; O-acetylhomoserine/O-acetylserine sulphydrylase [EC:2.5.1.49 2.5.1.47]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00920 Sulfur metabolism;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	-	TPX74596.1 O-acetylhomoserine aminocarboxypropyltransferase [Chytridiomycota confervae]	Homocysteine synthase OS=Emmericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) OX=227321 GN=cysD PE=1 SV=2
A8232	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At4g35780 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	XP_031025468.1 uncharacterized protein SmJEL517_g02575 [Synchytrium microbalum]	Serine/threonine-protein kinase STY17 OS=Arabidopsis thaliana OX=3702 GN=STY17 PE=1 SV=1
A8233	-	-	-	-	-	-	-	-
A8234	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding),GO:0003995(acyl-CoA dehydrogenase activity)	K00249 ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map03320 PPAR signaling pathway;map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map04936 Alcoholic liver disease;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG0139 Hs4501859 Short-chain acyl-CoA dehydrogenase	KXS13992.1 acyl-CoA dehydrogenase NM domain-like protein [Gonapodya prolifera JEL478]	Acyl-CoA dehydrogenase fadE12 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=fadE12 PE=3 SV=1
A8235	-	-	GO:0004842(ubiquitin-protein transferase activity),GO:0005515(protein binding),GO:0046872(metal ion binding)	-	-	KOG1426 Hs4557026 FOG:RCC1 domain	XP_031851879.1 uncharacterized protein SAPINGB_P001265 [Saprochaete ingens]	Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens OX=9606 GN=HERC1 PE=1 SV=2

A8236	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0043169(cation binding)	K07359 CAMKK2; calcium/calmodulin-dependent protein kinase kinase 2 [EC:2.7.11.17]	map04140 Autophagy - animal;map0421.1 Longevity regulating pathway;map05034 Alcoholism;map04936 Alcoholic liver disease;map04152 AMPK signaling pathway;map04920 Adipocytokine signaling pathway;map04921 Oxytocin signaling pathway	KOG0585 CE01146 Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	EPB86469.1 CAMKK/CAMKK-META protein kinase [Mucor circinelloides 1006PhL]	Calcium/calmodulin-dependent protein kinase kinase OS=Caenorhabditis elegans OX=6239 GN=ckk-1 PE=1 SV=2
A8237	-	-	GO:0005515(protein binding)	K14848 RRB1, GRWD1; ribosome assembly protein RRB1	-	KOG0302 At2g19540 Ribosome Assembly protein	KXS13583.1 WD40 repeat-like protein [Gonapodya prolifera JEL478]	Protein HEAT STRESS TOLERANT DWD 1 OS=Arabidopsis thaliana OX=3702 GN=HTD1 PE=1 SV=1
A8238	-	-	-	K00059 fabG, OAR1; 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	map01110 Biosynthesis of secondary metabolites;map00780 Biotin metabolism;map01240 Biosynthesis of cofactors;map00333 Prodigiosin biosynthesis;map00061 Fatty acid biosynthesis;map01100 Metabolic pathways;map01212 Fatty acid metabolism	KOG0725 At2g29260 Reductases with broad range of substrate specificities	PZC91345.1 hypothetical protein Ptr86124_11474 [Pyrenophora tritici-repentis]	Uncharacterized oxidoreductase Ymfl OS=Bacillus subtilis (strain 168) OX=224308 GN=ymfl PE=3 SV=2
A8239	GO:0006281(DNA repair)	GO:0005634(nucleus)	GO:0003684(damaged DNA binding)	K10849 ERCC1; DNA excision repair protein ERCC-1	map03420 Nucleotide excision repair;map01524 Platinum drug resistance;map03460 Fanconi anemia pathway	KOG2841 At3g05210 Structure-specific endonuclease ERCC1-XPF, ERCC1 component	XP_016609804.1 DNA repair protein rad10, variant [Spizellomyces punctatus DAOM BR117]	DNA excision repair protein ERCC-1 OS=Arabidopsis thaliana OX=3702 GN=ERCC1 PE=2 SV=1

A8240	GO:0009058(biosynthetic process), GO:0009094(L-phenylalanine biosynthetic process), GO:0006571(tyrosine biosynthetic process)	-	GO:0003824(catalytic activity), GO:0030170(pyridoxal phosphate binding), GO:0004664(prephenate dehydratase activity), GO:0004665(prephenate dehydrogenase (NADP+) activity), GO:0008977(prephenate dehydrogenase (NAD+) activity)	K14264 BNA3; kynurenine aminotransferase [EC:2.6.1.7]	map00380 Tryptophan metabolism; map01100 Metabolic pathways	KOG0257 At2g22250 Kynurenine aminotransferase, glutamine transaminase K	KAG1264013.1 hypothetical protein G6F65_014423 [Rhizopus oryzae]	Aspartate/prephenate aminotransferase OS=Chlorobaculum tepidum (strain ATCC 49652 / DSM 12025 / NBRC 103806 / TLS) OX=194439 GN=CT0966 PE=1 SV=1
A8241	GO:0006351(transcription, DNA-templated)	-	GO:0003899(DNA-directed 5'-3' RNA polymerase activity), GO:0046983(protein dimerization activity), GO:0001054(RNA polymerase I activity), GO:0001056(RNA polymerase III activity)	K03027 RPAC1, RPC40, POLR1C; DNA-directed RNA polymerases I and III subunit RPAC1	map03020 RNA polymerase; map04623 Cytosolic DNA-sensing pathway	KOG1521 At1g60850 RNA polymerase I and III, subunit RPA40/RPC40	KAG0006877.1 DNA-directed RNA polymerases I and III subunit RPAC1 [Modicella reniformis]	DNA-directed RNA polymerases I and III subunit rpac1 OS=Dictyostelium discoideum OX=44689 GN=polr1c PE=3 SV=1
A8242	-	-	-	-	-	-	-	-
A8243	-	-	-	-	-	-	-	-
A8244	-	-	GO:0003824(catalytic activity)	-	-	-	-	-
A8245	-	-	GO:0003676(nucleic acid binding), GO:0003723(RNA binding)	K14573 NOP4, RBM28; nucleolar protein 4	map03008 Ribosome biogenesis in eukaryotes	KOG0127 Hs8922388 Nucleolar protein fibrillarin NOP77 (RRM superfamily)	RKP07495.1 hypothetical protein THASP1DRAFT_30691 [Thamnocephalus sphaerospora]	RNA-binding protein 28 OS=Mus musculus OX=10090 GN=Rbm28 PE=1 SV=4
A8246	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity), GO:0005509(calcium ion binding)	K09578 PIN1; peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 [EC:5.2.1.8]	map03250 Viral life cycle - HIV-1; map04622 RIG-I-like receptor signaling pathway	KOG3259 At2g18040 Peptidyl-prolyl cis-trans isomerase	XP_001645783.1 hypothetical protein Kpol_1010p41 [Vanderwaltozyma polyspora DSM 70294]	Peptidyl-prolyl cis-trans isomerase Pin1 OS=Digitalis lanata OX=49450 GN=PARV12.8 PE=1 SV=1

A8247	-	-	GO:0016491(oxidoreductase activity),GO:0046872(metal ion binding)	K13954 yiaY; alcohol dehydrogenase [EC:1.1.1.1]	map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01220 Degradation of aromatic compounds;map00625 Chloroalkane and chloroalkene degradation;map00626 Naphthalene degradation;map00620 Pyruvate metabolism;map00350 Tyrosine metabolism;map01100 Metabolic pathways;map00	KOG3857 YGL256w Alcohol dehydrogenase, class IV	RMJ20703.1 alcohol dehydrogenase, partial [Aspergillus sp. HF37]	Long-chain-alcohol dehydrogenase 1 OS=Geobacillus thermodenitrificans (strain NG80-2) OX=420246 GN=adh1 PE=1 SV=1
A8248	GO:0006310(DNA recombination)	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding),GO:0004386(helicase activity)	K10899 RECQL; ATP-dependent DNA helicase Q1 [EC:5.6.2.4]	-	KOG0353 Hs14591902 ATP-dependent DNA helicase	ODV89963.1 hypothetical protein CANCADRAFT_24928, partial [Tortispora caseinolytica NRRL Y-17796]	ATP-dependent DNA helicase Q1 OS=Rattus norvegicus OX=10116 GN=Recql PE=1 SV=1
A8249	GO:0031145(anaphase-promoting complex-dependent catabolic process),GO:1990116(ribosome-associated ubiquitin-dependent protein catabolic process)	GO:0005680(anaphase-promoting complex),GO:1990112(RQC complex)	GO:0008270(zinc ion binding),GO:0061630(ubiquitin protein ligase activity),GO:0097602(cullin family protein binding)	K22377 LTN1; E3 ubiquitin-protein ligase listerin [EC:2.3.2.27]	-	KOG0803 Hs14780121 Predicted E3 ubiquitin ligase	KAF9921104.1 hypothetical protein BGZ65_010638, partial [Modicella reniformis]	E3 ubiquitin-protein ligase listerin OS=Xenopus tropicalis OX=8364 GN=ltn1 PE=2 SV=1
A8250	GO:0010468(regulation of gene expression),GO:0061780(mitotic cohesin loading)	-	GO:0003682(chromatin binding)	K06672 SCC2, NIPBL; cohesin loading factor subunit SCC2	map04111 Cell cycle - yeast;map04110 Cell cycle	KOG1020 Hs7661842 Sister chromatid cohesion protein SCC2/Nipped-B	GBC26280.1 Cohesin loading factor subunit SCC2 [Rhizophagus irregularis DAOM 181602=DAOM 197198]	Nipped-B-like protein OS=Homo sapiens OX=9606 GN=NIPBL PE=1 SV=2
A8251	-	-	GO:0005515(protein binding)	-	-	-	PMD12017.1 ankyrin, partial [Hyaloscypha hepaticicola]	-

A8252	GO:0006430(lysyl-tRNA aminoacylation),GO:0006418(tRNA aminoacylation for protein translation)	GO:0005737(cytoplasm)	GO:0004824(lysine-tRNA ligase activity),GO:0005524(ATP binding),GO:0001666(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0003676(nucleic acid binding)	K04567 KARS, lysS; lysyl-tRNA synthetase, class II [EC:6.1.1.6]	map00970 Aminoacyl-tRNA biosynthesis	KOG1885 7291073 Lysyl-tRNA synthetase (class II)	EPZ34923.1 Lysine--tRNA ligase [Rozella allomyces CSF55]	Lysine--tRNA ligase OS=Cricetulus griseus OX=10029 GN=KARS1 PE=1 SV=1
A8253	GO:0006913(nucleocytoplasmic transport)	GO:0005643(nuclear pore)	GO:0017056(structural constituent of nuclear pore)	K14312 NUP155, NUP170, NUP157; nuclear pore complex protein Nup155	map05014 Amyotrophic lateral sclerosis;map03013 Nucleocytoplasmic transport	KOG1900 At1g14850 Nuclear pore complex, Nup155 component (D Nup154, sc Nup157/Nup170)	KAG4105226.1 nucleoporin-domain-containing protein [Neocallimastix sp. JGI-2020a]	Nuclear pore complex protein NUP155 OS=Arabidopsis thaliana OX=3702 GN=NUP155 PE=1 SV=1
A8254	-	-	GO:0005515(protein binding),GO:0016787(hydrolase activity)	K14262 DUG2; di- and tripeptidase [EC:3.4.-.-]	-	KOG2276 CE12770 Metalloexopeptidases	RIA83883.1 hypothetical protein C1645_785306 [Glomus cerebriforme]	Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9606 GN=CNDP2 PE=1 SV=2
A8255	-	-	GO:0005515(protein binding)	-	-	-	KAG0171414.1 hypothetical protein DFQ30_000979 [Apophysomyces sp. BC1015]	2-aminoethylphosphonate dioxygenase OS=Uncultured bacterium HF130_AEPn_1 OX=663362 GN=phnY PE=1 SV=1
A8256	-	-	-	-	-	KOG4827 At1g65270 Uncharacterized conserved protein	TPX58707.1 hypothetical protein PhCBS80983_g02990 [Powellomyces hirtus]	-
A8257	GO:0007094(mitotic spindle assembly checkpoint signaling)	-	-	K02537 MAD2; mitotic spindle assembly checkpoint protein MAD2	map04914 Progesterone-mediated oocyte maturation;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04111 Cell cycle - yeast;map04110 Cell cycle;map05166 Human T-cell leukemia virus 1 infection	KOG3285 Hs4505067 Spindle assembly checkpoint protein	ORX91542.1 HORMA domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Mitotic spindle assembly checkpoint protein MAD2A OS=Dictyostelium discoideum OX=44689 GN=mad2 1-1 PE=3 SV=1
A8258	-	-	GO:0005544(calcium-dependent phospholipid binding)	-	-	KOG1327 Hs4503015 Copine	XP_016609497.1 hypothetical protein SPPG_03260 [Spizellomyces punctatus DAOM BR117]	Copine-2 OS=Homo sapiens OX=9606 GN=CPNE2 PE=1 SV=3

A8259	-	-	-	-	-	-	-	-
A8260	-	-	GO:0005515(protein binding)	-	-	KOG2084 Hs910274 Predicted histone tail methylase containing SET domain	RUP42399.1 hypothetical protein BC936DRAFT_138265 [Jimgerdemia flammicorona]	N-lysine methyltransferase SMYD2 OS=Sus scrofa OX=9823 GN=SMYD2 PE=2 SV=1
A8261	-	-	-	-	-	-	-	-
A8262	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	RPA77283.1 DUF803-domain-containing protein, partial [Ascobolus immersus RN42]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A8263	GO:0006508(proteolysis)	-	GO:0008236(serine-type peptidase activity),GO:0004252(serine-type endopeptidase activity)	K01322 PREP; prolyl oligopeptidase [EC:3.4.21.26]	map04614 Renin-angiotensin system	KOG2237 Hs14727117 Predicted serine protease	KAG0167250.1 hypothetical protein DFQ30_006240 [Apophysomyces sp. BC1015]	Dipeptidyl aminopeptidase BI OS=Pseudoxanthomonas mexicana OX=128785 GN=dapb1 PE=1 SV=1
A8264	GO:0006529(asparagine biosynthetic process)	-	GO:0004066(asparagine synthase (glutamine-hydrolyzing) activity)	K01953 asnB, ASNS; asparagine synthase (glutamine-hydrolyzing) [EC:6.3.5.4]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG0571 At5g65010 Asparagine synthase (glutamine-hydrolyzing)	KAF7114352.1 hypothetical protein CNMCM5793_008304 [Aspergillus hiratsukae]	Asparagine synthetase [glutamine-hydrolyzing] 2 OS=Arabidopsis thaliana OX=3702 GN=ASN2 PE=2 SV=1
A8265	-	-	GO:0016857(racemase and epimerase activity, acting on carbohydrates and derivatives)	-	-	-	PTD05974.1 hypothetical protein FCULG_00002212, partial [Fusarium culmorum]	L-rhamnose mutarotase OS=Oceanobacillus iheyensis (strain DSM 14371 / CIP 107618 / JCM 11309 / KCTC 3954 / HTE831) OX=221109 GN=rhaM PE=3 SV=1
A8266	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A8267	-	-	-	K14797 ENP1, BYSL; essential nuclear protein 1	-	KOG3871 Hs15208645 Cell adhesion complex protein bystin	ORY95736.1 Bystin-domain-containing protein [Syncephalaster racemosum]	Bystin OS=Mus musculus OX=10090 GN=BySL PE=1 SV=3
A8268	-	-	-	-	-	-	KXS21448.1 hypothetical protein M427DRAFT_150830 [Gonapodya prolifera JEL478]	-

A8269	GO:0006979(response to oxidative stress),GO:0034599(cellular response to oxidative stress)	-	GO:0004601(peroxidase activity),GO:0020037(heme binding)	K00428 E1.1.1.1.5; cytochrome c peroxidase [EC:1.1.1.1.5]	-	-	POY71032.1 cytochrome c peroxidase [Rhodotorula taiwanensis]	Cytochrome c peroxidase, mitochondrial OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=CCP1 PE=3 SV=1
A8270	-	-	-	-	-	-	OQS53519.1 hypothetical protein EHP00_2479 [Enterocytozoan hepatopenaei]	-
A8271	-	GO:0005634(nucleus)	GO:0005515(protein binding)	-	-	KOG4443 729022 Putative transcription factor HALR/MLL3, involved in embryonic development	RIB09800.1 F/Y rich C-terminus-domain-containing protein [Gigaspora rosea]	Histone-lysine N-methyltransferase trr OS=Drosophila melanogaster OX=7227 GN=trr PE=1 SV=2
A8272	GO:0006260(DNA replication),GO:0006281(DNA repair),GO:0006310(DNA recombination)	GO:0005634(nucleus)	GO:0003677(DNA binding)	-	-	-	GBB89705.1 hypothetical protein RclHR1_01650012 [Rhizophagus clarus]	Replication protein A 14 kDa subunit B OS=Arabidopsis thaliana OX=3702 GN=RPA3B PE=1 SV=1
A8273	-	-	-	K06950 K06950; uncharacterized protein	-	-	KAF9131879.1 hypothetical protein BGW39_001183 [Mortierella sp. 14UC]	Uncharacterized protein YpgQ OS=Bacillus subtilis (strain 168) OX=224308 GN=ypgQ PE=4 SV=1
A8274	GO:0006096(glycolytic process)	-	GO:0004619(phosphoglycerate mutase activity),GO:0016868(intramolecular transferase activity, phosphotransferases)	K01834 PGAM, gpmA; 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00680 Methane metabolism;map00260 Glycine, serine and threonine metabolism;map05230 Central carbon metabolism in cancer;map01110 Metabolic pathways;map04	KOG0235 At1g22170 Phosphoglycerate mutase	XP_025348444.1 phosphoglycerate mutase [Pseudomonas stroma glucosiphilum]	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2 OS=Arabidopsis thaliana OX=3702 GN=gpmA2 PE=2 SV=1
A8275	-	GO:0005758(mitochondrial intermembrane space)	-	-	-	KOG3336 Hs7705610 Predicted member of the intramitochondrial sorting protein family	ORX43094.1 MSF1-domain-containing protein [Hesseltinella vesiculosa]	PRELI domain containing protein 3B OS=Rattus norvegicus OX=10116 GN=Preli3b PE=1 SV=1
A8276	-	-	GO:0003677(DNA binding),GO:0008270(zinc ion binding)	-	-	-	-	-

A8277	GO:0034219(carbohydrate transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015144(carbohydrate transmembrane transporter activity)	-	-	-	-	Transmembrane protein 144 OS=Mus musculus OX=10090 GN=Tmem144 PE=2 SV=1
A8278	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0015301(anion:anion antiporter activity)	K14708 SLC26A11; solute carrier family 26 (sodium-independent sulfate anion transporter), member 11	-	KOG0236 At5g13550 Sulfate/bicarbonate/oxalate exchanger SAT-1 and related transporters (SLC26 family)	GBB94561.1 hypothetical protein RclHRI_02380020 [Rhizophagus clarus]	Sulfate transporter 4.1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=SULTR4;1 PE=1 SV=1
A8279	-	-	GO:0005509(calcium ion binding)	-	-	-	-	-
A8280	-	-	GO:0005515(protein binding)	-	-	-	XP_016604219.1 hypothetical protein SPPG_08334 [Spizellomyces punctatus DAOM BR117]	CBS domain-containing protein CBSCBSPB2 OS=Arabidopsis thaliana OX=3702 GN=CBSCBSPB2 PE=2 SV=1
A8281	GO:0006338(chromatin remodeling),GO:0006396(RNA processing)	GO:0005634(nucleus)	GO:0003723(RNA binding),GO:0016779(nucleotidyl transferase activity)	K11662 ACTR6, ARP6; actin-related protein 6	map03082 ATP-dependent chromatin remodeling	-	EWC44214.1 hypothetical protein DRE_06959 [Drechslerella stenobrocha 248]	Actin-related protein 6 OS=Gallus gallus OX=9031 GN=ACTR6 PE=1 SV=1
A8282	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	Ethylene-responsive transcription factor WRI1 OS=Arabidopsis thaliana OX=3702 GN=WRI1 PE=1 SV=1
A8283	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity),GO:0043169(cation binding)	K19704 PTC1; protein phosphatase PTC1 [EC:3.1.3.16]	map04011 MAPK signaling pathway - yeast	KOG0698 YDL006w Serine/threonine protein phosphatase	KAG0748386.1 hypothetical protein G6F23_001943 [Rhizopus oryzae]	Protein phosphatase 2C homolog 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PTC1 PE=1 SV=1
A8284	-	-	GO:0004364(glutathione transferase activity)	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis -	KOG1422 At1g75270 Intracellular Cl- channel CLIC, contains GST domain	TPX64507.1 hypothetical protein CcCBS67573_g08400 [Chytridiomycs confervae]	Glutathione S-transferase DHAR2 OS=Arabidopsis thaliana OX=3702 GN=DHAR2 PE=1 SV=1

A8285	-	-	GO:0005509(cal- cium ion binding)	K16466 CETN3, CDC31; centrin-3	-	KOG0028 Hs4 757976 Ca2+- binding protein (centrin/caltr- actin), EF- Hand superfamily protein	TPX67250.1 hypothetical protein SpCBS45565- g03964 [Spizellomyces sp. 'palustris']	Caltractin OS=Scherffelia dubia OX=3190 PE=1 SV=1
A8286	-	-	GO:0016620(oxi- doreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor),GO:00 16491(oxidore- ductase activity),GO:000 4491(methylmal- onate-semialdehyde dehydrogenase (acylating) activity)	K00140 mmsA, iolA, ALDH6A1; malonate- semialdehyde dehydrogenase (acylating)/ methylmalon- ate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]	map00410 beta- Alanine metabolism;map 01200 Carbon metabolism;map 00640 Propanoate metabolism;map 00280 Valine, leucine and isoleucine degradation;ma- p00562 Inositol phosphate metabolism;map 01100 Metabolic pathways	KOG2449 Hs1 1095441 Methylmalon- ate-semialdehyde dehydrogenase [acylating] mitochondria I [Rhizopus azgyosporus]	RCH88561.1 Methylmalon- ate-semialdehyde dehydrogenase [acylating] mitochondria I [Rhizopus azgyosporus]	Methylmalonate-semialdehyde/malonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Bos taurus OX=9913 GN=ALDH6A1 PE=1 SV=1
A8287	GO:00150 31(protein transport), GO:00421 47(retrograde transport, endosome to Golgi)	GO:00309 06(retromer, cargo- selective complex)	-	K18468 VPS35; vacuolar protein sorting- associated protein 35	map04144 Endocytosis	KOG1107 Hs1 7999541 Membrane coat complex Retromer, subunit VPS35	KAF9112984. 1 Vacuolar protein sorting- associated protein 35 [Mortierella sp. AM989]	Vacuolar protein sorting-associated protein 35A OS=Arabidopsis thaliana OX=3702 GN=VPS35A PE=1 SV=1
A8288	-	-	-	-	-	KOG1426 Hs1 9923519 FOG: RCC1 domain	-	RCC1 and BTB domain-containing protein 1 OS=Mus musculus OX=10090 GN=Rcbtb1 PE=1 SV=1
A8289	GO:00071 65(signal transduction)	-	GO:0005515(pro- tein binding)	-	-	-	XP_03102564. 6.1 uncharacteriz- ed protein SmJEL517_g0 2373 [Synchytrium microbalum]	-
A8290	-	-	-	-	-	-	-	-
A8291	GO:00065 08(proteol- ysis)	-	GO:0004252(seri- ne-type endopeptidase activity)	-	-	-	-	-
A8292	GO:00065 08(proteol- ysis)	-	GO:0004252(seri- ne-type endopeptidase activity),GO:000 8236(serine- type peptidase activity)	K01336 PRB1; cerevisin [EC:3.4.21.48 3.4.21.-]	map04138 Autophagy - yeast	-	KXX76973.1 Subtilisin-like protease 9 [Madurella mycetomatis]	Aqualysin-1 OS=Thermus aquaticus OX=271 GN=pstI PE=1 SV=2
A8293	GO:00064 68(protein phosphor- ylation)	-	GO:0004672(pro- tein kinase activity),GO:000 5524(ATP binding),GO:000 5515(protein binding)	-	-	KOG0194 CE 11430 Protein tyrosine kinase	XP_01899848 5.1 hypothetical protein L202_00578 [Cryptococcus amyloletus CBS 6039]	Cyclin-dependent kinase 9 OS=Danio rerio OX=7955 GN=cdk9 PE=2 SV=1
A8294	-	-	-	-	-	-	-	-
A8295	-	-	GO:0005515(pro- tein binding)	-	-	-	-	-

A8296	GO:0042732(D-xylose metabolic process)	-	GO:0048040(UDP-glucuronate decarboxylase activity),GO:0070403(NAD+ binding)	K08678 UXS1, uxs; UDP-glucuronate decarboxylase [EC:4.1.1.35]	map01250 Biosynthesis of nucleotide sugars;map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG1429[CE04302 dTDP-glucose 4-6-dehydratase/UDP-glucuronic acid decarboxylase	KZT55336.1 NAD(P)-binding protein [Calocera cornea HHB12733]	UDP-glucuronic acid decarboxylase 1 OS=Homo sapiens OX=9606 GN=UXS1 PE=1 SV=1
A8297	-	-	GO:0016787(hydrolase activity)	K06269 PPP1C; serine/threonine-protein phosphatase PP1 catalytic subunit. [EC:3.1.3.16]	map04390 Hippo signaling pathway;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05415 Diabetic cardiomyopathy; map04810 Regulation of actin cytoskeleton;map04510 Focal adhesion;map04218 Cellular senescence;map04910 Insulin signaling pathway;map04728 Dopaminergic synapse;map04720 Long-term potentiation;map05031 Amphetamine addiction;map04	-	KAF9992041.1 Serine/threonine-protein phosphatase pp1, partial [Entomortierella chlamydospora]	Serine/threonine-protein phosphatase PP1-1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=dis2 PE=1 SV=1
A8298	-	-	GO:0000166(nucleotide binding)	-	-	KOG2741[7295964 Dimeric dihydrodiol dehydrogenase	CDO73710.1 hypothetical protein BN946_scf185015.g38 [Trametes cinnabarina]	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase OS=Danio rerio OX=7955 GN=dhdh PE=2 SV=2
A8299	-	-	-	-	-	-	-	-
A8300	-	-	-	-	-	-	-	-
A8301	GO:0006413(translational initiation)	GO:0005852(eukaryotic translation initiation factor 3 complex)	GO:0003743(translation initiation factor activity),GO:0031369(translation initiation factor binding),GO:0005515(protein binding),GO:0008233(peptidase activity),GO:0008237(metallopeptidase activity)	K03249 EIF3F; translation initiation factor 3 subunit F	-	KOG2975[At2g39990 Translation initiation factor 3, subunit f (eIF-3f)	KAF9325429.1 hypothetical protein BG006_011094 [Podila minutissima]	Eukaryotic translation initiation factor 3 subunit F OS=Dictyostelium discoideum OX=44689 GN=eif3f PE=3 SV=1
A8302	GO:1902600(proton transmembrane transport)	GO:000587(integral component of plasma membrane)	GO:0030171(voltage-gated proton channel activity)	-	-	-	-	-
A8303	-	-	-	-	-	-	-	-

A8304	GO:0006355(regulation of transcription, DNA-templated);GO:0016573(histone acetylation)	-	GO:0004402(histone acetyltransferase activity)	K11304 TIP60, KAT5, ESA1; histone acetyltransferase HTATIP [EC:2.3.1.48]	map03082 ATP-dependent chromatin remodeling;map05017 Spinocerebellar ataxia;map05166 Human T-cell leukemia virus 1 infection	KOG2747 At5g64610 Histone acetyltransferase (MYST family)	EIE89546.1 hypothetical protein RO3G_14257 [Rhizopus delemar RA 99-880]	Histone acetyltransferase of the MYST family 1 OS=Arabidopsis thaliana OX=3702 GN=HAM1 PE=1 SV=1
A8305	-	-	GO:0019905(synaptotagmin binding)	-	-	KOG1850 Hs8922940 Myosin-like coiled-coil protein	-	-
A8306	GO:0000398(mRNA splicing, via spliceosome)	GO:0005688(U6 snRNP);GO:0046540(U4/U6 x U5 tri-snRNP complex)	-	K12627 LSM8; U6 snRNA-associated Sm-like protein LSM8	map03040 Spliceosome;map03018 RNA degradation	KOG1784 At1g65700 Small Nuclear ribonucleoprotein splicing factor	PIA18317.1 N-alpha-acetyltransferase 38, NatC auxiliary subunit [Coemansia reversa NRRL 1564]	Sm-like protein LSM8 OS=Arabidopsis thaliana OX=3702 GN=LSM8 PE=1 SV=1
A8307	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K06684 DBF2; cell cycle protein kinase DBF2 [EC:2.7.11.-]	map04392 Hippo signaling pathway - multiple species;map04111 Cell cycle - yeast	KOG0616 Hs4506057 cAMP-dependent protein kinase catalytic subunit (PKA)	KXN69972.1 kinase-like protein, partial [Conidiobolus coronatus NRRL 28638]	Spermatozoon-associated protein kinase OS=Aplysia californica OX=6500 PE=2 SV=1
A8308	GO:0006468(protein phosphorylation)	-	GO:0035091(phosphatidylinositol binding);GO:0004672(protein kinase activity);GO:0005524(ATP binding)	-	-	KOG0192 At1g73660 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAG0257413.1 hypothetical protein DFQ27_005157 [Actinomyces rella ambigua]	Probable serine/threonine-protein kinase SIS8 OS=Arabidopsis thaliana OX=3702 GN=SIS8 PE=1 SV=1
A8309	-	-	-	-	-	KOG1609 At4g34100 Protein involved in mRNA turnover and stability	RIB06064.1 hypothetical protein C2G38_542961 [Gigaspora rosea]	Probable E3 ubiquitin ligase SUD1 OS=Arabidopsis thaliana OX=3702 GN=SUD1 PE=1 SV=1
A8310	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding)	K03005 RPA49, POLR1E; DNA-directed RNA polymerase I subunit RPA49	map03020 RNA polymerase	KOG4183 Hs11968047 RNA polymerase I 49 kDa subunit	OSD00005.1 RNA polymerase I associated factor A49-like protein [Trametes coccinea BRFM310]	DNA-directed RNA polymerase I subunit RPA49 OS=Xenopus laevis OX=8355 GN=polr1e PE=2 SV=1
A8311	-	-	GO:0005524(ATP binding)	K06158 ABCF3; ATP-binding cassette, subfamily F, member 3	-	KOG0066 Hs10947135 eIF2-interacting protein ABC50 (ABC superfamily)	GFZ42543.1 Probable ATP-binding cassette sub-family F member 3 homolog [Saitozyma sp. JCM 24511]	ATP-binding cassette sub-family F member 1 OS=Mus musculus OX=10090 GN=Abcf1 PE=1 SV=1
A8312	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8313	-	-	GO:0005515(protein binding)	-	-	-	-	-

A8314	GO:0016579(protein deubiquitination).GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase)	K11841 USP10, UBP3; ubiquitin carboxyl-terminal hydrolase 10 [EC:3.4.19.12]	map04139 Mitophagy - yeast	-	KAB5525603.1 hypothetical protein GE09DRAFT_475731 [Coniochaeta sp. 2T2.1]	Ubiquitin hydrolase B OS=Dictyostelium discoideum OX=44689 GN=ubpB PE=1 SV=1
A8315	-	-	GO:0003676(nucleic acid binding).GO:0005524(ATP binding)	K14806 DDX31, DBP7; ATP-dependent RNA helicase DDX31/DBP7 [EC:3.6.4.13]	-	KOG0348 At2g40700 ATP-dependent RNA helicase	GES86699.1 DEAD-domain-containing protein [Rhizophagus clarus]	DEAD-box ATP-dependent RNA helicase 17 OS=Arabidopsis thaliana OX=3702 GN=RH17 PE=2 SV=1
A8316	GO:0006434(seryl-tRNA aminoacylation).GO:0006418(tRNA aminoacylation for protein translation)	-	GO:0000166(nucleotide binding).GO:0004828(serine-tRNA ligase activity).GO:0005524(ATP binding).GO:0004812(aminoacyl-tRNA ligase activity)	K01875 SARS, serS; seryl-tRNA synthetase [EC:6.1.1.11]	map00970 Aminoacyl-tRNA biosynthesis	KOG2509 At5g27470 Seryl-tRNA synthetase	XP_002562612.1 Pc20g00490 [Penicillium rubens Wisconsin 54-1255]	Serine--tRNA ligase, cytoplasmic OS=Dictyostelium discoideum OX=44689 GN=serS PE=1 SV=1
A8317	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1198 At1g23740 Zinc-binding oxidoreductase	KAG5362225.1 2-methylene-furan-3-one reductase [Yarrowia sp. C11]	2-methylene-furan-3-one reductase OS=Solanum lycopersicum OX=4081 GN=EO PE=1 SV=1
A8318	-	-	-	-	-	-	-	-
A8319	-	-	-	-	-	-	-	-
A8320	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity)	-	-	-	KAG0095046.1 hypothetical protein BGZ93_006400 [Podila epicladia]	-
A8321	-	-	-	-	-	-	-	-
A8322	-	-	-	-	-	-	-	-
A8323	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2157 Hs7661564 Predicted tubulin-tyrosine ligase	TPX72983.1 hypothetical protein SpCBS45565_g00142 [Spizellomyces sp. 'palustris']	Tubulin glycosylase 3A OS=Tetrahymena thermophila (strain SB210) OX=312017 GN=TTLL3A PE=1 SV=1
A8324	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8325	GO:0006265(DNA topological change)	GO:0005694(chromosome)	GO:0003677(DNA binding).GO:0003917(DNA topoisomerase type I (single strand cut, ATP-independent) activity)	K03163 TOP1; DNA topoisomerase I [EC:5.6.2.1]	-	KOG0981 At5g55310 DNA topoisomerase I	ORX47892.1 hypothetical protein BCR36DRAFT_355358 [Piromyces finnis]	DNA topoisomerase 1 OS=Dictyostelium discoideum OX=44689 GN=top1 PE=3 SV=1

A8326	GO:0008299(isoprenoid biosynthetic process)	-	GO:0004452(isopentenyl-diphosphate delta-isomerase activity)	K01823 idi, IDI; isopentenyl-diphosphate Delta-isomerase [EC:5.3.3.2]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis;map01100 Metabolic pathways	KOG0142 Hs4758584 Isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	TPX57189.1 isopentenyl-diphosphate Delta-isomerase [Spizellomyces sp. 'palustris']	Isopentenyl-diphosphate Delta-isomerase 1 OS=Macaca fascicularis OX=9541 GN=IDI1 PE=2 SV=2
A8327	-	-	-	-	-	-	-	-
A8328	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02871 RP-L13, MRPL13, rplM; large subunit ribosomal protein L13	map03010 Ribosome	KOG3203 YOR150w Mitochondrial/chloroplast ribosomal protein L13	KAG2177474.1 hypothetical protein INT44_007985 [Umbelopsis vinacea]	Large ribosomal subunit protein uL13 OS=Clostridioides difficile (strain 630) OX=272563 GN=rplM PE=3 SV=1
A8329	-	-	-	-	-	-	-	-
A8330	GO:0007165(signal transduction),GO:000160(phosphorelay signal transduction system),GO:0016310(phosphorylation)	-	GO:0000155(phosphorelay sensor kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	KOG0519 At5g35750 Sensory transduction histidine kinase	PHH67070.1 hypothetical protein CDD81_4465 [Ophiocordyceps australis]	Probable histidine kinase 1 OS=Oryza sativa subsp. indica OX=39946 GN=HK1 PE=3 SV=1
A8331	GO:0000160(phosphorelay signal transduction system),GO:0007165(signal transduction),GO:0016310(phosphorylation)	-	GO:0000155(phosphorelay sensor kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups)	K19691 NIK1, TCSC; osomolarity two-component system, sensor histidine kinase NIK1 [EC:2.7.13.3]	map02020 Two-component system	KOG0519 At5g10720 Sensory transduction histidine kinase	KAF9121300.1 hypothetical protein BGX30_002674 [Mortierella sp. GBA39]	Autoinducer 2 sensor kinase/phosphatase LuxQ OS=Vibrio vulnificus (strain CMCP6) OX=216895 GN=luxQ PE=3 SV=1
A8332	-	-	-	-	-	-	-	-
A8333	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A8334	-	-	-	-	-	-	ORY42512.1 CRAL/TRIO domain-containing protein [Rhizoclostium globosum]	-
A8335	-	-	-	-	-	-	-	-
A8336	GO:0031124(mRNA 3'-end processing),GO:0006396(RNA processing)	-	GO:0051731(polyribonucleotide 5'-hydroxyl-kinase activity)	K14399 CLP1, HERB; polyribonucleotide 5'-hydroxyl-kinase [EC:2.7.1.78]	map03015 mRNA surveillance pathway	KOG2749 At3g04680 mRNA cleavage and polyadenylation factor IA/II complex, subunit CLP1	CDH48990.1 polyribonucleotide 5'-hydroxyl-kinase clp1 [Lichtheimia corymbifera JMRC:FSU:9682]	Protein CLP1 homolog OS=Arabidopsis thaliana OX=3702 GN=CLP53 PE=1 SV=1
A8337	-	-	GO:0005515(protein binding)	-	-	-	-	-

A8338	-	-	GO:0005515(protein binding),GO:0005085(guanylnucleotide exchange factor activity)	K19842 ROM1_2; RHO1 GDP-GTP exchange protein 1/2	map04011 MAPK signaling pathway - yeast	KOG4424 Hs21245128 Predicted Rho/Rac guanine nucleotide exchange factor/faciogenital dysplasia protein 3	PVV02070.1 hypothetical protein BB560_00348 4, partial [Smittium megazygosporum]	FYVE, RhoGEF and PH domain-containing protein 4 OS=Mus musculus OX=10090 GN=Fgd4 PE=1 SV=1
A8339	-	-	-	-	-	-	SAM04862.1 hypothetical protein [Absidia glauca]	-
A8340	GO:0043461(proton-transporting ATP synthase complex assembly)	-	-	K07556 ATPeAF2, ATPAF2, ATP12; ATP synthase mitochondria I F1 complex assembly factor 2	-	KOG3015 Hs21735485 F1-ATP synthase assembly protein	KZT60360.1 ATP12-domain-containing protein [Calocera cornea HHB12733]	ATP synthase mitochondrial F1 complex assembly factor 2 OS=Homo sapiens OX=9606 GN=ATPAF2 PE=1 SV=1
A8341	GO:1902600(proton transmembrane transport)	GO:0016020(membrane)	GO:0004427(inorganic diphosphatase activity),GO:0009678(pyrophosphate hydrolysis-driven proton transmembrane transporter activity)	-	-	-	KAG1209907.1 hypothetical protein G6F35_010653 [Rhizopus oryzae]	Pyrophosphate-energized vacuolar membrane proton pump OS=Vigna radiata var. radiata OX=3916 PE=1 SV=4
A8342	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003723(RNA binding),GO:0003677(DNA binding),GO:0003676(nucleic acid binding),GO:0003700(DNA-binding transcription factor activity)	-	-	KOG1275 CE01269 PAB-dependent poly(A) ribonuclease, subunit PAN2	RLV92562.1 RNA exonuclease 1 [Spathaspora sp. JA1]	RNA exonuclease 1 homolog OS=Mus musculus OX=10090 GN=Rexo1 PE=1 SV=1
A8343	GO:0000160(phosphorelay signal transduction system),GO:0007165(signal transduction),GO:0016310(phosphorylation)	-	GO:0000155(phosphorelay sensor kinase activity),GO:0016772(transferase activity, transferring phosphorus-containing groups)	-	-	KOG0519 At1g66340 Sensory transduction histidine kinase	QRW26613.1 protein-histidine kinase [Rhizoctonia solani]	Hybrid signal transduction histidine kinase J OS=Dictyostelium discoideum OX=44689 GN=dhkj PE=3 SV=2
A8344	-	-	-	-	-	-	-	-
A8345	-	-	-	-	-	-	-	-
A8346	-	-	-	-	-	KOG4372 YOR059c Predicted alpha/beta hydrolase	XP_022391576.1 hypothetical protein ABOM_003318 [Aspergillus bombycis]	Lipid droplet phospholipase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LPL1 PE=1 SV=1
A8347	-	-	GO:0003676(nucleic acid binding),GO:0008270(zinc ion binding)	-	-	-	-	-

A8348	-	-	-	-	-	-	XP_031024894.1 uncharacterized protein SmJEL517_g03213 [Synchytrium microbalum]	-
A8349	-	GO:0016020(membrane)	-	-	-	-	KAF9123733.1 hypothetical protein BGX30_001279 [Mortierella sp. GBA39]	Mycolic acid-containing lipids exporter MmpL11 OS=Mycolicibacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=mmpL11 PE=3 SV=1
A8350	-	-	-	K23518 MACROD, ymdB; O-acetyl-ADP-ribose deacetylase [EC:3.1.1.106]	-	-	-	-
A8351	GO:0000778(mitotic cell cycle)	GO:0000775(chromosome, centromeric region),GO:0005634(nucleus)	-	-	-	KOG2163 Hs4759344 Centromere/kinetochore protein zw10 involved in mitotic chromosome segregation	TPX63586.1 hypothetical protein SpCBS45565_g06499 [Spizellomyces sp. 'palustris']	Centromere/kinetochore protein zw10 homolog OS=Mus musculus OX=10090 GN=Zw10 PE=1 SV=3
A8352	-	-	GO:0005515(protein binding)	-	-	KOG4234 Hs4507711 TPR repeat-containing protein	KAG2181860.1 hypothetical protein INT44_008676 [Umbelopsis vinacea]	Tetratricopeptide repeat protein 1 OS=Homo sapiens OX=9606 GN=TTC1 PE=1 SV=1
A8353	GO:0006508(proteolysis),GO:0071586(CAAX-box protein processing)	-	GO:0004222(metalloendopeptidase activity),GO:0008233(peptidase activity)	K06013 STE24; STE24 endopeptidase [EC:3.4.24.84]	map01110 Biosynthesis of secondary metabolites;map00900 Terpenoid backbone biosynthesis	KOG2719 At4g01320 Metalloprotease	RHZ47951.1 hypothetical protein Glove_564g28 [Diversispora epigaea]	CAAX prenyl protease 1 homolog OS=Arabidopsis thaliana OX=3702 GN=FACE1 PE=1 SV=1
A8354	-	-	GO:0005509(calcium ion binding)	K01613 psd, PISD; phosphatidylserine decarboxylase [EC:4.1.1.65]	map01110 Biosynthesis of secondary metabolites;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG1032 At1g03370.2 Uncharacterized conserved protein, contains GRAM domain	TPX43516.1 hypothetical protein SeLEV6574_g05020 [Synchytrium endobioticum]	C2 and GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana OX=3702 GN=At1g03370 PE=2 SV=4
A8355	-	-	-	-	-	-	-	-
A8356	-	-	-	-	-	-	-	-
A8357	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8358	-	-	-	-	-	-	-	-
A8359	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	-	XP_016608451.1 hypothetical protein SPPG_04735 [Spizellomyces punctatus DAOM BR117]	Magnetosome protein MamZ OS=Magnetospirillum gryphiswaldense (strain DSM 6361 / JCM 21280 / NBRC 15271 / MSR-1) OX=431944 GN=mamZ PE=1 SV=1

