



*** Welcome to DAVID (2021 Update) ***

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Functional Annotation Clustering

Current Gene List: [List_1](#)

Current Background: [Saccharomyces cerevisiae S288C](#)

613 DAVID IDs

Options

Classification Stringency

Medium ▼

Rerun using options

Create Sublist

64 Cluster(s)

Annotation Cluster 1

Enrichment Score: 2.91

G



- | | | | |
|---|--|--------------------|--|
| <input type="checkbox"/> GOTERM_BP_DIRECT | reciprocal meiotic recombination | RT | |
| <input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS | Meiosis | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | meiotic cell cycle | RT | |

Annotation Cluster 2

Enrichment Score: 1.64

G



- | | | | |
|---|--|--------------------|--|
| <input type="checkbox"/> INTERPRO | Glycoside hydrolase, superfamily | RT | |
| <input type="checkbox"/> UP_KW_MOLECULAR_FUNCTION | Glycosidase | RT | |
| <input type="checkbox"/> GOTERM_MF_DIRECT | hydrolase activity, acting on glycosyl bonds | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | carbohydrate metabolic process | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | metabolic process | RT | |

Annotation Cluster 3

Enrichment Score: 1.27

G



- | | | | |
|---|---|--------------------|--|
| <input type="checkbox"/> KEGG_PATHWAY | Nucleocytoplasmic transport | RT | |
| <input type="checkbox"/> GOTERM_CC_DIRECT | nuclear pore | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | mRNA transport | RT | |
| <input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS | mRNA transport | RT | |
| <input type="checkbox"/> UP_KW_CELLULAR_COMPONENT | Nuclear pore complex | RT | |
| <input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS | Translocation | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | NLS-bearing protein import into nucleus | RT | |

Annotation Cluster 4

Enrichment Score: 1.19

G



- | | | | |
|---|---|--------------------|--|
| <input type="checkbox"/> KEGG_PATHWAY | Starch and sucrose metabolism | RT | |
| <input type="checkbox"/> INTERPRO | Glycoside hydrolase, superfamily | RT | |
| <input type="checkbox"/> SMART | Amy | RT | |
| <input type="checkbox"/> INTERPRO | Glycosyl hydrolase, family 13, catalytic domain | RT | |
| <input type="checkbox"/> INTERPRO | Glycosyl hydrolase, family 13, all-beta | RT | |
| <input type="checkbox"/> UP_SEQ_FEATURE | SITE:Transition state stabilizer | RT | |
| <input type="checkbox"/> KEGG_PATHWAY | Galactose metabolism | RT | |
| <input type="checkbox"/> GOTERM_MF_DIRECT | alpha-amylase activity | RT | |
| <input type="checkbox"/> GOTERM_MF_DIRECT | oligo-1,6-glucosidase activity | RT | |
| <input type="checkbox"/> GOTERM_MF_DIRECT | maltose alpha-glucosidase activity | RT | |
| <input type="checkbox"/> GOTERM_MF_DIRECT | glucan 1,4-alpha-maltotriohydrolase activity | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | maltose catabolic process | RT | |
| <input type="checkbox"/> GOTERM_MF_DIRECT | sucrose alpha-glucosidase activity | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | sucrose catabolic process | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | oligosaccharide catabolic process | RT | |
| <input type="checkbox"/> UP_KW_BIOLOGICAL_PROCESS | Maltose metabolism | RT | |
| <input type="checkbox"/> GOTERM_BP_DIRECT | maltose metabolic process | RT | |

Annotation Cluster 1

Enrichment Score: 2.91

G

<input type="checkbox"/>	GOTERM_MF_DIRECT	transmembrane transporter activity	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	fructose transmembrane transporter activity	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	mannose transmembrane transporter activity	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	glucose transmembrane transporter activity	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	fructose transport	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	mannose transport	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	glucose transmembrane transport	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	hexose transport	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	sugar:proton symporter activity	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	carbohydrate transport	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Sugar transport	RT	
<input type="checkbox"/>	INTERPRO	Sugar transporter, conserved site	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=3	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=4	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Meiosis - yeast	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=11	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=12	RT	
<input type="checkbox"/>	INTERPRO	Sugar/inositol transporter	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=5	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=10	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=9	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=6	RT	
<input type="checkbox"/>	INTERPRO	General substrate transporter	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=8	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=1	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=2	RT	
<input type="checkbox"/>	INTERPRO	Major facilitator superfamily domain	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical; Name=7	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	hydrogen ion transmembrane transport	RT	

Annotation Cluster 8

Enrichment Score: 1.06

G

<input type="checkbox"/>	INTERPRO	DNA recombination/repair protein RecA/RadB, ATP-binding domain	RT	
<input type="checkbox"/>	INTERPRO	DNA recombination and repair protein Rad51, C-terminal	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA recombinase assembly	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	strand invasion	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	recombinase activity	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitotic recombination	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	heteroduplex formation	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	DNA-dependent ATPase activity	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	double-stranded DNA binding	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Homologous recombination	RT	
<input type="checkbox"/>	SMART	AAA	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	single-stranded DNA binding	RT	
<input type="checkbox"/>	INTERPRO	AAA+ ATPase domain	RT	