A8360	-	-	-	-	-	-	KAE8219169.1 hypothetical protein CF319_g7087 [Tilletia indica]	Translationally-controlled tumor protein homolog OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=YALI0E27071g PE=3 SV=1
A8361	-	-	-	-	-	-	-	-
A8362	GO:0031047(gene silencing by RNA)	GO:0016442(RISC complex)	-	K15979 SND1; staphylococcal nuclease domain-containing protein 1	map05203 Viral carcinogenesis	KOG2039 At5g61780 Transcriptional coactivator p100	PKY45758.1 hypothetical protein RhiirA4_517786 [Rhizophagus irregularis]	Ribonuclease TUDOR 1 OS=Arabidopsis thaliana OX=3702 GN=TSN1 PE=1 SV=1
A8363	-	-	-	K24940 CWF19L2; CWF19-like protein 2	-	KOG2477 At1g56290 Uncharacterized conserved protein	RKP26872.1 CwfJ C-terminus 1-domain-containing protein-like protein [Syncephalis pseudoplumigaleata]	CWF19-like protein 2 OS=Danio rerio OX=7955 GN=cwf19l2 PE=2 SV=1
A8364	-	-	-	K01069 gloB, gloC, HAGH; hydroxyacylglutathione hydrolase [EC:3.1.2.6]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG0813 Hs21703352 Glyoxylase	RKP24643.1 beta-lactamase-like protein, partial [Syncephalis pseudoplumigaleata]	Persulfide dioxygenase ETHE1, mitochondrial OS=Mus musculus OX=10090 GN=Ethe1 PE=1 SV=2
A8365	-	-	GO:0005515(protein binding)	-	-	KOG1337 At3g07670 N-methyltransferase	CAF9906832.1 hypothetical protein HETSPECPRED_006968 [Heterodermia speciosa]	[Fructose-bisphosphate aldolase]-lysine N-methyltransferase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=LSMT-L PE=1 SV=1
A8366	-	-	GO:0003676(nucleic acid binding),GO:0016787(hydrolase activity),GO:0046872(metal ion binding)	K01173 ENDOg; endonuclease G, mitochondrial	map04210 Apoptosis	KOG3721 Hs4758270 Mitochondrial endonuclease	KDR81381.1 hypothetical protein GALMADRAFT_134826 [Galerina marginata CBS 339.88]	Endonuclease G, mitochondrial OS=Mus musculus OX=10090 GN=Endog PE=1 SV=1
A8367	GO:0006511(ubiquitin-dependent protein catabolic process)	GO:0031461(cullin-RING ubiquitin ligase complex)	GO:0031625(ubiquitin protein ligase binding)	K03869 CUL3; cullin 3	map04340 Hedgehog signaling pathway;map04341 Hedgehog signaling pathway - fly;map04120 Ubiquitin mediated proteolysis	KOG2166 At4g02570 Cullins	ORY00785.1 Cullin-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Cullin-1 OS=Arabidopsis thaliana OX=3702 GN=CUL1 PE=1 SV=1
A8368	GO:0006621(protein retention in ER lumen)	GO:0016021(integral component of membrane)	GO:0046923(ER retention sequence binding)	K10949 KDELr; ER lumen protein retaining receptor	map05110 Vibrio cholerae infection	KOG3106 At1g75760 ER lumen protein retaining receptor	XP_006461390.1 hypothetical protein AGAB12DRAFT_192892 [Agaricus bisporus var. bisporus H97]	ER lumen protein-retaining receptor OS=Petunia hybrida OX=4102 GN=ERD2 PE=2 SV=1

A8369	-	-	-	-	-	-	XP_01661120.1 hypothetical protein SPPG_02224 [Spizellomyces punctatus DAOM BR117]	Dynein axonemal assembly factor 5 OS=Xenopus laevis OX=8355 GN=dnaaf5 PE=2 SV=1
A8370	GO:0008033(tRNA processing)	GO:0005739(mitochondrion)	GO:0005515(protein binding)	-	-	-	-	Proteinaceous RNase P 2 OS=Arabidopsis thaliana OX=3702 GN=PRORP2 PE=1 SV=1
A8371	-	-	-	-	-	-	-	UPF0301 protein MCA0413 1 OS=Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) OX=243233 GN=MCA0413 PE=3
A8372	-	-	-	-	-	-	SAL99006.1 hypothetical protein [Absidia glauca]	Uncharacterized FCP1 homology domain-containing protein C1271.03c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC1271.03c PE=4 SV=1
A8373	GO:0006260(DNA replication)	-	GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K10755 RFC2_4; replication factor C subunit 2/4	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03430 Mismatch repair	KOG0989[Hs4506491 Replication factor C, subunit RFC4	NP_594540.1 DNA replication factor C complex subunit Rfc2 [Schizosaccharomyces pombe]	Replication factor C subunit 4 OS=Homo sapiens OX=9606 GN=RFC4 PE=1 SV=2
A8374	-	-	-	-	-	-	RDW77812.1 NAD(P)-binding protein-34 [Coleophoma cylindrospora]	Zinc-type alcohol dehydrogenase-like protein C337.11 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC337.11 PE=3 SV=1
A8375	-	-	-	K00344 qor, CRYZ; NADPH:quinone reductase [EC:1.6.5.5]	-	KOG0025[7303260 Zn2+ - binding dehydrogenase (nuclear receptor binding factor-1)	KAF2459109.1 chaperonin 10-like protein [Lineolata rhizophorae]	Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=Drosophila melanogaster OX=7227 GN=CG16935 PE=3 SV=2
A8376	-	-	GO:0016491(oxidoreductase activity)	K00344 qor, CRYZ; NADPH:quinone reductase [EC:1.6.5.5]	-	KOG1198[At4g13010 Zinc-binding oxidoreductase	XP_019042976.1 NADPH2:quinone reductase [Kwoniella bestiolae CBS 10118]	Quinone oxidoreductase OS=Sus scrofa OX=9823 GN=CRYZ PE=2 SV=1
A8377	GO:0006457(protein folding)	-	GO:0031072(hot shock protein binding),GO:0051082(unfolded protein binding),GO:0030544(Hsp70 protein binding)	K09503 DNAJA2; DnaJ homolog subfamily A member 2	map04141 Protein processing in endoplasmic reticulum	KOG0712[At3g44110 Molecular chaperone (DnaJ superfamily)	ORX90055.1 dnaJ-like protein subfamily A member 2-like protein [Basidiobolus meristosporus CBS 931.73]	Chaperone protein dnaJ 2 OS=Arabidopsis thaliana OX=3702 GN=ATJ2 PE=1 SV=2

A8378	-	-	GO:0005506(iron ion binding),GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen),GO:0031418(L-ascorbic acid binding),GO:0016706(2-oxoglutarate-dependent dioxygenase activity)	K24029 OGFOD1, TPA1; prolyl 3-hydroxylase /prolyl 3,4-dihydroxylase [EC:1.14.11.-]	-	KOG3844 CE01785 Predicted component of NuA3 histone acetyltransferase complex	KAG0224933.1 Prolyl 3-hydroxylase ogfod1 [Actinomortierella wolfii]	Prolyl 3-hydroxylase OGFOD1 OS=Xenopus laevis OX=8355 GN=ogfod1 PE=2 SV=1
A8379	GO:0006207('de novo' pyrimidine nucleobase biosynthetic process), GO:0006520(cellular amino acid metabolic process)	-	GO:0004070(aspartate carbamoyltransferase activity),GO:0016597(amino acid binding),GO:0016743(carboxyl- or carbamoyltransferase activity)	K11541 URA2; carbamoyl-phosphate synthase / aspartate carbamoyltransferase [EC:6.3.5.5 2.1.3.2]	map00240 Pyrimidine metabolism;map01240 Biosynthesis of cofactors;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	KOG0370 Hs18105007 Multifunctional pyrimidine synthesis protein CAD (includes carbamoyl-phosphate synthetase, aspartate transcarbamylase, and glutamine amidotransferase)	KAF9995650.1 hypothetical protein BGZ80_007458, partial [Entomortierella chlamydospora]	Multifunctional protein pyr1-3 OS=Dictyostelium discoideum OX=44689 GN=pyr1-3 PE=1 SV=3
A8380	-	-	GO:0071949(FAD binding)	-	-	KOG2614 At5g67030 Kynurenine 3-monooxygenase and related flavoprotein monooxygenases	EPZ33981.1 Monooxygenase, FAD-binding domain-containing protein [Rozella allomyces CSF55]	Aurachin C monooxygenase/isomerase OS=Stigmatella aurantiaca OX=41 GN=auaG PE=1 SV=1
A8381	-	-	-	-	-	-	ORY64240.1 phosphotransferase enzyme family protein [Pseudomassaria vexata]	-
A8382	GO:0036211(protein modification process)	-	GO:0008641(ubiquitin-like modifier activating enzyme activity)	K03178 UBE1, UBA1; ubiquitin-activating enzyme E1 [EC:6.2.1.45]	map04120 Ubiquitin mediated proteolysis;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease	KOG2012 At5g06460 Ubiquitin activating enzyme UBA1	XP_028483544.1 ubiquitin-activating enzyme E1 1 [Byssoschlamys spectabilis]	Ubiquitin-activating enzyme E1 2 OS=Triticum aestivum OX=4565 GN=UBA2 PE=2 SV=1
A8383	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	Transcription factor BOA OS=Arabidopsis thaliana OX=3702 GN=BOA PE=2 SV=1
A8384	-	-	-	-	-	-	-	Vacuolar-sorting receptor 4 OS=Arabidopsis thaliana OX=3702

A8385	GO:0018193(peptidyl-amino acid modification)	-	-	-	-	KOG3696 Hs10092629 Aspartyl beta-hydroxylase	KGQ02391.1 Aspartyl/asparaginyl beta-hydroxylase [Beauveria bassiana D1-5]	Ornithine lipid ester-linked acyl 2-hydroxylase OS=Rhizobium tropici OX=398 GN=olsC PE=1 SV=1
A8386	-	-	-	-	-	-	-	-
A8387	-	-	GO:0003677(DNA binding)	K15178 RTF1; RNA polymerase-associated protein RTF1	-	KOG2402 Hs14749361 Paf1/RNA polymerase II complex, RTF1 component (involved in regulation of TATA box-binding protein)	KAG1184517.1 hypothetical protein G6F36_007636 [Rhizopus oryzae]	RNA polymerase-associated protein RTF1 homolog (Fragment) OS=Pongo abelii OX=9601 GN=RTF1 PE=2 SV=2
A8388	-	-	GO:0005515(protein binding)	K14319 RANGAP1; Ran GTPase-activating protein 1	map03013 Nucleocytoplasmic transport	-	TPX76944.1 hypothetical protein CcCBS67573_g01773 [Chytridiomycota confervae]	Ribonuclease inhibitor OS=Sus scrofa OX=9823 GN=RNH1 PE=1 SV=1
A8389	GO:0033014(tetrapyrrole biosynthetic process), GO:0018160(peptidyl-pyrromethane cofactor linkage)	-	GO:0004418(hydroxymethylbilane synthase activity)	K01749 hemC, HMBS; hydroxymethylbilane synthase [EC:2.5.1.61]	map01110 Biosynthesis of secondary metabolites;map00860 Porphyrin metabolism;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	KOG2892 Hs20149500 Porphobilinogen deaminase	KAG0164003.1 hypothetical protein DFQ30_010647 [Apophysomonas sp. BC1015]	Porphobilinogen deaminase OS=Thermosynechococcus vestitus (strain NIES-2133 / IAM M-273 / BP-1) OX=197221 GN=hemC PE=3 SV=1
A8390	-	-	GO:0003676(nucleic acid binding)	-	-	-	-	-
A8391	-	-	-	K14617 LMBRD1; LMBR1 domain-containing protein 1	map04977 Vitamin digestion and absorption	-	XP_016610558.1 hypothetical protein SPPG_02978 [Spizellomyces punctatus DAOM BR117]	UMR family protein DDB_G0293610 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0293610 PE=3 SV=1
A8392	-	GO:0017119(Golgi transport complex)	-	K20295 COG8; conserved oligomeric Golgi complex subunit 8	-	KOG2069 Hs21166361 Golgi transport complex subunit	ORX91000.1 Dor1-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Conserved oligomeric Golgi complex subunit 8 OS=Mus musculus OX=10090 GN=Cog8 PE=1 SV=3

A8393	GO:0006298(mismatch repair),GO:0006821(chloride transport),GO:0055085(transmembrane transport)	GO:0032300(mismatch repair complex),GO:0016020(membrane)	GO:0016887(ATP hydrolysis activity),GO:0005524(ATP binding),GO:0030983(mismatched DNA binding),GO:0005247(voltage-gated chloride channel activity)	K10858 PMS2; DNA mismatch repair protein PMS2	map03430 Mismatch repair;map03460 Fanconi anemia pathway	KOG1978 7303075 DNA mismatch repair protein - MLH2/PMS1/Pms2 family	SAM08383.1 hypothetical protein [Absidia glauca]	Mismatch repair endonuclease PMS2 OS=Homo sapiens OX=9606 GN=PMS2 PE=1 SV=2
A8394	GO:0006821(chloride transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0005247(voltage-gated chloride channel activity)	-	-	-	KGQ13837.1 Putative ion-transport protein yfeO [Beauveria bassiana D1-5]	Putative ion-transport protein YfeO OS=Escherichia coli O139:H28 (strain E24377A / ETEC) OX=331111 GN=yfeO PE=3 SV=1
A8395	GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015299(solute:proton antiporter activity)	K12041 SLC9A6_7, NHE6_7; solute carrier family 9 (sodium/hydrogen exchanger), member 6/7	map04260 Cardiac muscle contraction	KOG1965 At2g01980 Sodium/hydrogen exchanger protein	KAF9125069.1 hypothetical protein BGX30_000634, partial [Mortierella sp. GBA39]	Sodium/hydrogen exchanger 7 OS=Arabidopsis thaliana OX=3702 GN=NHX7 PE=1 SV=1
A8396	-	-	GO:0005515(protein binding)	-	-	KOG3602 CE27437 WD40 repeat-containing protein	TPX72575.1 hypothetical protein CcCBS67573_g05748 [Chytridiomycetes confervae]	NACHT domain- and WD repeat-containing protein 1 OS=Mus musculus OX=10090 GN=Nwd1 PE=2 SV=2
A8397	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015267(channel activity)	K03441 GLP-F; aquaglyceroporin related protein, other eukaryote	-	KOG0224 Hs4826645 Aquaporin (major intrinsic protein family)	ORY45159.1 putative glycerol uptake facilitator protein [Rhizoclostium globosum]	Glycerol uptake facilitator protein OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=glpF PE=3 SV=1
A8398	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015267(channel activity)	K03441 GLP-F; aquaglyceroporin related protein, other eukaryote	-	KOG0224 Hs4826645 Aquaporin (major intrinsic protein family)	TPX48008.1 hypothetical protein SeMB42_g03148 [Synchytium endobioticum]	Glycerol uptake facilitator protein OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=glpF PE=3 SV=2
A8399	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015267(channel activity)	K03441 GLP-F; aquaglyceroporin related protein, other eukaryote	-	KOG0224 CE04707 Aquaporin (major intrinsic protein family)	ORY45159.1 putative glycerol uptake facilitator protein [Rhizoclostium globosum]	Glycerol uptake facilitator protein OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=glpF PE=3 SV=2
A8400	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015267(channel activity)	K03441 GLP-F; aquaglyceroporin related protein, other eukaryote	-	-	ORY45159.1 putative glycerol uptake facilitator protein [Rhizoclostium globosum]	Glycerol uptake facilitator protein OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=glpF PE=3 SV=2

A8401	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015267(channel activity)	K03441 GLP-F; aquaglyceroporin related protein, other eukaryote	-	KOG0224 CE04707 Aquaporin (major intrinsic protein family)	ORY45159.1 putative glycerol uptake facilitator protein [Rhizoclostium globosum]	Glycerol uptake facilitator protein OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=glpF PE=3 SV=2
A8402	-	-	-	-	-	-	-	-
A8403	-	-	-	-	-	-	TPX54987.1 hypothetical protein SeMB42_g00013 [Synchytrium endobioticum]	Centrosomal protein of 120 kDa OS=Bos taurus OX=9913 GN=CEP120 PE=2 SV=2
A8404	-	-	-	-	-	-	-	-
A8405	-	-	-	-	-	-	-	-
A8406	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	K04536 GNB1; guanine nucleotide-binding protein G(i)/G(s)/G(t) subunit beta-1	map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724 Glutamatergic synapse;map04725 Cholinergic synapse;map04726 Serotonergic synapse;map04727 GABAergic synapse;map04723 Retrograde endocannabinoid signaling;map05032 Morphine addiction;map05034 Alcoholism;map04713 Circadian entrainment;map04014 Ras signaling pathway;map05	KOG0286 At4g34460 G-protein beta subunit	XP_033650683.1 guanine nucleotide-binding protein-like protein subunit beta 1 [Westerdykella ornata]	Guanine nucleotide-binding protein subunit beta OS=Cryphonectria parasitica OX=5116 GN=GB-1 PE=3 SV=1
A8407	-	-	-	-	-	-	-	-
A8408	-	-	-	-	-	-	-	Axin interactor, dorsalization-associated protein A OS=Xenopus laevis
A8409	-	-	-	-	-	-	-	-
A8410	-	-	-	-	-	-	-	-
A8411	-	-	GO:0003676(nucleic acid binding);GO:0005524(ATP binding)	K15271 HFM1, MER3; ATP-dependent DNA helicase HFM1/MER3 [EC:5.6.2.4]	-	KOG0952 At3g27730 DNA/RNA helicase MER3/SLH1, DEAD-box superfamily	RUS21409.1 Sec63 Brl domain-containing protein [Endogone sp. FLAS-F59071]	DExH-box ATP-dependent RNA helicase DExH17 OS=Arabidopsis thaliana OX=3702 GN=MER3 PE=2 SV=1
A8412	GO:0044237(cellular metabolic process)	-	-	K03754 eIF2B2; translation initiation factor eIF-2B subunit beta	map05168 Herpes simplex virus 1 infection	KOG1465 Hs7657058 Translation initiation factor 2B, beta subunit (eIF-2Bbeta/GCD7)	KAF9319436.1 Translation initiation factor eIF-2B subunit beta [Podila horticola]	Translation initiation factor eIF2B subunit beta OS=Dictyostelium discoideum OX=44689 GN=eif2b2 PE=3 SV=1
A8413	-	-	-	-	-	KOG3241 Hs17447811 Uncharacterized conserved protein	ORX67097.1 hypothetical protein DL89DRAFT_52140 [Linderina pennisporea]	Uncharacterized protein C9orf85 homolog OS=Mus musculus OX=10090 PE=2 SV=1
A8414	GO:0006886(intracellular protein transport);GO:0006606(protein import into nucleus)	-	GO:0031267(smooth muscle GTPase binding)	K20221 IPO4, RANBP4; importin-4	map03013 Nucleocytoplasmic transport	KOG2171 At4g27640 Karyopherin (importin) beta 3	XP_007008011.1 uncharacterized protein TREMEDRAFT_41072 [Tremella mesenterica DSM 1558]	Importin-4 OS=Homo sapiens OX=9606 GN=IPO4 PE=1 SV=2

A8415	-	-	GO:0005515(protein binding)	-	-	KOG1616 Hs19923359 Protein involved in Snf1 protein kinase complex assembly	ORY82247.1 AMPKBI-domain-containing protein, partial [Neocallimastix californiae]	5'-AMP-activated protein kinase subunit beta-1 OS=Mus musculus OX=10090 GN=Prkab1 PE=1 SV=2
A8416	-	-	-	-	-	-	-	-
A8417	-	-	-	-	-	-	ORY21538.1 hypothetical protein LY90DRAFT_676210 [Neocallimastix californiae]	-
A8418	GO:0007030(Golgi organization),GO:0015031(protein transport)	GO:0016020(membrane)	-	K20289 COG2; conserved oligomeric Golgi complex subunit 2	-	KOG2307 At4g24840 Low density lipoprotein receptor	ORY93523.1 oligomeric golgi complex component, COG2-domain-containing protein [Syncephalastrium racemosum]	Conserved oligomeric Golgi complex subunit 2 OS=Arabidopsis thaliana OX=3702 GN=COG2 PE=1 SV=1
A8419	GO:0000398(mRNA splicing, via spliceosome)	GO:0046540(U4/U6 x U5 tri-snRNP complex)	-	K12859 TXNL4A, DIB1; U5 snRNP protein, DIM1 family	map03040 Spliceosome	KOG3414 At5g08290 Component of the U4/U6.U5 snRNP/mitosis protein DIM1	XP_018989304.1 thioredoxin-like protein 4A [Cryptococcus amyloletus CBS 6039]	Thioredoxin-like protein YLS8 OS=Arabidopsis thaliana OX=3702 GN=YLS8 PE=1 SV=1
A8420	-	-	GO:0005509(calcium ion binding)	-	-	KOG0044 Hs13375787 Ca2+ sensor (EF-Hand superfamily)	-	Calaxin OS=Bos taurus OX=9913 GN=CLXN PE=1 SV=1
A8421	-	-	-	-	-	-	-	-
A8422	-	-	GO:0003924(GTPase activity),GO:0005525(GTP binding)	K07905 RAB11B; Ras-related protein Rab-11B	map04144 Endocytosis;map04152 AMPK signaling pathway;map04962 Vasopressin-regulated water reabsorption;map05164 Influenza A	KOG0087 YER031c GTPase Rab11/YPT3, small G protein superfamily	KAF9432677.1 Ras-protein Rab-11B [Entomortierella beljakovae]	Ras-related protein YPTC6 OS=Chlamydomonas reinhardtii OX=3055 GN=YPTC6 PE=3 SV=1
A8423	-	-	-	-	-	-	-	-
A8424	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	-	-	KOG0035 Hs12025678 Ca2+-binding actin-bundling protein (actinin), alpha chain (EF-Hand protein superfamily)	CCG81045.1 Alpha-actinin, sarcomeric [Taphrina deformans PYCC 5710]	Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2
A8425	-	-	-	-	-	-	-	-
A8426	-	-	-	-	-	-	-	-
A8427	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transporter activity)	K20989 DUR3; urea-proton symporter	-	KOG2349 Hs17941285 Na+:iodide/myo-inositol/multi-vitamin symporters	ORX85711.1 solute:sodium symporter family transporter [Anaeromyces robustus]	Sodium/myo-inositol cotransporter 2 OS=Bos taurus OX=9913 GN=SLC5A11 PE=2 SV=1

A8428	-	-	-	-	-	-	-	-
A8429	-	-	-	-	-	-	-	-
A8430	GO:0030036(actin cytoskeleton organization),GO:0016043(cellular component organization)	-	GO:0003779(actin binding),GO:0031267(small GTPase binding)	-	-	KOG1922[Hs21071077 Rho GTPase effector BNI1 and related formins	OAJ39966.1 hypothetical protein, variant [Batrachochytrium dendrobatidis JEL423]	Disheveled-associated activator of morphogenesis 1 OS=Mus musculus OX=10090 GN=Daam1 PE=1 SV=4
A8431	GO:0006412(translation)	GO:0005840(ribosome),GO:0015935(small ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02969 RP-S20e, RPS20; small subunit ribosomal protein S20e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0900[At3g45030 40S ribosomal protein S20	RUP46474.1 40S ribosomal protein S20 [Jimgerdennia flammicorona]	Small ribosomal subunit protein uS10y OS=Arabidopsis thaliana OX=3702 GN=RPS20B PE=2 SV=1
A8432	-	-	-	-	-	-	-	-
A8433	GO:0006427(histidyl-tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0004821(histidine-tRNA ligase activity),GO:0005524(ATP binding)	K01892 HARS, hisS; histidyl-tRNA synthetase [EC:6.1.1.21]	map00970 Aminoacyl-tRNA biosynthesis	KOG1936[At3g46100 Histidyl-tRNA synthetase	KAF9436478.1 hypothetical protein BGZ76_003805 [Entomortierella beljakovae]	Histidine--tRNA ligase OS=Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIMB 8255 / S1) OX=269796 GN=hisS PE=3 SV=1
A8434	-	-	-	-	-	-	-	-
A8435	GO:0016192(vesicle-mediated transport),GO:0090114(COPII-coated vesicle budding),GO:1904263(positive regulation of TORC1 signaling)	GO:0030127(COPII vesicle coat)	GO:0005515(protein binding),GO:0005198(structural molecule activity)	-	-	KOG1332[Hs134911164 Vesicle coat complex COPII, subunit SEC13	KAF9437956.1 GTPase-activating protein S13 [Entomortierella beljakovae]	Protein SEC13 homolog OS=Mus musculus OX=10090 GN=Sec13 PE=1 SV=3
A8436	-	-	GO:0005515(protein binding)	-	-	-	TPX75258.1 hypothetical protein CcCBS67573_g03479 [Chytridiomycetes confervae]	-
A8437	-	-	GO:0003824(catalytic activity)	-	-	-	-	-
A8438	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG0872[CE15565 Sterol C5 desaturase	OAD02716.1 hypothetical protein MUCCIDRAFT_48488 [Mucor lusitanicus CBS 277.49]	Alkylglycerol monooxygenase OS=Homo sapiens OX=9606 GN=AGMO PE=1 SV=1
A8439	-	-	-	-	-	-	-	-
A8440	-	-	-	-	-	-	PAV15596.1 mitochondria I tricarboxylate transporter [Pyrrhoderma noxium]	Tricarboxylate transporter FUM11 OS=Gibberella moniliformis (strain M3125 / FGSC 7600) OX=334819 GN=FUM11 PE=3 SV=2
A8441	-	-	GO:0070403(NAD+ binding)	-	-	KOG2684[Hs13787215 Sirtuin 5 and related class III sirtuins (SIR2 family)	-	NAD-dependent protein deacetylase OS=Thermococcus sibiricus (strain DSM 12597 / MM 739) OX=604354 GN=cobB PE=3 SV=1

A8442	-	-	-	K20242 EVI5; ecotropic viral integration site 5 protein	-	-	KAF7732155.1 hypothetical protein EC973_006410 [Apophysomyces ossiformis]	-
A8443	-	-	-	-	-	-	-	-
A8444	-	-	-	-	-	KOG1700 7298855 Regulatory protein MLP and related LIM proteins	TKA54758.1 hypothetical protein B0A53_02567 [Rhodotorula sp. CCFEE 5036]	Muscle LIM protein Mlp84B OS=Drosophila melanogaster OX=7227 GN=Mlp84B PE=1 SV=1
A8445	-	-	-	-	-	-	-	-
A8446	-	-	-	GO:0005524(ATP binding),GO:0140658(ATPase-dependent chromatin remodeler activity),GO:0016757(glycosyltransferase activity)	-	-	OAV87422.1 hypothetical protein PTTG_29440 [Puccinia tritici 1-1 BBBD Race 1]	Uncharacterized ATP-dependent helicase YwqA OS=Bacillus subtilis (strain 168) OX=224308 GN=ywqA PE=1 SV=2
A8447	-	-	-	-	-	-	-	-
A8448	GO:0015914(phospholipid transport)	GO:0016021(integral component of membrane),GO:0005739(mitochondrion)	GO:0000287(magnesium ion binding),GO:0005524(ATP binding),GO:0140326(ATPase-coupled intramembrane lipid transporter activity),GO:0000166(nucleotide binding),GO:0004408(holocytochrome-c synthase activity),GO:0005215(transporter activity),GO:0016887(ATP hydrolysis activity)	K14802 DRS2, ATP8A; phospholipid-transporting ATPase [EC:7.6.2.1]	-	KOG0206 At1g54280 P-type ATPase	TCD65572.1 hypothetical protein EIP91_002493 [Steccherinum ochraceum]	Phospholipid-transporting ATPase 6 OS=Arabidopsis thaliana OX=3702 GN=ALA6 PE=1 SV=2
A8449	-	-	-	-	-	-	KNE59416.1 hypothetical protein AMAG_03696 [Allomyces macrogynus ATCC 38327]	-
A8450	-	-	GO:0005515(protein binding)	-	-	KOG0166 Hs6912678 Karyopherin (importin) alpha	OON11396.1 hypothetical protein BSLG_00016 [Batrachochytrium salamandrivorans]	Sperm-associated antigen 6 OS=Mus musculus OX=10090 GN=Spag6 PE=1 SV=1
A8451	-	-	-	K07019 K07019; uncharacterized protein	-	KOG1838 At5g49950 Alpha/beta hydrolase	KAG2227042.1 hypothetical protein INT45_006449 [Mucor circinatus]	Protein ABHD1 OS=Bos taurus OX=9913 GN=ABHD1 PE=2 SV=1

A8452	-	-	GO:0003723(RNA binding),GO:0003676(nucleic acid binding)	-	-	-	KAG2182482.1 hypothetical protein INT43_007412 [Umbelopsis isabellina]	-
A8453	GO:0006418(tRNA aminoacylation for protein translation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding)	K01880 GARS, glyS1; glycyl-tRNA synthetase [EC:6.1.1.14]	map00970 Aminoacyl-tRNA biosynthesis	KOG2298[Hs6996010 Glycyl-tRNA synthetase and related class II tRNA synthetase	CAE6386183.1 unnamed protein product [Rhizoctonia solani]	Glycine--tRNA ligase OS=Leptospira borgpetersenii serovar Hardjo-bovis (strain JB197) OX=355277 GN=glyQS PE=3 SV=1
A8454	GO:0006413(translational initiation)	-	GO:0005515(protein binding),GO:0003743(translation initiation factor activity)	K03262 EIF5; translation initiation factor 5	map04214 Apoptosis - fly	KOG2767[Hs21361337 Translation initiation factor 5 (eIF-5)	KAF9364378.1 hypothetical protein BGX34_001692 [Mortierella sp. NVP85]	Eukaryotic translation initiation factor 5 OS=Mus musculus OX=10090 GN=EIF5 PE=1 SV=1
A8455	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A8456	-	-	-	-	-	-	GFZ51951.1 hypothetical protein JCM24511_09721 [Saitozyma sp. JCM 24511]	2-deoxy-scylo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A8457	-	-	GO:0003824(catalytic activity)	-	-	KOG1075[CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A8458	-	-	-	-	-	KOG1075[CE04575 FOG: Reverse transcriptase	OMJ12941.1 Transposon TX1 protein [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1
A8459	-	-	-	-	-	-	-	-
A8460	-	-	-	-	-	-	-	-
A8461	-	-	-	-	-	-	-	-
A8462	-	-	-	-	-	-	-	-
A8463	GO:0006284(base-excision repair)	-	GO:0003684(damaged DNA binding),GO:0003906(DNA-(apurinic or apyrimidinic site) endonuclease activity),GO:0008270(zinc ion binding),GO:0016799(hydrolase activity, hydrolyzing N-glycosyl compounds),GO:0003676(nucleic acid binding)	-	-	-	KXS17204.1 H2TH-domain-containing protein [Gonapodya prolifera JEL478]	Endonuclease 8 1 OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=nei1 PE=3 SV=3

A8464	-	-	GO:0005515(protein binding)	-	-	KOG4177 CE26238_1 Ankyrin	RWA14940.1 hypothetical protein EKO27_g228 [Xylaria grammica]	Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ANKHD1 PE=1 SV=1
A8465	-	-	-	K04648 DCTN1; dynactin 1	map05014 Amyotrophic lateral sclerosis;map05132 Salmonella infection;map04814 Motor proteins;map05022 Pathways of neurodegeneration - multiple diseases;map05016 Huntington disease;map04962 Vasopressin-regulated water reabsorption	KOG3206 Hs17456232 Alpha-tubulin folding cofactor B	KLU89556.1 dynactin ro-3, partial [Magnaporthe oryzae ATCC 64411]	Tubulin-folding cofactor B OS=Bos taurus OX=9913 GN=TBCB PE=2 SV=1
A8466	GO:0006401(RNA catabolic process)	GO:0055087(Ski complex)	-	-	-	-	-	-
A8467	-	-	GO:0005515(protein binding)	-	-	KOG1108 CE18831 Predicted heme/steroid binding protein	ORY43412.1 cytochrome b5 [Rhizoclostium globosum]	Neuferricin homolog OS=Caenorhabditis briggsae OX=6238 GN=tag-131 PE=3 SV=1
A8468	-	-	GO:0016491(oxidoreductase activity),GO:0046872(metal ion binding)	-	-	-	-	-
A8469	-	-	GO:0005515(protein binding),GO:0004842(ubiquitin-protein transferase activity)	K10591 NEDD4, RSP5; E3 ubiquitin-protein ligase NEDD4 [EC:2.3.2.26]	map04144 Endocytosis;map04120 Ubiquitin mediated proteolysis;map04530 Tight junction;map04011 MAPK signaling pathway - yeast;map05169 Epstein-Barr virus infection	KOG1426 Hs4758520 FOG:RCC1 domain	NP_595793.1 putative HECT-type ubiquitin-protein ligase Pub3 [Schizosaccharomyces pombe]	E3 ubiquitin-protein ligase HERC2 OS=Mus musculus OX=10090 GN=Herc2 PE=1 SV=3
A8470	-	-	GO:0005515(protein binding)	-	-	KOG2507 CE00392 Ubiquitin regulatory protein UBXD2, contains UAS and UBX domains	-	UBX domain-containing protein 1 OS=Xenopus tropicalis OX=8364 GN=ubxn1 PE=2 SV=1

A8471	GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0046872(metal ion binding),GO:0019829(ATPase-coupled cation transmembrane transporter activity),GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0000166(nucleotide binding)	K17686 copA, ctpA, ATP7; P-type Cu+ transporter [EC:7.2.2.8]	map01524 Platinum drug resistance;map04978 Mineral absorption;map04016 MAPK signaling pathway - plant	KOG0207 At4g30110 Cation transport ATPase	RYO74449.1 hypothetical protein DL763_011509 [Monosporascus cannonballus]	Cadmium/zinc-transporting ATPase HMA2 OS=Oryza sativa subsp. japonica OX=39947 GN=HMA2 PE=1 SV=1
A8472	-	-	-	-	-	KOG1327 At1g79380 Copine	-	-
A8473	GO:0072344(rescue of stalled ribosome)	-	GO:0061630(ubiquitin protein ligase activity)	K22381 ZNF598; E3 ubiquitin-protein ligase ZNF598 [EC:2.3.2.27]	-	KOG2231 At3g62240 Predicted E3 ubiquitin ligase	KAG2202501.1 hypothetical protein INT47_013117 [Mucor saturninus]	E3 ubiquitin-protein ligase hel2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC1223.01 PE=1 SV=2
A8474	-	-	-	-	-	-	-	-
A8475	GO:0006508(proteolysis)	-	GO:0008234(cysteine-type peptidase activity)	-	-	KOG1543 Hs14786522 Cysteine proteinase Cathepsin L	-	Cathepsin Z OS=Homo sapiens OX=9606 GN=CTSZ PE=1 SV=1
A8476	-	-	-	-	-	-	-	-
A8477	-	-	-	-	-	KOG4776 At5g30145 Uncharacterized conserved protein BCNT	OMH83591.1 SWR1-complex protein 5 [Zancudomyces culisetae]	Craniofacial development protein 1 OS=Gallus gallus OX=9031 GN=CFDP1 PE=2 SV=1
A8478	-	-	-	-	-	-	-	-
A8479	-	-	GO:0008168(methyltransferase activity)	-	-	-	CEL00930.1 hypothetical protein ASPCAL00522 [Aspergillus calidoustus]	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE OS=Shewanella baltica (strain OS223) OX=407976 GN=ubiE PE=3 SV=1
A8480	GO:0019310(inositol catabolic process)	GO:0005737(cytoplasm)	GO:0005506(iron ion binding),GO:0005113(inositol oxygenase activity)	K00469 MIOX; inositol oxygenase [EC:1.13.99.1]	map01250 Biosynthesis of nucleotide sugars;map00053 Ascorbate and aldarate metabolism;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG1573 7294608 Aldehyde reductase	XP_01334494.3.1 hypothetical protein AUExF2481D RAFT_38634 [Aureobasidium subglaciale EXF-2481]	Inositol oxygenase OS=Mus musculus OX=10090 GN=Miox PE=1 SV=2

A8481	GO:0008610(lipid biosynthetic process)	-	GO:0005506(iron ion binding),GO:0016491(oxidoreductase activity)	-	-	KOG0873 7292910 C-4 sterol methyl oxidase	XP_018274527.1 uncharacterized protein RHOBADRAFT_64416 [Rhodotorula graminis WP1]	Methylsterol monooxygenase 1 OS=Sus scrofa OX=9823 GN=MSMO1 PE=2 SV=1
A8482	-	-	-	K08341 GABARAP, ATG8, LC3; GABA(A) receptor-associated protein	map04140 Autophagy - animal;map04212 Longevity regulating pathway - worm;map04139 Mitophagy - yeast;map04138 Autophagy - yeast;map04137 Mitophagy - animal;map04136 Autophagy - other;map04727 GABAergic synapse;map04621 NOD-like receptor signaling pathway;map04068 FoxO signaling pathway	KOG1654 At2g45170 Microtubule-associated anchor protein involved in autophagy and membrane trafficking	KIO13249.1 hypothetical protein M404DRAFT_12250 [Pisolithus tinctorius Marx 270]	Autophagy-related protein 8 OS=Phytophthora infestans OX=4787 GN=ATG8 PE=3 SV=1
A8483	-	-	-	-	-	-	-	-
A8484	-	GO:0016021(integral component of membrane)	-	-	-	KOG2568 CE04256 Predicted membrane protein	XP_002499182.1 uncharacterized protein ZYRO0E05808g [Zygosaccharomyces rouxii]	Transmembrane protein 87B OS=Mus musculus OX=10090 GN=Tmem87b PE=2 SV=1
A8485	GO:0044341(sodium-dependent phosphate transport),GO:0035435(phosphate ion transmembrane transport)	GO:0016020(membrane)	GO:0005436(sodium:phosphate symporter activity),GO:0015114(phosphate ion transmembrane transporter activity)	-	-	-	-	Sodium-dependent phosphate transport protein 2B OS=Homo sapiens OX=9606 GN=SLC34A2 PE=1 SV=3
A8486	GO:0044341(sodium-dependent phosphate transport)	GO:0016020(membrane)	GO:0005436(sodium:phosphate symporter activity)	-	-	-	-	Sodium-dependent phosphate transport protein 2A OS=Rattus norvegicus OX=10116 GN=Slc34a1 PE=1 SV=1
A8487	GO:0035435(phosphate ion transmembrane transport),GO:0044341(sodium-dependent phosphate transport)	GO:0016020(membrane)	GO:0015114(phosphate ion transmembrane transporter activity),GO:0005436(sodium:phosphate symporter activity)	-	-	-	-	Sodium-dependent phosphate transport protein 2B OS=Bos taurus OX=9913 GN=SLC34A2 PE=1 SV=1
A8488	GO:0044341(sodium-dependent phosphate transport),GO:0035435(phosphate ion transmembrane transport)	GO:0016020(membrane)	GO:0005436(sodium:phosphate symporter activity),GO:0015114(phosphate ion transmembrane transporter activity)	-	-	-	-	Sodium-dependent phosphate transport protein 2B OS=Homo sapiens OX=9606 GN=SLC34A2 PE=1 SV=3

A8489	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0051603(proteolysis involved in cellular protein catabolic process)	GO:0019773(proteasome complex, alpha-subunit complex), GO:0005839(proteasome complex)	-	-	-	KOG0183 7293190 20S proteasome, regulatory subunit alpha type PSM A7/PRE6	RKP12138.1 N-terminal nucleophile aminohydrolase [Piptocephalis cylindrospora]	Proteasome subunit alpha type-7 OS=Dictyostelium discoideum OX=44689 GN=psmA7 PE=3 SV=1
A8490	-	-	-	K01054 MGLL; acylglycerol lipase [EC:3.1.1.23]	map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00561 Glycerolipid metabolism;map01100 Metabolic pathways;map04923 Regulation of lipolysis in adipocytes	KOG1455 Hs6005786 Lysophospholipase	XP_038800509.1 uncharacterized protein EKO05_002615 [Ascochyta rabiei]	Monoacylglyceride lipase OS=Mus musculus OX=10090 GN=Mgll PE=1 SV=1
A8491	-	-	-	-	-	KOG1455 Hs6005786 Lysophospholipase	KAF1937361.1 alpha/beta-hydrolase [Clathrospora elynae]	Monoacylglycerol lipase OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=MSMEG_0220 PE=1 SV=1
A8492	GO:0016042(lipid catabolic process)	-	GO:0005515(protein binding);GO:0003847(1-alkyl-2-acetylglycerophosphocholine esterase activity)	K01062 PLA2G7, PAFAH; platelet-activating factor acetylhydrolase [EC:3.1.1.47]	map00565 Ether lipid metabolism;map01100 Metabolic pathways	KOG3847 Hs4826884 Phospholipase A2 (platelet-activating factor acetylhydrolase in humans)	TPX75290.1 1-alkyl-2-acetylglycerophosphocholine esterase [Chytrium confervae]	Platelet-activating factor acetylhydrolase OS=Bos taurus OX=9913 GN=PLA2G7 PE=2 SV=1
A8493	-	-	-	-	-	-	-	-
A8494	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A8495	GO:0006364(rRNA processing)	GO:0032040(small-subunit processome)	GO:0005515(protein binding)	K14555 UTP13, TBL3; U3 small nucleolar RNA-associated protein 13	map03008 Ribosome biogenesis in eukaryotes	KOG0319 At5g16750 WD40-repeat-containing subunit of the 18S rRNA processing complex	XP_019022827.1 WD40 repeat-like protein [Saitoella complicata NRRL Y-17804]	Transducin beta-like protein 3 OS=Rattus norvegicus OX=10116 GN=Tbl3 PE=2 SV=1
A8496	-	-	-	-	-	-	-	-
A8497	-	-	-	-	-	-	-	-
A8498	-	-	GO:0005515(protein binding)	-	-	-	QDS73546.1 hypothetical protein FKW77_000360 [Venturia effusa]	IQ motif and ankyrin repeat domain-containing protein 1 OS=Mus musculus OX=10090 GN=lqank1 PE=1 SV=3
A8499	-	-	GO:0016787(hydrolase activity)	-	-	KOG4388 CE27859 Hormone-sensitive lipase HSL	BCR91441.1 hypothetical protein ACHE_70284A [Aspergillus chevalieri]	Esterase LipI OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=lipI PE=1 SV=1
A8500	-	-	GO:0005515(protein binding)	-	-	-	-	-

A8501	GO:0006629(lipid metabolic process)	-	-	-	-	KOG2624[CE18732 Triglyceride lipase-cholesterol esterase	XP_031864690.1 uncharacterized protein BP5553_10627 [Venustampulla echinocandica]	Lipase lip1-1 OS=Caenorhabditis elegans OX=6239 GN=lip1-1 PE=2 SV=2
A8502	-	-	-	-	-	KOG1398[At5g51150 Uncharacterized conserved protein	TPX65961.1 hypothetical protein SpCBS45565_g04824 [Spizellomyces sp. 'palustris']	-
A8503	-	-	-	-	-	-	-	-
A8504	GO:0006376(mRNA splice site selection)	GO:0005685(U1 snRNP)	GO:0003729(mRNA binding)	-	-	KOG2130[Hs14769286 Phosphatidylinositol-specific receptor PtdSerR, contains JmjC domain	RKP09981.1 hypothetical protein THASP1DRAFT_10514, partial [Thamnocephalus sphaerospora]	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6 OS=Danio rerio OX=7955 GN=jmjd6 PE=2 SV=2
A8505	-	GO:0016021(integral component of membrane)	-	K00799 GST, gst; glutathione S-transferase [EC:2.5.1.18]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map00983 Drug metabolism - other enzymes;map04212 Longevity regulating pathway - worm;map01524 Platinum drug resistance;map05418 Fluid shear stress and atherosclerosis; map00480 Glutathione metabolism;map05200 Pathways in cancer;map05204 Chemical carcinogenesis -	-	CDS12800.1 hypothetical protein LRAMOSA04984 [Lichtheimia ramosa]	Glutathione S-transferase 3, mitochondrial OS=Homo sapiens OX=9606 GN=MGST3 PE=1 SV=1
A8506	-	-	GO:0005085(guanyl-nucleotide exchange factor activity);GO:0005515(protein binding)	K20047 PAN1; actin cytoskeleton-regulatory complex protein PAN1	-	KOG4424[CE03899 Predicted Rho/Rac guanine nucleotide exchange factor/facilitating protein 3	RKO96702.1 hypothetical protein CAUPRSCDR AFT_11608, partial [Caulochytrium protostelioides]	Myosin-M heavy chain OS=Dictyostelium discoideum OX=44689 GN=myoM PE=1 SV=1
A8507	-	-	GO:0003676(nucleic acid binding);GO:0003723(RNA binding)	-	-	KOG4206[Hs4759156 Spliceosomal protein snRNP-U1A/U2B	KAF0493792.1 U2 small nuclear ribonucleoprotein B [Gigaspora margarita]	U1 small nuclear ribonucleoprotein A OS=Homo sapiens OX=9606 GN=SNRPA PE=1 SV=3
A8508	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	-	-	-
A8509	-	-	-	K24810 IBTK; inhibitor of Bruton tyrosine kinase	-	KOG1426[Hs4758520 FOG; RCC1 domain	ORY44469.1 RCC1/BLIP-II protein [Rhizoclostium globosum]	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens OX=9606 GN=HERC2 PE=1 SV=2

A8510	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10356 MYO1; myosin I	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0162 CE05763 Myosin class I heavy chain	XP_031027609.1 uncharacterized protein SmJEL517_g00731 [Synchytrium microbalum]	Myosin ID heavy chain OS=Dictyostelium discoideum OX=44689 GN=myoD PE=1 SV=2
A8511	-	-	-	-	-	KOG1579 At3g63250 Homocysteine S-methyltransferase	KAG1501936.1 hypothetical protein G6F52_012414 [Rhizopus delemar]	Homocysteine S-methyltransferase 4 OS=Zea mays OX=4577 GN=HMT-4 PE=2 SV=1
A8512	GO:0034755(iron ion transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005381(iron ion transmembrane transporter activity)	-	-	-	-	-
A8513	GO:0006629(lipid metabolic process)	-	GO:0008081(phosphoric diester hydrolase activity)	-	-	-	TGO32646.1 hypothetical protein BHYA_0299g00080 [Botrytis hyacinthi]	-
A8514	-	-	-	-	-	-	-	-
A8515	GO:0006396(RNA processing),GO:0030488(tRNA methylation)	-	GO:0003723(RNA binding),GO:0008173(RNA methyltransferase activity),GO:0016423(tRNA (guanine) methyltransferase activity)	-	-	KOG0839 At4g17610 RNA Methylase, SpoU family	PJF18627.1 hypothetical protein PSACC_01573 [Paramicrosporidium saccamoebae]	Probable methyltransferase TARBP1 OS=Homo sapiens OX=9606 GN=TARBP1 PE=1 SV=1
A8516	GO:0022904(respiratory electron transport chain)	-	-	K03949 NDUFA5; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 5	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04723 Retrograde endocannabinoid signaling;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map050	KOG3365 At5g52840 NADH:ubiquinone oxidoreductase, NDUFA5/B13 subunit	OMJ07198.1 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 [Smittium culicis]	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At5g52840 PE=1 SV=1
A8517	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0015297(antiporter activity),GO:0042910(xenobiotic transmembrane transporter activity)	K03327 TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family	-	KOG1347 At1g73700 Uncharacterized membrane protein, predicted efflux pump	XP_013024511.1 MatE family transporter [Schizosaccharomyces cryophilus OY26]	Protein DETOXIFICATION 17 OS=Arabidopsis thaliana OX=3702 GN=DTX17 PE=2 SV=1
A8518	-	-	-	-	-	KOG1177 CE20812 Long chain fatty acid acyl-CoA ligase	ORY02209.1 AMP-binding domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Putative acyl-CoA synthetase YngI OS=Bacillus subtilis (strain 168) OX=224308 GN=yngI PE=3 SV=1

A8519	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005515(protein binding)	-	-	KOG0192 At1g14000 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KXS19920.1 kinase-like protein [Gonapodya prolifera JEL478]	Serine/threonine-protein kinase VIK OS=Arabidopsis thaliana OX=3702 GN=VIK PE=1 SV=1
A8520	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	-	-
A8521	GO:0006334(nucleosome assembly)	GO:0005634(nucleus)	-	K11279 NAP1L1, NRP; nucleosome assembly protein 1-like 1	-	KOG1507 At2g19480 Nucleosome assembly protein NAP-1	XP_003709662.1 nucleosome assembly protein [Pyricularia oryzae 70-15]	Nucleosome assembly protein 1,4 OS=Nicotiana tabacum OX=4097 GN=NAP1,4 PE=1 SV=1
A8522	-	-	-	-	-	-	TPX56409.1 hypothetical protein PhCBS80983_g04545 [Powellomyces hirtus]	-
A8523	-	-	-	-	-	-	-	-
A8524	-	-	-	-	-	-	-	-
A8525	GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase)	K05609 UCHL3, YUH1; ubiquitin carboxyl-terminal hydrolase L3 [EC:3.4.19.12]	-	KOG1415 Hs5174741 Ubiquitin C-terminal hydrolase UCHL1	RKP37199.1 hypothetical protein BJ085DRAFT_31677 [Dimargaris cristalligena]	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Sus scrofa OX=9823 GN=UCHL3 PE=2 SV=1
A8526	GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport), GO:0006890(retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum)	-	GO:0005484(SNAP receptor activity)	K08517 SEC22; vesicle transport protein SEC22	map04145 Phagosome;map05134 Legionellosis;map04130 SNARE interactions in vesicular transport	KOG0862 Hs4759086 Synaptobrevin/VAMP-like protein SEC22	EPZ33749.1 Longin domain-containing protein [Rozella allomycis CSF55]	Vesicle-traffic protein SEC22b OS=Homo sapiens OX=9606 GN=SEC22B PE=1 SV=5
A8527	GO:0016070(RNA metabolic process)	-	GO:0004523(RNA-DNA hybrid ribonuclease activity),GO:0003676(nucleic acid binding),GO:0003723(RNA binding)	K10743 RNASEH2A; ribonuclease H2 subunit A [EC:3.1.26.4]	map03030 DNA replication	KOG2299 Hs5454010 Ribonuclease HI	KAG0046936.1 Ribonuclease H2 subunit A [Gryganskiella cystojenkinii]	Ribonuclease H2 subunit A OS=Bos taurus OX=9913 GN=RNASEH2A PE=1 SV=1
A8528	GO:0097428(protein maturation by iron-sulfur cluster transfer)	-	-	K15075 MET18, MMS19; DNA repair/transcription protein MET18/MMS19	-	KOG1967 Hs13375626 DNA repair/transcription protein Mms19	ORX91539.1 ARM repeat-containing protein [Basidiobolus meristosporus CBS 931.73]	MMS19 nucleotide excision repair protein homolog OS=Homo sapiens OX=9606 GN=MMS19 PE=1 SV=2

A8529	-	-	GO:0005509(cal cium ion binding)	-	-	KOG1326[Hs4 758856 Membrane- associated protein FER- 1 and related ferlins, contain multiple C2 domains	KNE72792.1 phosphatidyl serine decarboxylase [Allomyces macrogynus ATCC 38327]	Fer-1-like protein 6 OS=Homo sapiens OX=9606 GN=FER1L6 PE=2 SV=2
A8530	-	-	GO:0005524(AT P binding),GO:001 6887(ATP hydrolysis activity)	K22766 FIGNL1: fidgetin-like protein 1 [EC:5.6.2.-]	-	KOG0740[Hs1 1545833 AAA+ -type ATPase	RIA89557.1 P-loop containing nucleoside triphosphate hydrolase protein [Glomus cerebriforme]	Fidgetin-like protein 1 OS=Xenopus laevis OX=8355 GN=fign1 PE=2 SV=1
A8531	GO:00322 59(methyl ation)	-	GO:0003676(nu cleic acid binding),GO:000 8168(methyltran sferase activity)	-	-	-	KGQ02252.1 Putative protein methyltransfe rase [Beauveria bassiana D1- 5]	Ribosomal RNA large subunit methyltransferase G OS=Shewanella amazonensis (strain ATCC BAA-1098 / SB2B) OX=326297 GN=rlmG PE=3 SV=1
A8532	-	-	-	-	-	-	-	-
A8533	GO:00065 08(proteo lysis)	-	GO:0008236(seri ne-type peptidase activity),GO:000 4252(serine- type endopeptidase activity)	-	-	-	KAF8645749. 1 hypothetical protein AX16_007616 [Volvariella volvacea WC 439]	Aqualysin-1 OS=Thermus aquaticus OX=271 GN=pstI PE=1 SV=2
A8534	GO:00068 07(nitroge n compoun d metaboli c process), GO:00065 42(glutam ine biosynthe tic process)	-	GO:0003824(cat alytic activity),GO:000 4356(glutamate -ammonia ligase activity)	K01915 glnA, GLUL; glutamine synthetase [EC:6.3.1.2]	map00910 Nitrogen metabolism;map 04217 Necroptosis;map 01120 Microbial metabolism in diverse environments;m ap04724 Glutamatergic synapse;map047 27 GABAergic synapse;map012 30 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map 02020 Two- component system;map0022 0 Arginine biosynthesis;ma p01100 Metabolic pathways;map00 630 Glyoxylate	KOG0683[At3 g53180 Glutamine synthetase	OBT41947.1 glutamine synthetase [Pseudogymn oascus sp. WSF 3629]	Gamma-glutamylethanolamide synthetase GlnA4 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=glnA4 PE=1 SV=1
A8535	-	-	GO:0005085(gu anyl-nucleotide exchange factor activity)	K19842 ROM1_2; RHO1 GDP- GTP exchange protein 1/2	map04011 MAPK signaling pathway - yeast	KOG3519[Hs4 507501 Invasion- inducing protein TIAM1/CDC2 4 and related RhoGEF GTPases	EXX56347.1 Rom2p [Rhizophagus irregularis DAOM 197198w]	RhoGEF domain-containing protein gxc OS=Dictyostelium discoideum OX=44689 GN=gxc PE=3 SV=1

A8536	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032[Hs4502553 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KAG2227790.1 hypothetical protein INT45_002028 [Mucor circinatus]	Calcium/calmodulin-dependent protein kinase type 1 OS=Homo sapiens OX=9606 GN=CAMK1 PE=1 SV=1
A8537	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8538	-	-	-	-	-	-	-	-
A8539	-	-	-	-	-	-	-	-
A8540	-	-	-	-	-	-	-	-
A8541	GO:0055085(transmembrane transport)	GO:0016020(membrane)	-	-	-	-	RYO78308.1 hypothetical protein DL763_00970.1 [Monosporascus cannonballus]	Small-conductance mechanosensitive channel MscMj OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=MJ0170 PE=1 SV=1
A8542	-	-	-	-	-	-	-	-
A8543	-	-	GO:0005524(ATP binding),GO:0004329(formate-tetrahydrofolate ligase activity)	K00288 MTHFD; methylenetetrahydrofolate dehydrogenase (NADP+) / methylenetetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase [EC:1.5.1.5 3.5.4.9 6.3.4.3]	map00670 One carbon pool by folate;map01240 Biosynthesis of cofactors;map01120 Microbial metabolism in diverse environments;map01100 Metabolic pathways	-	CDS14530.1 hypothetical protein LRAMOSA06699 [Lichtheimia ramosa]	Formate--tetrahydrofolate ligase OS=Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1) OX=391165 GN=fhs PE=3 SV=1
A8544	GO:0060271(cilium assembly)	-	GO:0005515(protein binding)	K03246 EIF3I; translation initiation factor 3 subunit I	-	KOG1538[Hs16554619 Uncharacterized conserved protein WDR10, contains WD40 repeats	TPX63995.1 hypothetical protein SpCBS45565_g06180 [Spizellomyces sp. 'palustris']	Intraflagellar transport protein 122 homolog OS=Xenopus tropicalis OX=8364 GN=ift122 PE=2 SV=1
A8545	-	-	-	-	-	KOG1124[CE09867 FOG:TPR repeat	-	Protein O-mannosyl-transferase TMTC4 OS=Mus musculus OX=10090 GN=Tmtc4 PE=2 SV=1
A8546	-	-	GO:0016702(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen)	K17842 carT, CAO-2; torulene dioxygenase [EC:1.13.11.5 9]	map01110 Biosynthesis of secondary metabolites;map00906 Carotenoid biosynthesis;map01100 Metabolic pathways	KOG1285[CE07263 Beta, beta-carotene 15,15'-dioxygenase and related enzymes	KFZ03515.1 hypothetical protein V502_10880 [Pseudogymnoascus sp. VKM F-4520 (FW-2644)]	Carotenoid dioxygenase OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) OX=367110 GN=cao-2 PE=2 SV=1
A8547	-	-	-	-	-	-	TPX56764.1 hypothetical protein PhCBS80983_g04286 [Powellomyces hirtus]	tRNA1(Val) (adenine(37)-N6)-methyltransferase OS=Porphyromonas gingivalis (strain ATCC 33277 / DSM 20709 / CIP 103683 / JCM 12257 / NCTC 11834 / 2561) OX=431947 GN=PGN_1201 PE=3 SV=2
A8548	-	-	GO:0005515(protein binding)	-	-	-	-	-

A8549	-	-	-	-	-	-	KAF8346717.1 hypothetical protein F5887DRAFT_1180532 [Amanita rubescens]	-
A8550	-	-	-	-	-	-	-	-
A8551	GO:0006886(intracellular protein transport) GO:0007033(vacuole organization)	GO:0005737(cytoplasm)	-	K20180 VPS16; vacuolar protein sorting-associated protein 16	map04140 Autophagy - animal;map05132 Salmonella infection;map04138 Autophagy - yeast	KOG2280 At2g38020 Vacuolar assembly/sorting protein VPS16	XP_023462564.1 vacuolar protein sorting vps16 [Rhizopus microsporus ATCC 52813]	Protein VACUOLELESS1 OS=Arabidopsis thaliana OX=3702 GN=VCL1 PE=1 SV=1
A8552	GO:0070072(vacuolar proton-transporting V-type ATPase complex assembly)	-	GO:0016279(protein-lysine N-methyltransferase activity)	-	-	-	KAG0251000.1 hypothetical protein BG011_007914 [Mortierella polycephala]	Protein-lysine N-methyltransferase OS=Sulfolobus islandicus (strain REY15A) OX=930945 GN=SiRe_1449 PE=1 SV=1
A8553	GO:0015914(phospholipid transport)	GO:0016021(integral component of membrane)	GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0000166(nucleotide binding),GO:0000287(magnesium ion binding),GO:0140326(ATPase-coupled intramembrane lipid transporter activity)	K14802 DRS2, ATP8A; phospholipid-transporting ATPase [EC:7.6.2.1]	-	KOG0206 At3g25610 P-type ATPase	KNE71012.1 phospholipid-transporting P-type ATPase, flippase [Allomyces macrogynus ATCC 38327]	Phospholipid-transporting ATPase 10 OS=Arabidopsis thaliana OX=3702 GN=ALA10 PE=3 SV=1
A8554	-	-	GO:0004842(ubiquitin-protein transferase activity)	K12232 HECTD2; E3 ubiquitin-protein ligase HECTD2 [EC:2.3.2.26]	-	KOG0941 7292061 E3 ubiquitin protein ligase	ORY01705.1 HECT-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Probable E3 ubiquitin-protein ligase HERC3 OS=Homo sapiens OX=9606 GN=HERC3 PE=1 SV=1
A8555	-	-	GO:0005525(GTP binding)	-	-	-	ORY42075.1 P-loop containing nucleoside triphosphate hydrolase protein [Neocallimastix californiae]	-

A8556	-	-	GO:0003824(catalytic activity)	K07511 ECHS1: enoyl-CoA hydratase [EC:4.2.1.17]	map00410 beta-Alanine metabolism;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00930 Caprolactam degradation;map00280 Valine, leucine and isoleucine degradation;map00650 Butanoate metabolism;map00062 Fatty acid elongation;map00627 Aminobenzoate	KOG1680 CE00318 Enoyl-CoA hydratase	XP_031026385.1 uncharacterized protein SmJEL517_g01792 [Synchytrium microbalum]	Probable enoyl-CoA hydratase, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=echs1 PE=3 SV=1
A8557	-	-	-	-	-	-	KAF9116574.1 hypothetical protein BGX27_001430 [Mortierella sp. AM989]	Isonitrile hydratase OS=Pseudomonas putida OX=303 GN=inhA PE=1 SV=1
A8558	GO:0006418(tRNA aminoacylation for protein translation),GO:0006434(seryl-tRNA aminoacylation)	-	GO:0000166(nucleotide binding),GO:0004812(aminoacyl-tRNA ligase activity),GO:0005524(ATP binding),GO:0005085(guanyl-nucleotide exchange factor activity),GO:0004828(serine-tRNA ligase activity)	K01875 SARS, serS; seryl-tRNA synthetase [EC:6.1.1.11]	map00970 Aminoacyl-tRNA biosynthesis	KOG2509 At1g11870 Seryl-tRNA synthetase	ORZ03635.1 seryl-tRNA synthetase [Syncephalaster racemosum]	Serine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana OX=3702 GN=OVA7 PE=2 SV=1
A8559	-	-	GO:0003682(chromatin binding)	K25931 NKAP; NF-kappa-B-activating protein	-	KOG2812 Hs13375676 Uncharacterized conserved protein	KAG4087819.1 DUF926-domain-containing protein [Neocallimastix sp. JGI-2020a]	NF-kappa-B-activating protein OS=Homo sapiens OX=9606 GN=NKAP PE=1 SV=1
A8560	-	GO:0005871(kinesin complex)	GO:0005515(protein binding),GO:0005509(calcium ion binding)	K14556 DIP2, UTP12, WDR3; U3 small nucleolar RNA-associated protein 12	map03008 Ribosome biogenesis in eukaryotes	KOG0319 At5g16750 WD40-repeat-containing subunit of the 18S rRNA processing complex	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	Protein TORMOZ EMBRYO DEFECTIVE OS=Arabidopsis thaliana OX=3702 GN=TOZ PE=1 SV=1
A8561	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	-	-
A8562	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08294 MKK1.2; mitogen-activated protein kinase kinase [EC:2.7.12.2]	map04139 Mitogen-activated protein kinase pathway - yeast;map04011 MAPK signaling pathway - yeast	KOG0581 At4g26070 Mitogen-activated protein kinase kinase (MAP2K)	SAM09416.1 hypothetical protein [Absidia glauca]	Mitogen-activated protein kinase kinase 1a OS=Physcomitrium patens OX=3218 GN=MKK1a PE=2 SV=1
A8563	-	-	-	-	-	-	-	-

A8564	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8565	-	GO:0016020(membrane)	-	-	-	KOG3776 7292180 Plasma membrane glycoprotein CD36 and related membrane receptors	-	Lysosome membrane protein 2 OS=Rattus norvegicus OX=10116 GN=Scarb2 PE=1 SV=2
A8566	-	-	-	-	-	-	-	-
A8567	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1619 CE00212 Cytochrome b	RKO88984.1 eukaryotic cytochrome b561-domain-containing protein [Blyttiomycetes helicus]	Putative transmembrane ascorbate-dependent reductase CYB561 homolog OS=Caenorhabditis elegans OX=6239 GN=F55H2.5 PE=3 SV=1
A8568	-	-	-	K14002 SCJ1; DnaJ-related protein SCJ1	map04141 Protein processing in endoplasmic reticulum	-	KZT67946.1 DnaJ-domain-containing protein [Daedalea quercina L-15889]	Chaperone protein DnaJ OS=Thermoplasma volcanium (strain ATCC 51530 / DSM 4299 / JCM 9571 / NBRC 15438 / GSS1) OX=273116 GN=dnaJ PE=3 SV=1
A8569	-	-	-	-	-	-	-	-
A8570	-	-	GO:0016787(hydrolase activity)	-	-	-	-	-
A8571	GO:0009058(biosynthetic process)	-	GO:0030170(pyridoxal phosphate binding),GO:0003824(catalytic activity)	K14265 Tam1; tryptophan aminotransferase [EC:2.6.1.27]	map00380 Tryptophan metabolism:map01100 Metabolic pathways	KOG0634 Hs7705897 Aromatic amino acid aminotransferase and related proteins	XP_031027067.1 uncharacterized protein SmJEL517_g01044 [Synchytrium microbalum]	Kynurenine/alpha-amino adipate aminotransferase, mitochondrial OS=Mus musculus OX=10090 GN=Aadat PE=1 SV=1
A8572	-	GO:0016020(membrane)	-	K23544 SERINC1; serine incorporator 1	-	KOG2592 7294110 Tumor differentially expressed (TDE) protein	RKP20934.1 TMS membrane protein/tumor differentially expressed protein, partial [Rozella allomyces CSF55]	Probable serine incorporator OS=Nematostella vectensis OX=45351 GN=serinc PE=3 SV=1
A8573	-	-	-	-	-	-	KNE69215.1 ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent [Allomyces macrogynus ATCC 38327]	Probable adenosylcobalamin-dependent ribonucleoside-triphosphate reductase OS=Dictyostelium discoideum OX=44689 GN=rtpR PE=3 SV=1
A8574	-	-	-	-	-	KOG1205 7301818 Predicted dehydrogenase	KZL82088.1 amp-binding enzyme [Colletotrichum incanum]	Fatty acyl-CoA reductase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=acr1 PE=1 SV=2
A8575	GO:0006890(retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum)	-	GO:0005515(protein binding),GO:0005198(structural molecule activity)	K17268 COPE; coatomer subunit epsilon	-	KOG3081 At1g30630 Vesicle coat complex COPI, epsilon subunit	ORY01163.1 hypothetical protein K493DRAFT_278255 [Basidiobolus meristosporus CBS 931.73]	Coatomer subunit epsilon-1 OS=Arabidopsis thaliana OX=3702 GN=At1g30630 PE=2 SV=1

A8576	-	GO:0016021(integral component of membrane)	-	-	-	KOG1688 At2g21600 Golgi proteins involved in ER retention (RER)	KAF9952391.1 retention in endoplasmic reticulum protein 1 [Mortierella alpina]	Protein RER1 OS=Bos taurus OX=9913 GN=RER1 PE=2 SV=2
A8577	GO:0005975(carbohydrate metabolic process)	-	GO:0005515(protein binding),GO:0016757(glycosyltransferase activity)	-	-	KOG3916 Hs994175 UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase	ORY39011.1 nucleotide-diphospho-sugar transferase [Rhizoclostium globosum]	Beta-1,4-galactosyltransferase 4 OS=Homo sapiens OX=9606 GN=B4GALT4 PE=1 SV=1
A8578	-	-	-	K17279 REEP5_6; receptor expression-enhancing protein 5/6	-	KOG1725 Hs19923919 Protein involved in membrane traffic (YOP1/TB2/DPI1/HVA22 family)	KNE59931.1 hypothetical protein AMAG_05380 [Allomyces macrogynus ATCC 38327]	Protein YOP1 homolog OS=Plasmodium berghei (strain Anka) OX=5823 GN=YOP1 PE=1 SV=1
A8579	-	-	GO:0005515(protein binding),GO:0003676(nucleic acid binding)	-	-	-	-	-
A8580	-	-	GO:0051537(2 iron, 2 sulfur cluster binding)	-	-	-	-	-
A8581	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1198 At1g23740 Zinc-binding oxidoreductase	KXL50638.1 hypothetical protein FE78DRAFT_84851 [Acidomyces sp. 'richmondensis']	2-methylene-furan-3-one reductase OS=Solanum lycopersicum OX=4081 GN=EO PE=1 SV=1
A8582	-	-	GO:0016757(glycosyltransferase activity)	-	-	-	-	-
A8583	-	-	GO:0005515(protein binding)	-	-	-	RUP42697.1 hypothetical protein BC936DRAFT_138210, partial [Jimgerdennia flammicorona]	Proliferation marker protein Ki-67 OS=Mus musculus OX=10090 GN=Mki67 PE=1 SV=1
A8584	GO:0006260(DNA replication)	-	GO:0004748(ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor),GO:005524(ATP binding)	K10807 RRM1; ribonucleoside-diphosphate reductase subunit M1 [EC:1.17.4.1]	map00983 Drug metabolism - other enzymes;map00230 Purine metabolism;map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG1112 At2g21790 Ribonucleotide reductase, alpha subunit	XP_021881877.1 ribonucleotide reductase [Lobosporangium transversale]	Ribonucleoside-diphosphate reductase large subunit OS=Mus musculus OX=10090 GN=Rrm1 PE=1 SV=2

A8585	-	GO:0016459(myosin complex)	GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 ECU09g1970 Myosin class V heavy chain	GAW06906.1 myosin 5 [Lentinula edodes]	Unconventional myosin-Vb OS=Mus musculus OX=10090 GN=Myo5b PE=1 SV=2
A8586	GO:0055085(transmembrane transport),GO:0006816(calcium ion transport)	GO:0016021(integral component of membrane),GO:0016020(membrane)	GO:0005432(calcium:sodium antiporter activity)	K13754 SLC24A6, NCKX6; solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	-	KOG1307 Hs9966787 K+-dependent Ca2+/Na+ exchanger NCKX1 and related proteins	KLO11555.1 hypothetical protein SCHPADRAFT_998804 [Schizopora paradoxa]	Sodium/potassium/calcium exchanger 2 OS=Gallus gallus OX=9031 GN=SLC24A2 PE=2 SV=1
A8587	-	-	GO:0005509(calcium ion binding)	-	-	KOG0027 At3g03410 Calmodulin and related proteins (EF-Hand superfamily)	-	-
A8588	-	-	-	-	-	-	-	-
A8589	-	-	-	K07019 K07019; uncharacterized protein	-	KOG1838 At1g34340 Alpha/beta hydrolase	ORZ25429.1 Alpha/Beta hydrolase protein [Absidia repens]	Protein ABHD1 OS=Mus musculus OX=10090 GN=Abhd1 PE=1 SV=2
A8590	-	-	-	K01669 phr, PHR1; deoxyribodipyrimidine photo-lyase [EC:4.1.99.3]	-	KOG0133 7304148 Deoxyribodipyrimidine photolyase/cryptochrome	AAU11091.1 class-II photolyase [Antonospora locustae]	Deoxyribodipyrimidine photo-lyase OS=Carassius auratus OX=7957 GN=phr PE=2 SV=1
A8591	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922 At3g26670 Uncharacterized conserved protein	EPR80014.1 hypothetical protein SLOPH_2238 [Spraguea lophii 42_110]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A8592	-	-	-	-	-	-	ORZ35140.1 hypothetical protein BCR44DRAFT_130074 [Catenaria anguillulae PL171]	Dynein regulatory complex subunit 7 OS=Xenopus tropicalis OX=8364 GN=drc7 PE=2 SV=1
A8593	-	-	-	-	-	-	-	-
A8594	GO:0016192(vesicle-mediated transport)	GO:0016021(integral component of membrane)	-	-	-	KOG2887 7296331 Membrane protein involved in ER to Golgi transport	KAG0244636.1 Vesicle transport protein [Actinomortierella wolffii]	Vesicle transport protein SFT2A OS=Mus musculus OX=10090 GN=Sft2d1 PE=1 SV=1
A8595	GO:0048870(cell motility)	GO:0031514(motile cilium)	GO:0008017(microtubule binding),GO:0031267(small GTPase binding)	-	-	-	ORY36463.1 hypothetical protein BCR33DRAFT_855207 [Rhizoclostium globosum]	Dynein regulatory complex subunit 4 OS=Chlamydomonas reinhardtii OX=3055 GN=DRC4 PE=1 SV=1

A8596	-	-	GO:0008374(O-acyltransferase activity)	-	-	KOG0831 At3g51520 Acyl-CoA:diacylglycerol acyltransferase (DGAT)	XP_016611326.1 hypothetical protein SPPG_09014 [Spizellomyces punctatus DAOM BR117]	Diacylglycerol O-acyltransferase 2 OS=Arabidopsis thaliana OX=3702 GN=DGAT2 PE=1 SV=1
A8597	-	-	-	-	-	-	-	-
A8598	GO:0006270(DNA replication initiation)	-	GO:0003690(double-stranded DNA binding),GO:0003697(single-stranded DNA binding)	K10736 MCM10; minichromosome maintenance protein 10	-	KOG3056 Hs19923534 Protein required for S-phase initiation or completion	TPX58689.1 hypothetical protein PhCBS80983.g02964 [Powellomyces hirtus]	Protein MCM10 homolog OS=Xenopus tropicalis OX=8364 GN=mcm10 PE=2 SV=1
A8599	-	-	GO:0005515(protein binding),GO:0005509(calcium ion binding)	-	-	KOG0027 YBR109c Calmodulin and related proteins (EF-Hand superfamily)	THY35806.1 EF-hand protein [Aureobasidium pullulans]	Calmodulin OS=Colletotrichum gloeosporioides OX=474922 PE=2 SV=2
A8600	GO:000958(biosynthetic process)	-	GO:0003824(catalytic activity),GO:0016740(transferase activity),GO:0030170(pyridoxal phosphate binding)	K00654 SPT; serine palmitoyltransferase [EC:2.3.1.50]	map04071 Sphingolipid signaling pathway;map00600 Sphingolipid metabolism;map04138 Autophagy - yeast;map01100 Metabolic pathways	KOG1357 At5g23670 Serine palmitoyltransferase	XP_016609061.1 hypothetical protein SPPG_04116 [Spizellomyces punctatus DAOM BR117]	Long chain base biosynthesis protein 2d OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0928800 PE=2 SV=1
A8601	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8602	-	-	GO:0106370(protein-L-histidine N-pros-methyltransferase activity)	-	-	KOG3987 Hs19923449 Uncharacterized conserved protein DREV/CGI-81	-	Protein-L-histidine N-pros-methyltransferase OS=Mus musculus OX=10090 GN=Mettl9 PE=1 SV=1
A8603	-	-	-	-	-	-	XP_031023949.1 uncharacterized protein SmJEL517_g04139 [Synchytrium microbalum]	Dynein regulatory complex subunit 7 OS=Xenopus tropicalis OX=8364 GN=drc7 PE=2 SV=1
A8604	-	-	GO:0070403(NA D+ binding)	-	-	KOG2684 7298007 Sirtuin 5 and related class III sirtuins (SIR2 family)	OLY80635.1 NAD-dependent histone deacetylase SIR2 [Smittium mucronatum]	NAD-dependent histone deacetylase sirtuin-1 OS=Drosophila melanogaster OX=7227 GN=Sirt1 PE=1 SV=1
A8605	GO:0034975(protein folding in endoplasmic reticulum)	GO:0005783(endoplasmic reticulum)	GO:0010181(FMN binding),GO:0016491(oxidoreductase activity),GO:0015035(protein-disulfide reductase activity),GO:0016972(thiol oxidase activity),GO:0071949(FAD binding)	-	-	-	TBU38795.1 Flavocytochrome c [Dichomitus squalens]	Fumarate reductase OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=osm1 PE=3 SV=1
A8606	-	-	-	-	-	-	-	-

A8607	-	-	-	K10573 UBE2A, UBC2, RAD6A; ubiquitin- conjugating enzyme E2 A [EC:2.3.2.23]	map04120 Ubiquitin mediated proteolysis	KOG0419 At2 g02760 Ubiquitin- protein ligase	KAG0309690. 1 Ubiquitin- conjugating enzyme E2 2 [Dissophora globulifera]	Ubiquitin-conjugating enzyme E2 2 OS=Medicago sativa OX=3879 GN=UBC2 PE=2 SV=1
A8608	GO:00715 62(nucleu s-vacuole junction assembly)	-	GO:0005515(pro tein binding),GO:004 3495(protein- membrane adaptor activity)	-	-	-	-	-
A8609	-	GO:00058 71(kinesin complex)	GO:0005515(pro tein binding),GO:001 9894(kinesin binding)	-	-	KOG1222 Hs1 8105054 Kinesin associated protein KAP	RKO93016.1 kinesin- associated protein- domain- containing protein, partial [Blyttomyces helicus]	Kinesin-associated protein 3 OS=Strongylocentrotus purpuratus OX=7668 GN=KAP115 PE=1 SV=1
A8610	-	-	-	-	-	KOG1090 Hs2 2061701 Predicted dual- specificity phosphatase	-	Myotubularin-related protein 13 OS=Mus musculus OX=10090 GN=Sbf2 PE=1 SV=1
A8611	-	-	-	-	-	-	-	-
A8612	-	-	-	-	-	-	-	-
A8613	-	-	GO:0003676(nu cleic acid binding)	K11135 PINX1; Pin2- interacting protein X1	-	KOG2809 Hs1 6975486 Telomerase elongation inhibitor/RNA maturation protein PINX1	PJF17412.1 hypothetical protein PSACC_0277 2 [Paramicrosp oridium saccamoebae]	PIN2/TERF1-interacting telomerase inhibitor 1 OS=Rattus norvegicus OX=10116 GN=Pinx1 PE=1 SV=1
A8614	-	-	GO:0005515(pro tein binding)	-	-	-	-	-
A8615	GO:00063 64(rRNA processin g)	-	GO:0005515(pro tein binding),GO:003 4511(U3 snoRNA binding)	K14793 RRP9; ribosomal RNA- processing protein 9	-	-	RKP12811.1 RNA, U3 small nucleolar interacting protein 2, isoform CRA_b [Piptocephali s cylindrospora]	U3 snoRNP-associated protein-like EMB2271 OS=Arabidopsis thaliana OX=3702 GN=EMB2271 PE=2 SV=1
A8616	-	-	GO:0008374(O- acyltransferase activity)	K14457 MOGAT2, MGAT2; 2- acylglycerol O- acyltransferas e 2 [EC:2.3.1.22]	map04975 Fat digestion and absorption;map 00561 Glycerolipid metabolism;map 01100 Metabolic pathways	KOG0831 Hs1 4211871 Acyl- CoA:diacylgly cerol acyltransferas e (DGAT)	XP_01661191. 5.1 hypothetical protein SPPG_01328 [Spizellomyce s punctatus DAOM BR117]	Diacylglycerol O-acyltransferase 2 OS=Dictyostelium discoideum OX=44689 GN=dgat2 PE=3 SV=1
A8617	GO:00069 13(nucleo cytoplasm ic transport)	GO:00056 43(nuclea r pore)	GO:0008139(nu clear localization sequence binding),GO:001 7056(structural constituent of nuclear pore)	-	-	-	-	Nucleoporin p58/p45 OS=Homo sapiens OX=9606 GN=NUP58 PE=1 SV=1

A8618	-	-	GO:0005515(protein binding)	-	-	KOG0644 7301145 Uncharacterized conserved protein, contains WD40 repeat and BROMO domains	ORY00993.1 YVTN repeat-like/Quino protein amine dehydrogenase [Basidiobolus meristosporus CBS 931.73]	PH-interacting protein OS=Mus musculus OX=10090 GN=Phip PE=1 SV=2
A8619	GO:0006807(nitrogen compound metabolic process)	-	GO:0003924(GTPase activity),GO:0016151(nickel cation binding)	K03189 ureG; urease accessory protein	-	-	KAF8420108.1 CobW/HypB/UreG, nucleotide-binding domain-containing protein [Tirmania nivea]	Uncharacterized urease accessory protein ureG-like OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCPB16A4.05c PE=3 SV=1
A8620	GO:0009165(nucleotide biosynthetic process)	-	GO:0000287(magnesium ion binding),GO:0004749(ribose phosphate diphosphokinase activity)	K00948 PRPS, prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG1448 At2g35390 Ribose-phosphate pyrophosphokinase	KAG0094207.1 hypothetical protein BGZ92_000003 [Podila epiciadia]	Ribose-phosphate pyrophosphokinase OS=Listeria ivanovii OX=1638 GN=prs PE=3 SV=1
A8621	GO:0006412(translation)	GO:0015935(small ribosomal subunit),GO:0005840(ribosome)	GO:0003723(RNA binding),GO:0003735(structural constituent of ribosome),GO:0008270(zinc ion binding)	K02980 RP-S29e, RPS29; small subunit ribosomal protein S29e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3506 YLR388w 40S ribosomal protein S29	XP_003955168.1 hypothetical protein KAFR_0A05980 [Kazachstania africana CBS 2517]	Small ribosomal subunit protein uS14 OS=Eremothecium gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=RPS29 PE=3 SV=1
A8622	GO:0006568(tryptophan metabolic process)	-	GO:0004640(phosphoribosylanthranilate isomerase activity),GO:0004425(indole-3-glycerol-phosphate synthase activity)	K13501 TRP1; anthranilate synthase / indole-3-glycerol phosphate synthase / phosphoribosylanthranilate isomerase [EC:4.1.3.27 4.1.1.48 5.3.1.24]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map01100 Metabolic pathways	-	KAF9973163.1 bifunctional tryptophan synthase trp1 [Actinomortierella ambigua]	Tryptophan biosynthesis protein TRP1 OS=Phytophthora parasitica OX=4792 GN=TRP1 PE=3 SV=1
A8623	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8624	-	-	-	-	-	-	-	-
A8625	-	-	-	-	-	-	-	-

A8626	-	-	-	-	-	KOG1161 YG R233c_1 Protein involved in vacuolar polyphosphat e accumulation , contains SPX domain	-	-
A8627	-	-	-	-	-	-	-	-
A8628	GO:00064 68(protein phosphor ylation)	-	GO:0005524(AT P binding),GO:000 4672(protein kinase activity)	K02218 CSNK1, CKI; casein kinase 1 [EC:2.7.11.1]	map04392 Hippo signaling pathway - multiple species:map040 11 MAPK signaling pathway - yeast	-	RCH88226.1 casein kinase I [Rhizopus stolonifer]	Casein kinase I OS=Plasmodium yoelii yoelii OX=73239 GN=CK1 PE=3 SV=1
A8629	-	-	GO:0005515(pro tein binding)	K09529 DNAJC9; DnaJ homolog subfamily C member 9	-	-	XP_00783684 8.1 hypothetical protein PFIC1_10076 [Pestalotiopsi s fici W106- 1]	Chaperone protein DnaJ OS=Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / DSM 15643 / BCRC 10681 / CIP 101130 / JCM 8532 / KCTC 2640 / LMG 13131 / VPI 4355) OX=190304 GN=dnaJ PE=3 SV=1
A8630	-	-	-	-	-	-	-	-
A8631	-	-	-	-	-	-	-	-
A8632	-	-	-	K17878 NNT1; EEF1A N-terminal glycine/lysine methyltransfe rase [EC:2.1.1.-]	-	-	KAG0199364. 1 hypothetical protein BGX28_00735 3 [Mortierella sp. GBA30]	Protein N-terminal and lysine N-methyltransferase efm7 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=nnt1 PE=3 SV=1
A8633	-	-	GO:0005515(pro tein binding)	-	-	KOG1839 Hs2 2062896 Uncharacteriz ed protein CLU1/cluA/TI F31 involved in mitochondria l morphology/ distribution, also found associated with eIF-3	TQV91394.1 tetratricopept ide repeat domain- containing protein [Cordyceps javanica]	-
A8634	-	-	-	-	-	-	-	-
A8635	-	-	GO:0003676(nu cleic acid binding)	-	-	KOG0922 Hs4 826690 DEAH-box RNA helicase	PVU92243.1 hypothetical protein BB559_00377 7 [Furculomyce s boomerangu s]	ATP-dependent RNA helicase DHX8 OS=Homo sapiens OX=9606 GN=DHX8 PE=1 SV=1
A8636	-	-	-	-	-	-	-	-
A8637	-	-	GO:0003676(nu cleic acid binding),GO:000 5524(ATP binding),GO:000 4386(helicase activity)	K12818 DHX8, PRP22; ATP - dependent RNA helicase DHX8/PRP22 [EC:3.6.4.13]	map03040 Spliceosome	KOG0922 At3 g26560 DEAH-box RNA helicase	ORX59963.1 P-loop containing nucleoside triphosphate hydrolase protein [Piromyces finnis]	Probable pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH5 OS=Arabidopsis thaliana OX=3702 GN=At3g26560 PE=1 SV=2
A8638	-	-	-	-	-	-	-	-
A8639	-	-	-	-	-	-	-	-
A8640	-	-	-	-	-	-	-	-

A8641	-	GO:0016021(integral component of membrane)	GO:0016757(glycosyltransferase activity)	K05531 MNN10; mannan polymerase II complex MNN10 subunit [EC:2.4.1.-]	map00513 Various types of N-glycan biosynthesis;map01100 Metabolic pathways	KOG4748 At1g74380 Subunit of Golgi mannosyltransferase complex	KAF9178583.1 hypothetical protein BGZ50_007619 [Haplosporangium sp. Z11]	Probable xyloglucan 6-xylosyltransferase 5 OS=Arabidopsis thaliana OX=3702 GN=XXT5 PE=1 SV=1
A8642	GO:0006457(protein folding)	-	GO:0005515(protein binding);GO:0030544(Hsp70 protein binding);GO:0051879(Hsp90 protein binding)	K09553 STIP1; stress-induced-phosphoprotein 1	map05020 Prion disease	KOG0548 Hs5803181 Molecular co-chaperone ST11	KAF8165112.1 chaperone [Crassisporium funariophilum]	Stress-induced-phosphoprotein 1 OS=Mus musculus OX=10090 GN=Stip1 PE=1 SV=1
A8643	-	-	GO:0008168(methyltransferase activity)	K17803 OMS1; methyltransferase OMS1, mitochondria I [EC:2.1.1.-]	-	KOG4300 YDR316w Predicted methyltransferase	RKO89184.1 S-adenosyl-L-methionine-dependent methyltransferase [Blyttiomycetes helicus]	Methyltransferase OMS1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OMS1 PE=1 SV=1
A8644	-	-	GO:0005515(protein binding);GO:0016301(kinase activity)	K06640 ATR; serine/threonine-protein kinase ATR [EC:2.7.11.1]	map04214 Apoptosis - fly;map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04115 p53 signaling pathway;map04110 Cell cycle;map03460 Fanconi anemia pathway;map05165 Human papillomavirus infection;map05166 Human T-cell leukemia virus 1 infection	KOG0890 Hs2041606 Protein kinase of the PI-3 kinase family involved in mitotic growth, DNA repair and meiotic recombination	XP_007365056.1 uncharacterized protein DICSQDRAFT_58492 [Dichomitus squalens LYAD-421 SS1]	Serine/threonine-protein kinase ATR OS=Homo sapiens OX=9606 GN=ATR PE=1 SV=3
A8645	-	-	-	-	-	-	-	-
A8646	-	-	GO:0005524(ATP binding)	-	-	KOG0055 CE06485 Multidrug/phenomone exporter, ABC superfamily	KAF6758086.1 P-loop containing nucleoside triphosphate hydrolase protein [Coprinellus angulatus]	ATP-dependent lipid A-core flippase OS=Bordetella avium (strain 197N) OX=360910 GN=msbA PE=3 SV=1
A8647	-	-	-	-	-	-	-	-
A8648	-	GO:0016021(integral component of membrane)	GO:0005524(ATP binding)	-	-	KOG0055 At4g18050 Multidrug/phenomone exporter, ABC superfamily	KAG0773258.1 hypothetical protein G6F22_015027 [Rhizopus oryzae]	ATP-dependent lipid A-core flippase OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) OX=233412 GN=msbA PE=3 SV=1
A8649	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding);GO:0140359(ABC-type transporter activity)	-	-	KOG0055 CE06485 Multidrug/phenomone exporter, ABC superfamily	KAG0773258.1 hypothetical protein G6F22_015027 [Rhizopus oryzae]	ATP-dependent lipid A-core flippase OS=Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) OX=257310 GN=msbA PE=3 SV=2