Annotation Cluster 9












Enrichment Score: 0.98






G





<input type="checkbox"/>	GOTERM_BP_DIRECT	fatty acid metabolic process	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Fatty acid degradation	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Fatty acid metabolism	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Fatty acid metabolism	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	lipid metabolic process	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Lipid metabolism	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Fatty acid metabolism	RT	





Annotation Cluster 1		Enrichment Score: 2.91	G	
<input type="checkbox"/>	INTERPRO	Aldo/keto reductase, conserved site	RT	
<input type="checkbox"/>	INTERPRO	Aldo/keto reductase subgroup	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	SITE:Lowers pKa of active site Tyr	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	D-threo-aldose 1-dehydrogenase activity	RT	
<input type="checkbox"/>	INTERPRO	NADP-dependent oxidoreductase domain	RT	
Annotation Cluster 14		Enrichment Score: 0.8	G	
<input type="checkbox"/>	UP_SEQ_FEATURE	TOPO_DOM:Mitochondrial intermembrane	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TOPO_DOM:Mitochondrial matrix	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	mitochondrial inner membrane	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Mitochondrion inner membrane	RT	
Annotation Cluster 15		Enrichment Score: 0.78	G	
<input type="checkbox"/>	GOTERM_CC_DIRECT	integral component of membrane	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	membrane	RT	
<input type="checkbox"/>	UP_KW_DOMAIN	Transmembrane	RT	
<input type="checkbox"/>	UP_KW_DOMAIN	Transmembrane helix	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Membrane	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TOPO_DOM:Cytoplasmic	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSMEM:Helical	RT	
Annotation Cluster 16		Enrichment Score: 0.75	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	meiotic joint molecule formation	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	condensed nuclear chromosome	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	double-stranded DNA binding	RT	
Annotation Cluster 17		Enrichment Score: 0.68	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	U1 snRNA 3'-end processing	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	U5 snRNA 3'-end processing	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	rRNA catabolic process	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	U4 snRNA 3'-end processing	RT	
Annotation Cluster 18		Enrichment Score: 0.65	G	
<input type="checkbox"/>	GOTERM_CC_DIRECT	spindle pole body	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	cytoskeleton	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Cytoskeleton	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Microtubule	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	microtubule	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	spindle	RT	
Annotation Cluster 19		Enrichment Score: 0.64	G	
<input type="checkbox"/>	GOTERM_MF_DIRECT	metal ion binding	RT	
<input type="checkbox"/>	UP_KW_LIGAND	Zinc	RT	
<input type="checkbox"/>	UP_KW_LIGAND	Metal-binding	RT	
Annotation Cluster 20		Enrichment Score: 0.63	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	cell wall organization	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Cell wall biogenesis/degradation	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Cell wall biogenesis/degradation	RT	
Annotation Cluster 21		Enrichment Score: 0.63	G	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Glycogen biosynthesis	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycogen biosynthetic process	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	transferase activity, transferring glycosyl groups	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Glycosyltransferase	RT	
Annotation Cluster 22		Enrichment Score: 0.62	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	ion transport	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Ion transport	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	integral component of plasma membrane	RT	

Annotation Cluster 1		Enrichment Score: 2.91	G	
<input type="checkbox"/>	INTERPRO	Transcription factor, fungi	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription, DNA-templated	RT	





Annotation Cluster 26		Enrichment Score: 0.52	G	
<input type="checkbox"/>	KEGG_PATHWAY	Spliceosome	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	U1 snRNP	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	U2-type prespliceosome	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA splicing, via spliceosome	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA splicing	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	mRNA splicing	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA processing	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	mRNA processing	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	spliceosomal complex	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Spliceosome	RT	





Annotation Cluster 27		Enrichment Score: 0.51	G	
<input type="checkbox"/>	GOTERM_CC_DIRECT	U2-type prespliceosome	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	catalytic step 2 spliceosome	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	U2 snRNP	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA processing	RT	





Annotation Cluster 28		Enrichment Score: 0.5	G	
<input type="checkbox"/>	KEGG_PATHWAY	mRNA surveillance pathway	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	mRNA cleavage and polyadenylation specificity factor complex	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	mRNA polyadenylation	RT	





Annotation Cluster 29		Enrichment Score: 0.48	G	
<input type="checkbox"/>	GOTERM_MF_DIRECT	transferase activity, transferring acyl groups other than amino-acyl groups	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	transferase activity, transferring acyl groups	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Acyltransferase	RT	






Annotation Cluster 30		Enrichment Score: 0.47	G	
<input type="checkbox"/>	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	glycolytic process	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Glycolysis	RT	




















































Annotation Cluster 31		Enrichment Score: 0.45	G	
<input type="checkbox"/>	INTERPRO	Zinc finger, FYVE/PHD-type	RT	
<input type="checkbox"/>	INTERPRO	Zinc finger, PHD-type, conserved site	RT	
<input type="checkbox"/>	INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT	




















