A8650	GO:0006468(protein phosphorylation)	-	GO:0005515(protein binding),GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K00916 CTK1; CTD kinase subunit alpha [EC:2.7.11.22 2.7.11.23]	-	KOG0194[CE11430 Protein tyrosine kinase	XP_02888994.5.1 uncharacterized protein CJI97_002687 [[Candida auris]	Cyclin-dependent kinase 9 OS=Danio rerio OX=7955 GN=cdk9 PE=2 SV=1
A8651	GO:0007165(signal transduction)	-	-	-	-	-	ORY46062.1 hypothetical protein BCR33DRAFT_159571 [Rhizoclostium globosum]	-
A8652	GO:0016226(iron-sulfur cluster assembly)	GO:0097361(CIA complex)	GO:0005515(protein binding)	K24730 CIAO1, CIA1; cytosolic iron-sulfur protein assembly protein CIAO1	-	-	PVG04639.1 WD40 repeat-like protein [Serendipita vermifera 'subsp. besicii']	Probable cytosolic iron-sulfur protein assembly protein 1 OS=Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) OX=306901 GN=CIA1 PE=3 SV=2
A8653	-	GO:0016021(integral component of membrane)	GO:0005524(ATP binding)	K05658 ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:7.6.2.2]	map04976 Bile secretion;map02010 ABC transporters;map05226 Gastric cancer;map05206 MicroRNAs in cancer	KOG0055[At4g18050 Multidrug/pheromone exporter, ABC superfamily	KNE72357.1 hypothetical protein AMAG_16841 [Allomyces macrogynus ATCC 38327]	ABC transporter B family member 9 OS=Arabidopsis thaliana OX=3702 GN=ABCB9 PE=3 SV=2
A8654	-	GO:0016021(integral component of membrane)	GO:0005524(ATP binding)	K05658 ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:7.6.2.2]	map04976 Bile secretion;map02010 ABC transporters;map05226 Gastric cancer;map05206 MicroRNAs in cancer	KOG0055[CE06485 Multidrug/pheromone exporter, ABC superfamily	XP_00739447.1.1 uncharacterized protein PHACADRAFT_253850 [Phanerochaete carnosae HHB-10118-sp]	ATP-dependent lipid A-core flippase OS=Bordetella avium (strain 197N) OX=360910 GN=msbA PE=3 SV=1
A8655	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05658 ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:7.6.2.2]	map04976 Bile secretion;map02010 ABC transporters;map05226 Gastric cancer;map05206 MicroRNAs in cancer	KOG0055[At1g02520 Multidrug/pheromone exporter, ABC superfamily	KNE72357.1 hypothetical protein AMAG_16841 [Allomyces macrogynus ATCC 38327]	ATP-dependent lipid A-core flippase OS=Histophilus somni (strain 129Pt) OX=205914 GN=msbA PE=3 SV=1
A8656	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05658 ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:7.6.2.2]	map04976 Bile secretion;map02010 ABC transporters;map05226 Gastric cancer;map05206 MicroRNAs in cancer	KOG0057[YM R301c Mitochondrial Fe/S cluster exporter, ABC superfamily	KAF2715325.1 hypothetical protein K504DRAFT_497197 [Pleiomassaria siparia CBS 279.74]	Probable multidrug resistance ABC transporter ATP-binding/permease protein YheI OS=Bacillus subtilis (strain 168) OX=224308 GN=yheI PE=1 SV=1
A8657	-	GO:0016021(integral component of membrane)	GO:0005524(ATP binding)	K05658 ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:7.6.2.2]	map04976 Bile secretion;map02010 ABC transporters;map05226 Gastric cancer;map05206 MicroRNAs in cancer	KOG0055[At1g02530 Multidrug/pheromone exporter, ABC superfamily	ODQ69913.1 hypothetical protein LIPSTDRAFT_6576 [Lipomyces starkeyi NRRL Y-11557]	ABC transporter B family member 12 OS=Arabidopsis thaliana OX=3702 GN=ABCB12 PE=2 SV=2

A8658	-	-	GO:0005515(protein binding)	-	-	KOG4842 At5g35690 Protein involved in sister chromatid separation and/or segregation	GBB91986.1 hypothetical protein RclHR1_19490003 [Rhizophagus clarus]	DNA-dependent metalloprotease WSS1 homolog 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=wss2 PE=1 SV=1
A8659	-	-	-	-	-	-	-	-
A8660	-	-	-	-	-	-	-	-
A8661	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8662	GO:0006099(tricarboxylic acid cycle)	-	GO:0005524(ATP binding),GO:0046872(metal ion binding),GO:0003824(catalytic activity)	K01900 LSC2; succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00640 Propanoate metabolism;map00020 Citrate cycle (TCA cycle);map01100 Metabolic pathways	KOG2799 At2g20420 Succinyl-CoA synthetase, beta subunit	KAG2179685.1 hypothetical protein INT44_006533 [Umbelopsis vinacea]	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Dictyostelium discoideum OX=44689 GN=scsC PE=3 SV=1
A8663	GO:0006805(xenobiotic metabolic process), GO:0009410(response to xenobiotic stimulus)	-	-	-	-	-	-	-
A8664	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG4254 At5g49550 Phytoene desaturase	XP_016607885.1 hypothetical protein SPPG_05219 [Spizellomyces punctatus DAOM BR117]	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 OS=Homo sapiens OX=9606 GN=PYROXD2 PE=1 SV=2
A8665	GO:0006886(intracellular protein transport), GO:0016192(vesicle-mediated transport)	GO:0071439(clathrin complex), GO:0030130(clathrin coat of trans-Golgi network vesicle),GO:0030132(clathrin coat of coated pit)	GO:0032051(clathrin light chain binding),GO:0005198(structural molecule activity),GO:0005515(protein binding)	K04646 CLTC, clathrin heavy chain	map04144 Endocytosis;map04142 Lysosome;map04721 Synaptic vesicle cycle;map05100 Bacterial invasion of epithelial cells;map05016 Huntington disease;map04961 Endocrine and other factor-regulated calcium reabsorption	KOG0985 Hs4758012 Vesicle coat protein clathrin, heavy chain	KAF9165116.1 hypothetical protein BGX20_000714 [Mortierella sp. AD010]	Clathrin heavy chain 1 OS=Mus musculus OX=10090 GN=Cltc PE=1 SV=3

A8666	-	GO:0016020(membrane)	-	-	-	KOG2718 Hs4506973 Na+-bile acid cotransporter	OUM63302.1 hypothetical protein PIROE2DRAFT_10203 [Piromyces sp. E2]	Ileal sodium/bile acid cotransporter OS=Oryctolagus cuniculus OX=9986 GN=SLC10A2 PE=2 SV=1
A8667	-	-	-	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0697 Hs10337595 Protein phosphatase 1B (formerly 2C)	KAG0934529.1 hypothetical protein G6F30_009774 [Rhizopus oryzae]	Probable protein phosphatase 1N OS=Mus musculus OX=10090 GN=Ppm1n PE=2 SV=1
A8668	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8669	-	GO:0016459(myosin complex)	GO:0005515(protein binding),GO:0003774(motor activity),GO:0005524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG0160 At4g28710 Myosin class V heavy chain	XP_002417916.1 myosin V myo2, putative [Candida dubliniensis CD36]	Myosin-5 OS=Arabidopsis thaliana OX=3702 GN=XI-1 PE=1 SV=1
A8670	-	-	-	-	-	-	-	-
A8671	-	GO:0016021(integral component of membrane)	GO:0009922(fatty acid elongase activity)	-	-	KOG3071 Hs12232379 Fatty acyl-CoA elongase/Pol yunsaturated fatty acid specific elongation enzyme	GEQ66676.1 hypothetical protein JCM33374_g339 [Metschnikowia sp. JCM 33374]	Fatty acid elongase A OS=Dictyostelium discoideum OX=44689 GN=eloA PE=2 SV=1
A8672	-	-	-	-	-	-	-	-
A8673	-	-	-	-	-	KOG1516 At3g02410 Carboxylesterase and related proteins	RGB30762.1 Alpha/Beta hydrolase protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Probable isoprenylcysteine alpha-carbonyl methylesterase ICME OS=Oryza sativa subsp. japonica OX=39947 GN=IMCE PE=2 SV=1
A8674	-	-	-	-	-	-	-	-
A8675	-	-	-	-	-	-	-	-
A8676	-	-	-	-	-	-	-	-
A8677	GO:0006352(DNA-templated transcription, initiation)	GO:0005634(nucleus)	-	K03134 TAF10; transcription initiation factor TFIID subunit 10	map03022 Basal transcription factors	KOG3423 At4g31720 Transcription initiation factor TFIID, subunit TAF10 (also component of histone acetyltransferase SAGA)	KAF9560001.1 Transcription initiation factor TFIID subunit 10 [Mortierella alpina]	Transcription initiation factor TFIID subunit 10 OS=Arabidopsis thaliana OX=3702 GN=TAF10 PE=1 SV=1
A8678	GO:0043631(RNA polyadenylation)	GO:0031499(TRANP complex)	GO:0016779(nucleotidyltransferase activity),GO:0004652(polynucleotide adenylyltransferase activity)	K03514 PAPD5_7, TRF4; non-canonical poly(A) RNA polymerase PAPD5/7 [EC:2.7.7.19]	map03018 RNA degradation	KOG1906 7290950 DNA polymerase sigma	KAF8924646.1 hypothetical protein BGZ58_001585 [Dissophora ornata]	Non-canonical poly(A) RNA polymerase protein Trf4-1 OS=Drosophila melanogaster OX=7227 GN=Trf4-1 PE=1 SV=1
A8679	GO:0030433(ubiquitin-dependent ERAD pathway), GO:0030968(endoplasmic reticulum unfolded protein response)	-	-	-	-	KOG3394 CE25700 Protein OS-9	ODV91612.1 hypothetical protein CANCADRAFT_73584 [Tortispora caseinolytica NRRL Y-17796]	Protein OS-9 homolog OS=Oryza sativa subsp. japonica OX=39947 GN=OS9 PE=2 SV=1

A8680	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	-	KZO94955.1 hypothetical protein CALVIDRAFT_565074 [Calocera viscosa TUFC12733]	-
A8681	-	GO:0016021(integral component of membrane)	-	-	-	KOG1162 Z95413 Predicted small molecule transporter	XP_016270486.1 protein-ER retention-related protein [Rhodotorula toruloides NP11]	Solute carrier family 53 member 1 OS=Drosophila melanogaster OX=7227 GN=PXo PE=1 SV=1
A8682	GO:0006542(glutamine biosynthetic process), GO:0006807(nitrogen compound metabolic process)	-	GO:0004356(glutamate-ammonia ligase activity), GO:0003824(catalytic activity)	K01915 glnA, GLUL; glutamine synthetase [EC:6.3.1.2]	map00910 Nitrogen metabolism;map04217 Necroptosis;map01120 Microbial metabolism in diverse environments;map04724 Glutamatergic synapse;map04727 GABAergic synapse;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map02020 Two-component system;map00220 Arginine biosynthesis;map01100 Metabolic pathways;map00630 Glyoxylate	KOG0683 At5g37600 Glutamine synthetase	RIA88022.1 glutamine synthetase 1 [Glomus cerebriforme]	Glutamine synthetase cytosolic isozyme OS=Daucus carota OX=4039 GN=GLN1 PE=2 SV=1
A8683	-	-	-	-	-	-	-	-
A8684	-	-	-	-	-	-	-	-
A8685	-	-	GO:0005524(ATP binding), GO:0140658(ATPase-dependent chromatin remodeler activity), GO:0005515(protein binding)	-	-	KOG0384 Hs22047966 Chromodomain-helicase DNA-binding protein	KAG0243186.1 hypothetical protein BGX31_011141, partial [Mortierella sp. GBA43]	Chromodomain-helicase-DNA-binding protein 8 OS=Danio rerio OX=7955 GN=chd8 PE=3 SV=2
A8686	-	-	GO:0005515(protein binding)	K14855 RSA4, NLE1; ribosome assembly protein 4	-	-	KAF7506539.1 hypothetical protein GJ744_011685 [Endocarpon pusillum]	-

A8687	GO:0009298(GDP-mannose biosynthetic process), GO:0005975(carbohydrate metabolic process)	-	GO:0004476(mannose-6-phosphate isomerase activity), GO:0008270(zinc ion binding)	K01809 manA, MPI; mannose-6-phosphate isomerase [EC:5.3.1.8]	map01250 Biosynthesis of nucleotide sugars; map0111.0 Biosynthesis of secondary metabolites; map00541 O-Antigen nucleotide sugar biosynthesis; map01240 Biosynthesis of cofactors; map00051 Fructose and mannose metabolism; map00520 Amino sugar and nucleotide sugar metabolism; map01100 Metabolic pathways	KOG2757 At3g02570 Mannose-6-phosphate isomerase	KJA19592.1 hypothetical protein HYP5UDRAFT_44152 [Hypholoma sublateritium FD-334 SS-4]	Mannose-6-phosphate isomerase OS=Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) OX=214684 GN=MAN1 PE=3 SV=2
A8688	-	-	GO:0140575(transmembrane monodehydroascorbate reductase activity)	-	-	-	ORX89295.1 hypothetical protein K493DRAFT_267265 [Basidiobolus meristosporus CBS 931.73]	-
A8689	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity)	-	-	-	ORX97933.1 phosphatases II [Basidiobolus meristosporus CBS 931.73]	Putative tyrosine phosphatase 197R OS=Invertebrate iridescent virus 6 OX=176652 GN=IIV6-197R PE=3 SV=1
A8690	-	-	GO:0005525(GTP binding), GO:0003924(GTPase activity)	K07952 ARFRP1; ADP-ribosylation factor related protein 1	-	KOG0076 At5g52210 GTP-binding ADP-ribosylation factor-like protein yARL3	ORX88605.1 P-loop containing nucleoside triphosphate hydrolase protein [Basidiobolus meristosporus CBS 931.73]	ADP-ribosylation factor-related protein 1 OS=Bos taurus OX=9913 GN=ARFRP1 PE=2 SV=1
A8691	GO:0006397(mRNA processing), GO:0006406(mRNA export from nucleus)	GO:0000347(THO complex)	-	K12879 THOC2; THO complex subunit 2	map03040 Spliceosome; map03013 Nucleocytoplasmic transport	KOG1874 Hs2055158 KEKE-like motif-containing transcription regulator (Rlr1)/suppressor of sin4	OAQ27251.1 hypothetical protein K457DRAFT_643166 [Linnemannia elongata AG-77]	THO complex subunit 2 OS=Mus musculus OX=10090 GN=Thoc2 PE=1 SV=1
A8692	-	-	GO:0008270(zinc ion binding)	-	-	KOG1940 At1g74760 Zinc-finger protein	KAF9381371.1 hypothetical protein CPC16_009880 [Podila verticillata]	Zinc finger protein BRUTUS OS=Arabidopsis thaliana OX=3702 GN=BTS PE=1 SV=1
A8693	-	-	-	-	-	-	-	-
A8694	-	-	GO:0008270(zinc ion binding), GO:0016491(oxidoreductase activity)	-	-	KOG1198 At1g23740 Zinc-binding oxidoreductase	KAG2178473.1 hypothetical protein INT44_001625 [Umbelopsis vinacea]	Zinc-type alcohol dehydrogenase-like protein SERP1785 OS=Staphylococcus epidermidis (strain ATCC 35984 / RP62A) OX=176279 GN=SERP1785 PE=3 SV=1

A8695	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11251 H2A; histone H2A	map04217 Necroptosis;map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map03082 ATP-dependent chromatin remodeling	KOG1756(CE04501A Histone 2A	RUO96772.1 histone-fold-containing protein [Jimgerdennia flammicorona]	Histone H2A-III OS=Volvox carteri OX=3067 PE=3 SV=1
A8696	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11252 H2B; histone H2B	map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG1744(YBL002w Histone H2B	ORE18420.1 histone H2b, partial [Rhizopus microsporus]	Histone H2B OS=Olisthodiscus luteus OX=83000 PE=1 SV=2
A8697	GO:0006555(methionine metabolic process)	-	GO:0004489(methylenetetrahydrofolate reductase (NAD(P)H) activity)	-	-	KOG0564(Hs6631098 5,10-methylenetetrahydrofolate reductase	RKP09411.1 methylenetetrahydrofolate reductase-domain-containing protein [Thamnocephalis sphaerospora]	Methylenetetrahydrofolate reductase (NADPH) OS=Macaca fascicularis OX=9541 GN=MTHFR PE=2 SV=1
A8698	-	-	-	-	-	-	-	-
A8699	GO:0032012(regulation of ARF protein signal transduction)	-	GO:0005085(guanyl-nucleotide exchange factor activity),GO:0000062(fatty-acyl-CoA binding)	K18442 ARFGEF, BIG; brefeldin A-inhibited guanine nucleotide-exchange protein	map04144 Endocytosis	KOG0929(Hs453571 Guanine nucleotide exchange factor	XP_007000601.1 uncharacterized protein TREMEDRAFT_25229 [Tremella mesenterica DSM 1558]	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Mus musculus OX=10090 GN=Arfgf1 PE=1 SV=1
A8700	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K20872 NEK2; serine/threonine-protein kinase Nek2 [EC:2.7.11.1]	-	KOG0589(Hs4507277_1 Serine/threonine protein kinase	EPZ31422.1 Protein kinase, catalytic domain-containing protein [Rozella allomycis CSF55]	Serine/threonine-protein kinase Nek4 OS=Mus musculus OX=10090 GN=Nek4 PE=1 SV=1
A8701	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08838 STK24_25_MST4; serine/threonine-protein kinase 24/25/MST4 [EC:2.7.11.1]	-	KOG0574(Hs16178962 STE20-like serine/threonine kinase MST	TXT10669.1 hypothetical protein VHUM_02174 [Vanrija humicola]	Serine/threonine-protein kinase 3 OS=Homo sapiens OX=9606 GN=STK3 PE=1 SV=2
A8702	GO:0006364(rRNA processing)	GO:0032040(small-subunit processome)	GO:0005515(protein binding)	K14554 UTP21, WDR36; U3 small nucleolar RNA-associated protein 21	map03008 Ribosome biogenesis in eukaryotes	KOG1539(At4g04940 WD repeat protein	KAF9538934.1 hypothetical protein EC957_006019 [Mortierella hygrophila]	U3 small nucleolar RNA-associated protein 21 homolog OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPCC1672.07 PE=3 SV=1
A8703	-	-	GO:0005515(protein binding)	-	-	-	-	-

A8704	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8705	GO:0016579(protein deubiquitination),GO:0006511(ubiquitin-dependent protein catabolic process)	-	GO:0004843(thiol-dependent deubiquitinase)	K11872 UBP9_13; ubiquitin carboxyl-terminal hydrolase 9/13 [EC:3.4.19.12]	-	KOG1864[Hs20548613 Ubiquitin-specific protease	KAF8077825.1 hypothetical protein FPV67DRAFT_1557276 [Lyophyllum atratum]	Ubiquitin carboxyl-terminal hydrolase 44-B OS=Xenopus laevis OX=8355 GN=usp44-b PE=2 SV=1
A8706	-	-	-	-	-	-	-	-
A8707	GO:0006621(protein retention in ER lumen)	GO:0016021(integral component of membrane)	GO:0046923(ER retention sequence binding)	K10949 KDELR; ER lumen protein retaining receptor	map05110 Vibrio cholerae infection	KOG3106[At1g29330 ER lumen protein retaining receptor	KAF9167208.1 endoplasmic reticulum retention protein [Mortierella sp. AD010]	ER lumen protein-retaining receptor OS=Petunia hybrida OX=4102 GN=ERD2 PE=2 SV=1
A8708	GO:0045047(protein targeting to ER)	GO:0005783(endoplasmic reticulum)	-	-	-	-	XP_017995292.1 Inorganic phosphate transport protein PHO88 [Phialophora atrinum]	-
A8709	-	-	-	-	-	-	-	-
A8710	-	-	-	-	-	-	-	-
A8711	-	-	GO:0005515(protein binding)	-	-	KOG0504[Hs4885087 FOG: Ankyrin repeat	KAF5016624.1 hypothetical protein F66182_11638 [Fusarium sp. NRRL 66182]	B-cell lymphoma 3 protein homolog OS=Mus musculus OX=10090 GN=Bcl3 PE=1 SV=2
A8712	GO:0015693(magnesium ion transport)	GO:0016021(integral component of membrane)	GO:0015095(magnesium ion transmembrane transporter activity)	K22733 NIPA, SLC57A2S; magnesium transporter	-	KOG2922[At3g26670 Uncharacterized conserved protein	KNE72038.1 hypothetical protein AMAG_15981 [Allomyces macrogynus ATCC 38327]	Probable magnesium transporter NIPA8 OS=Arabidopsis thaliana OX=3702 GN=At3g26670 PE=2 SV=1
A8713	-	-	-	-	-	-	-	-
A8714	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0619[7300644_2 FOG: Leucine rich repeat	XP_019035926.1 hypothetical protein WICANDRAFT_36790 [Wickerhamomyces anomalus NRRL Y-366-8]	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A8715	-	-	-	-	-	-	-	-
A8716	-	-	-	-	-	-	-	-
A8717	-	-	GO:0003824(catalytic activity)	-	-	KOG0234[At1g12850 Fructose-6-phosphate 2-kinase/fructose-2,6-biphosphatase	SCU82442.1 LADA_0C05314g1_1 [Lachancea dasiensis]	Probable phosphoglycerate mutase GpmB OS=Salmonella paratyphi C (strain RKS4594) OX=476213 GN=gpmB PE=3 SV=1
A8718	GO:0006812(cation transport),GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	-	-	-	-	-

A8719	GO:0006491(N-glycan processing)	-	-	-	-	KOG2397 At5g56360 Protein kinase C substrate, 80 KD protein, heavy chain	RGB33082.1 glucosidase II beta subunit-like protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Glucosidase 2 subunit beta OS=Arabidopsis thaliana OX=3702 GN=PSL4 PE=2 SV=1
A8720	GO:0005975(carbohydrate metabolic process)	-	GO:0008061(chitin binding)	K01183 E3.2.1.14; chitinase [EC:3.2.1.14]	map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG2806 Hs4758092 Chitinase	CEP08410.1 hypothetical protein [Parasitella parasitica]	Di-N-acetylchitinase OS=Homo sapiens OX=9606 GN=CTBS PE=1 SV=1
A8721	GO:0006265(DNA topological change),GO:0006259(DNA metabolic process)	GO:0005694(chromosome)	GO:0003677(DNA binding),GO:0003918(DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity),GO:0003824(catalytic activity),GO:0005524(ATP binding)	K10878 SPO11; meiotic recombination protein SPO11	map04113 Meiosis - yeast	KOG2795 At5g02820 Catalytic subunit of the meiotic double strand break transesterase	RIB24673.1 Spo11/DNA topoisomerase VI subunit A [Gigaspora rosea]	DNA topoisomerase 6 subunit A OS=Arabidopsis thaliana OX=3702 GN=TOP6A PE=1 SV=1
A8722	-	-	-	K08495 GOSR1, GOS1; golgi SNAP receptor complex member 1	map04130 SNARE interactions in vesicular transport	KOG3251 Hs16905522 Golgi SNAP receptor complex member	ORX96376.1 V-snare-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Golgi SNAP receptor complex member 2 homolog memb-1 OS=Caenorhabditis briggsae OX=6238 GN=memb-1 PE=3 SV=1
A8723	-	GO:0005643(nuclear pore)	GO:0017056(structural constituent of nuclear pore)	K14301 NUP107, NUP84; nuclear pore complex protein Nup107	map05014 Amyotrophic lateral sclerosis;map03013 Nucleocytoplasmic transport	KOG1964 Hs9966881 Nuclear pore complex, rNup107 component (sc Nup84)	EJU04993.1 nuclear pore protein 84/107 [Dacryopinax primogenitus]	Nuclear pore complex protein Nup107 OS=Mus musculus OX=10090 GN=Nup107 PE=1 SV=1
A8724	GO:0036158(outer dynein arm assembly),GO:0036159(inner dynein arm assembly)	GO:0005930(axoneme)	GO:0005515(protein binding),GO:0070840(dynein complex binding)	-	-	-	RKP00068.1 hypothetical protein CXG81DRAFT_27203 [Caulochytrium protostelioides]	Dynein axonemal assembly factor 1 homolog OS=Drosophila erecta OX=7220 GN=dtr PE=3 SV=1
A8725	GO:0065003(protein containing complex assembly)	GO:0005739(mitochondrion)	-	-	-	KOG3281 7300175 Mitochondrial F1-ATPase assembly protein	PVU87699.1 hypothetical protein BB561_006217 [Smittium simuli]	ATP synthase mitochondrial F1 complex assembly factor 1 OS=Xenopus tropicalis OX=8364 GN=atpaf1 PE=2 SV=1
A8726	-	-	-	-	-	-	-	-
A8727	GO:0016192(vesicle-mediated transport)	-	-	K20182 VPS33A; vacuolar protein sorting-associated protein 33A	map04140 Autophagy - animal;map05132 Salmonella infection;map04138 Autophagy - yeast	KOG1302 Hs18105056 Vacuolar sorting protein VPS33/slp1 (Sec1 family)	RGB36801.1 Sec1-like protein [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Vacuolar protein sorting-associated protein 33A OS=Rattus norvegicus OX=10116 GN=Vps33a PE=1 SV=1
A8728	-	-	-	-	-	-	-	-

A8729	-	-	-	-	-	KOG3706[Hs20127655 Uncharacterized conserved protein	-	Ribosomal oxygenase 2 OS=Rattus norvegicus OX=10116 GN=Riox2 PE=2 SV=1
A8730	-	-	-	-	-	-	-	-
A8731	GO:0006306(DNA methylation)	-	GO:0003677(DNA binding),GO:0008170(N-methyltransferase activity),GO:0005515(protein binding)	-	-	-	-	-
A8732	-	GO:0016021(integral component of membrane)	-	K17086 TM9SF2_4; transmembrane 9 superfamily member 2/4	-	KOG1277[At2g01970 Endosomal membrane proteins, EMP70	GES73082.1 transmembrane 9 superfamily member 3 [Rhizophagus clarus]	Transmembrane 9 superfamily member 4 OS=Arabidopsis thaliana OX=3702 GN=TMN4 PE=2 SV=1
A8733	-	-	-	K12864 CTNBL1; beta-catenin-like protein 1	map03040 Spliceosome	KOG2734[Hs18644734 Uncharacterized conserved protein	SAL95439.1 hypothetical protein [Absidia glauca]	Beta-catenin-like protein 1 OS=Homo sapiens OX=9606 GN=CTNBL1 PE=1 SV=1
A8734	GO:0030036(actin cytoskeleton organization),GO:0032456(endocytic recycling),GO:0006508(proteolysis),GO:0032049(cardiolipin biosynthetic process)	-	GO:0008234(cysteine-type peptidase activity),GO:0005515(protein binding),GO:0004605(phosphatidate cytidyltransferase activity),GO:0005525(GTP binding)	K17807 TAM41, MMP37; mitochondria l translocator assembly and maintenance protein 41	-	KOG1954[CE28509 Endocytosis/signaling protein EHD1	OAQ23009.1 hypothetical protein K457DRAFT_83959 [Linnemania elongata AG-77]	EH domain-containing protein 1 OS=Mus musculus OX=10090 GN=Ehd1 PE=1 SV=1
A8735	-	-	GO:0020037(heme binding)	K23490 CYB5; cytochrome b5	-	KOG0537[At2g32720 Cytochrome b5	OWB58350.1 hypothetical protein B5528_g4371 [[Candida] boidinii]	Cytochrome b5 OS=Candida tropicalis OX=5482 GN=Cytb5 PE=3 SV=1
A8736	-	-	-	-	-	-	-	-
A8737	-	-	GO:0003676(nucleic acid binding),GO:0005524(ATP binding)	K20103 DDX60; ATP-dependent RNA helicase DDX60 [EC:3.6.4.13]	-	-	KDQ07343.1 hypothetical protein BOTBODRAFT_140104 [Botryobasidium botryosum FD-172 SS1]	Uncharacterized helicase C694.02 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPAC694.02 PE=3 SV=1
A8738	-	-	-	-	-	KOG0619[7300644_2 FOG; Leucine rich repeat	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A8739	GO:0006974(cellular response to DNA damage stimulus)	-	GO:0005515(protein binding)	K24755 WDR76, CMR1; WD repeat-containing protein 76	-	KOG4328[Hs13376367 WD40 protein	RHZ89761.1 hypothetical protein Glove_11g70 [Diversispora epigaea]	WD repeat-containing protein 76 OS=Xenopus laevis OX=8355 GN=wdr76 PE=2 SV=1

A8740	GO:0006654(phosphatidic acid biosynthetic process), GO:0048017(inositol lipid-mediated signaling)	-	GO:0003824(catalytic activity),GO:0004630(phospholipase D activity)	K01115 PLD1_2; phospholipase D1/2 [EC:3.1.4.4]	map04024 cAMP signaling pathway;map04144 Endocytosis;map01110 Biosynthesis of secondary metabolites;map04071 Shingolipid signaling pathway;map04072 Phospholipase D signaling pathway;map04912 GnRH signaling pathway;map04724 Glutamatergic synapse;map05212 Pancreatic cancer;map04666 Fc gamma R-mediated phagocytosis;map04014 Ras signaling	KOG1329 At3g16785 Phospholipase D1	RIA88545.1 hypothetical protein C1645_725863 [Glomus cerebriforme]	Phospholipase D zeta 1 OS=Arabidopsis thaliana OX=3702 GN=PLDZETA1 PE=1 SV=1
A8741	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8742	-	-	-	-	-	KOG4001 7299529 Axonemal dynein light chain	XP_006678959.1 uncharacterized protein BATDEDRAFT_24899 [Batrachochytrium dendrobatidis JAM81]	28 kDa inner dynein arm light chain, axonemal OS=Chlamydomonas reinhardtii OX=3055 GN=IDA4 PE=1 SV=1
A8743	-	-	GO:0005515(protein binding)	-	-	-	TBU50449.1 ankyrin repeat-containing domain protein [Dichomitus squalens]	-
A8744	-	-	-	-	-	-	-	-
A8745	-	-	-	-	-	-	-	-
A8746	-	-	-	-	-	-	-	-
A8747	-	-	-	-	-	-	-	-
A8748	GO:0006409(tRNA export from nucleus), GO:0071528(tRNA re-export from nucleus)	-	GO:0000049(tRNA binding),GO:0031267(small GTPase binding)	K14288 XPOT; exportin-T	map03013 Nucleocytoplasmic transport	KOG2021 Hs8051636 Nuclear mRNA export factor receptor LOS1/Exportin-t (importin beta superfamily)	KAG2177879.1 hypothetical protein INT43_003126, partial [Umbelopsis isabellina]	Exportin-T OS=Dictyostelium discoideum OX=44689 GN=xpot PE=3 SV=1
A8749	-	-	GO:0005515(protein binding)	-	-	-	ERS97387.1 hypothetical protein HMPREF1624_05554 [Sporothrix schenckii ATCC 58251]	-
A8750	-	-	-	K15285 SLC35E3; solute carrier family 35, member E3	-	KOG1441 At1g06890 Glucose-6-phosphate and phosphoenolpyruvate/phosphate antiporter	RKP27535.1 triose-phosphate transporter family-domain-containing protein [Syncephalis pseudoplumigaleata]	UDP-xylose transporter 2 OS=Arabidopsis thaliana OX=3702 GN=UXT2 PE=1 SV=1
A8751	-	-	-	-	-	-	-	-

A8752	GO:003001(metal ion transport) GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	K14713 SLC39A7, KE4, ZIP7; solute carrier family 39 (zinc transporter), member 7	map05010 Alzheimer disease;map05012 Parkinson disease	KOG2693 7294338 Putative zinc transporter	ORZ34480.1 Zinc/iron permease [Catenaria anguillulae PL171]	Zinc transporter ZIP4 OS=Bos taurus OX=9913 GN=SLC39A4 PE=1 SV=1
A8753	GO:0006351(transcription, DNA-templated)	-	GO:0003677(DNA binding);GO:0003899(DNA-directed 5'-3' RNA polymerase activity)	K03018 RPC1, POLR3A; DNA-directed RNA polymerase III subunit RPC1 [EC:2.7.7.6]	map03020 RNA polymerase;map04623 Cytosolic DNA-sensing pathway	KOG0261 Hs5902062 RNA polymerase III, large subunit	ORY04347.1 RNA polymerase III largest subunit Rpc1 [Basidiobolus meristosporus CBS 931.73]	DNA-directed RNA polymerase III subunit rpc1 OS=Dictyostelium discoideum OX=44689 GN=polr3a PE=3 SV=1
A8754	-	-	GO:0005515(protein binding);GO:0005509(calcium ion binding)	-	-	KOG2106 Hs4758268 Uncharacterized conserved protein, contains HELP and WD40 domains	EPZ36884.1 Quinonprotein alcohol dehydrogenase-like superfamily domain-containing protein [Rozella allomyces CSF55]	Echinoderm microtubule-associated protein-like 5 OS=Homo sapiens OX=9606 GN=EML5 PE=2 SV=3
A8755	-	-	GO:0071949(FAD binding)	K00486 KMO; kynurenine 3-monooxygenase [EC:1.14.13.9]	map01240 Biosynthesis of cofactors;map00380 Tryptophan metabolism;map01100 Metabolic pathways	KOG2614 Hs4504891 Kynurenine 3-monooxygenase and related flavoprotein monooxygenases	PIA14919.1 FAD/NAD(P)-binding domain-containing protein [Coemansia reversa NRRL 1564]	Kynurenine 3-monooxygenase OS=Mus musculus OX=10090 GN=Kmo PE=1 SV=1
A8756	GO:0006457(protein folding)	-	GO:0005524(ATP binding);GO:0016887(ATP hydrolysis activity);GO:0051082(unfolded protein binding)	K09500 CCT8; T-complex protein 1 subunit theta	-	KOG0362 Hs6005727 Chaperonin complex component, TCP-1 theta subunit (CCT8)	TPX57701.1 hypothetical protein PhCBS80983.g03631 [Powellomyces hirtus]	T-complex protein 1 subunit theta OS=Bos taurus OX=9913 GN=CCT8 PE=1 SV=3
A8757	-	-	-	-	-	-	-	-
A8758	GO:0015986(ATP synthesis coupled proton transport)	GO:0000276(mitochondrial proton-transporting ATP synthase complex, coupling factor F(o))	GO:0015078(proton transmembrane transporter activity)	-	-	-	-	-
A8759	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8760	-	-	-	-	-	-	-	-
A8761	-	-	GO:0005515(protein binding)	-	-	-	-	NACHT, LRR and PYD domains-containing protein 13 OS=Homo sapiens OX=9606 GN=NLRP13 PE=2 SV=2
A8762	-	-	-	-	-	-	-	-
A8763	-	-	GO:0005515(protein binding)	K10752 RBBP4, HAT2, CAF1, MIS16; histone-binding protein RBBP4	map04218 Cellular senescence;map03082 ATP-dependent chromatin remodeling;map03083 Polycomb repressive complex	KOG0264 At5g58230 Nucleosome remodeling factor, subunit CAF1/NURF55/MSI1	KAF9901631.1 CCR4-Not complex caf1 ribonuclease subunit Caf1, partial [Lobosporangium transversale]	Histone-binding protein MSI1 OS=Arabidopsis thaliana OX=3702 GN=MSI1 PE=1 SV=1
A8764	-	-	-	-	-	-	-	-
A8765	-	-	-	-	-	-	-	-

A8766	GO:0008380(RNA splicing)	GO:0005681(spliceosomal complex)	-	K12817 PRPF18, PRP18; pre-mRNA-splicing factor 18	map03040 Spliceosome	KOG2808 At1g03140 U5 snRNP-associated RNA splicing factor	XP_025357469.1 Prp18-domain-containing protein, partial [Meiramlonrushii]	Pre-mRNA-splicing factor 18 OS=Danio rerio OX=7955 GN=prpf18 PE=2 SV=1
A8767	-	-	-	-	-	-	-	-
A8768	-	-	-	-	-	-	-	-
A8769	-	-	-	-	-	-	-	-
A8770	-	-	-	K01083 E3.1.3.8; 3-phytase [EC:3.1.3.8]	map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	-	KAF1943970.1 thermostable phytase [Clathrospora elyinae]	-
A8771	GO:0006470(protein dephosphorylation)	-	GO:0004722(protein serine/threonine phosphatase activity)	K14803 PTC2_3; protein phosphatase PTC2/3 [EC:3.1.3.16]	-	KOG0698 7291977 Serine/threonine protein phosphatase	KAG0005972.1 hypothetical protein BGZ65_009736 [Modicella reniformis]	Probable protein phosphatase 2C 60 OS=Arabidopsis thaliana OX=3702 GN=At4g31860 PE=2 SV=1
A8772	-	-	-	-	-	-	KAG0172419.1 hypothetical protein DFQ30_010487 [Apophysomyces sp. BC1015]	Sec14 cytosolic factor OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=sec14 PE=4 SV=1
A8773	GO:0006412(translation)	GO:0005840(ribosome)	GO:0005515(protein binding);GO:0003735(structural constituent of ribosome)	K02977 RP-S27Ae, RPS27A, UBA80; ubiquitin-small subunit ribosomal protein S27Ae	map04140 Autophagy - animal;map05131 Shigellosis;map05171 Coronavirus disease - COVID-19;map04137 Mitophagy - animal;map04120 Ubiquitin mediated proteolysis;map03010 Ribosome;map05022 Pathways of neurodegeneration - multiple diseases;map05012 Parkinson disease;map05167 Kaposi sarcoma-associated herpesvirus infection	KOG0004 ECU02g1080 Ubiquitin/40S ribosomal protein S27a fusion	ETS62592.1 ubiquitin-carboxy extension protein fusion [Moesziomyces aphidis DSM 70725]	Ubiquitin OS=Camelus dromedarius OX=9838 PE=3 SV=2
A8774	-	-	-	K03039 PSMD13, RPN9; 26S proteasome regulatory subunit N9	map05014 Amyotrophic lateral sclerosis;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map03050 Proteasome;map05010 Alzheimer disease;map05012 Parkinson disease;map05017 Spinocerebellar ataxia;map05016 Huntington disease;map05169 Epstein-Barr virus infection	KOG2908 Hs14774537 26S proteasome regulatory complex, subunit RPN9/PSMD13	RKP09871.1 hypothetical protein THASP1DRAFT_13660 [Thamnocephalus sphaerospora]	26S proteasome non-ATPase regulatory subunit 13 homolog B OS=Arabidopsis thaliana OX=3702 GN=RPN9B PE=1 SV=1

A8775	-	-	-	K14997 SLC38A11; solute carrier family 38 (sodium- coupled neutral amino acid transporter), member 11	-	KOG1305 At3 g56200 Amino acid transporter protein	XP_01627142 2.1 amino acid transmembra ne transporter [Rhodotorula toruloides NP11]	Sodium-coupled neutral amino acid transporter 7 OS=Xenopus laevis OX=8355 GN=slc38a7 PE=2 SV=1
A8776	-	-	-	-	-	-	KAG1255927. 1 hypothetical protein G6F68_01002 3 [Rhizopus microsporus]	-
A8777	-	-	-	-	-	-	-	-
A8778	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	-	-	-	KAF8926465. 1 hypothetical protein BGZ47_00270 6 [Haplosporani um gracile]	-
A8779	-	-	-	-	-	KOG0907 At1 g19730 Thioredoxin	KAE8167821. 1 thioredoxin [Aspergillus tamarii]	Thioredoxin H1 OS=Oryza sativa subsp. japonica OX=39947 GN=TRXH PE=1 SV=1
A8780	GO:00064 01(RNA catabolic process)	GO:00322 99(ribonu clease H2 complex)	-	K10745 RNASEH2C; ribonuclease H2 subunit C	map03030 DNA replication	-	XP_03102808 5.1 uncharacteriz ed protein SmJEL517_g0 0369 [Synchytrium microbalum]	-
A8781	GO:00702 86(axone mal dynein complex assembly)	GO:00057 37(cytopl asm)	-	-	-	KOG4356 730 4153 Uncharacteriz ed conserved protein	XP_03102688 8.1 uncharacteriz ed protein SmJEL517_g0 1190 [Synchytrium microbalum]	Protein kintoun OS=Drosophila sechellia OX=7238 GN=Nop17I PE=3 SV=1
A8782	-	-	-	K11600 RRP41, EXOSC4, SKI6; exosome complex component RRP41	map03018 RNA degradation	KOG1068 Hs9 506689 Exosomal 3'- 5' exoribonucle ase complex, subunit Rrp41 and related exoribonucle ases	RKP07866.1 ribosomal protein S5 domain 2- type protein [Thamnoceph alis sphaerospora]	Exosome complex component RRP41 OS=Bos taurus OX=9913 GN=EXOSC4 PE=2 SV=3
A8783	GO:00064 12(translation)	GO:00058 40(riboso me)	GO:0003735(str uctural constituent of ribosome),GO:0 019843(rRNA binding)	K02940 RP- L9e, RPL9; large subunit ribosomal protein L9e	map05171 Coronavirus disease - COVID- 19;map03010 Ribosome	KOG3255 Hs1 4720157 60S ribosomal protein L9	KAF7726901. 1 hypothetical protein EC973_00819 6 [Apophysom yces ossiformis]	Large ribosomal subunit protein uL6 OS=Mus musculus OX=10090 GN=Rpl9 PE=1 SV=2
A8784	-	GO:00058 56(cytosk eleton),G O:001645 9(myosin complex)	GO:0005515(pro tein binding),GO:000 3774(motor activity),GO:000 5524(ATP binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04 814 Motor proteins	KOG0160 At1 g54560 Myosin class V heavy chain	RKO94560.1 myosin VIIA, isoform CRA_d, partial [Blyttiomycetes helicus]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1

A8785	-	-	GO:0016810(hydroxylase activity, acting on carbon-nitrogen (but not peptide) bonds)	-	-	KOG3035 At5g62930 Isoamyl acetate-hydrolyzing esterase	KAF9126973.1 hypothetical protein BGX30_014997 [Mortierella sp. GBA39]	Putative amidohydrolase YtcJ OS=Bacillus subtilis (strain 168) OX=224308 GN=ytcJ PE=3 SV=1
A8786	GO:0006086(acetyl-CoA biosynthetic process from pyruvate)	GO:0045254(pyruvate dehydrogenase complex)	GO:0005515(protein binding)	-	-	KOG0557 At3g13930 Dihydrolipoamide acetyltransferase	-	Dihydrolipoalysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex OS=Rickettsia bellii (strain RML369-C) OX=336407 GN=sucB PE=3 SV=1
A8787	-	-	-	-	-	-	-	-
A8788	GO:0019243(methylglyoxal catabolic process to D-lactate via S-lactoylglutathione)	-	GO:0004416(hydroxyacylglutathione hydrolase activity)	K01069 gloB, gloC, HAGH; hydroxyacylglutathione hydrolase [EC:3.1.2.6]	map00620 Pyruvate metabolism;map01100 Metabolic pathways	KOG0813 Hs4885389 Glyoxylase	KXS10408.1 hydroxyacylglutathione hydrolase [Gonapodya prolifera JEL478]	Hydroxyacylglutathione hydrolase, mitochondrial OS=Xenopus tropicalis OX=8364 GN=hagh PE=2 SV=1
A8789	-	-	-	-	-	-	-	-
A8790	-	-	-	-	-	-	-	-
A8791	-	-	-	-	-	-	-	-
A8792	-	-	-	K09503 DNAJA2; DnaJ homolog subfamily A member 2	map04141 Protein processing in endoplasmic reticulum	KOG0712 At3g44110 Molecular chaperone (DnaJ superfamily)	CDH50023.1 predicted protein [Lichtheimia corymbifera JMR:FSU:9682]	Chaperone protein dnaJ 3 OS=Arabidopsis thaliana OX=3702 GN=ATJ3 PE=1 SV=2
A8793	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8794	-	-	-	-	-	-	-	-
A8795	-	-	-	-	-	-	-	-
A8796	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0619 7300644_2 FOG; Leucine rich repeat	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A8797	GO:0007021(tubulin complex assembly), GO:0007023(post-chaperonin tubulin folding pathway)	-	GO:0005096(GTPase activator activity), GO:0048487(beta-tubulin binding)	K21767 TBCD; tubulin-specific chaperone D	-	KOG1943 Hs8400736 Beta-tubulin folding cofactor D	PKC61437.1 ARM repeat-containing protein [Rhizophagus irregularis]	Tubulin-specific chaperone D OS=Mus musculus OX=10090 GN=Tbcd PE=1 SV=1
A8798	GO:0006357(regulation of transcription by RNA polymerase II)	GO:0032777(Piccolo NuA4 histone acetyltransferase complex), GO:0035267(NuA4 histone acetyltransferase complex)	-	K11322 EPC; enhancer of polycomb-like protein	map03082 ATP-dependent chromatin remodeling	KOG2261 At1g79020 Polycomb enhancer protein, EPC	CRK35676.1 hypothetical protein BN1708_001308 [Verticillium longisporum]	Enhancer of polycomb homolog 1 OS=Homo sapiens OX=9606 GN=EPC1 PE=1 SV=1
A8799	GO:0009190(cyclic nucleotide biosynthetic process), GO:0035556(intracellular signal transduction)	-	-	-	-	-	ORX52156.1 adenylyl cyclase [Piromyces finnis]	Adenylyl cyclase type 10 OS=Homo sapiens OX=9606 GN=ADCY10 PE=1 SV=3
A8800	-	-	-	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1234 At4g01660 ABC (ATP binding cassette) 1 protein	ORX69763.1 ABC1-domain-containing protein [Linderina pennisporea]	Protein ABC transporter 1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=ABC1 PE=2 SV=1

A8801	-	GO:0016459(myosin complex), GO:0005856(cytoskeleton)	GO:0003774(motor activity),GO:0005524(ATP binding),GO:0005515(protein binding)	K10357 MYO5; myosin V	map05130 Pathogenic Escherichia coli infection;map04814 Motor proteins	KOG4229[Hs4505307 Myosin VII, myosin IxB and related myosins	RKO94560.1 myosin VIIA, isoform CRA_d, partial [Blyttiomycetes helicus]	High molecular weight form of myosin-1 OS=Acanthamoeba castellanii OX=5755 PE=3 SV=1
A8802	-	-	GO:0008146(sulfotransferase activity)	-	-	KOG3704[Hs5174465 Heparan sulfate D-glucosaminyl 3-O-sulfotransferase	KAG2177966.1 hypothetical protein [INT43_003213 [Umbelopsis isabellina]	Membrane-associated sulfotransferase kil1 OS=Dictyostelium discoideum OX=44689 GN=kil1 PE=3 SV=1
A8803	-	-	-	-	-	-	-	-
A8804	-	-	-	-	-	-	-	-
A8805	-	-	-	-	-	-	-	-
A8806	-	GO:0016021(integral component of membrane)	-	-	-	-	ORX96267.1 YhhN-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	-
A8807	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8808	GO:0007034(vacuolar transport)	-	-	K12193 VPS24, CHMP3; charged multivesicular body protein 3	map04144 Endocytosis;map04217 Necroptosis	KOG3229[Hs7706353 Vacuolar sorting protein VPS24	KAF9186772.1 Vacuolar protein-sorting-associated protein 24 [Haplosporangium sp. Z 11]	Charged multivesicular body protein 3 OS=Homo sapiens OX=9606 GN=CHMP3 PE=1 SV=3
A8809	-	-	-	-	-	-	ORY81276.1 nucleotide-diphospho-sugar transferase-domain-containing protein [Leucosporidium creatinivorum]	-
A8810	-	-	-	-	-	-	-	-
A8811	-	-	-	-	-	-	RMV87869.1 hypothetical protein D0864_06764 [Hortaea werneckii]	-
A8812	-	GO:0016021(integral component of membrane)	GO:0000166(nucleotide binding),GO:0005215(transporter activity),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K05853 ATP2A; P-type Ca2+ transporter type 2A [EC:7.2.2.10]	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05415 Diabetic cardiomyopathy; map05414 Dilated cardiomyopathy; map05410 Hypertrophic cardiomyopathy; map05412 Arrhythmogenic right ventricular cardiomyopathy; map04919 Thyroid hormone signaling pathway;map04380 Osteoclast differentiation;map04261 Adrenergic	KOG0202[At4g00900 Ca2+ transporting ATPase	XP_018296061.1 hypothetical protein PHYBLDRAFT_185726 [Phycomyces blakesleeanus NRRL 1555(-)]	Calcium-transporting ATPase 2, endoplasmic reticulum-type OS=Arabidopsis thaliana OX=3702 GN=ECA2 PE=1 SV=1

A8813	GO:0006226(dUMP biosynthetic process), GO:0046081(dUTP catabolic process)	-	GO:0000287(magnesium ion binding),GO:0004170(dUTP diphosphatase activity)	K01520 dut, DUT; dUTP diphosphatase [EC:3.6.1.23]	map00983 Drug metabolism - other enzymes;map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG3370 At3g46940 dUTPase	XP_006696419.1 hypothetical protein CHTT_0061030 [Chaetomium thermophilum var. thermophilum DSM 1495]	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Arabidopsis thaliana OX=3702 GN=DUT PE=1 SV=1
A8814	-	-	-	-	-	-	OZJ06172.1 hypothetical protein BZG36_00999 [Bifiguratus adalaidae]	-
A8815	-	-	-	K10579 UBE2M, UBC12; ubiquitin-conjugating enzyme E2 M [EC:2.3.2.34]	map04120 Ubiquitin mediated proteolysis	KOG0420 At2g18600 Ubiquitin-protein ligase	ORY72423.1 E2 ubiquitin-conjugating enzyme [Leucosporidium creatinivorum]	Probable NEDD8-conjugating enzyme Ubc12-like OS=Arabidopsis thaliana OX=3702 GN=RCE2 PE=2 SV=1
A8816	-	-	-	-	-	-	-	-
A8817	-	-	-	-	-	-	-	-
A8818	GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K11835 USP4_11, UBP12; ubiquitin carboxyl-terminal hydrolase 4/11 [EC:3.4.19.12]	-	KOG1870 Hs14149627 Ubiquitin C-terminal hydrolase	KAF9930415.1 CSN-associated deubiquitinating enzyme Ubp12 [Mortierella alpina]	Ubiquitin carboxyl-terminal hydrolase 5 OS=Arabidopsis thaliana OX=3702 GN=UBP5 PE=1 SV=2
A8819	GO:0034755(iron ion transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005381(iron ion transmembrane transporter activity)	K14685 SLC40A1, FPN1; solute carrier family 40 (iron-regulated transporter), member 1	map04216 Ferroptosis;map04978 Mineral absorption	KOG2601 Hs7657100 Iron transporter	OJJ37341.1 hypothetical protein ASPWEDRAFT_107452 [Aspergillus wentii DTO 134E9]	Solute carrier family 40 member 1 OS=Danio rerio OX=7955 GN=slc40a1 PE=1 SV=3
A8820	-	GO:0031417(NatC complex)	-	K20824 NAA38; N-alpha-acetyltransferase 38, NatC auxiliary subunit	-	-	XP_019024057.1 uncharacterized protein SAICODRAFT_7546 [Saitoella complicata NRRL Y-17804]	-
A8821	GO:0019346(transsulfuration)	-	GO:0030170(pyridoxal phosphate binding),GO:0003824(catalytic activity)	-	-	KOG0053 7302582 Cystathionine beta-lyases/cystathionine gamma-synthases	GBC05130.1 hypothetical protein RclHR1_06050008 [Rhizophagus clarus]	Cystathionine gamma-lyase OS=Bacillus subtilis (strain 168) OX=224308 GN=mccB PE=1 SV=1
A8822	GO:0071108(protein K48-linked deubiquitination)	-	GO:0005509(calcium ion binding),GO:0004843(thiol-dependent deubiquitinase), GO:1990380(Lys48-specific deubiquitinase activity)	-	-	KOG2871 Hs13376431 Uncharacterized conserved protein	OON07431.1 hypothetical protein, variant [Batrachochytrium salamandrivorans]	Ubiquitin carboxyl-terminal hydrolase MINDY-3 OS=Homo sapiens OX=9606 GN=MINDY3 PE=1 SV=1

A8823	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867[Hs4503899 Sulfatase	KAF5010842.1 hypothetical protein FDECE_3015 [Fusarium decemcellulare]	N-acetylglactosamine-6-O-sulfatase OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / JCM 5827 / CCUG 10774 / NCTC 10582 / VPI-5482 / E50) OX=226186 GN=BT_3333 PE=1 SV=1
A8824	-	-	GO:0005509(calcium ion binding),GO:0005515(protein binding)	-	-	KOG0504[CE27598 FOG: Ankyrin repeat	KJK61165.1 ANK ankyrin repeat protein [Aspergillus parasiticus SU-1]	Putative ankyrin repeat protein L371 OS=Acanthamoeba polyphaga mimivirus OX=212035 GN=MIMI_L371 PE=4 SV=1
A8825	GO:0006694(steroid biosynthetic process)	-	GO:0003854(3-beta-hydroxy-delta5-steroid dehydrogenase activity),GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)	K07748 NSDHL, ERG26; sterol-4alpha-carboxylate 3-dehydrogenase (decarboxylating) [EC:1.1.1.170]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG1430[Hs19923621 C-3 sterol dehydrogenase/3-beta-hydroxysteroid dehydrogenase and related dehydrogenases	TPX45856.1 hypothetical protein SeMB42_g03881 [Synchytrium endobioticum]	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Mus musculus OX=10090 GN=Nsdhl PE=1 SV=1
A8826	-	-	-	-	-	-	-	-
A8827	-	-	GO:0005515(protein binding)	-	-	-	-	NACHT, LRR and PYD domains-containing protein 3 OS=Mus musculus OX=10090 GN=Nlrp3 PE=1 SV=1
A8828	-	-	-	-	-	-	-	-
A8829	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8830	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8831	-	-	-	-	-	-	-	-
A8832	-	-	-	-	-	-	-	-
A8833	-	GO:0005871(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY36122.1 hypothetical protein BCR33DRAFT_770394 [Rhizoclostium globosum]	-
A8834	-	-	-	-	-	-	KZM27989.1 hypothetical protein ST47_g860 [Ascochyta rabiei]	2-deoxy-scyllo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1
A8835	-	-	-	-	-	-	-	-
A8836	-	-	-	-	-	KOG2942[At4g28020 Uncharacterized conserved protein	ORY41869.1 hypothetical protein BCR33DRAFT_718539 [Rhizoclostium globosum]	tRNA (adenine(37)-N6)-methyltransferase OS=Mus musculus OX=10090 GN=Trmo PE=2 SV=2
A8837	-	-	-	-	-	-	-	-
A8838	-	-	-	-	-	-	-	-
A8839	-	-	GO:0003824(catalytic activity)	-	-	KOG1075[CE04575 FOG: Reverse transcriptase	OMJ10672.1 RNA-directed DNA polymerase from mobile element jockey [Smittium culicis]	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Fragment) OS=Popillia japonica OX=7064 PE=4 SV=1

A8840	-	-	GO:0016491(oxidoreductase activity),GO:0016628(oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor)	-	-	KOG1196 Hs18597326 Predicted NAD-dependent oxidoreductase	POS75020.1 hypothetical protein DHEL01_v206579 [Diaporthe helianthi]	Prostaglandin reductase 2 OS=Bos taurus OX=9913 GN=PTGR2 PE=2 SV=1
A8841	-	-	-	-	-	-	CEJ01154.1 hypothetical protein RMCBS34429_2_15190 [Rhizopus microsporus]	-
A8842	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0605 At4g33080 NDR and related serine/threonine kinases	RKP09497.1 serine/threonine-protein kinase orb6 [Thamnocephalis sphaerospora]	Serine/threonine-protein kinase tricorned OS=Drosophila pseudoobscura pseudoobscura OX=46245 GN=trc PE=3 SV=1
A8843	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG1330 CE05393 Sugar transporter/s pinster transmembrane protein	RPD54546.1 MFS general substrate transporter [Lentinus tigrinus ALCF2SS1-6]	Cis,cis-muconate transport protein OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=mucK PE=3 SV=1
A8844	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity),GO:0008138(protein tyrosine/serine/threonine phosphatase activity)	-	-	-	-	-
A8845	GO:0045292(mRNA cis splicing, via spliceosome)	-	GO:0005515(protein binding)	-	-	-	-	-
A8846	-	-	GO:0005524(ATP binding)	-	-	KOG0061 At2g37010 Transporter, ABC superfamily (Breast cancer resistance protein)	KAF9116038.1 hypothetical protein BGX27_005271 [Mortierella sp. AM989]	ABC transporter G family member 28 OS=Arabidopsis thaliana OX=3702 GN=ABCG28 PE=3 SV=1
A8847	-	-	GO:0061630(ubiquitin protein ligase activity)	-	-	KOG3039 Hs7705716 Uncharacterized conserved protein	QDS75002.1 hypothetical protein FKW77_005602 [Venturia effusa]	Nitric oxide synthase-interacting protein OS=Bos taurus OX=9913 GN=NOSIP PE=2 SV=1
A8848	-	-	GO:0004518(nuclease activity)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518 YO R033c 5'-3' exonuclease	KAF8515840.1 PIN domain-like protein [Hysterangium stoloniferum]	Exodeoxyribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EXO1 PE=1 SV=2
A8849	-	-	-	-	-	-	-	-

A8850	-	-	-	-	-	KOG4842 At5g35690 Protein involved in sister chromatid separation and/or segregation	-	-
A8851	-	-	GO:0005509(cal cium ion binding)	-	-	KOG0027 Hs4885109 Calmodulin and related proteins (EF-Hand superfamily)	KAG5357677.1 Calmodulin [Yarrowia sp. C11]	Dynein 18 kDa light chain, flagellar outer arm OS=Chlamydomonas reinhardtii OX=3055 PE=1 SV=1
A8852	GO:0010756(positive regulation of plasminogen activation)	GO:0005887(integral component of plasma membrane)	-	-	-	-	TPX64815.1 hypothetical protein SpCBS45565_g05571 [Spizellomyces sp. 'palustris']	Plasminogen receptor (KT) OS=Mus musculus OX=10090 GN=Plgrkt PE=1 SV=1
A8853	-	-	-	-	-	-	-	-
A8854	-	-	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K24512 VWA8; von Willebrand factor A domain-containing protein 8	-	KOG1808 Hs22053093 AAA ATPase containing von Willebrand factor type A (VWA) domain	GBC32829.1 von willebrand factor a domain-containing protein 8-like [Rhizophagus irregularis DAOM 181602=DAOM 197198]	von Willebrand factor A domain-containing protein 8 OS=Danio rerio OX=7955 GN=sidkey-1811.1 PE=3 SV=1
A8855	-	-	-	K14816 REI1; pre-60S factor REI1	-	KOG2785 YBR267w C2H2-type Zn-finger protein	KAF0528296.1 C2H2 type zinc-finger-domain-containing protein [Gigaspora margarita]	Cytoplasmic 60S subunit biogenesis factor REI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=REI1 PE=1 SV=3
A8856	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity),GO:0005515(protein binding)	K09568 FKBP1; FK506-binding protein 1 [EC:5.2.1.8]	-	KOG0544 Hs4503725 FKBP-type peptidyl-prolyl cis-trans isomerase	KAF9071179.1 peptidyl-prolyl isomerase [Rhodocollybia butyracea]	FK506-binding protein 1 OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) OX=246409 GN=FKBP1 PE=3 SV=1
A8857	GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport),GO:0006890(retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum)	GO:0070939(Dsl1/NZR complex)	-	K20474 RINT1, TIP20; RAD50-interacting protein 1	-	KOG2218 7295261 ER to golgi transport protein/RAD50-interacting protein 1	KAF9229614.1 hypothetical protein BS17DRAFT_805254 [Gyrodont lividus]	RINT1-like protein OS=Drosophila melanogaster OX=7227 GN=Rint1 PE=2 SV=2
A8858	-	-	-	-	-	-	-	-
A8859	-	-	GO:0003676(nucleic acid binding)	K11135 PINX1; Pin2-interacting protein X1	-	KOG2809 Hs18549312 Telomerase elongation inhibitor/RNA maturation protein PINX1	KNE57077.1 hypothetical protein AMAG_02831 [Allomyces macrogynus ATCC 38327]	G patch domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GPATCH4 PE=1 SV=2

A8860	-	-	-	K26736 PA2G4, EBP1; ERBB-3 binding protein	-	KOG2776 Hs5 453842 Metallopepti dase	TPX55258.1 hypothetical protein PhCBS80983. g05479 [Powellomyce s hirtus]	ERBB-3 BINDING PROTEIN 1 OS=Solanum tuberosum OX=4113 GN=EBP1 PE=2 SV=1
A8861	-	GO:00057 77(peroxis ome)	-	-	-	-	-	-
A8862	-	-	-	-	-	-	-	-
A8863	GO:00550 85(transm embrane transport)	GO:00160 21(integra l compone nt of membran e)	GO:0005524(AT p binding),GO:014 0359(ABC-type transporter activity)	K05657 ABCB10; ATP-binding cassette, subfamily B (MDR/TAP), member 10	map02010 ABC transporters	KOG0058 Hs9 961244 Peptide exporter, ABC superfamily	CEG68405.1 Putative ATP- binding cassette, subfamily B (MDR/TAP), member 10 [Rhizopus microsporus]	ABC transporter B family member 1 OS=Dictyostelium discoideum OX=44689 GN=abcB1 PE=3 SV=1
A8864	-	-	-	-	-	-	-	-
A8865	GO:00062 81(DNA repair),GO :0019985(translesio n synthesis)	GO:00160 35(zeta DNA polymerase complex)	GO:0000166(nu cleotide binding),GO:000 3676(nucleic acid binding),GO:000 3887(DNA- directed DNA polymerase activity),GO:000 3677(DNA binding)	K02350 REV3L, POLZ; DNA polymerase zeta [EC:2.7.7.7]	map01524 Platinum drug resistance;map0 3460 Fanconi anemia pathway	KOG0968 At1 g67500 DNA polymerase zeta, catalytic subunit	KMU81655.1 DNA polymerase zeta catalytic subunit [Coccidioides immitis RMSCC 3703]	DNA polymerase zeta catalytic subunit OS=Arabidopsis thaliana OX=3702 GN=REV3 PE=2 SV=1
A8866	GO:00068 91(intra- Golgi vesicle- mediated transport)	GO:00301 73(integra l compone nt of Golgi membran e)	-	K09313 CUTL; homeobox protein cut- like	-	KOG0963 At3 g18480 Transcription factor/CCAAT displacement protein CDP1	XP_03102566 1.1 uncharacteriz ed protein SmJEL517_g0 2488 [Synchytrium microbalum]	Protein CASP OS=Arabidopsis thaliana OX=3702 GN=CASP PE=1 SV=2
A8867	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	-	-	KOG0583 YPL 026c Serine/threon ine protein kinase	XP_03722107 2.1 Protein kinase domain- containing protein [Mycena indigotica]	Serine/threonine-protein kinase RUNKEL OS=Arabidopsis thaliana OX=3702 GN=RUKE PE=1 SV=1
A8868	-	-	-	-	-	-	-	-
A8869	-	-	GO:0005515(pro tein binding)	-	-	KOG4014 728 9028 Uncharacteriz ed conserved protein (contains TPR repeat)	KNE60015.1 hypothetical protein AMAG_05454 [Allomyces macrogynus ATCC 38327]	Cytochrome c oxidase assembly factor 7 homolog OS=Drosophila melanogaster OX=7227 GN=Cox7 PE=2 SV=1
A8870	-	GO:00014 01(SAM complex)	-	-	-	KOG3027 Hs5 729937 Mitochondria l outer membrane protein Metaxin 2, Metaxin 1- binding protein	OON09235.1 hypothetical protein BSLG_01682 [Batrachochyt rium salamandrivo rans]	Metaxin-3 OS=Danio rerio OX=7955 GN=mtx3 PE=2 SV=2

A8871	-	-	GO:0004605(phosphatidate cytidyltransferase activity)	K00981 E2.7.7.41, CDS1, CDS2, cdsA; phosphatidate cytidyltransferase [EC:2.7.7.41]	map01110 Biosynthesis of secondary metabolites;map04070 Phosphatidylinositol signaling system;map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG1440 At1g62430 CDP-diacylglycerol synthase	KAG0228554.1 hypothetical protein BGW42_002098 [Actinomortierella wolffii]	Phosphatidate cytidyltransferase 1 OS=Arabidopsis thaliana OX=3702 GN=CDS1 PE=1 SV=1
A8872	GO:0006355(regulation of transcription, DNA-templated),GO:0016573(histone acetylation)	-	GO:0004402(histone acetyltransferase activity),GO:0005515(protein binding)	K11684 BDF1; bromodomain-containing factor 1	-	KOG1778 At1g16710 CREB binding protein/P300 and related TAZ Zn-finger proteins	OUM65932.1 hypothetical protein PIR0E2DRAFT_41243, partial [Piromyces sp. E2]	Histone acetyltransferase HAC12 OS=Arabidopsis thaliana OX=3702 GN=HAC12 PE=3 SV=2
A8873	GO:0006355(regulation of transcription, DNA-templated),GO:0016573(histone acetylation)	-	GO:0005515(protein binding),GO:0008270(zinc ion binding),GO:0004402(histone acetyltransferase activity)	K11684 BDF1; bromodomain-containing factor 1	-	KOG1778 At1g16710 CREB binding protein/P300 and related TAZ Zn-finger proteins	KAF2460373.1 Bromodomain-containing protein [Lineolata rhizophorae]	Histone acetyltransferase HAC12 OS=Arabidopsis thaliana OX=3702 GN=HAC12 PE=3 SV=2
A8874	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0005509(calcium ion binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At2g17890 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	TIA86774.1 hypothetical protein E3P99_03573 [Wallemia hederae]	Probable myosin light chain kinase DDB_G0292624 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0292624 PE=3 SV=1
A8875	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 At3g10660 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORX53708.1 Pkinase-domain-containing protein [Piromyces finnis]	Calcium-dependent protein kinase 2 OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=CDPK2 PE=1 SV=4
A8876	-	-	-	-	-	-	KAF9428474.1 hypothetical protein BGZ94_002265 [Podila epigama]	Acidic fibroblast growth factor intracellular-binding protein OS=Homo sapiens OX=9606 GN=FIBP PE=1 SV=3

A8877	-	-	GO:0005515(protein binding)	-	-	KOG2162 At5g19400 Nonsense-mediated mRNA decay protein	RGB26150.1 hypothetical protein C1646_430686 [Rhizophagus diaphanus] [Rhizophagus sp. MUCL 43196]	Nonsense-mediated mRNA decay factor SMG7 OS=Arabidopsis thaliana OX=3702 GN=SMG7 PE=1 SV=1
A8878	-	-	-	K01904 4CL; 4-coumarate--CoA ligase [EC:6.2.1.12]	map01110 Biosynthesis of secondary metabolites;map00940 Phenylpropanoid biosynthesis;map00130 Ubiquinone and other terpenoid-quinone biosynthesis;map01100 Metabolic pathways	KOG1176 YBR222c Acyl-CoA synthetase	KAE8243748.1 hypothetical protein A4X03_0g7683 [Tilletia caries]	Medium-chain fatty-acid--CoA ligase OS=Escherichia coli (strain K12) OX=83333 GN=fadK PE=1 SV=4
A8879	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K12761 SNF1; carbon catabolite-derepressing protein kinase [EC:2.7.11.1]	map04138 Autophagy - yeast;map04113 Meiosis - yeast	KOG0583 At3g01090 Serine/threonine protein kinase	XP_006680638.1 uncharacterized protein BATDEDRAFT_13136, partial [Batrachochytrium dendrobatidis JAM81]	Serine/threonine protein kinase OSK1 OS=Oryza sativa subsp. japonica OX=39947 GN=OSK1 PE=1 SV=1
A8880	-	-	-	-	-	-	-	-
A8881	GO:0000413(protein peptidyl-prolyl isomerization)	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K12734 PP1L3; peptidyl-prolyl cis-trans isomerase-like 3 [EC:5.2.1.8]	-	KOG0881 At2g36130 Cyclophilin type peptidyl-prolyl cis-trans isomerase	CCG81591.1 Peptidyl-prolyl cis-trans isomerase-like 3 [Taphrina deformans PYCC 5710]	Peptidyl-prolyl cis-trans isomerase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=rotA PE=3 SV=1
A8882	GO:0006537(glutamate biosynthetic process)	-	GO:0015930(glutamate synthase activity),GO:0016638(oxidoreductase activity, acting on the CH-NH2 group of donors)	K00264 GLT1; glutamate synthase (NADH) [EC:1.4.1.14]	map00910 Nitrogen metabolism;map01110 Biosynthesis of secondary metabolites;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00250 Alanine, aspartate and glutamate metabolism;map01100 Metabolic pathways	-	ORY53645.1 FMN-linked oxidoreductase [Rhizoclostridium globosum]	Glutamate synthase large subunit-like protein YerD OS=Bacillus subtilis (strain 168) OX=224308 GN=yerD PE=3 SV=1

A8883	GO:0006139(nucleobase-containing compound metabolic process), GO:0000467(exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA))	-	GO:0003676(nucleic acid binding),GO:0008408(3'-5' exonuclease activity),GO:0000175(3'-5'-exoribonuclease activity)	K12591 RRP6, EXOSC10; exosome complex exonuclease RRP6 [EC:3.1.13.-]	map03018 RNA degradation	KOG2206 YOR001w Exosome 3'-5' exoribonuclease complex, subunit PM/SCL-100 (Rrp6)	OBZ84967.1 Exosome complex exonuclease rrp6 [Choanephora cucurbitarum]	Exosome complex exonuclease RRP6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP6 PE=1 SV=1
A8884	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity),GO:0008236(serine-type peptidase activity)	-	-	-	XP_023624697.1 related to Cuticle-degrading protease [Ramularia collo-cygni]	Aqualysin-1 OS=Thermus aquaticus OX=271 GN=pstI PE=1 SV=2
A8885	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity),GO:0008236(serine-type peptidase activity)	-	-	-	XP_023624697.1 related to Cuticle-degrading protease [Ramularia collo-cygni]	Aqualysin-1 OS=Thermus aquaticus OX=271 GN=pstI PE=1 SV=2
A8886	-	-	-	K15113 SLC25A28_37, MFRN; solute carrier family 25 (mitochondrial iron transporter), member 28/37	-	KOG0760 At1g07030 Mitochondrial carrier protein MRS3/4	KAF9978092.1 asparaginyl-tRNA synthetase [Mortierella antarctica]	Mitoferrin OS=Dictyostelium discoideum OX=44689 GN=mcfF PE=3 SV=1
A8887	-	-	GO:0016409(palmitoyltransferase activity)	K20003 ZDHHC4, SWF1; palmitoyltransferase ZDHHC4 [EC:2.3.1.225]	-	KOG1312 At3g04970 DHHC-type Zn-finger proteins	XP_016609512.1 hypothetical protein SPPG_03274 [Spizellomyces punctatus DAOM BR117]	Probable protein S-acyltransferase 17 OS=Arabidopsis thaliana OX=3702 GN=PAT17 PE=2 SV=1
A8888	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	-	XP_025173902.1 kinase-like domain-containing protein [Rhizophagus irregularis DAOM 181602=DAOM 197198]	-
A8889	-	-	GO:0016746(acyltransferase activity),GO:0008374(O-acyltransferase activity)	-	-	KOG4666 7291068_2 Predicted phosphate acyltransferase, contains PlsC domain	KNE86455.1 hypothetical protein PSTG_20184, partial [Puccinia striiformis f. sp. tritici PST-78]	Lysophosphatidylcholine acyltransferase 2 OS=Mus musculus OX=10090 GN=Lpcat2 PE=1 SV=1
A8890	-	-	-	-	-	-	-	-

A8891	-	GO:0000786(nucleosome)	GO:0003677(DNA binding),GO:0030527(structural constituent of chromatin),GO:0046982(protein heterodimerization activity)	K11252 H2B; histone H2B	map05322 Systemic lupus erythematosus; map04613 Neutrophil extracellular trap formation;map05034 Alcoholism;map05203 Viral carcinogenesis	KOG1744 Hs10800138 Histone H2B	RKP27388.1 hypothetical protein SYNPS1DRAFT_21074 [Syncephalis pseudoplumigaleata]	Histone H2B OS=Olisthodiscus luteus OX=83000 PE=1 SV=2
A8892	-	-	-	-	-	KOG1924 Hs4885183 RhoA GTPase effector DIA/Diaphanous	RKP01507.1 hypothetical protein CXG81DRAFT_25836 [Caulochytrium protostelioides]	Protein diaphanous homolog 1 OS=Homo sapiens OX=9606 GN=DIAPH1 PE=1 SV=2
A8893	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004674(protein serine/threonine kinase activity)	K19800 SCH9; serine/threonine protein kinase SCH9 [EC:2.7.11.1]	map04213 Longevity regulating pathway - multiple species;map04138 Autophagy - yeast	KOG0598 CE22045 Ribosomal protein S6 kinase and related proteins	KXN66960.1 Pkinase-domain-containing protein [Conidiobolus coronatus NRRL 28638]	RAC family serine/threonine-protein kinase homolog OS=Dictyostelium discoideum OX=44689 GN=pkbA PE=1 SV=1
A8894	-	-	-	-	-	KOG2381 At3g56600 Phosphatidylinositol 4-kinase	-	Phosphatidylinositol 4-kinase gamma 8 OS=Arabidopsis thaliana OX=3702 GN=PI4KG8 PE=2 SV=2
A8895	-	-	-	-	-	-	-	-
A8896	-	-	GO:0016746(acyltransferase activity)	K00624 E2.3.1.7; carnitine O-acetyltransferase [EC:2.3.1.7]	map04146 Peroxisome	KOG3717 Hs21618336 Carnitine O-acyltransferase CRAT	TPX71179.1 hypothetical protein SpCBS45565_g01373 [Spizellomyces sp. 'palustris']	Carnitine O-acetyltransferase OS=Homo sapiens OX=9606 GN=CRAT PE=1 SV=5
A8897	-	-	GO:0016746(acyltransferase activity)	K08766 E2.3.1.21; carnitine O-palmitoyltransferase 2 [EC:2.3.1.21]	map00071 Fatty acid degradation	KOG3719 Hs4503023 Carnitine O-acyltransferase CPT2/YAT1	KKY18466.1 putative carnitine acetyltransferase [Phaeomonielachlamydispora]	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Mus musculus OX=10090 GN=Cpt2 PE=1 SV=2
A8898	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8899	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	-	-	KOG0192 At1g18160 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	KAG0233310.1 hypothetical protein BGW42_007508 [Actinomortierella wolfii]	Serine/threonine-protein kinase CTR1 OS=Arabidopsis thaliana OX=3702 GN=CTR1 PE=1 SV=1
A8900	-	-	-	K17818 ARD1; D-arabinitol dehydrogenase (NADP+) [EC:1.1.1.287]	map00040 Pentose and glucuronate interconversions; map01100 Metabolic pathways	-	KIM52504.1 hypothetical protein SCLCIDRAFT_1223705 [Scleroderma citrinum Foug A]	2-deoxy-scyllo-inosamine dehydrogenase OS=Streptomyces fradiae OX=1906 GN=neoA PE=1 SV=1

A8901	-	GO:000571(kinesin complex)	GO:0005515(protein binding)	-	-	-	ORY31577.1 TPR-like protein [Rhizoclostium globosum]	-
A8902	-	-	GO:0005509(calcium ion binding)	K06268 PPP3R, CNB; serine/threonine-protein phosphatase 2B regulatory subunit	map04360 Axon guidance;map05014 Amyotrophic lateral sclerosis;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis;map04218 Cellular senescence;map05170 Human immunodeficiency virus 1 infection;map04650 Natural killer cell mediated cytotoxicity;map04658 Th1 and Th2 cell differentiation;map04659 Th17 cell	KOG0044 CE24845 Ca2+ sensor (EF-Hand superfamily)	KAG0377794.1 Neuronal calcium sensor 1 [Mortierella sp. AD032]	Calsenilin OS=Mus musculus OX=10090 GN=Kcnip3 PE=1 SV=2
A8903	GO:0006979(response to oxidative stress),GO:0034599(cellular response to oxidative stress)	-	GO:0004601(peroxidase activity),GO:0020037(heme binding)	K00428 E1.1.1.1.5; cytochrome c peroxidase [EC:1.11.1.5]	-	-	RKP19149.1 heme peroxidase [Rozella allomyces CSF55]	Cytochrome c peroxidase, mitochondrial OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=ccp1 PE=3 SV=1
A8904	-	-	GO:0005515(protein binding)	K15442 TAD3, ADAT3; tRNA-specific adenosine deaminase 3	-	-	KAF8650125.1 hypothetical protein AX16_005362 [Volvariella volvacea WC 439]	Histone-lysine N-methyltransferase, H3 lysine-37 specific OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=set7 PE=1 SV=1
A8905	-	-	-	-	-	-	-	-
A8906	-	-	-	-	-	-	-	-
A8907	-	-	-	-	-	-	-	-
A8908	-	-	-	-	-	-	-	-
A8909	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome),GO:0019843(rRNA binding)	-	-	KOG4707 At1g16740 Mitochondrial/chloroplast ribosomal protein L20	KAG0323187.1 hypothetical protein BGZ97_012346 [Linnemannia gamsii]	Large ribosomal subunit protein bL20 OS=Ehrlichia chaffeensis (strain ATCC CRL-10679 / Arkansas) OX=205920 GN=rpIT PE=3 SV=1
A8910	-	-	GO:0016491(oxidoreductase activity)	-	-	-	KAF7759522.1 hypothetical protein DSO57_018053 [Entomophthora muscae]	-
A8911	-	-	-	K00761 upp, UPRT; uracil phosphoribosyltransferase [EC:2.4.2.9]	map00240 Pyrimidine metabolism;map01232 Nucleotide metabolism;map01100 Metabolic pathways	KOG4203 At4g26510 Armadillo/beta-Catenin/plakoglobin	KXS17370.1 PRTase-like protein [Gonapodya prolifera JEL478]	Uridine kinase-like protein 3 OS=Arabidopsis thaliana OX=3702 GN=UKL3 PE=2 SV=1

A8912	GO:0016567(protein ubiquitination)	-	GO:0004842(ubiquitin-protein transferase activity)	K21804 METTL21A; protein N-lysine methyltransferase METTL21A [EC:2.1.1.-]	-	KOG2793 CE02891_1 Putative N2.N2-dimethylguanosine tRNA methyltransferase	OON06713.1 hypothetical protein BSLG_03671 [Batrachochytrium salamandrivorans]	E3 ubiquitin-protein ligase ipaH3 OS=Shigella flexneri OX=623 GN=ipaH3 PE=1 SV=1
A8913	-	GO:0016021(integral component of membrane)	-	-	-	KOG1623 At2g39060 Multitransmembrane protein	KXS17721.1 hypothetical protein M427DRAFT_54321 [Gonapodya prolifera JEL478]	Bidirectional sugar transporter SWEET17 OS=Arabidopsis thaliana OX=3702 GN=SWEET17 PE=1 SV=2
A8914	-	GO:0016021(integral component of membrane)	-	-	-	KOG1623 At5g50790 Multitransmembrane protein	XP_006677490.1 uncharacterized protein BATDEDRAFT_36766 [Batrachochytrium dendrobatidis JAM81]	Bidirectional sugar transporter SWEET11 OS=Oryza sativa subsp. indica OX=39946 GN=SWEET11 PE=2 SV=1
A8915	-	GO:0016021(integral component of membrane)	-	-	-	-	KNE61201.1 hypothetical protein AMAG_06951 [Allomyces macrogynus ATCC 38327]	Bidirectional sugar transporter SWEET11 OS=Oryza sativa subsp. indica OX=39946 GN=SWEET11 PE=2 SV=1
A8916	-	GO:0016021(integral component of membrane)	GO:0005515(protein binding)	-	-	KOG1623 CE08976 Multitransmembrane protein	KXS17721.1 hypothetical protein M427DRAFT_54321 [Gonapodya prolifera JEL478]	Tetratricopeptide repeat protein 38 OS=Xenopus laevis OX=8355 GN=ttc38 PE=2 SV=1
A8917	-	-	GO:0005515(protein binding)	-	-	-	KAG0211160.1 T-complex-associated testis-expressed protein 1 [Mortierella sp. NVP41]	-
A8918	GO:0006457(protein folding)	-	GO:0005515(protein binding),GO:0043014(alpha-tubulin binding)	K21768 TBCE; tubulin-specific chaperone E	-	KOG3207 Hs4507375 Beta-tubulin folding cofactor E	PKC15693.1 L domain-like protein [Rhizophagus irregularis]	Tubulin-folding cofactor E OS=Arabidopsis thaliana OX=3702 GN=TFCE PE=2 SV=1
A8919	-	-	-	-	-	-	KAF9399557.1 hypothetical protein BGX21_006012 [Mortierella sp. AD011]	Embryogenesis-like protein OS=Arabidopsis thaliana OX=3702 GN=EML PE=1 SV=1
A8920	-	-	-	-	-	-	-	-
A8921	-	-	GO:0008270(zinc ion binding)	-	-	-	-	-
A8922	-	-	-	-	-	KOG3544 Hs2045683 Collagens (type IV and type XIII), and related proteins	-	Collagen alpha-4(VI) chain OS=Mus musculus OX=10090 GN=Col6a4 PE=1 SV=2
A8923	-	-	-	-	-	-	-	Collagen alpha-1(XIV) chain OS=Homo sapiens OX=9606 GN=COL14A1

A8924	GO:0006508(proteolysis)	GO:0005576(extracellular region)	GO:0005515(protein binding)	-	-	-	KAF4994524.1 hypothetical protein FGRMN_5733 [Fusarium gramineum]	-
A8925	GO:0006508(proteolysis)	GO:0005576(extracellular region)	GO:0005515(protein binding)	-	-	-	-	-
A8926	-	-	-	-	-	-	-	-
A8927	GO:0006508(proteolysis)	GO:0005576(extracellular region)	GO:0005515(protein binding)	-	-	KOG3637 Hs20562592 Vitronectin receptor, alpha subunit	-	-
A8928	GO:0006508(proteolysis)	GO:0005576(extracellular region)	GO:0005515(protein binding)	-	-	-	-	-
A8929	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0008569(minus-end-directed microtubule motor activity)	-	-	KOG3595 Hs17864092 Dyneins, heavy chain	TPX78372.1 hypothetical protein CcCBS67573_g00338 [Chytridiomycetes confervae]	Dynein axonemal heavy chain 7 OS=Homo sapiens OX=9606 GN=DNAH7 PE=1 SV=2
A8930	-	-	-	K17989 SDS, SDH, CHA1; L-serine/L-threonine ammonia-lyase [EC:4.3.1.17 4.3.1.19]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01230 Biosynthesis of amino acids;map00260 Glycine, serine and threonine metabolism;map00290 Valine, leucine and isoleucine biosynthesis;map01100 Metabolic pathways;map00270 Cysteine and methionine metabolism	KOG1250 Hs5803161 Threonine/serine dehydratases	KAG0087505.1 hypothetical protein BGZ92_007283 [Podila epicladia]	L-serine dehydratase/L-threonine deaminase OS=Homo sapiens OX=9606 GN=SDS PE=1 SV=2
A8931	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 Hs9966875 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	KAG0366372.1 hypothetical protein BGZ54_005428 [Gamsiella multidivariata]	Calcium-dependent protein kinase 7 OS=Arabidopsis thaliana OX=3702 GN=CPK7 PE=2 SV=1
A8932	-	-	GO:0016407(acyltransferase activity)	-	-	-	-	-
A8933	-	-	GO:0005515(protein binding)	-	-	KOG1611 CE09002 Predicted short chain-type dehydrogenase	XP_018380985.1 NAD(P)-binding protein [Alternaria alternata]	1-hydroxy-2-glutathionyl-2-methyl-3-butene dehydrogenase OS=Rhodococcus sp. (strain AD45) OX=103808 GN=isoH PE=1 SV=1

A8934	-	-	-	-	-	KOG1611 CE09002 Predicted short chain-type dehydrogenase	CCO35427.1 C-factor AltName: Full=C signal [Rhizoctonia solani AG-1 IB]	C-signal OS=Myxococcus xanthus OX=34 GN=csgA PE=1 SV=1
A8935	-	-	-	-	-	-	-	-
A8936	-	-	-	-	-	KOG0909 Hs21314690 Peptide:N-glycanase	ORY38370.1 hypothetical protein BCR33DRAFT_429443 [Rhizoclostium globosum]	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase OS=Mus musculus OX=10090 GN=Ngly1 PE=1 SV=2
A8937	-	-	-	-	-	-	-	-
A8938	GO:0006665(sphingolipid metabolic process)	-	GO:0004348(glucosylceramidase activity)	K22276 NEG1; glucan endo-1,6-beta-glucosidase [EC:3.2.1.75]	-	KOG2566 CE20669 Beta-glucocerebrosidase	RFU32833.1 hypothetical protein B7463_g3482, partial [Scytalidium lignicola]	Putative glucosylceramidase 3 OS=Caenorhabditis elegans OX=6239 GN=gba-3 PE=3 SV=1
A8939	GO:0044341(sodium-dependent phosphate transport); GO:0035435(phosphate ion transmembrane transport)	GO:0016020(membrane)	GO:0005436(sodium:phosphate symporter activity); GO:0015114(phosphate ion transmembrane transporter activity)	-	-	-	-	Sodium-dependent phosphate transport protein 2B OS=Pongo abelii OX=9601 GN=SLC34A2 PE=2 SV=1
A8940	GO:0043039(tRNA aminoacylation)	-	GO:0000166(nucleotide binding); GO:0003824(catalytic activity); GO:0004812(aminoacyl-tRNA ligase activity); GO:0005524(ATP binding)	K04487 iscS, NFS1; cysteine desulfurase [EC:2.8.1.7]	map00730 Thiamine metabolism; map01240 Biosynthesis of cofactors; map04122 Sulfur relay system; map01100 Metabolic pathways	KOG1549 Hs19923803 Cysteine desulfurase NFS1	KAF1991120.1 ThrRS/AlaRS common domain-containing protein [Aulographum hederarum CBS 113979]	Selenocysteine lyase OS=Xenopus laevis OX=8355 GN=scly PE=2 SV=1
A8941	GO:0044341(sodium-dependent phosphate transport); GO:0035435(phosphate ion transmembrane transport)	GO:0016020(membrane)	GO:0005436(sodium:phosphate symporter activity); GO:0015114(phosphate ion transmembrane transporter activity)	-	-	-	-	Sodium-dependent phosphate transport protein 2B OS=Pongo abelii OX=9601 GN=SLC34A2 PE=2 SV=1
A8942	-	-	-	K14786 KRI1; protein KRI1	-	KOG2409 7294617 KRR1-interacting protein involved in 40S ribosome biogenesis	XP_031026113.1 uncharacterized protein SmJEL517_g01900 [Synchytrium microbalum]	Protein KRI1 homolog OS=Drosophila melanogaster OX=7227 GN=CG5645 PE=1 SV=1
A8943	GO:0008033(tRNA processing)	-	GO:0000166(nucleotide binding); GO:0005524(ATP binding); GO:0016879(ligase activity, forming carbon-nitrogen bonds)	K04075 ttiS, mesJ; tRNA(Ile)-lysidine synthase [EC:6.3.4.19]	-	-	TID30520.1 hypothetical protein CANINC_000873 [[Candida] inconspicua]	tRNA(Ile)-lysidine synthase OS=Chlamydia caviae (strain ATCC VR-813 / DSM 19441 / 03DC25 / GPIC) OX=227941 GN=ttiS PE=3 SV=1

A8944	GO:0000398(mRNA splicing, via spliceosome),GO:0000956(nuclear-transcribed mRNA catabolic process)	-	-	K12626 LSM7; U6 snRNA-associated Sm-like protein LSM7	map03040 Spliceosome;map03018 RNA degradation	KOG1781 At2g03870 Small Nuclear ribonucleoprotein splicing factor	TPX72882.1 hypothetical protein SpCBS45565.g00213 [Spizellomyces sp. 'palustris']	Probable U6 snRNA-associated Sm-like protein LSM7 OS=Dictyostelium discoideum OX=44689 GN=lsm7 PE=3 SV=1
A8945	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02893 RP-L23Ae, RPL23A; large subunit ribosomal protein L23Ae	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG1751 Hs17105394 60S ribosomal protein L23	KAF8636229.1 hypothetical protein AX17_003715 [Amanita inopinata Kibby_2008]	Large ribosomal subunit protein uL23 OS=Daucus carota OX=4039 GN=RPL23A PE=2 SV=1
A8946	-	-	-	K02863 RP-L1, MRPL1, rplA; large subunit ribosomal protein L1	map03010 Ribosome	KOG1569 At3g63490 50S ribosomal protein L1	KAG0084169.1 hypothetical protein BGZ92_010140, partial [Podila epiciadia]	Large ribosomal subunit protein uL1 OS=Rickettsia akari (strain Hartford) OX=293614 GN=rplA PE=3 SV=1
A8947	GO:0006096(glycolytic process)	-	GO:0004807(triose-phosphate isomerase activity)	K01803 TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00051 Fructose and mannose metabolism;map00710 Carbon fixation in photosynthetic organisms;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG1643 At2g21170 Triosephosphate isomerase	XP_009224188.1 triosephosphate isomerase [Gaeumannomyces tritici R3-111a-1]	Triosephosphate isomerase, cytosolic OS=Hordeum vulgare OX=4513 PE=1 SV=3
A8948	GO:0030001(metal ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	K14709 SLC39A1_2_3, ZIP1_2_3; solute carrier family 39 (zinc transporter), member 1/2/3	map05010 Alzheimer disease;map05012 Parkinson disease	KOG1558 At3g12750 Fe2+/Zn2+ regulated transporter	CDS14543.1 hypothetical protein LRAMOSA06712 [Lichtheimia ramosa]	Zinc-regulated transporter 1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ZRT101 PE=1 SV=1
A8949	-	-	GO:0005515(protein binding)	-	-	KOG1081 Hs13699811 Transcription factor NSD1 and related SET domain proteins	-	Histone-lysine N-methyltransferase NSD3 OS=Mus musculus OX=10090 GN=Nsd3 PE=1 SV=2

A8950	-	GO:0005739(mitochondrion), GO:0045277(respiratory chain complex IV)	-	K02267 COX6B; cytochrome c oxidase subunit 6b	map05014 Amyotrophic lateral sclerosis;map05415 Diabetic cardiomyopathy; map04260 Cardiac muscle contraction;map04714 Thermogenesis; map00190 Oxidative phosphorylation; map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05208 Chemical carcinogenesis - reactive oxygen species;map04932 Non-alcoholic fatty liver disease;map05010 Alzheimer disease;map050	KOG3057 At1g22450 Cytochrome c oxidase, subunit VIb/COX12	KAF9122683.1 Cytochrome c oxidase subunit 6B [Mortierella sp. 14UC]	Cytochrome c oxidase subunit 6b-3 OS=Arabidopsis thaliana OX=3702 GN=COX6B-3 PE=2 SV=2
A8951	GO:0006310(DNA recombination)	-	GO:0000150(DNA strand exchange activity),GO:0003677(DNA binding)	-	-	-	RHZ50113.1 hypothetical protein Glove_505g19 [Diversispora epigaea]	Putative transposase A625R OS=Paramecium bursaria Chlorella virus 1 OX=10506 GN=A625R PE=3 SV=1
A8952	-	GO:0030014(CCR4-NOT complex)	-	-	-	KOG4508 Hs8922110 Uncharacterized conserved protein	RKO90227.1 hypothetical protein BDK51DRAFT_30456 [Blyttomyces helicus]	CCR4-NOT transcription complex subunit 11 OS=Danio rerio OX=7955 GN=cnot11 PE=2 SV=1
A8953	GO:0006468(protein phosphorylation)	-	GO:0005524(ATP binding),GO:0004672(protein kinase activity)	K08794 CAMK1; calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17]	map04020 Calcium signaling pathway;map05214 Glioma;map04921 Oxytocin signaling pathway;map04925 Aldosterone synthesis and secretion	KOG0032 CE25046 Ca2+/calmodulin-dependent protein kinase, EF-Hand protein superfamily	ORX54885.1 calcium/calmodulin-dependent protein kinase I delta short [Piromyces finnis]	Calcium/calmodulin-dependent protein kinase type 1 OS=Caenorhabditis briggsae OX=6238 GN=cmk-1 PE=3 SV=4
A8954	-	GO:0016021(integral component of membrane)	GO:0008146(sulfotransferase activity)	-	-	-	-	-
A8955	-	-	-	-	-	KOG4265 Hs14042925 Predicted E3 ubiquitin ligase	EPZ36198.1 hypothetical protein O9G_002264 [Rozella allomycis CSF55]	E3 ubiquitin-protein ligase RNF26 OS=Mus musculus OX=10090 GN=Rnf26 PE=2 SV=1
A8956	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-

A8957	GO:0007165(signal transduction),GO:0046856(phosphatidyl inositol dephosphorylation)	-	GO:0016791(phosphatase activity),GO:0003824(catalytic activity)	K01099 INPP5B_F; inositol polyphosphate 5-phosphatase INPP5B/F [EC:3.1.3.36]	map04070 Phosphatidylinositol signaling system;map00562 Inositol phosphate metabolism;map01100 Metabolic pathways	KOG0565[Hs13325070 Inositol polyphosphate 5-phosphatase and related proteins	KAF7740738.1 hypothetical protein DSO57_012749 [Entomophthora muscae]	Inositol polyphosphate 5-phosphatase OCRL OS=Rattus norvegicus OX=10116 GN=Ocr1 PE=1 SV=1
A8958	-	-	-	K18342 OTUD6; OTU domain-containing protein 6 [EC:3.4.19.12]	-	KOG2606[Hs7706314 OTU (ovarian tumor)-like cysteine protease	XP_024663887.1 Ubiquitin thioesterase otu2 [Wickerhamia sorbophila]	Deubiquitinase OTUD6B OS=Gallus gallus OX=9031 GN=OTUD6B PE=2 SV=1
A8959	-	-	GO:0005515(protein binding)	-	-	-	-	-
A8960	-	-	-	-	-	KOG2130[Hs14769286 Phosphatidyserine-specific receptor PtdSerR, contains JmjC domain	KAF9954537.1 hypothetical protein BGZ70_010535 [Mortierella alpina]	Arginine-specific demethylase JMJ20 OS=Arabidopsis thaliana OX=3702 GN=JMJ20 PE=1 SV=1
A8961	-	-	-	K23796 PLEKHA1_2; pleckstrin homology domain-containing family A member 1/2	-	-	KAF8519524.1 hypothetical protein JB92DRAFT_2710689 [Gautieria morchelliformis]	Pleckstrin homology domain-containing family A member 2 OS=Mus musculus OX=10090 GN=Plekha2 PE=1 SV=1
A8962	-	-	GO:0016787(hydrolase activity)	-	-	KOG2679[Hs4501873 Purple (tartrate-resistant) acid phosphatase	ORY30966.1 Metallo-dependent phosphatase [Rhizoclostium globosum]	Tartrate-resistant acid phosphatase type 5 OS=Homo sapiens OX=9606 GN=ACP5 PE=1 SV=3
A8963	GO:0006281(DNA repair),GO:0000724(double-strand break repair via homologous recombination)	GO:0033063(Rad51B-Rad51C-Rad51D-XRCC2 complex)	GO:0003677(DNA binding),GO:0005524(ATP binding)	K10872 DMC1; meiotic recombination protein DMC1	map04113 Meiosis - yeast	KOG1433[Hs10835029 DNA repair protein RAD51/RHP55	RUS19596.1 P-loop containing nucleoside triphosphate hydrolase protein [Endogone sp. FLAS-F59071]	DNA repair protein RAD51 homolog 2 OS=Arabidopsis thaliana OX=3702 GN=RAD51B PE=2 SV=2
A8964	-	-	-	-	-	-	-	-
A8965	-	-	-	-	-	-	-	-
A8966	-	-	-	-	-	-	-	Katanin-interacting protein OS=Homo sapiens OX=9606 GN=KATNIP
A8967	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1236[YPL109c Predicted unusual protein kinase	OJJ33136.1 hypothetical protein ASPWEDRAFT_609733 [Aspergillus wentii DTO134E9]	ABC1 family protein YPL109C, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPL109C PE=1 SV=2
A8968	-	-	GO:0003824(catalytic activity),GO:0030151(molybdenum ion binding),GO:0030170(pyridoxal phosphate binding)	-	-	KOG2362[At1g30910 Uncharacterized Fe-S protein	GES74158.1 MOSC domain-containing protein [Rhizophagus clarus]	Uncharacterized protein YcbX OS=Escherichia coli (strain K12) OX=83333 GN=ycbX PE=1 SV=1

A8969	GO:0006086(acetyl-CoA biosynthetic process from pyruvate)	GO:0045254(pyruvate dehydrogenase complex)	GO:0016746(acyltransferase activity)	K00627 DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12]	map01110 Biosynthesis of secondary metabolites;map00785 Lipoic acid metabolism;map01200 Carbon metabolism;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00020 Citrate cycle (TCA cycle);map00620 Pyruvate metabolism;map01100 Metabolic pathways;map01210 2-Oxocarboxylic acid metabolism	-	KAF7750885.1 pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase component (E2) [Entomophthora muscae]	Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate dehydrogenase complex, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At1g54220 PE=1 SV=1
A8970	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10396 KIF5; kinesin family member 5	map05014 Amyotrophic lateral sclerosis;map04144 Endocytosis;map05132 Salmonella infection;map04814 Motor proteins;map05223 Non-small cell lung cancer;map04728 Dopaminergic synapse;map05020 Prion disease;map05022 Pathways of neurodegeneration - multiple diseases;map05010 Alzheimer disease;map05012 Parkinson disease;map05016 Huntington disease	KOG0240[Hs4758650 Kinesin (SMY1 subfamily)	OAC98528.1 hypothetical protein MUCCIDRAFT_44717, partial [Mucor lusitanicus CBS 277.49]	Kinesin heavy chain OS=Syncephalastrum racemosum OX=13706 PE=2 SV=1
A8971	GO:0001510(RNA methylation)	-	GO:0003924(GTPase activity),GO:0005525(GTP binding),GO:0008168(methyltransferase activity)	-	-	KOG0098[Hs20535925 GTPase Rab2, small G protein superfamily	ORY36860.1 P-loop containing nucleoside triphosphate hydrolase protein [Rhizoclostium globosum]	DnaJ homolog subfamily C member 27 OS=Danio rerio OX=7955 GN=dnajc27 PE=2 SV=1
A8972	GO:0007018(microtubule-based movement)	-	GO:0003777(microtubule motor activity),GO:0005524(ATP binding),GO:0008017(microtubule binding)	K10401 KIF18A; kinesin family member 18A	map04814 Motor proteins	KOG0242[At3g10180 Kinesin-like protein	PVV01030.1 hypothetical protein BB560_004568 [Smittium megazygosporum]	Kinesin-like protein KIN-70 OS=Arabidopsis thaliana OX=3702 GN=KIN70 PE=3 SV=1
A8973	-	-	-	-	-	-	-	-
A8974	-	-	GO:0005515(protein binding)	-	-	KOG4567[Hs21361637 GTPase-activating protein	RKP05074.1 rab-GTPase-TBC domain-containing protein [Thamnocephalus sphaerosporus]	TBC1 domain family member 13 OS=Mus musculus OX=10090 GN=Tbc1d13 PE=1 SV=1

A8975	-	-	GO:0005506(iron ion binding);GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen);GO:0031418(L-ascorbic acid binding)	K00472 P4HA; prolyl 4-hydroxylase [EC:1.14.11.2]	map00330 Arginine and proline metabolism;map01100 Metabolic pathways	KOG1591 At3g06300 Prolyl 4-hydroxylase alpha subunit	RKP09243.1 hypothetical protein THASP1DRAFT_28974 [Thamnocephalis sphaerospora]	Prolyl 4-hydroxylase 2 OS=Arabidopsis thaliana OX=3702 GN=P4H2 PE=1 SV=1
A8976	-	-	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors);GO:0050660(flavin adenine dinucleotide binding);GO:0003995(acyl-CoA dehydrogenase activity)	K09478 ACADSB; short-chain 2-methylacyl-CoA dehydrogenase [EC:1.3.8.5]	map01110 Biosynthesis of secondary metabolites;map00280 Valine, leucine and isoleucine degradation;map01100 Metabolic pathways;map01212 Fatty acid metabolism;map00071 Fatty acid degradation	KOG0139 CE11776 Short-chain acyl-CoA dehydrogenase	KAF9308949.1 hypothetical protein BG003_010381 [Podila horticola]	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus OX=10090 GN=Acadsb PE=1 SV=1
A8977	GO:0006457(protein folding)	GO:0016272(prefoldin complex)	GO:0051082(unfolded protein binding)	K09550 PFDN4; prefoldin subunit 4	-	KOG1760 Hs12408677 Molecular chaperone Prefoldin, subunit 4	KAF2657642.1 Prefoldin, subunit 4 [Lophiostoma macrostomum CBS 122681]	Prefoldin subunit 4 OS=Bos taurus OX=9913 GN=PFDN4 PE=2 SV=1
A8978	-	-	GO:0003824(catalytic activity)	K12603 CNOT6, CCR4; CCR4-NOT transcription complex subunit 6 [EC:3.1.13.4]	map03018 RNA degradation	KOG2338 Hs14784709 Transcriptional effector CCR4-related protein	XP_007376967.1 hypothetical protein SPAPADRAFT_68158 [Spathaspora passalidarum NRRL Y-27907]	CCR4-Not complex 3'-5'-exoribonuclease subunit Ccr4 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CCR4 PE=3 SV=2
A8979	-	GO:0005634(nucleus)	GO:0004721(phosphoprotein phosphatase activity)	K17618 UBLCP1; ubiquitin-like domain-containing CTD phosphatase 1 [EC:3.1.3.16]	-	KOG1605 Hs21450802_2 TFIIF-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	KAG0256790.1 hypothetical protein DFQ27_005495 [Actinomyces rella ambigua]	Ubiquitin-like domain-containing CTD phosphatase 1 OS=Xenopus laevis OX=8355 GN=ublc1 PE=2 SV=1
A8980	-	-	-	-	-	-	-	-
A8981	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity)	-	-	KOG1330 At5g64500 Sugar transporter/spinster transmembrane protein	ORY52517.1 hypothetical protein BCR33DRAFT_711810, partial [Rhizoclostium globosum]	Probable sphingolipid transporter spinster homolog 1 OS=Arabidopsis thaliana OX=3702 GN=At5g65687 PE=1 SV=1
A8982	-	-	-	-	-	-	-	-

A8983	GO:1990547(mitochondrial phosphate ion transmembrane transport)	-	GO:0005315(organic phosphate transmembrane transporter activity)	K15102 SLC25A3, PHC, PIC; solute carrier family 25 (mitochondrial phosphate transporter), member 3	-	KOG0767 At3g48850 Mitochondrial phosphate carrier protein	XP_00668114.1.1 uncharacterized protein BATDEDRAFT_35739 [Batrachochytrium dendrobatidis JAM81]	Mitochondrial phosphate carrier protein 2, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MPT2 PE=2 SV=1
A8984	GO:0055085(transmembrane transport), GO:0006812(cation transport)	GO:0016021(integral component of membrane)	GO:0008324(cation transmembrane transporter activity)	K07300 chaA, CAX; Ca2+:H+ antiporter	-	-	KAF9431084.1 hypothetical protein BGZ94_009470 [Podila epigama]	Vacuolar calcium ion transporter OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=vex1 PE=3 SV=1
A8985	-	-	-	-	-	-	-	-
A8986	GO:0016311(dephosphorylation)	-	GO:0016791(phosphatase activity)	K01110 PTEN; phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN [EC:3.1.3.16 3.1.3.48 3.1.3.67]	map04361 Axon regeneration;map05415 Diabetic cardiomyopathy; map04140 Autophagy - animal;map05222 Small cell lung cancer;map04510 Focal adhesion;map04212 Longevity regulating pathway - worm;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04071 Sphingolipid signaling pathway;map01521 EGFR tyrosine kinase inhibitor resistance;map05215 Prostate cancer;map0521	KOG2283 Hs4885251_2 Clathrin coat dissociation kinase GAK/PTEN/Auxilin and related tyrosine phosphatases	XP_031023735.1 uncharacterized protein SmJEL517_g04398 [Synchytrium microbalum]	Tensin-3 OS=Homo sapiens OX=9606 GN=TNS3 PE=1 SV=2
A8987	GO:0006812(cation transport), GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0015299(solute:proton antiporter activity)	K12041 SLC9A6_7, NHE6_7; solute carrier family 9 (sodium/hydrogen exchanger), member 6/7	map04260 Cardiac muscle contraction	KOG1965 At2g01980 Sodium/hydrogen exchanger protein	RYO79157.1 hypothetical protein DL763_009381 [Monosporascus cannonballus]	Sodium/hydrogen exchanger 7 OS=Arabidopsis thaliana OX=3702 GN=NHX7 PE=1 SV=1
A8988	-	-	GO:0003824(catalytic activity)	K08726 EPHX2; soluble epoxide hydrolase / lipid-phosphate phosphatase [EC:3.3.2.10 3.1.3.76]	map04146 Peroxisome;map01120 Microbial metabolism in diverse environments;map00590 Arachidonic acid metabolism;map05207 Chemical carcinogenesis - receptor activation;map05208 Chemical carcinogenesis - reactive oxygen species;map00625 Chloroalkane and chloroalkene degradation;map01100 Metabolic pathways	KOG4178 Hs4503585_2 Soluble epoxide hydrolase	ORY06579.1 alpha/beta-hydrolase [Basidiobolus meristosporus CBS 931.73]	Bifunctional epoxide hydrolase 2 OS=Homo sapiens OX=9606 GN=EPHX2 PE=1 SV=2

A8989	GO:1902600(proton transmembrane transport)	GO:0033178(proton-transporting two-sector ATPase complex, catalytic domain)	GO:0046961(proton-transporting ATPase activity, rotational mechanism)	K02150 ATPeV1E, ATP6E; V-type H+-transporting ATPase subunit E	map04145 Phagosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation;map05110 Vibrio cholerae infection;map04150 mTOR signaling pathway;map05120 Epithelial cell signaling in Helicobacter pylori infection;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG1664 At4g11150 Vacuolar H+-ATPase V1 sector, subunit E	KAF2847694.1 vacuolar ATP synthase subunit E [Plenodomus tracheiphilus IPT5]	V-type proton ATPase subunit E OS=Dictyostelium discoideum OX=44689 GN=vatE PE=1 SV=1
A8990	-	GO:0016020(membrane)	-	K10082 LMAN2, VIP36; lectin, mannose-binding 2	map04141 Protein processing in endoplasmic reticulum	KOG3839 7301116 Lectin VIP36, involved in the transport of glycoproteins carrying high mannose-type glycans	XP_01799923.6.1 L-type lectin-like domain-containing protein [Phialophora attinorum]	VIP36-like protein OS=Mus musculus OX=10090 GN=Lman2l PE=1 SV=1
A8991	GO:0006364(rRNA processing)	GO:0005730(nucleolus)	GO:0005515(protein binding)	K14549 UTP15; U3 small nucleolar RNA-associated protein 15	map03008 Ribosome biogenesis in eukaryotes	-	ORY94368.1 WD40-repeat-containing domain protein [Syncephalaster racemosus]	U3 small nucleolar RNA-associated protein 15 homolog OS=Xenopus laevis OX=8355 GN=utp15 PE=2 SV=1
A8992	GO:0036211(protein modification process)	-	-	-	-	-	-	Protein polyglycylase TTL10 OS=Mus musculus OX=10090 GN=Ttl10 PE=1 SV=1
A8993	-	-	-	-	-	KOG3245 Hs17463505 Uncharacterized conserved protein	OMJ29776.1 Succinate dehydrogenase assembly factor 4, mitochondria I [Smittium culicis]	Succinate dehydrogenase assembly factor 4, mitochondrial OS=Homo sapiens OX=9606 GN=SDHAF4 PE=1 SV=1
A8994	-	-	-	-	-	-	KAG2181575.1 hypothetical protein INT44_008390 [Umbelopsis vinacea]	[Skp1-protein]-hydroxyproline N-acetylglucosaminyltransferase OS=Dictyostelium discoideum OX=44689 GN=gnt1 PE=1 SV=2
A8995	GO:0006396(rRNA processing)	-	GO:0003723(RNA binding);GO:0016779(nucleotidyltransferase activity)	K00974 cca; tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.72 3.1.3.- 3.1.4.-]	-	KOG2159 At1g22660 tRNA nucleotidyltransferase/poly(A) polymerase	TRM65648.1 hypothetical protein BD626DRAFT_485438 [Auriculariopsis amplaj]	CCA tRNA nucleotidyltransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCA1 PE=1 SV=1
A8996	-	-	-	-	-	-	-	-

A8997	GO:0006886 (intracellular protein transport)	-	GO:0003924 (GTPase activity), GO:0005525 (GTP binding)	K07953 SAR1: GTP-binding protein SAR1 [EC:3.6.5.-]	map04141 Protein processing in endoplasmic reticulum; map05134 Legionellosis	KOG0077 At1g56330 Vesicle coat complex COPII, GTPase subunit SAR1	KAG2218805.1 hypothetical protein INT45_005452 [Mucor circinatus]	GTP-binding protein SAR2 OS=Solanum lycopersicum OX=4081 GN=SAR2 PE=2 SV=1
A8998	-	-	-	K26405 CCDC25; coiled-coil domain-containing protein 25	-	KOG3272 At5g11500 Predicted coiled-coil protein	SMR42646.1 unnamed protein product [Zymoseptoria tritici ST99CH_1E4]	Coiled-coil domain-containing protein 25 OS=Danio rerio OX=7955 GN=ccdc25 PE=1 SV=1
A8999	-	-	-	-	-	-	-	-
A9000	GO:0006979 (response to oxidative stress), GO:0034599 (cellular response to oxidative stress)	-	GO:0004601 (peroxidase activity), GO:0020037 (heme binding)	K00428 E1.1.1.1.5; cytochrome c peroxidase [EC:1.11.1.5]	-	-	KNE67634.1 hypothetical protein AMAG_12087 [Allomyces macrogynus ATCC 38327]	Putative heme-binding peroxidase OS=Pyricularia oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) OX=242507 GN=MGG_10368 PE=3 SV=1
A9001	GO:0051603 (proteolysis involved in cellular catabolic process)	GO:0005839 (proteasome core complex)	-	K02736 PSMB4; 20S proteasome subunit beta 7 [EC:3.4.25.1]	map05014 Amyotrophic lateral sclerosis; map05020 Prion disease; map05022 Pathways of neurodegeneration - multiple diseases; map03050 Proteasome; map05010 Alzheimer disease; map05012 Parkinson disease; map05017 Spinocerebellar ataxia; map05016 Huntington disease	KOG0185 At1g56450 20S proteasome, regulatory subunit beta type PSMB4/PRE4	XP_018288178.1 hypothetical protein PHYBLDRAFT_135279 [Phycomyces blakesleeana NRRL 1555(-)]	Proteasome subunit beta type-4 (Fragment) OS=Xenopus laevis OX=8355 GN=psmb4 PE=2 SV=2
A9002	GO:0006139 (nucleobase-containing compound metabolic process)	-	GO:0003678 (DNA helicase activity), GO:0003676 (nucleic acid binding), GO:0004386 (helicase activity), GO:0005524 (ATP binding), GO:0016818 (hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides), GO:0003677 (DNA binding)	K11136 RTEL1; regulator of telomere elongation helicase 1 [EC:5.6.2.3]	-	KOG1132 Hs7706541_1 Helicase of the DEAD superfamily	XP_016613137.1 DNA repair helicase (rad3) [Spizellomyces punctatus DAOM BR117]	Regulator of telomere elongation helicase 1 OS=Bos taurus OX=9913 GN=RTEL1 PE=2 SV=1
A9003	-	-	-	-	-	-	-	-
A9004	-	-	-	-	-	-	-	-

A9005	GO:0046907(intracellular transport), GO:0006913(nucleocytoplasmic transport)	-	GO:0004869(cysteine-type endopeptidase inhibitor activity)	K15306 RANBP1; Ran-binding protein 1	map05203 Viral carcinogenesis; map05166 Human T-cell leukemia virus 1 infection	KOG0864 YDR002w Ran-binding protein RANBP1 and related RanBD domain proteins	ODV91727.1 hypothetical protein CANCADRAFT_16113, partial [Tortispora caseinolytica NRRL Y-17796]	Ran-specific GTPase-activating protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRB1 PE=1 SV=1
A9006	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity), GO:0005524(ATP binding)	K07359 CAMKK2; calcium/calmodulin-dependent protein kinase kinase 2 [EC:2.7.11.17]	map04140 Autophagy - animal; map0421.1 Longevity regulating pathway; map05034 Alcoholism; map04936 Alcoholic liver disease; map04152 AMPK signaling pathway; map04920 Adipocytokine signaling pathway; map04921 Oxytocin signaling pathway	KOG0585 Hs17933758 Ca2+/calmodulin-dependent protein kinase kinase beta and related serine/threonine protein kinases	XP_003346457.1 uncharacterized protein SMAC_05352 [Sordaria macrospora k-hell]	Calcium/calmodulin-dependent protein kinase kinase 2 OS=Rattus norvegicus OX=10116 GN=Camkk2 PE=1 SV=1
A9007	GO:0036211(protein modification process)	-	-	K06047 TTL; tubulin--tyrosine ligase [EC:6.3.2.25]	-	KOG2157 Hs11068135 Predicted tubulin-tyrosine ligase	KNE70960.1 hypothetical protein AMAG_15224 [Allomyces macrogynus ATCC 38327]	Probable tubulin polyglutamylase TTL9 OS=Rattus norvegicus OX=10116 GN=Ttl9 PE=2 SV=1
A9008	-	-	GO:0003723(RNA binding), GO:0003676(nucleic acid binding)	-	-	KOG0123 ECU10g1110 Polyadenylation-binding protein (RRM superfamily)	XP_021875241.1 hypothetical protein BCR41DRAFT_402427 [Lobosporangium transversale]	-
A9009	-	-	-	-	-	-	-	-
A9010	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02879 RP-L17, MRPL17, rplQ; large subunit ribosomal protein L17	map03010 Ribosome	KOG3280 At5g09770 Mitochondrial/chloroplast ribosomal protein L17	KIM33166.1 hypothetical protein M408DRAFT_61200 [Serendipita vermifera MAFF 305830]	Large ribosomal subunit protein bL17 OS=Anaeromyxobacter sp. (strain Fw109-5) OX=404589 GN=rplQ PE=3 SV=1

A9011	GO:0006096(glycolytic process), GO:0006002(fructose 6-phosphate metabolic process)	GO:0005737(cytoplasm)	GO:0003872(6-phosphofructokinase activity),GO:0005524(ATP binding)	K00850 pfkA, PFK, 6-phosphofructokinase 1 [EC:2.7.1.11]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map04919 Thyroid hormone signaling pathway;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map01230 Biosynthesis of amino acids;map00052 Galactose metabolism;map00051 Fructose and mannose metabolism;map00680 Methane metabolism;map03018 RNA degradation;map	KOG2440[Hs1321601 Pyrophosphate-dependent phosphofructo-1-kinase	XP_018283425.1 hypothetical protein PHYBLDRAFT_137735 [Phycomyces blakesleeanus NRRL 1555(-)]	ATP-dependent 6-phosphofructokinase, liver type OS=Bos taurus OX=9913 GN=PFKL PE=2 SV=1
A9012	-	-	-	K13335 PEX16; peroxin-16	map04146 Peroxisome	KOG4546[At2g45690 Peroxisomal biogenesis protein (peroxin 16)	KAF7755863.1 Peroxisomal membrane protein pex16 [Entomophthora muscae]	Peroxisomal membrane protein PEX16 OS=Xenopus laevis OX=8355 GN=pex16 PE=2 SV=1
A9013	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K04563 CDC28, CDC2; cyclin-dependent kinase [EC:2.7.11.22]	map04011 MAPK signaling pathway - yeast;map04113 Meiosis - yeast;map04111 Cell cycle - yeast	KOG0594[Hs4557439 Protein kinase PCTAIRE and related kinases	KAF9097115.1 Cyclin-dependent kinase 3 [Mortierella sp. GBA35]	Cyclin-dependent kinase 3 OS=Homo sapiens OX=9606 GN=CDK3 PE=1 SV=1
A9014	GO:0006468(protein phosphorylation)	GO:0016021(integral component of membrane)	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004252(serine-type endopeptidase activity),GO:0005515(protein binding)	K08850 AURKX; aurora kinase, other [EC:2.7.11.1]	-	KOG0580[At4g32830 Serine/threonine protein kinase	RKP10390.1 kinase-like domain-containing protein [Thamnocephalus sphaerosporus]	Aurora kinase A OS=Mus musculus OX=10090 GN=Aurka PE=1 SV=1
A9015	-	-	-	-	-	KOG3213[Hs20469614 Transcription factor IIB	OON06117.1 hypothetical protein BSLG_04147 [Batrachochytrium salamandrivorans]	Protein CFAP20DC OS=Mus musculus OX=10090 GN=Cfap20dc PE=2 SV=2
A9016	-	-	-	-	-	-	-	-
A9017	GO:0030042(actin filament depolymerization)	GO:0015629(actin cytoskeleton)	GO:0003779(actin binding)	K05765 CFL; cofilin	map04360 Axon guidance;map05133 Pertussis;map04810 Regulation of actin cytoskeleton;map05170 Human immunodeficiency virus 1 infection;map04666 Fc gamma R-mediated phagocytosis	KOG1735[At4g34970 Actin depolymerizing factor	CDH13597.1 probable Cofilin [Zygosaccharomyces bailii ISA1307]	Cofilin OS=Zygosaccharomyces rouxii OX=4956 GN=cof1 PE=2 SV=1

A9018	-	-	-	K15030 EIF3M; translation initiation factor 3 subunit M	-	KOG2753 At5 g15610 Uncharacteriz ed conserved protein, contains PCI domain	XP_01661132 9.1 hypothetical protein SPPG_02339 [Spizellomyces punctatus DAOM BR117]	Eukaryotic translation initiation factor 3 subunit M OS=Dictyostelium discoideum OX=44689 GN=eif3m PE=1 SV=1
A9019	-	-	-	-	-	-	-	-
A9020	-	-	-	-	-	-	-	-
A9021	-	-	GO:0005515(pro tein binding)	K03671 trxA; thioredoxin 1	map05132 Salmonella infection;map05 418 Fluid shear stress and atherosclerosis; map04621 NOD-like receptor signaling pathway;map05 012 Parkinson disease	KOG0907 Hs1 4740408 Thioredoxin	XP_00776363 1.1 thioredoxin- domain- containing protein [Coniophora puteana RWD-64-598 SS2]	Thioredoxin OS=Ophiophagus hannah OX=8665 GN=TXN PE=3 SV=3
A9022	-	-	-	-	-	-	-	-
A9023	-	-	-	-	-	-	XP_00667727 0.1 uncharacteriz ed protein BATDEDRAFT _23388 [Batrachochyt rium dendrobatidis JAM81]	-
A9024	-	-	-	-	-	-	-	-
A9025	-	-	-	-	-	-	-	-
A9026	-	-	-	-	-	-	-	-
A9027	-	-	GO:0016787(hy drolase activity)	K15423 PPP4C; serine/threon ine-protein phosphatase 4 catalytic subunit [EC:3.1.3.16]	map04922 Glucagon signaling pathway	KOG0372 At5 g55260 Serine/threon ine specific protein phosphatase involved in glycogen accumulation , PP2A- related	OON08385.1 serine/threon ine-protein phosphatase 4 catalytic subunit, variant [Batrachochyt rium salamandrivo rans]	Serine/threonine-protein phosphatase PP-X isozyme 2 OS=Arabidopsis thaliana OX=3702 GN=PPX2 PE=2 SV=2
A9028	-	-	GO:0005525(GT P binding);GO:000 3924(GTPase activity)	-	-	KOG1486 At1 g17470 GTP- binding protein DRG2 (ODN superfamily)	RIB04186.1 development ally regulated GTP-binding protein 2 [Gigaspora rosea]	Developmentally-regulated G-protein 1 OS=Arabidopsis thaliana OX=3702 GN=DRG1 PE=1 SV=1
A9029	-	-	-	-	-	-	-	-

A9030	GO:0006351(transcription, DNA-templated)	GO:0005634(nucleus)	GO:0005509(calcium ion binding);GO:0005515(protein binding)	K02183 CALM; calmodulin	map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04020 Calcium signaling pathway;map05417 Lipid and atherosclerosis; map05133 Pertussis;map04722 Neurotrophin signaling pathway;map04218 Cellular senescence;map04070 Phosphatidylinositol signaling system;map04915 Estrogen signaling pathway;map04912 GnRH signaling pathway;map04910 Insulin	KOG0027(CE01908 Calmodulin and related proteins (EF-Hand superfamily)	KAF9465904.1 calmodulin-like protein [Lepista nuda]	Putative calmodulin-like protein 6 OS=Oryza sativa subsp. japonica OX=39947 GN=CML6 PE=3 SV=1
A9031	-	-	-	-	-	-	-	-
A9032	GO:000079(regulation of cyclin-dependent protein serine/threonine kinase activity)	-	GO:0019901(protein kinase binding)	K24113 PCL6.7; PHO85 cyclin-6/7	-	KOG1674(At3g21870 Cyclin	ORX89589.1 cyclin-domain-containing protein [Basidiobolus meristosporus CBS 931.73]	Cyclin-U1-1 OS=Arabidopsis thaliana OX=3702 GN=CYCU1-1 PE=1 SV=1
A9033	GO:0006633(fatty acid biosynthetic process)	-	GO:0016874(ligase activity);GO:0005524(ATP binding);GO:0046872(metal ion binding);GO:0003989(acetyl-CoA carboxylase activity)	-	-	KOG0368(Hs4826637 Acetyl-CoA carboxylase	OZJ03120.1 hypothetical protein BZG36_03869 [Bifiguratus adelaidae]	Acetyl-CoA carboxylase 1 OS=Rattus norvegicus OX=10116 GN=Acaca PE=1 SV=1
A9034	-	-	-	-	-	-	-	-
A9035	-	-	-	K19703 FA2H, SCS7; 4-hydroxysphinganine ceramide fatty acyl 2-hydroxylase [EC:1.14.18.6]	-	KOG0537(Hs21389413 Cytochrome b5	XP_016605530.1 hypothetical protein SPPG_07405 [Spizellomyces punctatus DAOM BR117]	Cytochrome b5 domain-containing protein 1 OS=Xenopus tropicalis OX=8364 GN=cyb5d1 PE=2 SV=1
A9036	-	-	-	-	-	-	-	-
A9037	GO:0006281(DNA repair)	-	GO:0043138(3'-5' DNA helicase activity);GO:0003677(DNA binding);GO:0005524(ATP binding);GO:0016787(hydrolase activity)	K14635 MPH1; ATP-dependent DNA helicase MPH1 [EC:5.6.2.4]	-	KOG0354(At1g35530 DEAD-box like helicase	XP_018287928.1 hypothetical protein PHYBLDRAFT_115863, partial [Phycomyces blakesleeanus NRRL 1555(-)]	DEAD-box ATP-dependent RNA helicase FANCM OS=Arabidopsis thaliana OX=3702 GN=FANCM PE=2 SV=1
A9038	GO:0009058(biosynthetic process)	-	GO:0016747(acyltransferase activity, transferring groups other than amino-acyl groups)	-	-	-	TPX73238.1 homoserine O-acetyltransferase [Chytridiomycetes confervae]	Homoserine O-acetyltransferase OS=Deferribacter desulfuricans (strain DSM 14783 / JCM 11476 / NBRC 101012 / SSM1) OX=639282 GN=metXA PE=1 SV=1
A9039	-	-	-	-	-	-	-	Protein ENHANCED DISEASE RESISTANCE 2-like OS=Arabidopsis

A9040	GO:0000105(histidine biosynthetic process), GO:0009058(biosynthetic process)	-	GO:0004424(imidazoleglycerol-phosphate dehydratase activity),GO:0003824(catalytic activity),GO:0004400(histidinol-phosphate transaminase activity),GO:0030170(pyridoxal phosphate binding)	K01693 hisB; imidazoleglycerol-phosphate dehydratase [EC:4.2.1.19]	map00340 Histidine metabolism;map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map01100 Metabolic pathways	KOG0633 At1g71920 Histidinol phosphate aminotransferase	KAF9518387.1 hypothetical protein BS47DRAFT_1338319 [Hydnum rufescens UP504]	Imidazoleglycerol-phosphate dehydratase OS=Phytophthora parasitica OX=4792 GN=HIS3 PE=3 SV=1
A9041	-	-	-	-	-	-	ORY50478.1 hypothetical protein BCR33DRAFT_846941 [Rhizoclostium globosum]	Tiny macrocysts protein C OS=Dictyostelium discoideum OX=44689 GN=tmcC PE=2 SV=1
A9042	-	-	-	-	-	-	TPX77702.1 hypothetical protein CcCBS67573_g01047 [Chytridiomycetes confervae]	Tiny macrocysts protein B OS=Dictyostelium discoideum OX=44689 GN=tmcB PE=2 SV=1
A9043	-	-	-	-	-	-	-	-
A9044	-	-	GO:0005515(protein binding)	-	-	-	ORY50598.1 TPR-like protein [Rhizoclostium globosum]	-
A9045	-	-	-	-	-	KOG1444 At5g19980 Nucleotide-sugar transporter VRG4/SQV-7	KAG0090149.1 hypothetical protein BGZ92_003596 [Podila epicladia]	GDP-fucose transporter 1 OS=Arabidopsis thaliana OX=3702 GN=GFT1 PE=1 SV=1
A9046	-	-	GO:0005525(GTP binding),GO:0003924(GTPase activity)	K07874 RAB1A; Ras-related protein Rab-1A	map05014 Amyotrophic lateral sclerosis;map04140 Autophagy - animal;map05134 Legionellosis;map05130 Pathogenic Escherichia coli infection;map05022 Pathways of neurodegeneration - multiple diseases	KOG0084 Hs4758988 GTPase Rab1/YPT1, small G protein superfamily, and related GTP-binding proteins	KAF8308915.1 ras-related protein ypt1 [Clavulina sp. PMI_390]	Ras-like GTP-binding protein YPT1 OS=Phytophthora infestans OX=4787 GN=YPT1 PE=3 SV=1

A9047	GO:0006412(translation)	GO:0015934(large ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02911 RP-L32, MRPL32, rpmF; large subunit ribosomal protein L32	map03010 Ribosome	-	RKP11703.1 hypothetical protein BJ684DRAFT_4873, partial [Piptocephalis cylindrospora]	-
A9048	-	-	-	-	-	-	-	-
A9049	-	-	-	-	-	-	-	-
A9050	GO:0030163(protein catabolic process)	GO:0005737(cytoplasm)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity),GO:0036402(proteasome-activating activity)	-	-	KOG0726 7301070 26S proteasome regulatory complex, ATPase RPT2	ORX58211.1 26S proteasome subunit P45 [Hesseltinella vesiculosa]	26S proteasome regulatory subunit 4 OS=Drosophila melanogaster OX=7227 GN=Rpt2 PE=1 SV=2
A9051	GO:0006457(protein folding)	-	GO:0005515(protein binding),GO:0030544(Hsp70 protein binding),GO:0051879(Hsp90 protein binding)	K16365 SGTA; small glutamine-rich tetratricopeptide repeat-containing protein alpha	-	KOG0548 YOR027w Molecular co-chaperone ST11	XP_031024190.1 uncharacterized protein SmJEL517_g03939 [Synchytrium microbalum]	Stress-induced-phosphoprotein 1 OS=Xenopus laevis OX=8355 GN=stip1 PE=2 SV=1
A9052	-	-	-	-	-	-	KAF9527398.1 hypothetical protein CPB83DRAFT_934328 [Crepidotus variabilis]	-
A9053	-	-	-	-	-	-	KAF8217711.1 hypothetical protein K438DRAFT_7822 [Mycena galopus ATCC 62051]	-
A9054	-	-	-	-	-	-	-	-
A9055	GO:0032008(positive regulation of TOR signaling)	-	GO:0005515(protein binding)	K20408 WDR24, SEA2; SEA/GATOR complex protein SEA2/WDR24	map04150 mTOR signaling pathway	KOG0269 Hs14149987 WD40 repeat-containing protein	RKO86430.1 WD40-repeat-containing domain protein, partial [Blyttiomycetes helicis]	GATOR2 complex protein WDR24 OS=Homo sapiens OX=9606 GN=WDR24 PE=1 SV=2
A9056	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02951 RP-S12e, RPS12; small subunit ribosomal protein S12e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG3406 Hs14277700 40S ribosomal protein S12	ORX93745.1 L30e-like protein [Basidiobolus meristosporus CBS 931.73]	Small ribosomal subunit protein eS12 OS=Cyanophora paradoxa OX=2762 GN=RPS12 PE=2 SV=1
A9057	-	-	GO:0046982(protein heterodimerization activity)	-	-	KOG1088 At1g22270_1 Uncharacterized conserved protein	XP_038913041.1 uncharacterized protein E190DRAFT_3146497 [Cantharellus anzutake]	Multifunctional methyltransferase subunit TRM112 homolog A OS=Arabidopsis thaliana OX=3702 GN=TRM112A PE=1 SV=1
A9058	-	-	-	-	-	-	-	-
A9059	-	GO:0005634(nucleus)	GO:0005515(protein binding)	K14788 NOL10, ENP2; ribosome biogenesis protein ENP2	-	KOG2321 At3g56990 WD40 repeat protein	XP_016611521.1 hypothetical protein SPPG_00966 [Spizellomyces punctatus DAOM BR117]	Nucleolar protein 10 OS=Xenopus tropicalis OX=8364 GN=nol10 PE=2 SV=1

A9060	-	-	-	-	-	-	-	EF-hand domain-containing family member B OS=Homo sapiens
A9061	GO:0036066(protein O-linked fucosylation)	-	GO:0046922(peptide-O-fucosyltransferase activity)	-	-	-	KAF9438467.1 hypothetical protein BGZ76_00772.1 [Entomortierella beljakovae]	-
A9062	GO:0006289(nucleotide-excision repair),GO:0006351(transcription, DNA-templated)	GO:0000439(transcription factor TFIIF core complex)	-	K03141 TFIIF1, GTF2H1, TFB1; transcription initiation factor TFIIF subunit 1	map03420 Nucleotide excision repair;map03022 Basal transcription factors;map05203 Viral carcinogenesis	-	XP_006679876.1 uncharacterized protein BATDERAFT_25771 [Batrachochytrium dendrobatidis JAM81]	-
A9063	GO:0015031(protein transport)	-	-	K26678 MON2; protein MON2	-	KOG1848 At5g27970 Uncharacterized conserved protein	GES88442.1 hypothetical protein RCL_jg5346.t1 [Rhizophagus clarus]	Protein MON2 homolog OS=Drosophila melanogaster OX=7227 GN=mon2 PE=2 SV=4
A9064	-	-	-	-	-	-	-	-
A9065	-	-	-	-	-	-	-	-
A9066	GO:0006281(DNA repair)	-	GO:0004518(nuclease activity),GO:0046872(metal ion binding),GO:0035312(5'-3' exodeoxyribonuclease activity),GO:0016788(hydrolase activity, acting on ester bonds)	K10746 EXO1; exonuclease 1 [EC:3.1.-.-]	map03430 Mismatch repair	KOG2518 At1g29630 5'-3' exonuclease	TNY20010.1 PIN domain-like protein [Rhodotorula diobovata]	Exonuclease 1 OS=Arabidopsis thaliana OX=3702 GN=EXO1 PE=2 SV=2
A9067	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	K14556 DIP2, UTP12, WDR3; U3 small nucleolar RNA-associated protein 12	map03008 Ribosome biogenesis in eukaryotes	KOG0619 7300644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase pats1 OS=Dictyostelium discoideum OX=44689 GN=pats1 PE=3 SV=1
A9068	-	-	-	-	-	-	XP_031024007.1 uncharacterized protein SmJEL517_g04073 [Synchytrium microbalum]	-
A9069	-	-	-	-	-	KOG4722 Hs16507198 Zn-finger protein	KXS11623.1 hypothetical protein M427DRAFT_425231 [Gonapodya prolifera JEL478]	S phase cyclin A-associated protein in the endoplasmic reticulum OS=Homo sapiens OX=9606 GN=SCAPER PE=1 SV=2
A9070	-	-	-	-	-	-	-	-
A9071	-	-	GO:0005515(protein binding)	-	-	-	-	-

A9072	-	-	-	-	-	KOG1426[Hs4557445 FOG: RCC1 domain	RKP27547.1 regulator of chromosome condensation 1/beta-lactamase-inhibitor protein II [Syncephalis pseudoplumigaleata]	RCC1 and BTB domain-containing protein 2 OS=Homo sapiens OX=9606 GN=RCBTB2 PE=1 SV=1
A9073	GO:0016226(iron-sulfur cluster assembly)	-	GO:0051536(iron-sulfur cluster binding)	K22063 ISCA1; iron-sulfur cluster assembly 1	-	KOG1120[CE21678 Fe-S cluster biosynthesis protein ISA1 (contains a HesB-like domain)	OZJ02936.1 hypothetical protein BZG36_04559 [Bifiguratus adalaidae]	Iron-sulfur cluster assembly 1 homolog, mitochondrial OS=Columbia livia OX=8932 GN=ISCA1 PE=1 SV=1
A9074	-	-	-	-	-	-	-	-
A9075	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity),GO:0003677(DNA binding)	-	-	-	-	-
A9076	-	-	-	-	-	-	-	-
A9077	GO:0006511(ubiquitin-dependent protein catabolic process), GO:0016579(protein deubiquitination)	-	GO:0004843(thiol-dependent deubiquitinase)	K11853 USP34; ubiquitin carboxyl-terminal hydrolase 34 [EC:3.4.19.12]	-	KOG1866[Hs2043041 Ubiquitin carboxyl-terminal hydrolase	RUS20937.1 hypothetical protein BC937DRAFT_93997 [Endogone sp. FLAS-F59071]	Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens OX=9606 GN=USP34 PE=1 SV=2
A9078	-	-	GO:0020037(heme binding)	-	-	KOG0537[YM L054c_1 Cytochrome b5	RKP09846.1 cytochrome b5-like heme/steroid binding domain-containing protein [Thamnocephalis sphaerospora]	L-lactate dehydrogenase (cytochrome) OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYB2 PE=1 SV=1
A9079	GO:0000387(spliceosomal snRNP assembly),GO:0006396(RNA processing)	GO:0005681(spliceosomal complex)	-	K11088 SNRPD3, SMD3; small nuclear ribonucleoprotein D3	map03040 Spliceosome;map04139 Mitophagy - yeast;map05322 Systemic lupus erythematosus	KOG3172[At1g76300 Small nuclear ribonucleoprotein Sm D3	RKP37783.1 hypothetical protein BJ085DRAFT_38896 [Dimargaris cristalligena]	Small nuclear ribonucleoprotein SmD3a OS=Arabidopsis thaliana OX=3702 GN=SMD3A PE=2 SV=1
A9080	-	-	-	-	-	-	-	-
A9081	-	-	-	-	-	-	-	-
A9082	-	GO:0016020(membrane)	-	K23564 EMC3, TMEM111; ER membrane protein complex subunit 3	-	KOG3188[At4g12590 Uncharacterized conserved protein	KXS12160.1 transmembrane protein [Gonapodya prolifera JEL478]	ER membrane protein complex subunit 3 OS=Homo sapiens OX=9606 GN=EMC3 PE=1 SV=3
A9083	-	-	GO:0016799(hydrolase activity, hydrolyzing N-glycosyl compounds)	-	-	-	NP_595062.1 putative uridine ribohydrolase [Schizosaccharomyces pombe]	Uncharacterized protein C1683.06c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=SPBC1683.06c PE=3 SV=1

A9084	GO:0042373(vitamin K metabolic process)	-	GO:0047057(vitamin-K-epoxide reductase (warfarin-sensitive) activity)	-	-	-	-	Vitamin K epoxide reductase complex subunit 1-like protein 1 OS=Takifugu rubripes OX=31033 GN=vkorc1l1 PE=1 SV=1
A9085	GO:0009231(riboflavin biosynthetic process)	-	GO:0003935(GTP cyclohydrolase II activity)	K01497 ribA, RIB1; GTP cyclohydrolase II [EC:3.5.4.25]	map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map02024 Quorum sensing;map00740 Riboflavin metabolism;map01100 Metabolic pathways;map00790 Folate biosynthesis	KOG1284 At5g59750 Bifunctional GTP cyclohydrolase II/3,4-dihydroxy-2butanone-4-phosphate synthase	KAG0186389.1 hypothetical protein DFCQ28_007942 [Apophysomycetes sp. BC1034]	GTP cyclohydrolase-2 OS=Burkholderia mallei (strain ATCC 23344) OX=243160 GN=ribA PE=3 SV=1
A9086	-	-	-	-	-	-	-	-
A9087	-	-	-	-	-	-	-	-
A9088	-	-	-	-	-	KOG4198 At5g25490 RNA-binding protein Ran Zn-finger protein and related proteins	ORX60528.1 hypothetical protein DM01DRAFT_265442 [Hesseltinella vesiculosa]	RNA-binding protein FUS OS=Bos taurus OX=9913 GN=FUS PE=2 SV=2
A9089	-	-	-	-	-	-	-	-
A9090	GO:0006044(N-acetylglucosamine metabolic process), GO:0005975(carbohydrate metabolic process)	-	GO:0004342(glucosamine-6-phosphate deaminase activity)	K02564 nagB, GNPDA; glucosamine-6-phosphate deaminase [EC:3.5.99.6]	map00520 Amino sugar and nucleotide sugar metabolism;map01100 Metabolic pathways	KOG3148 7296992 Glucosamine-6-phosphate isomerase	RIB11534.1 glucosamine-6-phosphate isomerase [Gigaspora rosea]	Glucosamine-6-phosphate isomerase OS=Aedes aegypti OX=7159 GN=Gnpda1 PE=3 SV=1
A9091	-	-	-	K12592 C1D, LRP1; exosome complex protein LRP1	map03018 RNA degradation	KOG4835 Hs5453583 DNA-binding protein C1D involved in regulation of double-strand break repair	PIA19222.1 hypothetical protein COEREDRAFT_20805, partial [Coemansia reversa NRRL 1564]	Nuclear nucleic acid-binding protein C1D OS=Danio rerio OX=7955 GN=c1d PE=2 SV=1
A9092	-	-	-	-	-	KOG4154 730136 Arginine-rich protein	-	Mesencephalic astrocyte-derived neurotrophic factor homolog OS=Drosophila ananassae OX=7217 GN=Manf PE=3 SV=1

A9093	-	-	GO:0005524(ATP binding)	K03283 HSPA1_6_8; heat shock 70kDa protein 1/6/8	map03040 Spliceosome;map05417 Lipid and atherosclerosis; map04144 Endocytosis;map04141 Protein processing in endoplasmic reticulum;map05134 Legionellosis;map04213 Longevity regulating pathway - multiple species;map04915 Estrogen signaling pathway;map04612 Antigen processing and presentation;map05145 Toxoplasmosis; map05020 Prion disease;map04010 MAPK	KOG0101 CE18679A Molecular chaperones HSP70/HSC70, HSP70 superfamily	ORY77876.1 heat shock 70 kDa protein 1-like protein [Neocallimastix californiae]	Heat shock cognate HSP70 protein OS=Trypanosoma brucei brucei OX=5702 PE=3 SV=1
A9094	-	-	-	-	-	KOG4781 Hs17474989 Uncharacterized conserved protein	TPX62618.1 hypothetical protein PhCBS80983.g00393 [Powellomyces hirtus]	Acyl-coenzyme A thioesterase THEM4 OS=Homo sapiens OX=9606 GN=THEM4 PE=1 SV=1
A9095	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding);GO:0008569(minus-end-directed microtubule motor activity)	-	-	KOG3595 Hs17864092 Dyneins, heavy chain	TPX68770.1 hypothetical protein SpCBS45565.g02893 [Spizellomyces sp. 'palustris']	Dynein-1-beta heavy chain, flagellar inner arm I1 complex OS=Chlamydomonas reinhardtii OX=3055 GN=DHC10 PE=1 SV=1
A9096	GO:0016126(sterol biosynthetic process)	GO:0016020(membrane)	GO:0016628(oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor)	K00222 TM7SF2, ERG24; Delta14-sterol reductase [EC:1.3.1.70]	map01110 Biosynthesis of secondary metabolites;map00100 Steroid biosynthesis;map01100 Metabolic pathways	KOG1435 Hs20537133 Sterol reductase/lamin B receptor	XP_031024630.1 uncharacterized protein SmJEL517_g03422 [Synchytrium microbalum]	Delta(14)-sterol reductase LBR OS=Gallus gallus OX=9031 GN=LBR PE=1 SV=1
A9097	-	-	-	-	-	-	XP_031027443.1 uncharacterized protein SmJEL517_g0491 [Synchytrium microbalum]	-
A9098	-	-	-	-	-	-	-	-
A9099	GO:0007165(signal transduction)	-	GO:0005515(protein binding)	-	-	KOG0619 7300644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase roco5 OS=Dictyostelium discoideum OX=44689 GN=roco5 PE=3 SV=1
A9100	-	-	-	-	-	-	-	-
A9101	-	-	-	-	-	-	-	-
A9102	GO:0006468(protein phosphorylation).GO:0005975(carbohydrate metabolic process)	-	GO:0004672(protein kinase activity).GO:0005524(ATP binding).GO:0016773(phosphotransferase activity, alcohol group as acceptor)	K00875 rbtK, FGGY; D-ribulokinase [EC:2.7.1.47]	map00040 Pentose and glucuronate interconversions; map01100 Metabolic pathways	KOG2517 7292419 Ribulose kinase and related carbohydrate kinases	KAG2189149.1 hypothetical protein INT44_004291 [Umbelopsis vinacea]	FGGY carbohydrate kinase domain-containing protein OS=Homo sapiens OX=9606 GN=FGGY PE=1 SV=2

A9103	-	-	-	-	-	KOG0048 At5g40360 Transcription factor, Myb superfamily	KAF9986420.1 hypothetical protein BGZ65_007682, partial [Modicella reniformis]	Myb-related protein B OS=Xenopus laevis OX=8355 GN=mybl2 PE=2 SV=2
A9104	-	-	GO:0005515(protein binding)	-	-	-	-	-
A9105	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0054 Hs4826838 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	ORY38590.1 P-loop containing nucleoside triphosphate hydrolase protein [Rhizoclostium globosum]	Multidrug resistance-associated protein 1 OS=Homo sapiens OX=9606 GN=ABCC1 PE=1 SV=3
A9106	-	-	-	-	-	-	-	-
A9107	-	-	-	-	-	-	-	-
A9108	-	-	-	-	-	-	-	-
A9109	GO:0002949(tRNA threonylcarbamoyl adenosine modification)	GO:0000408(EKC/K EOPS complex)	-	K01409 OSGEP, KAE1, QRI7; N6-L-threonylcarbamoyladenine synthase [EC:2.3.1.234]	-	KOG2708 Hs8923380 Predicted metalloproteinase with chaperone activity (RNAse H/HSP70 fold)	KAF7721068.1 putative tRNA threonylcarbamoyladenine biosynthesis protein kae1 [Apophysomyces ossiformis]	Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Nematostella vectensis OX=45351 GN=osgep PE=3 SV=1
A9110	-	-	GO:0008146(sulfotransferase activity)	-	-	KOG4157 7293063 beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	XP_014571395.1 hypothetical protein L969DRAFT_92244 [Mixia osmundae IAM 14324]	WSCD family member GA21586 OS=Drosophila pseudoobscura pseudoobscura OX=46245 GN=GA21586 PE=3 SV=2
A9111	GO:0006614(SRP-dependent cotranslational protein targeting to membrane),GO:0006886(intracellular protein transport)	GO:0005785(signal recognition particle receptor complex)	GO:0005525(GTP binding),GO:0003924(GTPase activity),GO:0005047(signal recognition particle binding)	-	-	KOG0781 At4g30600 Signal recognition particle receptor, alpha subunit	KAG0168419.1 hypothetical protein DFQ30_004780 [Apophysomyces sp. BC1015]	Signal recognition particle receptor subunit alpha OS=Dictyostelium discoideum OX=44689 GN=srpra PE=3 SV=1
A9112	-	GO:0005634(nucleus)	GO:0003676(nucleic acid binding),GO:0005515(protein binding)	K14401 CPSF1, CFT1; cleavage and polyadenylation specificity factor subunit 1	map03015 mRNA surveillance pathway	KOG1896 Hs9558725 mRNA cleavage and polyadenylation factor II complex, subunit CFT1 (CPSF subunit)	RIB01623.1 CPSF A subunit region-domain-containing protein [Gigaspora rosea]	Cleavage and polyadenylation specificity factor subunit 1 OS=Mus musculus OX=10090 GN=Cpsf1 PE=1 SV=1
A9113	-	-	GO:0005524(ATP binding)	K06174 ABCE1, Rli1; ATP-binding cassette, sub-family E, member 1	-	KOG0063 Hs20532766 RNAse L inhibitor, ABC superfamily	KAG0046903.1 Fe-S cluster-binding ribosome biosynthesis protein [Gryganskiella cystojenkini]	ATP-binding cassette sub-family E member 1 OS=Homo sapiens OX=9606 GN=ABCE1 PE=1 SV=1

A9114	GO:000079(regulation of cyclin-dependent protein serine/threonine kinase activity)	-	GO:0019901(protein kinase binding)	-	-	KOG1675 7297875 Predicted cyclin	XP_016604798.1 hypothetical protein SPPG_07965 [Spizellomyces punctatus DAOM BR117]	Cyclin-Y-like protein 1 OS=Danio rerio OX=7955 GN=ccny1 PE=2 SV=1
A9115	-	-	GO:0005515(protein binding)	K04536 GNB1; guanine nucleotide-binding protein G(i)/G(s)/G(t) subunit beta-1	map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724 Glutamatergic synapse;map04725 Cholinergic synapse;map04726 Serotonergic synapse;map04727 GABAergic synapse;map04723 Retrograde endocannabinoid signaling;map05032 Morphine addiction;map05034 Alcoholism;map04713 Circadian entrainment;map04014 Ras signaling pathway;map05	KOG0313 7297759 Microtubule binding protein YTM1 (contains WD40 repeats)	EPZ32275.1 LNS2, Lipin/Ned1/Smpp2 domain-containing protein [Rozella allomycis CSF55]	Ribosome biogenesis protein WDR12 homolog OS=Drosophila ananassae OX=7217 GN=GF14067 PE=3 SV=1
A9116	-	-	-	-	-	-	-	-
A9117	-	-	GO:0016787(hydrolase activity)	-	-	-	-	-
A9118	-	-	GO:0016409(palmitoyltransferase activity)	-	-	-	-	-
A9119	-	-	GO:0080048(GDP-D-glucose phosphorylase activity)	-	-	KOG2720 7294934 Predicted hydrolase (HIT family)	-	-
A9120	-	-	GO:0005096(GTPase activator activity)	-	-	KOG0702 At1g08680 Predicted GTPase-activating protein	KAG0338633.1 ArfGAP with FG repeats 1 [Podila humilis]	Probable ADP-ribosylation factor GTPase-activating protein AGD14 OS=Arabidopsis thaliana OX=3702 GN=AGD14 PE=1 SV=2
A9121	-	-	-	K14833 NOC2; nucleolar complex protein 2	-	KOG2256 At2g18220 Predicted protein involved in nuclear export of pre-ribosomes	ORY31319.1 Noc2-domain-containing protein [Neocallimastix californiae]	Nucleolar complex protein 2 homolog OS=Bos taurus OX=9913 GN=NOC2L PE=2 SV=1
A9122	-	-	-	-	-	-	-	-
A9123	-	-	-	-	-	-	KAG0195475.1 hypothetical protein BGX28_001302, partial [Mortierella sp. GBA30]	-
A9124	-	-	-	-	-	-	-	-
A9125	-	-	-	-	-	-	-	-
A9126	-	-	GO:0005515(protein binding)	K16743 ASPM, ASP; abnormal spindle-like microcephaly-associated protein	-	KOG0165 Hs18546106 Microtubule-associated protein Asp	RUS18329.1 LOW QUALITY PROTEIN: hypothetical protein BC937DRAFT_88916 [Endogone sp. FLAS-F59071]	Abnormal spindle-like microcephaly-associated protein homolog OS=Saimiri boliviensis boliviensis OX=39432 GN=ASPM PE=2 SV=1

A9127	GO:0005975(carbohydrate metabolic process)	GO:0016020(membrane)	GO:0004571(mannosyl-oligosaccharide 1,2-alpha-mannosidase activity),GO:0005509(calcium ion binding)	K23741 MAN1B, MNS3; endoplasmic reticulum Man9GlcNAc2 1,2-alpha-mannosidase [EC:3.2.1.209]	map04141 Protein processing in endoplasmic reticulum;map00513 Various types of N-glycan biosynthesis;map00510 N-Glycan biosynthesis;map01100 Metabolic pathways	KOG2431 Hs6005808 1, 2-alpha-mannosidase	KAG0173894.1 mannosyl-oligosaccharide alpha-1,2-mannosidase [Apophysomyces sp. BC1015]	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN1B1 PE=1 SV=2
A9128	-	-	-	-	-	-	-	-
A9129	GO:0007018(microtubule-based movement)	GO:0030286(dynein complex)	GO:0005524(ATP binding),GO:0008569(minus-end-directed microtubule motor activity)	K10413 DYNC1H; dynein cytoplasmic 1 heavy chain	map04145 Phagosome;map05132 Salmonella infection;map04814 Motor proteins;map04962 Vasopressin-regulated water reabsorption	KOG3595 Hs17864092 Dyneins, heavy chain	ORY51831.1 hypothetical protein BCR33DRAFT_712026 [Rhizoclostium globosum]	Dynein axonemal heavy chain 7 OS=Homo sapiens OX=9606 GN=DNAH7 PE=1 SV=2
A9130	GO:1902600(proton transmembrane transport)	GO:0033180(proton-transporting V-type ATPase, V1 domain)	GO:0046961(proton-transporting ATPase activity, rotational mechanism),GO:0015078(proton transmembrane transporter activity)	K02148 ATPeV1C, ATP6C; V-type H+-transporting ATPase subunit C	map04145 Phagosome;map04721 Synaptic vesicle cycle;map05323 Rheumatoid arthritis;map00190 Oxidative phosphorylation;map05110 Vibrio cholerae infection;map04150 mTOR signaling pathway;map05120 Epithelial cell signaling in Helicobacter pylori infection;map04966 Collecting duct acid secretion;map01100 Metabolic pathways;map05165 Human papillomavirus infection	KOG2909 Hs4502315 Vacuolar H+-ATPase V1 sector, subunit C	ORY05996.1 ATPase, V1 complex, subunit C [Basidiobolus meristosporus CBS 931.73]	V-type proton ATPase subunit C 1 OS=Mus musculus OX=10090 GN=Atp6v1c1 PE=1 SV=4
A9131	-	GO:0005743(mitochondrial inner membrane),GO:0061617(MICOS complex)	-	-	-	-	-	-
A9132	-	-	-	-	-	-	XP_025335828.1 uncharacterized protein CXQ87_005164 [[Candida] duobushaemulonis]	-
A9133	-	-	-	-	-	-	ORY23763.1 hypothetical protein BCR33DRAFT_727882 [Rhizoclostium globosum]	-
A9134	-	-	GO:0005515(protein binding)	-	-	-	-	-

A9135	-	-	-	K08869 ADCK, ABC1; aarF domain- containing kinase	-	KOG1235 At5 g24810 Predicted unusual protein kinase	KXS09410.1 beta- lactamase/tra nspeptidase- like protein [Gonapodya prolifera JEL478]	Probable protein kinase UbiB OS=Delftia acidovorans (strain DSM 14801 / SPH-1) OX=398578 GN=ubiB PE=3 SV=1
A9136	-	-	-	-	-	-	-	-
A9137	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K14430 PHO87_91; phosphate transporter	-	KOG1281 At5 g47560 Na+/dicarboxylate, Na+/tricarboxylate and phosphate transporters	KAG2419351.1 hypothetical protein HFD88_004146 [Aspergillus terreus]	Tonoplast dicarboxylate transporter OS=Arabidopsis thaliana OX=3702 GN=TDT PE=2 SV=2
A9138	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K14430 PHO87_91; phosphate transporter	-	KOG1281 At5 g47560 Na+/dicarboxylate, Na+/tricarboxylate and phosphate transporters	XP_014565586.1 hypothetical protein L969DRAFT_96586 [Mixia osmundae IAM 14324]	Tonoplast dicarboxylate transporter OS=Arabidopsis thaliana OX=3702 GN=TDT PE=2 SV=2
A9139	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K14430 PHO87_91; phosphate transporter	-	KOG1281 At5 g47560 Na+/dicarboxylate, Na+/tricarboxylate and phosphate transporters	KAG2419351.1 hypothetical protein HFD88_004146 [Aspergillus terreus]	Tonoplast dicarboxylate transporter OS=Arabidopsis thaliana OX=3702 GN=TDT PE=2 SV=2
A9140	GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0022857(transmembrane transporter activity)	K14430 PHO87_91; phosphate transporter	-	KOG1281 At5 g47560 Na+/dicarboxylate, Na+/tricarboxylate and phosphate transporters	SCZ87939.1 BZ3500_MvS of-1268-A1-R1 Chr2- 3g05407 [Microbotryum saponariae]	Sodium-dependent dicarboxylate transporter SdcS OS=Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229 / NCIMB 8711 / NCTC 7292 / S-41) OX=342451 GN=sdcS PE=3 SV=1
A9141	-	-	-	-	-	KOG4038 Hs4 505671 cGMP-phosphodiesterase, delta subunit	ORY51463.1 delta subunit of GMP phosphodiesterase [Rhizoclosium globosum]	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta OS=Bos taurus OX=9913 GN=PDE6D PE=1 SV=1
A9142	GO:190466(positive regulation of ubiquitin protein ligase activity)	-	GO:0005515(protein binding);GO:0010997(anaphase-promoting complex binding);GO:0097027(ubiquitin-protein transferase activator activity)	K03364 CDH1, FZR1; cell division cycle 20-like protein 1, cofactor of APC complex	map04914 Progesterone-mediated oocyte maturation;map 04120 Ubiquitin mediated proteolysis;map 04111 Cell cycle - yeast;map04110 Cell cycle	KOG0305 At4 g22910 Anaphase promoting complex, Cdc20, Cdh1, and Ama1 subunits	KAF8545442.1 quinon protein alcohol dehydrogenase-like superfamily [Trichophaea hybrida]	B-type cell cycle switch protein ccs52A OS=Medicago truncatula OX=3880 GN=CCS52A PE=1 SV=1
A9143	-	-	-	-	-	-	TPX43015.1 hypothetical protein SeLEV6574_g 05292 [Synchytrium endobioticum]	-

A9144	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding),GO:0004707(MAP kinase activity)	K04371 ERK, MAPK1_3; mitogen-activated protein kinase 1/3 [EC:2.7.11.24]	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map05417 Lipid and atherosclerosis; map04140 Autophagy - animal;map04730 Long-term depression;map05135 Yersinia infection;map05132 Salmonella infection;map05133 Pertussis;map05130 Pathogenic Escherichia coli infection;map05131 Shigellosis;map04350 TGF-beta signaling pathway;map04810 Regulation of	KOG0660 At2g43790 Mitogen-activated protein kinase	KXN68118.1 MAP kinase 1 [Conidiobolus coronatus NRRL 28638]	Mitogen-activated protein kinase 4b OS=Physcomitrium patens OX=3218 GN=MPK4b PE=1 SV=1
A9145	GO:0006979(response to oxidative stress),GO:0034599(cellular response to oxidative stress)	-	GO:0004601(peroxidase activity),GO:0020037(heme binding)	K00428 E1.11.1.5; cytochrome c peroxidase [EC:1.11.1.5]	-	-	CZS93410.1 probable cytochrome-c peroxidase precursor [Rhynchosporium agropyri]	Putative heme-binding peroxidase OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=AFUA_6G13570 PE=3 SV=1
A9146	-	-	-	-	-	-	RKO92696.1 hypothetical protein BDK51DRAFT_43510 [Blyttomyces helicus]	-
A9147	-	-	-	-	-	KOG0048 At3g09370 Transcription factor, Myb superfamily	ORX44765.1 hypothetical protein DM01DRAFT_257984, partial [Hesseltinella vesiculosa]	Transcription factor MYB3R-3 OS=Arabidopsis thaliana OX=3702 GN=MYB3R3 PE=1 SV=1
A9148	-	-	-	-	-	-	-	-
A9149	-	-	GO:0005515(protein binding)	-	-	-	OSD03302.1 galactose oxidase [Trametes coccinea BRFM310]	Leucine-zipper-like transcriptional regulator 1 homolog OS=Drosophila melanogaster OX=7227 GN=Lztr1 PE=1 SV=1
A9150	-	GO:0016021(integral component of membrane)	-	-	-	-	-	Sulfite exporter TauE/SafE family protein 4 OS=Arabidopsis thaliana OX=3702 GN=At2g36630 PE=2 SV=1
A9151	-	-	-	-	-	-	-	Ribitol-5-phosphate xylosyltransferase 1 OS=Danio rerio OX=7955
A9152	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	-	-	KOG3419 At5g56940 Mitochondrial/chloroplast ribosomal protein S16	TPX77273.1 hypothetical protein CcCBS67573_g01432 [Chytridiomycetes confervae]	Small ribosomal subunit protein bS16 OS=Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) OX=246200 GN=rpsP PE=3 SV=1
A9153	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1235 At3g24190 Predicted unusual protein kinase	KAF9132471.1 hypothetical protein BGX30_012641 [Mortierella sp. GBA39]	Uncharacterized protein sli0005 OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=sli0005 PE=3 SV=1
A9154	-	-	-	-	-	-	-	-

A9155	GO:0000278(mitotic cell cycle),GO:0030261(chromosome condensation),GO:007076(mitotic chromosome condensation),GO:0006629(lipid metabolic process)	GO:0005634(nucleus)	-	K06677 YCS4, CNAP1, CAPD2; condensin complex subunit 1	map04111 Cell cycle - yeast	KOG0414 At3g57060 Chromosome condensation complex Condensin, subunit D2	KAF9977027.1 Condensin complex subunit [Actinomortierella ambigua]	Condensin complex subunit 1 OS=Xenopus laevis OX=8355 GN=ncapd2 PE=1 SV=1
A9156	GO:0009058(biosynthetic process), GO:0009073(aromatic amino acid family biosynthetic process)	-	GO:0003849(3-deoxy-7-phosphoheptulonate synthase activity)	K01626 E2.5.1.54, aroF, aroG, aroH; 3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map02024 Quorum sensing;map01100 Metabolic pathways	-	ORZ00475.1 3-deoxy-7-phosphoheptulonate synthase [Syncephalastrum racemosum]	Phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive OS=Escherichia coli O157:H7 OX=83334 GN=aroG PE=3 SV=1
A9157	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transporter activity)	-	-	KOG0253 At3g13050 Synaptic vesicle transporter SV2 (major facilitator superfamily)	XP_01324578.1 MFS general substrate transporter [Tilletiaria anomala UBC 951]	Organic cation/carnitine transporter 7 OS=Arabidopsis thaliana OX=3702 GN=OCT7 PE=2 SV=1
A9158	-	-	GO:0016836(hydro-lyase activity)	-	-	-	KAE8371687.1 enolase 2-phosphoglycerate dehydratase [Aspergillus bertholletiae]	Cis-3-hydroxy-L-proline dehydratase OS=Starkeya novella (strain ATCC 8093 / DSM 506 / JCM 20403 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIMB 10456) OX=639283 GN=Snov_0156 PE=1 SV=1
A9159	GO:0006098(pentose-phosphate shunt)	-	GO:0004616(6-phosphogluconate dehydrogenase (decarboxylating) activity),GO:0016491(oxidoreductase activity),GO:0050661(NADP binding)	K00033 PGD, gnd, gntZ; 6-phosphogluconate dehydrogenase [EC:1.1.1.44 1.1.1.343]	map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map01120 Microbial metabolism in diverse environments;map00480 Glutathione metabolism;map00030 Pentose phosphate pathway;map01100 Metabolic pathways	KOG2653 At1g64190 6-phosphogluconate dehydrogenase	CAE6422774.1 unnamed protein product [Rhizoctonia solani]	6-phosphogluconate dehydrogenase, decarboxylating 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PGD1 PE=1 SV=1

A9160	-	-	GO:0005515(protein binding)	K11092 SNRPA1; U2 small nuclear ribonucleoprotein A'	map03040 Spliceosome	KOG0531 7295647 Protein phosphatase 1, regulatory subunit, and related proteins	RKO84887.1 hypothetical protein BDK51DRAFT_15741, partial [Blyttiomycetes helicus]	Dynein axonemal assembly factor 11 OS=Danio rerio OX=7955 GN=dnaaf11 PE=1 SV=1
A9161	-	-	-	-	-	-	-	-
A9162	-	-	GO:0005515(protein binding)	-	-	-	-	-
A9163	GO:0006139(nucleobase-containing compound metabolic process)	-	GO:0004017(adenylate kinase activity),GO:0005524(ATP binding),GO:0019205(nucleobase-containing compound kinase activity),GO:0016776(phosphotransferase activity, phosphate group as acceptor)	K00944 AK3; nucleoside-triphosphate --adenylate kinase [EC:2.7.4.10]	map00230 Purine metabolism;map01110 Biosynthesis of secondary metabolites;map01240 Biosynthesis of cofactors;map01232 Nucleotide metabolism	KOG3078 Hs19923437 Adenylate kinase	XP_016605961.1 adenylate kinase [Spizellomyces punctatus DAOM BR117]	GTP:AMP phosphotransferase AK3, mitochondrial OS=Bos taurus OX=9913 GN=AK3 PE=1 SV=3
A9164	GO:0006369(termination of RNA polymerase II transcription),GO:0006378(mRNA polyadenylation),GO:0006379(mRNA cleavage)	-	GO:0000993(RNA polymerase II complex binding),GO:0003729(mRNA binding)	K14400 PCF11; pre-mRNA cleavage complex 2 protein Pcf11	map03015 mRNA surveillance pathway	KOG2071 YDR228c mRNA cleavage and polyadenylation factor I/II complex, subunit Pcf11	KAG0254382.1 hypothetical protein BG011_005800, partial [Mortierella polycephala]	Protein PCF11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PCF11 PE=1 SV=2
A9165	-	GO:0016021(integral component of membrane)	-	-	-	KOG4474 Hs20558849 Uncharacterized conserved protein	-	TLC domain-containing protein 5 OS=Homo sapiens OX=9606 GN=TLCD5 PE=2 SV=2
A9166	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K02208 CDK8_11; cyclin-dependent kinase 8/11 [EC:2.7.11.22 2.7.11.23]	-	KOG0666 At5g63610 Cyclin C-dependent kinase CDK8	ORX83096.1 Pkinase-domain-containing protein [Anaeromyces robustus]	Probable cyclin-dependent kinase 8 OS=Dictyostelium discoideum OX=44689 GN=cdk8 PE=2 SV=1
A9167	-	-	-	-	-	KOG0769 YPR128c Predicted mitochondrial carrier protein	ORY84753.1 peroxisomal adenine nucleotide transporter 1 [Protomyces lactucaedebilis]	Mitochondrial substrate carrier family protein Q OS=Dictyostelium discoideum OX=44689 GN=mcfQ PE=2 SV=1
A9168	-	-	-	K09022 ridA, tdcF, RIDA; 2-iminobutanoate/2-iminopropanoate deaminase [EC:3.5.99.10]	-	KOG2317 Hs5032215 Putative translation initiation inhibitor UK114/IBM1	RKP36403.1 endoribonuclease L-PSP [Dimargaris cristalligena]	2-iminobutanoate/2-iminopropanoate deaminase OS=Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1) OX=186497 GN=ridA PE=1 SV=1
A9169	-	-	-	-	-	-	-	-
A9170	-	-	-	-	-	-	-	-

A9171	-	-	GO:0005515(protein binding)	K09527 DNAJC7; DnaJ homolog subfamily C member 7	-	KOG0624 Hs5453980 dsRNA-activated protein kinase inhibitor P58, contains TPR and DnaJ domains	RIB14192.1 hypothetical protein C2G38_16762.75 [Gigaspora rosea]	DnaJ homolog subfamily C member 3 OS=Gallus gallus OX=9031 GN=DNAJC3 PE=2 SV=1
A9172	-	-	-	K26544 SEC14, SEC14L; phosphatidylinositol/phosphatidylcholine transfer protein	-	KOG1471 At4g34580 Phosphatidylinositol transfer protein SEC14 and related proteins	TPX57783.1 hypothetical protein PhCBS80983_g03595 [Powellomyces hirtus]	Phosphatidylinositol/phosphatidylcholine transfer protein SFH1 OS=Arabidopsis thaliana OX=3702 GN=SFH1 PE=2 SV=1
A9173	GO:0006508(proteolysis)	-	GO:0004252(serine-type endopeptidase activity)	K01312 PRSS1_2_3; trypsin [EC:3.4.21.4]	map04974 Protein digestion and absorption;map04972 Pancreatic secretion;map04080 Neuroactive ligand-receptor interaction;map05164 Influenza A	KOG3627 7299159 Trypsin	KFH43498.1 Trypsin-like protein [Acromonium chrysogenum ATCC 11550]	Trypsin 5G1 OS=Aedes aegypti OX=7159 GN=AAEL013712 PE=2 SV=2
A9174	GO:0009166(nucleotide catabolic process)	-	GO:0005509(calcium ion binding);GO:0016787(hydrolase activity)	-	-	-	ORY53862.1 Metallo-dependent phosphatase [Rhizoclostium globosum]	Endonuclease YhcR OS=Bacillus subtilis (strain 168) OX=224308 GN=yhcR PE=1 SV=1
A9175	-	-	-	-	-	-	-	-
A9176	-	-	-	-	-	-	-	-
A9177	-	-	GO:0005515(protein binding)	-	-	-	ORX49689.1 hypothetical protein BCR36DRAFT_291719 [Piromyces finnis]	Centrosomal protein of 164 kDa OS=Mus musculus OX=10090 GN=Cep164 PE=1 SV=2
A9178	-	-	-	-	-	-	-	-
A9179	GO:0007186(G protein-coupled receptor signaling pathway), GO:0007165(signal transduction)	-	GO:0003924(GTPase activity);GO:0019001(guanylnucleotide binding);GO:0031683(G-protein beta/gamma-subunit complex binding)	K04630 GNAI; guanine nucleotide-binding protein G(i) subunit alpha	map04360 Axon guidance;map04024 cAMP signaling pathway;map04022 cGMP-PKG signaling pathway;map04730 Long-term depression;map05133 Pertussis;map04071 Sphingolipid signaling pathway;map04915 Estrogen signaling pathway;map04914 Progesterone-mediated oocyte maturation;map05170 Human immunodeficiency virus 1 infection;map04728 Dopaminergic synapse;map04724	KOG0082 7303740 G-protein alpha subunit (small G protein superfamily)	KAG2189664.1 hypothetical protein INT46_010847 [Mucor plumbeus]	Guanine nucleotide-binding protein G(o) subunit alpha OS=Locusta migratoria OX=7004 PE=3 SV=1

A9180	-	-	GO:0003824(catalytic activity),GO:0030151(molybdenum ion binding),GO:0030170(pyridoxal phosphate binding)	-	-	KOG2362 At5g44720 Uncharacterized Fe-S protein	KXN70542.1 hypothetical protein CONCODRAFT_78793 [Conidiobolus coronatus NRRL 28638]	Mitochondrial amidoxime-reducing component 1 OS=Homo sapiens OX=9606 GN=MTARC1 PE=1 SV=1
A9181	GO:0055085(transmembrane transport)	-	GO:0022857(transmembrane transporter activity),GO:0005515(protein binding),GO:0016407(acetyltransferase activity),GO:0010485(H4 histone acetyltransferase activity),GO:0043998(H2A histone acetyltransferase activity)	K20794 NAA40, NAT4; N-alpha-acetyltransferase 40 [EC:2.3.1.257]	-	KOG1330 At4g36790 Sugar transporter/suspenser transmembrane protein	KAF9015226.1 acyl-CoA N-acyltransferase [Cyathus striatus]	N-alpha-acetyltransferase 40 OS=Xenopus laevis OX=8355 GN=naa40 PE=2 SV=1
A9182	-	-	GO:0005515(protein binding)	-	-	-	-	-
A9183	-	-	-	-	-	KOG2620 At3g01290 Prohibitins and stomatins of the PID superfamily	OUM64622.1 hypothetical protein PIROE2DRAFT_8542 [Piromyces sp. E2]	Hypersensitive-induced response protein 1 OS=Oryza sativa subsp. japonica OX=39947 GN=HIR1 PE=1 SV=1
A9184	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0140359(ABC-type transporter activity)	K05665 ABCC1; ATP-binding cassette, subfamily C (CFTR/MRP), member 1 [EC:7.6.2.3]	map04071. Sphingolipid signaling pathway;map01523 Antifolate resistance;map04977 Vitamin digestion and absorption;map02010 ABC transporters;map05206 MicroRNAs in cancer	KOG0054 Hs5031915 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	KAF9224518.1 metal resistance protein YCF1 [Gyrodont lividus]	ATP-binding cassette sub-family C member 4 OS=Homo sapiens OX=9606 GN=ABCC4 PE=1 SV=3
A9185	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0005524(ATP binding),GO:0005515(protein binding),GO:0140359(ABC-type transporter activity)	-	-	KOG0054 Hs4557481 Multidrug resistance-associated protein/mitoxantrone resistance protein, ABC superfamily	XP_007869060.1 multidrug resistance-associated ABC transporter [Gloeophyllum trabeum ATCC 11539]	ATP-binding cassette sub-family C member 2 OS=Homo sapiens OX=9606 GN=ABCC2 PE=1 SV=3

A9186	GO:0007165(signal transduction)	GO:0000159(protein phosphatase type 2A complex)	GO:0019888(protein phosphatase regulator activity)	K11584 PPP2R5; serine/threonine-protein phosphatase 2A regulatory subunit B'	map04071 Sphingolipid signaling pathway;map04728 Dopaminergic synapse;map04660 T cell receptor signaling pathway;map04261 Adrenergic signaling in cardiomyocytes;map03015 mRNA surveillance pathway;map04152 AMPK signaling pathway;map04151 PI3K-Akt signaling pathway;map04114 Oocyte meiosis;map04113 Meiosis - yeast;map04110 Cell cycle-map05165	KOG2085 At3g26020 Serine/threonine protein phosphatase 2A, regulatory subunit	ORY64720.1 protein phosphatase 2A regulatory B subunit [Neocallimastix californiae]	Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' eta isoform OS=Arabidopsis thaliana OX=3702 GN=B'ETA PE=1 SV=1
A9187	-	GO:0016021(integral component of membrane)	-	K24195 XPR1, PHO1; xenotropic and polytropic retrovirus receptor 1	-	KOG1162 Hs19923272 Predicted small molecule transporter	ORX45357.1 EXS-domain-containing protein [Piromyces finnis]	SPX and EXS domain-containing protein 1 OS=Dictyostelium discoideum OX=44689 GN=DDb_G0271664 PE=3 SV=2
A9188	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding);GO:0004674(protein serine/threonine kinase activity)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration;map04024 cAMP signaling pathway;map04020 Calcium signaling pathway;map05414 Dilated cardiomyopathy;map04140 Autophagy - animal;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map01522 Endocrine resistance;map04919 Thyroid hormone signaling pathway;map04918 Thyroid hormone synthesis;map04	KOG0614 Hs10835242 cGMP-dependent protein kinase	ORY42342.1 kinase-like protein [Rhizoclostium globosum]	cGMP-dependent protein kinase OS=Plasmodium vivax (strain Salvador I) OX=126793 GN=PKG PE=1 SV=1
A9189	-	-	GO:0008146(sulfotransferase activity)	-	-	KOG3704 7293568 Heparan sulfate D-glucosaminyl 3-O-sulfotransferase	-	Heparan sulfate glucosamine 3-O-sulfotransferase 3B1 OS=Homo sapiens OX=9606 GN=HS3ST3B1 PE=1 SV=1
A9190	GO:0055085(transmembrane transport)	GO:0016021(integral component of membrane)	GO:0022857(transmembrane transporter activity)	-	-	KOG2533 At4g25220 Permease of the major facilitator superfamily	KQG13517.1 Regulatory protein uhpC [Beauveria bassiana D1-5]	Putative glycerol-3-phosphate transporter 2 OS=Arabidopsis thaliana OX=3702 GN=At4g25220 PE=2 SV=1
A9191	GO:0006261(DNA-dependent DNA replication);GO:0006260(DNA replication)	-	GO:0003887(DNA-directed DNA polymerase activity);GO:0003677(DNA binding);GO:0003676(nucleic acid binding)	-	-	KOG0950 At1g50840 DNA polymerase theta/eta, DEAD-box superfamily	KAG0777045.1 hypothetical protein G6F22_01214 [Rhizopus oryzae]	DNA polymerase I B, chloroplastic/mitochondrial OS=Arabidopsis thaliana OX=3702 GN=POLIB PE=2 SV=1
A9192	-	-	-	-	-	-	-	-

A9193	GO:0032456(endocytic recycling), GO:0042147(retrograde transport, endosome to Golgi)	GO:1990745(EARP complex)	-	-	-	KOG2939 At2g27910 Uncharacterized conserved protein	-	Syndetin OS=Rattus norvegicus OX=10116 GN=Vps50 PE=1 SV=1
A9194	GO:0006614(SRP-dependent cotranslational protein targeting to membrane)	-	GO:0005515(protein binding)	K03108 SRP72; signal recognition particle subunit SRP72	map03060 Protein export	KOG2376 Hs5902124 Signal recognition particle, subunit Srp72	KAG2185150.1 hypothetical protein INT44_001940 [Umbelopsis vinacea]	Signal recognition particle subunit SRP72 OS=Homo sapiens OX=9606 GN=SRP72 PE=1 SV=3
A9195	-	-	-	K08869 ADCK, ABC1; aarF domain-containing kinase	-	KOG1235 At1g65950 Predicted unusual protein kinase	KAF9358646.1 hypothetical protein BGX34_008831 [Mortierella sp. NVP85]	AarF domain-containing protein kinase 1 OS=Mus musculus OX=10090 GN=Adck1 PE=1 SV=1
A9196	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08867 WNK, PRKWNK; WNK lysine deficient protein kinase [EC:2.7.11.1]	-	KOG0584 At3g51630 Serine/threonine protein kinase	XP_021878627.1 kinase-like domain-containing protein, partial [Lobosporangium transversale]	Probable serine/threonine-protein kinase WNK3 OS=Arabidopsis thaliana OX=3702 GN=WNK3 PE=2 SV=1
A9197	-	-	-	-	-	-	-	-
A9198	-	-	GO:0005515(protein binding),GO:0005096(GTPase activator activity)	K12486 SMAP; stromal membrane-associated protein	map04144 Endocytosis	-	KU16285.1 hypothetical protein PAXINDRAFT_168446, partial [Paxillus involutus ATCC 200175]	Stromal membrane-associated protein 2 OS=Gallus gallus OX=9031 GN=SMAP2 PE=2 SV=1
A9199	-	-	GO:0005515(protein binding),GO:0003676(nucleic acid binding)	K12571 PAN2; PAB-dependent poly(A)-specific ribonuclease subunit 2 [EC:3.1.13.4]	map03018 RNA degradation	KOG1275 Hs7662258 PAB-dependent poly(A) ribonuclease, subunit PAN2	KAG0202360.1 poly(A)-specific ribonuclease [Mortierella sp. GBA30]	PAN2-PAN3 deadenylation complex catalytic subunit PAN2 OS=Gallus gallus OX=9031 GN=PAN2 PE=2 SV=1
A9200	-	-	GO:0003723(RNA binding)	K07575 MCTS, TMA20; malignant T-cell-amplified sequence	-	KOG2523 7290666 Predicted RNA-binding protein with PUA domain	ORX64560.1 hypothetical protein BCR32DRAFT_238763 [Anaeromyces robustus]	Malignant T-cell-amplified sequence 1 OS=Danio rerio OX=7955 GN=mcts1 PE=2 SV=1
A9201	-	-	-	-	-	-	PIA19389.1 FAD/NAD(P)-binding domain-containing protein [Coemansia reversa NRRL 1564]	-

A9202	GO:0070481(nuclear-transcribed mRNA catabolic process, non-stop decay),GO:0070966(nuclear-transcribed mRNA catabolic process, no-go decay),GO:0071025(RNA surveillance)	-	-	K06965 PELO, DOM34, pelA; protein pelota	map03015 mRNA surveillance pathway	KOG2869 7297544 Meiotic cell division protein Pelota/DOM34	XP_018285729.1 hypothetical protein PHYBLDRAFT_136746 [Phycomyces blakesleeanus NRRL 1555(-)]	Protein pelota OS=Drosophila melanogaster OX=7227 GN=pelo PE=1 SV=2
A9203	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004930(G protein-coupled receptor activity),GO:0004965(G protein-coupled GABA receptor activity)	-	-	KOG1055 Hs20127671 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	TPX74487.1 hypothetical protein CcCBS67573_g04236 [Chytridiomycetes confervae]	Gamma-aminobutyric acid type B receptor subunit 2 OS=Mus musculus OX=10090 GN=Gabbr2 PE=1 SV=2
A9204	GO:0007186(G protein-coupled receptor signaling pathway)	GO:0016021(integral component of membrane)	GO:0004965(G protein-coupled GABA receptor activity),GO:0004930(G protein-coupled receptor activity)	-	-	KOG1055 Hs20127671 GABA-B ion channel receptor subunit GABABR1 and related subunits, G-protein coupled receptor superfamily	KNE72869.1 hypothetical protein AMAG_16969 [Allomyces macrogynus ATCC 38327]	Gamma-aminobutyric acid type B receptor subunit 2 OS=Mus musculus OX=10090 GN=Gabbr2 PE=1 SV=2
A9205	-	-	-	-	-	-	-	-
A9206	-	-	-	-	-	-	-	-
A9207	-	-	GO:0005515(protein binding)	-	-	KOG3617 Hs7662194 WD40 and TPR repeat-containing protein	TPX69392.1 hypothetical protein SpCBS45565_g02472 [Spizellomyces sp. 'palustris']	Intraflagellar transport protein 140 homolog OS=Mus musculus OX=10090 GN=Ift140 PE=1 SV=1
A9208	-	-	GO:0005515(protein binding)	-	-	KOG0619 7300644_2 FOG; Leucine rich repeat	-	Probable serine/threonine-protein kinase roco5 OS=Dictyostelium discoideum OX=44689 GN=roco5 PE=3 SV=1
A9209	-	-	GO:0004488(methylenetetrahydrofolate dehydrogenase (NADP+) activity)	K00295 MTD1; methylenetetrahydrofolate dehydrogenase (NAD+) [EC:1.5.1.15]	map00670 One carbon pool by folate;map01100 Metabolic pathways	-	RKO94649.1 hypothetical protein BDK51DRAFT_43523 [Blyttomyces helicus]	Methylenetetrahydrofolate dehydrogenase [NAD(+)] OS=Dictyostelium discoideum OX=44689 GN=thfA PE=3 SV=1
A9210	-	-	GO:0005509(calcium ion binding)	-	-	KOG0027 At1g66410 Calmodulin and related proteins (EF-Hand superfamily)	AOW06370.1 hypothetical protein YALI1_E40467g [Yarrowia lipolytica]	Dynein 18 kDa light chain, flagellar outer arm OS=Chlamydomonas reinhardtii OX=3055 PE=1 SV=1
A9211	GO:0000027(ribosomal large subunit assembly)	GO:0005634(nucleus)	GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K14572 MDN1, REA1; midasin	map03008 Ribosome biogenesis in eukaryotes	KOG1808 YLR106c AAA ATPase containing von Willebrand factor type A (vWA) domain	KAG2177510.1 hypothetical protein INT44_008021 [Umbelopsis vinacea]	Midasin OS=Dictyostelium discoideum OX=44689 GN=mdn1 PE=3 SV=2

A9212	GO:0006364(rRNA processing)	-	GO:0005515(protein binding)	K14791 PWP1; periodic tryptophan protein 1	-	KOG0270[Hs5902034 WD40 repeat-containing protein	RKP07218.1 WD40-repeat-containing domain protein [Thamnocephalus sphaerosporus]	Periodic tryptophan protein 1 homolog OS=Mus musculus OX=10090 GN=Pwp1 PE=1 SV=1
A9213	GO:0006508(proteolysis)	-	GO:0004185(serine-type carboxypeptidase activity)	K13289 CTSA, CPY; cathepsin A (carboxypeptidase C) [EC:3.4.16.5]	map04142 Lysosome;map04614 Renin-angiotensin system	KOG1282[YM R297w Serine carboxypeptidases (lysosomal cathepsin A)	ORX84975.1 peptidase S10, serine carboxypeptidase [Basidiobolus meristosporus CBS 931.73]	Carboxypeptidase Y homolog A OS=Fusarium vanettenii (strain ATCC MYA-4622 / CBS 123669 / FGSC 9596 / NRRL 45880 / 77-13-4) OX=660122 GN=CPYA PE=3 SV=1
A9214	-	-	GO:0005515(protein binding)	-	-	-	XP_016611226.1 hypothetical protein SPPG_09006 [Spizellomyces punctatus DAOM BR117]	Cilia- and flagella-associated protein 251 OS=Tetrahymena thermophila (strain SB210) OX=312017 GN=CFAP251 PE=4 SV=2
A9215	GO:0006412(translation)	GO:0005840(ribosome)	GO:0003735(structural constituent of ribosome)	K02955 RP-S14e, RPS14; small subunit ribosomal protein S14e	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	KOG0407[At3g11510 40S ribosomal protein S14	RIA92457.1 ribosomal protein S11-domain-containing protein [Glomus cerebriforme]	Small ribosomal subunit protein uS11y OS=Zea mays OX=4577 PE=3 SV=1
A9216	-	-	-	-	-	-	-	-
A9217	-	-	-	-	-	KOG0656[HsM4502615 G1/S-specific cyclin D	ORX90880.1 A/B/D/E cyclin [Basidiobolus meristosporus CBS 931.73]	G1/S-specific cyclin-D2 OS=Sus scrofa OX=9823 GN=CCND2 PE=2 SV=1
A9218	-	-	-	-	-	KOG0867[7299606 Glutathione S-transferase	OCK79119.1 thioredoxin-like protein, partial [Lepidopterella palustris CBS 459.81]	Glutathione S-transferase A OS=Pleuronectes platessa OX=8262 PE=2 SV=1
A9219	GO:0006468(protein phosphorylation)	-	GO:0004674(protein serine/threonine kinase activity),GO:0005524(ATP binding),GO:0004672(protein kinase activity),GO:0004692(cGMP-dependent protein kinase activity)	K04345 PKA; protein kinase A [EC:2.7.11.11]	map04361 Axon regeneration;map04024 cAMP signaling pathway;map04020 Calcium signaling pathway;map05414 Dilated cardiomyopathy;map04140 Autophagy - animal;map04211 Longevity regulating pathway;map04213 Longevity regulating pathway - multiple species;map01522 Endocrine resistance;map04919 Thyroid hormone signaling pathway;map04918 Thyroid hormone synthesis;map04	KOG0614[Hs10835242 cGMP-dependent protein kinase	ORZ30315.1 camp-dependent protein kinase [Catenaria anguillulae PL171]	cGMP-dependent protein kinase 1 OS=Homo sapiens OX=9606 GN=PRKG1 PE=1 SV=3

A9220	-	-	GO:0016702(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen)	K17842 carT, CAO-2; torulene dioxygenase [EC:1.13.11.59]	map01110 Biosynthesis of secondary metabolites;map00906 Carotenoid biosynthesis;map01100 Metabolic pathways	KOG1285 Hs4506591 Beta, beta-carotene 15,15'-dioxygenase and related enzymes	KAF8927535.1 hypothetical protein BGZ58_010337 [Dissophoromata]	Carotenoid cleavage dioxygenase 8, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=CCD8 PE=1 SV=1
A9221	GO:0006383(transcription by RNA polymerase III)	GO:0005666(RNA polymerase III complex)	GO:0003677(DNA binding)	-	-	-	-	-
A9222	-	-	-	-	-	-	-	-
A9223	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity);GO:0005524(ATP binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0192 At1g62400 Tyrosine kinase specific for activated (GTP-bound) p21cdc42Hs	RKP06665.1 kinase-like domain-containing protein, partial [Thamnocephalis sphaerospora]	Probable serine/threonine-protein kinase drkD OS=Dictyostelium discoideum OX=44689 GN=drkD PE=2 SV=1
A9224	-	-	-	-	-	KOG3589 Hs4506519 G protein signaling regulators	RIA85537.1 hypothetical protein C1645_830654 [Glomus cerebriiforme]	Regulator of G-protein signaling 21 OS=Homo sapiens OX=9606 GN=RGS21 PE=2 SV=1
A9225	GO:0036211(protein modification process)	-	-	K03800 lplA, lplJ, lplL1; lipoate--protein ligase [EC:6.3.1.20]	map00785 Lipoic acid metabolism;map01240 Biosynthesis of cofactors;map01100 Metabolic pathways	KOG3159 At3g29010 Lipoate-protein ligase A	-	Inactive lipoate--protein ligase 2 OS=Plasmodium falciparum (isolate 3D7) OX=36329 GN=LipL2 PE=1 SV=1
A9226	GO:0007165(signal transduction)	-	-	-	-	KOG0619 7300644_2 FOG: Leucine rich repeat	-	Probable serine/threonine-protein kinase roco5 OS=Dictyostelium discoideum OX=44689 GN=roco5 PE=3 SV=1
A9227	GO:0006751(glutathione catabolic process)	-	GO:0003839(gamma-glutamylcyclotransferase activity)	K07232 CHAC, chaC; glutathione-specific gamma-glutamylcyclotransferase [EC:4.3.2.7]	map00480 Glutathione metabolism;map01100 Metabolic pathways	KOG3182 Hs13129126 Predicted cation transporter	KAG0228460.1 Cation transport regulator-like protein 2 [Actinomyces rella wolffii]	Glutathione-specific gamma-glutamylcyclotransferase 1 OS=Rattus norvegicus OX=10116 GN=Chac1 PE=2 SV=1
A9228	-	-	-	-	-	-	-	-
A9229	-	-	-	-	-	-	-	-

A9230	GO:0006631(fatty acid metabolic process), GO:0006635(fatty acid beta-oxidation)	GO:0005777(peroxisome)	GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0003997(acyl-CoA oxidase activity),GO:0071949(FAD binding),GO:0050660(flavin adenine dinucleotide binding)	K00232 E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00410 beta-Alanine metabolism;map03320 PPAR signaling pathway;map04024 cAMP signaling pathway;map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00640 Propanoate metabolism;map01040 Biosynthesis of unsaturated fatty acids;map04936 Alcoholic liver disease;map00592 alpha-Linolenic acid metabolism;map	KOG0136 Hs6031155 Acyl-CoA oxidase	XP_016607254.1 hypothetical protein SPPG_05470 [Spizellomyces punctatus DAOM BR117]	Peroxisomal acyl-coenzyme A oxidase 1 OS=Cavia porcellus OX=10141 GN=ACOX1 PE=2 SV=1
A9231	GO:0007015(actin filament organization)	GO:0015629(actin cytoskeleton)	GO:0003779(actin binding)	-	-	-	RUP51938.1 hypothetical protein BC936DRAFT_144338 [Jimgerdennia flammicorona]	KICSTOR complex protein kaptin OS=Homo sapiens OX=9606 GN=KPTN PE=1 SV=2
A9232	-	-	GO:0016491(oxidoreductase activity)	K13953 adhP; alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]	map00980 Metabolism of xenobiotics by cytochrome P450;map00982 Drug metabolism - cytochrome P450;map01110 Biosynthesis of secondary metabolites;map00010 Glycolysis / Gluconeogenesis;map01120 Microbial metabolism in diverse environments;map00830 Retinol metabolism;map01220 Degradation of aromatic compounds;map00625 Chloroalkane and chloroalkene	KOG0023 YMR303c Alcohol dehydrogenase, class V	KXS18111.1 alcohol dehydrogenase superfamily, zinc-containing protein [Gonapodya prolifera JEL478]	Acrylyl-CoA reductase Acul OS=Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) OX=246200 GN=acul PE=1 SV=1
A9233	-	-	GO:0005515(protein binding)	-	-	-	KAG0343224.1 cysteinyl-tRNA synthetase [Podila horticola]	-
A9234	-	-	-	-	-	-	-	-
A9235	-	-	-	-	-	-	-	-
A9236	-	-	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)	K09568 FKBP1; FK506-binding protein 1 [EC:5.2.1.8]	-	KOG0544 YNL135c FKBP-type peptidyl-prolyl cis-trans isomerase	XP_019015745.1 hypothetical protein PICMEDRAFT_74347 [Pichia membranifaciens NRRL Y-2026]	FK506-binding protein 1 OS=Candida glabrata (strain ATCC 2001 / BCRC 20586 / JCM 3761 / NBRC 0622 / NRRL Y-65 / CBS 138) OX=284593 GN=FPR1 PE=1 SV=1
A9237	-	-	-	-	-	-	KNE62878.1 hypothetical protein AMAG_08055 [Allomyces macrogynus ATCC 38327]	-

A9238	-	-	-	K09539 DNAJC19; DnaJ homolog subfamily C member 19	-	KOG0723 At3 g09700 Molecular chaperone (DnaJ superfamily)	TPX66557.1 hypothetical protein SpCBS45565_ g04404 [Spizellomyces sp. 'palustris']	Mitochondrial import inner membrane translocase subunit TIM14-2 OS=Arabidopsis thaliana OX=3702 GN=TIM14-2 PE=3 SV=1
A9239	-	-	GO:0016787(hy drolase activity)	K06128 LYPLA1; lysophosphol ipase I [EC:3.1.1.5]	map00564 Glycerophospho lipid metabolism;map 05231 Choline metabolism in cancer	KOG2112 Hs5 453722 Lysophosphol ipase	PIA19596.1 acyl-protein thioesterase- 1 [Coemansia reversa NRRL 1564]	Acyl-protein thioesterase 1 OS=Gibberella zeae (strain ATCC MYA-4620 / CBS 123657 / FGSC 9075 / NRRL 31084 / PH-1) OX=229533 GN=FGRAMPH1_01T20223 PE=3 SV=1
A9240	-	-	GO:0016787(hy drolase activity)	-	-	KOG1515 At5 g06570 Arylacetamid e deacetylase	PBL00723.1 hypothetical protein ARMGADRAFT_ 1006850 [Armillaria gallica]	Acetyl-hydrolase OS=Streptomyces hygroscopicus OX=1912 GN=bah PE=3 SV=3
A9241	-	-	-	K02975 RP- S25e, RPS25; small subunit ribosomal protein S25e	map05171 Coronavirus disease - COVID- 19;map03010 Ribosome	KOG1767 Hs4 506707 40S ribosomal protein S25	XP_01903292 9.1 30S small subunit ribosomal protein S25e [Cryptococcus wingfieldii CBS 7118]	Small ribosomal subunit protein eS25 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=RPS25B PE=1 SV=1
A9242	GO:00421 47(retrogr ade transport, endosome to Golgi)	GO:00309 04(retrom er complex)	-	K18467 VPS29; vacuolar protein sorting- associated protein 29	map04144 Endocytosis	KOG3325 Hs7 706441 Membrane coat complex Retromer, subunit VPS29/PEP11	RIB08417.1 Metallo- dependent phosphatase -like protein [Gigaspora rosea]	Vacuolar protein sorting-associated protein 29 OS=Rattus norvegicus OX=10116 GN=Vps29 PE=1 SV=2
A9243	-	-	-	-	-	-	-	-
A9244	-	-	-	-	-	-	XP_03102203 9.1 uncharacteriz ed protein SmJEL517_g0 6054 [Synchytrium microbalum]	-
A9245	GO:00064 68(protein phosphor ylation)	-	GO:0004672(pro tein kinase activity),GO:000 5524(ATP binding)	-	-	KOG0198 At1 g54960 MEK and related serine/threon ine protein kinases	XP_01829877 2.1 hypothetical protein PHYBLDRAFT_ 88191, partial [Phycomyces blakesleeanu s NRRL 1555(-)]	Mitogen-activated protein kinase kinase 2 OS=Arabidopsis thaliana OX=3702 GN=ANP2 PE=2 SV=1
A9246	-	GO:00057 37(cytopl asm),GO: 0005852(e ukaryotic translatio n initiation factor 3 complex)	GO:0003743(tra nslation initiation factor activity)	-	-	KOG4813 730 3820 Translation initiation factor eIF3, p35 subunit	-	Eukaryotic translation initiation factor 3 subunit J OS=Drosophila persimilis OX=7234 GN=eIF3j PE=3 SV=1
A9247	GO:00092 31(ribofla vin biosynthe tic process)	-	GO:0008686(3,4 -dihydroxy-2- butanone-4- phosphate synthase activity)	-	-	KOG1284 YD R487c Bifunctional GTP cyclohydrolas e II/3,4- dihydroxy- 2butanone- 4-phosphate synthase	XP_02889131 8.1 3,4- dihydroxy-2- butanone 4- phosphate synthase [[Candida] auris]	3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) OX=243232 GN=ribB PE=1 SV=1

A9248	GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport)	-	-	K20363 YIPF5_7, YIP1; protein YIPF5/7	-	KOG3103 7297993 Rab GTPase interacting factor, Golgi membrane protein	RIB11837.1 hypothetical protein C2G38_18872.13, partial [Gigaspora rosea]	Protein YIPF5 homolog OS=Dictyostelium discoideum OX=44689 GN=yipf5 PE=3 SV=1
A9249	-	-	-	-	-	KOG0048 At3g09370 Transcription factor, Myb superfamily	KAF9981062.1 Transcription factor myb3r-5 [Mortierella antarctica]	Transcription factor MYB3R-3 OS=Arabidopsis thaliana OX=3702 GN=MYB3R3 PE=1 SV=1
A9250	-	-	GO:0003678(DNA helicase activity),GO:0016818(hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides),GO:0005524(ATP binding),GO:0003677(DNA binding)	K11136 RTEL1; regulator of telomere elongation helicase 1 [EC:5.6.2.3]	-	KOG1132 ECU02g1090 Helicase of the DEAD superfamily	ORZ14489.1 helicase C-terminal domain-containing protein [Absidia repens]	Regulator of telomere elongation helicase 1 homolog OS=Drosophila erecta OX=7220 GN=GG18780 PE=3 SV=1
A9251	GO:0006427(histidyl-tRNA aminoacylation)	GO:0005737(cytoplasm)	GO:0004821(histidine-tRNA ligase activity),GO:0005524(ATP binding)	K01892 HARS, hisS; histidyl-tRNA synthetase [EC:6.1.1.21]	map00970 Aminoacyl-tRNA biosynthesis	KOG1936 Hs6996014 Histidyl-tRNA synthetase	ORY04836.1 histidyl-tRNA synthetase [Basidiobolus meristosporus CBS 931.73]	Histidine-tRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=HARS1 PE=2 SV=1
A9252	-	-	-	-	-	-	-	-
A9253	GO:0006281(DNA repair)	-	GO:0004518(nuclease activity),GO:0003824(catalytic activity)	-	-	KOG1294 At3g48420.2 Apurinic/apurimidinic endonuclease and related enzymes	KIP08846.1 hypothetical protein PHLGIDRAFT_29324 [Phlebiopsis gigantea 11061_1 CR5-6]	DNA-(apurinic or apyrimidinic site) endonuclease OS=Arabidopsis thaliana OX=3702 GN=APE1L PE=1 SV=1
A9254	-	-	-	K09425 K09425; Myb-like DNA-binding protein FlbD	-	KOG0048 At4g18770 Transcription factor, Myb superfamily	EOB15043.1 Myb proto-oncogene protein [Nosema bombycis CQ1]	Transcription factor MYB98 OS=Arabidopsis thaliana OX=3702 GN=MYB98 PE=2 SV=1
A9255	GO:0051260(protein homooligomerization)	-	-	-	-	KOG2716 CE09558 Polymerase delta-interacting protein PDIP1 and related proteins, contain BTB/POZ domain	ORY91280.1 BTB/POZ protein [Syncephalaster racemosus]	BTB/POZ domain-containing protein KCTD16 OS=Homo sapiens OX=9606 GN=KCTD16 PE=1 SV=1
A9256	-	-	-	-	-	-	XP_006680352.1 uncharacterized protein BATDEDRAFT_26295 [Batrachochytrium dendrobatidis JAM81]	-

A9257	GO:0030001(metal ion transport),GO:0055085(transmembrane transport)	GO:0016020(membrane)	GO:0046873(metal ion transmembrane transporter activity)	-	-	KOG2474 Hs21040273 Zinc transporter and related ZIP domain-containing proteins	KAG1235733.1 hypothetical protein G6F68_018900 [Rhizopus microsporus]	Zinc transporter ZIP11 OS=Mus musculus OX=10090 GN=Slc39a11 PE=1 SV=1
A9258	-	-	-	-	-	-	-	-
A9259	-	-	-	-	-	-	-	-
A9260	-	-	-	-	-	-	-	-
A9261	-	-	-	-	-	-	-	-
A9262	GO:0009190(cyclic nucleotide biosynthetic process),GO:0035556(intracellular signal transduction)	-	-	-	-	-	KAG4098900.1 adenylyl cyclase [Neocallimastix sp. JGI-2020a]	Adenylate cyclase type 10 OS=Homo sapiens OX=9606 GN=ADCY10 PE=1 SV=3
A9263	-	-	-	K10580 UBE2N, BLU, UBC13; ubiquitin-conjugating enzyme E2 N [EC:2.3.2.23]	map05131 Shigellosis;map04624 Toll and Imd signaling pathway;map04120 Ubiquitin mediated proteolysis	KOG0417 At1g16890 Ubiquitin-protein ligase	KAG0734657.1 hypothetical protein G6F23_012200 [Rhizopus oryzae]	Ubiquitin-conjugating enzyme E2 36 OS=Arabidopsis thaliana OX=3702 GN=UBC36 PE=1 SV=1
A9264	-	-	-	-	-	-	-	-
A9265	GO:0016226(iron-sulfur cluster assembly)	-	GO:0005506(iron ion binding),GO:0051536(iron-sulfur cluster binding)	K22068 ISCU; iron-sulfur cluster assembly enzyme ISCU, mitochondrial	-	KOG3361 7299098 Iron binding protein involved in Fe-S cluster formation	EJW01541.1 iron sulfur cluster assembly protein 1 [Edhazardia aedis USNM 41457]	Iron-sulfur cluster assembly enzyme ISCU OS=Homo sapiens OX=9606 GN=ISCU PE=1 SV=2
A9266	GO:0006811(ion transport),GO:0055085(transmembrane transport),GO:0030317(flagellated sperm motility)	GO:0016020(membrane),GO:0036128(CatSper complex)	GO:0005216(ion channel activity),GO:0005227(calcium activated cation channel activity)	-	-	KOG2301 Hs16876443 Voltage-gated Ca2+ channels, alpha1 subunits	KNE71767.1 hypothetical protein AMAG_16071 [Allomyces macrogynus ATCC 38327]	Cation channel sperm-associated protein 2 OS=Homo sapiens OX=9606 GN=CATSPER2 PE=1 SV=2
A9267	-	-	-	-	-	-	-	-
A9268	GO:0006355(regulation of transcription, DNA-templated)	-	GO:0003700(DNA-binding transcription factor activity)	-	-	-	-	-
A9269	-	-	GO:0005515(protein binding)	-	-	-	-	-
A9270	-	-	GO:0005515(protein binding)	-	-	-	-	-
A9271	-	-	-	-	-	-	PHH74134.1 hypothetical protein CDD80_3293 [Ophiocordyceps camponoti-rufipedis]	Inactive C-alpha-formylglycine-generating enzyme 2 OS=Pongo abelii OX=9601 GN=SUMF2 PE=2 SV=1
A9272	-	-	GO:0008270(zinc ion binding),GO:0003677(DNA binding)	-	-	KOG3173 Hs21359918 Predicted Zn-finger protein	CDS05159.1 hypothetical protein LRAMOSA07688 [Lichtheimia ramosa]	AN1-type zinc finger protein 6 OS=Homo sapiens OX=9606 GN=ZFAND6 PE=1 SV=2

A9273	GO:0006414(translational elongation),GO:0002182(cytoplasmic translation elongation)	GO:0005840(ribosome),GO:0022625(cytosolic large ribosomal subunit)	GO:0003735(structural constituent of ribosome)	K02943 RP-LP2, RPLP2; large subunit ribosomal protein LP2	map05171 Coronavirus disease - COVID-19;map03010 Ribosome	-	XP_02559223.1.1 uncharacterized protein FVRRES_08593 [Fusarium venenatum]	Large ribosomal subunit protein P2 OS=Aspergillus fumigatus (strain ATCC MYA-4609 / CBS 101355 / FGSC A1100 / Af293) OX=330879 GN=AFUA_2G10100 PE=1 SV=2
A9274	-	-	GO:0016788(hydrolase activity, acting on ester bonds)	K05294 PGAP1; GPI inositol-deacylase [EC:3.-.-.-]	map00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis;map01100 Metabolic pathways	KOG3724 Hs13376494 Negative regulator of COPII vesicle formation	XP_01828596.7.1 hypothetical protein PHYBLDRAFT_127912, partial [Phycomyces blakesleeanus NRRL 1555(-)]	Putative GPI inositol-deacylase C OS=Yarrowia lipolytica (strain CLIB 122 / E 150) OX=284591 GN=BST1C PE=3 SV=1
A9275	-	-	GO:0008484(sulfuric ester hydrolase activity)	-	-	KOG3867 Hs4557333 Sulfatase	XP_02466333.7.1 Arylsulfatase I [Wickerhamiella sorbophila]	Arylsulfatase B OS=Rattus norvegicus OX=10116 GN=Arsl PE=2 SV=2
A9276	-	-	-	-	-	-	-	-
A9277	-	GO:0016021(integral component of membrane)	-	K13348 MPV17; protein Mpv17	map04146 Peroxisome	KOG1944 Hs4505241 Peroxisomal membrane protein MPV17 and related proteins	TPX60727.1 hypothetical protein PhCBS80983_g01629 [Powellomyces hirtus]	PXMP2/4 family protein 2 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0278529 PE=3 SV=1
A9278	-	-	-	K13354 SLC25A17, PMP34; solute carrier family 25 (peroxisomal adenine nucleotide transporter), member 17	map04146 Peroxisome	KOG0769 7292482.2 Predicted mitochondrial carrier protein	XP_019042629.1 solute carrier family 25 (peroxisomal adenine nucleotide transporter), member 17 [Kwoniella bestiolae CBS 10118]	Peroxisomal membrane protein PMP34 OS=Mus musculus OX=10090 GN=Slc25a17 PE=1 SV=1
A9279	-	-	-	-	-	-	-	-
A9280	GO:0006468(protein phosphorylation)	-	GO:0004672(protein kinase activity),GO:0005524(ATP binding)	K08286 E2.7.11.-; protein-serine/threonine kinase [EC:2.7.11.-]	-	KOG0612 CE11916 Rho-associated, coiled-coil containing protein kinase	TKA56602.1 hypothetical protein B0A53_01794 [Rhodotorula sp. CCFEE 5036]	Serine/threonine-protein kinase mrck-1 OS=Caenorhabditis elegans OX=6239 GN=mrck-1 PE=1 SV=3
A9281	-	-	-	-	-	KOG3695 Hs2055651 Uncharacterized conserved protein	-	FHF complex subunit HOOK-interacting protein 2B OS=Xenopus tropicalis OX=8364 GN=fhip2b PE=2 SV=1
A9282	-	-	-	-	-	-	-	-
A9283	GO:0045892(negative regulation of transcription, DNA-templated)	-	-	-	-	KOG0403 At5g63190 Neoplastic transformation suppressor Pdc4/MA-3, contains MA3 domain	EPB91951.1 hypothetical protein HMPREF1544_01245 [Mucor circinelloides 1006PhL]	MA3 DOMAIN-CONTAINING TRANSLATION REGULATORY FACTOR 1 OS=Arabidopsis thaliana OX=3702 GN=MRF1 PE=1 SV=1

A9284	GO:000341(cilium movement),GO:0060271(cilium assembly)	-	-	-	-	-	XP_031022980.1 uncharacterized protein SmJEL517_g05091 [Synchytrium microbalum]	Cilia- and flagella-associated protein 53 OS=Mus musculus OX=10090 GN=Cfap53 PE=1 SV=3
A9285	-	-	-	-	-	-	-	-
A9286	GO:0005975(carbohydrate metabolic process)	-	-	-	-	-	-	-
A9287	GO:0006260(DNA replication)	-	GO:0003677(DNA binding),GO:0005524(ATP binding),GO:0016887(ATP hydrolysis activity)	K10756 RFC3_5; replication factor C subunit 3/5	map03420 Nucleotide excision repair;map03030 DNA replication;map03410 Base excision repair;map03430 Mismatch repair	KOG0990[Hs6677723 Replication factor C, subunit RFC5	XP_016612495.1 hypothetical protein SPPG_00185 [Spizellomyces punctatus DAOM BR117]	Probable replication factor C subunit 5 OS=Dictyostelium discoideum OX=44689 GN=rfc5 PE=3 SV=1
A9288	-	-	-	-	-	KOG1764[YG L056c 5'-AMP-activated protein kinase, gamma subunit	GAN06993.1 conserved hypothetical protein [Mucor ambiguus]	Protein SDS23 OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=SDS23 PE=3 SV=1
A9289	-	-	-	-	-	-	-	-
A9290	-	-	GO:0005509(calcium ion binding)	K03017 RPB9, POLR2l; DNA-directed RNA polymerase II subunit RPB9	map03420 Nucleotide excision repair;map03020 RNA polymerase;map05016 Huntington disease	KOG0044[Hs19913441 Ca2+ sensor (EF-Hand superfamily)	XP_025508739.1 putative calcium-binding signaling protein Frq1 [Aspergillus aculeatinus CBS 121060]	Hippocalcin-like protein 1 OS=Mus musculus OX=10090 GN=Hpcal1 PE=1 SV=2
A9291	-	-	-	-	-	-	-	-
A9292	-	-	-	-	-	KOG3599[CE25589 Ca2+-modulated nonselective cation channel polycystin	-	-
A9293	-	-	GO:0005515(protein binding)	-	-	KOG0001[Hs20473312 Ubiquitin and ubiquitin-like proteins	XP_021884111.1 ubiquitin-related domain-containing protein [Lobosporangium transversale]	Ubiquitin-ribosomal protein eL40 fusion protein OS=Caenorhabditis elegans OX=6239 GN=ubq-2 PE=3 SV=2
A9294	-	-	GO:0003677(DNA binding)	-	-	KOG0724[At3g09600 Zuotin and related molecular chaperones (Dna) superfamily), contains DNA-binding domains	ORX93100.1 hypothetical protein K493DRAFT_262785 [Basidiobolus meristosporus CBS 931.73]	Protein REVEILLE 1 OS=Arabidopsis thaliana OX=3702 GN=RVE1 PE=1 SV=1

A9295	GO:0005992(trehalose biosynthetic process)	-	GO:0003824(catalytic activity)	K22337 TSL1; TPS3; trehalose 6-phosphate synthase complex regulatory subunit	map01110 Biosynthesis of secondary metabolites;map00500 Starch and sucrose metabolism;map01100 Metabolic pathways	KOG1050 At1g68020 Trehalose-6-phosphate synthase component TPS1 and related subunits	KAG2189464.1 hypothetical protein INT44_004606 [Umbelopsis vinacea]	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabidopsis thaliana OX=3702 GN=TPS5 PE=1 SV=2
A9296	-	-	GO:0003824(catalytic activity)	K22966 HINT4; sulfate adenylyltransferase (ADP) / adenylylsulfatase [EC:2.7.7.5 3.6.2.1]	map01120 Microbial metabolism in diverse environments;map00920 Sulfur metabolism;map01100 Metabolic pathways	KOG3275 Hs14211923 Zinc-binding protein of the histidine triad (HIT) family	KAG4095614.1 histidine triad nucleotide-binding protein 3-like protein [Neocallimastix sp. JGI-2020a]	Adenosine 5'-monophosphoramidase HINT3 OS=Xenopus tropicalis OX=8364 GN=hint3 PE=2 SV=1
A9297	-	-	-	-	-	-	-	-
A9298	-	-	GO:0005515(protein binding)	-	-	-	-	-
A9299	GO:0006631(fatty acid metabolic process), GO:0006635(fatty acid beta-oxidation)	GO:0005777(peroxisome)	GO:0003997(acyl-CoA oxidase activity),GO:0071949(FAD binding),GO:0016627(oxidoreductase activity, acting on the CH-CH group of donors),GO:0050660(flavin adenine dinucleotide binding)	K00232 E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00410 beta-Alanine metabolism;map03320 PPAR signaling pathway;map04024 cAMP signaling pathway;map04146 Peroxisome;map01110 Biosynthesis of secondary metabolites;map01200 Carbon metabolism;map00640 Propanoate metabolism;map01040 Biosynthesis of unsaturated fatty acids;map04936 Alcoholic liver disease;map00592 alpha-Linolenic acid metabolism;map	KOG0136 Hs6031155 Acyl-CoA oxidase	KAF8142701.1 acyl-CoA dehydrogenase/oxidase [Mycena galopus ATCC 62051]	Peroxisomal acyl-coenzyme A oxidase 1 OS=Bos taurus OX=9913 GN=ACOX1 PE=2 SV=1
A9300	-	-	-	-	-	-	-	-
A9301	-	-	-	-	-	-	-	-
A9302	-	-	-	-	-	KOG1420 Hs4504853 Ca2+-activated K+ channel Slowpoke, alpha subunit	RIA82227.1 hypothetical protein C1645_835709 [Glomus cerebriforme]	Calcium-activated potassium channel subunit alpha-1a OS=Danio rerio OX=7955 GN=kcnma1a PE=1 SV=1
A9303	GO:0006891(intra-Golgi vesicle-mediated transport)	GO:0017119(Golgi transport complex)	-	K20293 COG6, COD2; conserved oligomeric Golgi complex subunit 6	-	KOG3758 At1g31780 Uncharacterized conserved protein	XP_016613172.1 hypothetical protein SPPG_00803 [Spizellomyces punctatus DAOM BR117]	Conserved oligomeric Golgi complex subunit 6 OS=Arabidopsis thaliana OX=3702 GN=COG6 PE=1 SV=1
A9304	-	-	GO:0005515(protein binding)	-	-	KOG4308 Hs1436853 LRR-containing protein	KAG1206324.1 hypothetical protein G6F35_011247 [Rhizopus oryzae]	Ribonuclease inhibitor OS=Mus musculus OX=10090 GN=Rnh1 PE=1 SV=1

A9305	-	-	GO:0005515(protein binding)	-	-	KOG0531 7297577 Protein phosphatase 1, regulatory subunit, and related proteins	TPX74014.1 hypothetical protein CcCBS67573_g04721 [Chytridiomycota confervae]	Dynein regulatory complex subunit 3 OS=Chlamydomonas reinhardtii OX=3055 GN=DRC3 PE=1 SV=1
A9306	-	-	-	-	-	-	-	-
A9307	-	-	-	-	-	-	-	-
A9308	GO:000973(aromatic amino acid family biosynthetic process)	GO:0005737(cytoplasm)	GO:0003856(3-dehydroquinase synthase activity)	K13830 ARO1; pentafunctional AROM polypeptide [EC:4.2.3.4 4.2.1.10 1.1.1.25 2.7.1.71 2.5.1.19]	map01110 Biosynthesis of secondary metabolites;map01230 Biosynthesis of amino acids;map00400 Phenylalanine, tyrosine and tryptophan biosynthesis;map00999 Biosynthesis of various plant secondary metabolites;map01100 Metabolic pathways	KOG0692 At5g66120 Pentafunctional AROM protein	KAG0165542.1 hypothetical protein DFQ30_008319 [Apophysomonas sp. BC1015]	3-dehydroquinase synthase OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) OX=243277 GN=aroB PE=1 SV=2
A9309	GO:000079(regulation of cyclin-dependent protein serine/threonine kinase activity)	-	GO:0019901(protein kinase binding)	-	-	KOG1674 At2g45080 Cyclin	TPX58719.1 hypothetical protein PhCBS80983_g02958 [Powellomyces hirtus]	Cyclin-U2-1 OS=Arabidopsis thaliana OX=3702 GN=CYCU2-1 PE=1 SV=1
A9310	-	-	GO:0016491(oxidoreductase activity)	-	-	KOG1201 Hs705905 Hydroxysteroid 17-beta dehydrogenase 11	KAF8639862.1 hypothetical protein AX17_001117 [Amanita inopinata Kibby_2008]	Estradiol 17-beta-dehydrogenase 11 OS=Mus musculus OX=10090 GN=Hsd17b11 PE=1 SV=1
A9311	-	-	GO:0005515(protein binding)	-	-	KOG0543 Hs4758384 FKBP-type peptidyl-prolyl cis-trans isomerase	XP_007882063.1 hypothetical protein PFL1_06331 [Anthracocystis flocculosa PF-1]	-
A9312	-	-	-	-	-	KOG0725 7295487 Reductases with broad range of substrate specificities	ORY06562.1 short chain dehydrogenase/reductase family [Basidiobolus meristosporus CBS 931.73]	Rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] reductase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=rhIG PE=1 SV=1
A9313	-	-	-	K00866 CK1; choline kinase [EC:2.7.1.32]	map00564 Glycerophospholipid metabolism;map01100 Metabolic pathways	KOG4720 At2g26830 Ethanolamine kinase	XP_016610513.1 hypothetical protein SPPG_09071 [Spizellomyces punctatus DAOM BR117]	Probable ethanolamine kinase OS=Arabidopsis thaliana OX=3702 GN=EMB1187 PE=2 SV=1

A9314	-	-	-	-	-	-	PKC70369.1 hypothetical protein RhiirA1_3392 85 [Rhizophagus irregularis]	-
A9315	-	-	GO:0016491(oxi doreductase activity);GO:003 0151(molybden um ion binding);GO:002 0037(heme binding)	K00387 SUOX; sulfite oxidase [EC:1.8.3.1]	map01120 Microbial metabolism in diverse environments;m ap00920 Sulfur metabolism;map 01100 Metabolic pathways	KOG0535 Hs4 557867_2 Sulfite oxidase, molybdopteri n-binding component	XP_01660629 0.1 hypothetical protein SPPG_06649 [Spizellomyces punctatus DAOM BR117]	Sulfite oxidase OS=Gallus gallus OX=9031 GN=SUOX PE=1 SV=3
A9316	-	-	-	-	-	-	-	Sex-regulated protein janus-A OS=Drosophila teissieri OX=7243
A9317	GO:00071 65(signal transducti on)	-	GO:0008081(ph osphoric diester hydrolase activity);GO:000 4114(3',5'- cyclic- nucleotide phosphodiester ase activity)	K18436 PDE7; high affinity cAMP- specific 3',5'- cyclic phosphodiester ase 7 [EC:3.1.4.53]	map00230 Purine metabolism;map 05032 Morphine addiction;map01 100 Metabolic pathways	KOG3689 Hs5 453862 Cyclic nucleotide phosphodiester ase	ORZ38093.1 hypothetical protein BCR44DRAFT _141090 [Catenaria anguillulae PL171]	3',5'-cyclic-AMP phosphodiesterase 4C (Fragment) OS=Rattus norvegicus OX=10116 GN=Pde4c PE=2 SV=2
A9318	-	-	-	K06990 MEMO1; MEMO1 family protein	-	KOG3086 729 9707 Predicted dioxxygenase	XP_00741005 3.1 uncharacteriz ed protein MELLADRAFT _48375 [Melampsora larici- populina 98AG31]	Protein MEMO1 OS=Xenopus laevis OX=8355 GN=memo1 PE=2 SV=1
A9319	-	-	-	K22684 MCA1; metacaspase -1 [EC:3.4.22.-]	-	-	ORX92922.1 metacaspase [Basidiobolus meristosporus CBS 931.73]	Metacaspase-1 OS=Ustilago maydis (strain 521 / FGSC 9021) OX=237631 GN=MCA1 PE=3 SV=1
A9320	-	-	-	-	-	-	-	-
A9321	-	-	-	-	-	-	-	-
A9322	GO:00422 74(riboso mal small subunit biogenesis)	-	-	-	-	KOG2637 730 3692 Uncharacteriz ed conserved protein	ORZ41147.1 Low temperature viability protein- domain- containing protein [Catenaria anguillulae PL171]	Protein LTV1 homolog OS=Drosophila melanogaster OX=7227 GN=LTV1 PE=1 SV=1
A9323	-	-	GO:0016407(ace tyltransferase activity)	-	-	-	TPX42580.1 hypothetical protein SeLEV6574_g 05531 [Synchytrium endobioticu m]	Actin maturation protease OS=Bos taurus OX=9913 PE=2 SV=3
A9324	-	-	-	-	-	-	-	-
A9325	-	GO:00058 71(kinesin complex)	GO:0005515(pro tein binding)	-	-	-	ORY44048.1 TPR-like protein [Rhizoclosma tium globosum]	-

A9326	-	-	-	-	-	-	KAF5345350.1 hypothetical protein D9758_00846 6 [Tetrapyrgos nigripes]	L-threonine 3-dehydrogenase OS=Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087) OX=3042615 GN=tdh PE=3 SV=1
A9327	-	-	-	-	-	-	PVU87440.1 hypothetical protein BB561_00632 9, partial [Smittium simulii]	-