Annotation Cluster 32		Enrichment Score: 0.42	G	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Transport	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein transport	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Protein transport	RT	







































Annotation Cluster 33		Enrichment Score: 0.4	G	
<input type="checkbox"/>	GOTERM_CC_DIRECT	endosome	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Endosome	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	endosome membrane	RT	

Annotation Cluster 34		Enrichment Score: 0.39	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromatin silencing at telomere	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromosome, telomeric region	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	telomeric heterochromatin assembly	RT	

Annotation Cluster 35		Enrichment Score: 0.39	G	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:1-4	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:1-3	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:2-1	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:2-2	RT	

Annotation Cluster 1		Enrichment Score: 2.91	G	
<input type="checkbox"/>	SMART	S TKc	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleotide binding	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	phosphorylation	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	peptidyl-serine phosphorylation	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	NP_BIND:ATP	RT	
<input type="checkbox"/>	INTERPRO	Serine/threonine-protein kinase, active site	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	ATP binding	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein serine/threonine kinase activity	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	BINDING:ATP	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Serine/threonine-protein kinase	RT	
<input type="checkbox"/>	INTERPRO	Protein kinase, catalytic domain	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	ACT_SITE:Proton acceptor	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	intracellular signal transduction	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	protein kinase activity	RT	
<input type="checkbox"/>	INTERPRO	Protein kinase, ATP binding site	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Protein kinase	RT	
<input type="checkbox"/>	INTERPRO	Protein kinase-like domain	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	protein phosphorylation	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	transferase activity	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Transferase	RT	
<input type="checkbox"/>	UP_KW_LIGAND	Nucleotide-binding	RT	
<input type="checkbox"/>	UP_KW_LIGAND	ATP-binding	RT	
Annotation Cluster 39		Enrichment Score: 0.3	G	
<input type="checkbox"/>	INTERPRO	DNA/RNA helicase, DEAD/DEAH box type, N-terminal	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	RNA helicase activity	RT	
<input type="checkbox"/>	SMART	DEXDc	RT	
<input type="checkbox"/>	INTERPRO	RNA helicase, DEAD-box type, Q motif	RT	
<input type="checkbox"/>	INTERPRO	Helicase, superfamily 1/2, ATP-binding domain	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:Q motif	RT	
<input type="checkbox"/>	SMART	HELICc	RT	
<input type="checkbox"/>	INTERPRO	Helicase, C-terminal	RT	
<input type="checkbox"/>	INTERPRO	RNA helicase, ATP-dependent, DEAD-box, conserved site	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:DEAD box	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	MOTIF:DEAH box	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Helicase C-terminal	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Helicase	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	helicase activity	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Helicase ATP-binding	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	nucleic acid binding	RT	
Annotation Cluster 40		Enrichment Score: 0.3	G	
<input type="checkbox"/>	KEGG_PATHWAY	Autophagy - yeast	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	late nucleophagy	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	autophagy	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	piecemeal microautophagy of nucleus	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	mitophagy	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Autophagy	RT	
Annotation Cluster 41		Enrichment Score: 0.3	G	
<input type="checkbox"/>	UP_SEQ_FEATURE	ZN_FING:RING-type; atypical	RT	
<input type="checkbox"/>	INTERPRO	Zinc finger, RING/FYVE/PHD-type	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	ubiquitin-protein transferase activity	RT	

Annotation Cluster 1		Enrichment Score: 2.91	G	
<input type="checkbox"/>	UP_KW_PTM	Prenylation	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	LIPID:S-geranylgeranyl cysteine	RT	
<input type="checkbox"/>	INTERPRO	Small GTP-binding protein domain	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	NP_BIND:GTP	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTPase activity	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	GTP binding	RT	
<input type="checkbox"/>	UP_KW_PTM	Methylation	RT	
<input type="checkbox"/>	UP_KW_LIGAND	GTP-binding	RT	
Annotation Cluster 46		Enrichment Score: 0.25	G	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Elongation factor	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	translation elongation factor activity	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Protein biosynthesis	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	translational elongation	RT	
Annotation Cluster 47		Enrichment Score: 0.23	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	GPI anchor biosynthetic process	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	GPI-anchor biosynthesis	RT	
Annotation Cluster 48		Enrichment Score: 0.22	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	phospholipid biosynthetic process	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Phospholipid biosynthesis	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Glycerophospholipid metabolism	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Phospholipid metabolism	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Lipid biosynthesis	RT	
Annotation Cluster 49		Enrichment Score: 0.22	G	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Solcar 3	RT	
<input type="checkbox"/>	INTERPRO	Mitochondrial substrate/solute carrier	RT	
<input type="checkbox"/>	INTERPRO	Mitochondrial carrier protein	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Solcar 1	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:Solcar 2	RT	
<input type="checkbox"/>	INTERPRO	Mitochondrial carrier domain	RT	
Annotation Cluster 50		Enrichment Score: 0.22	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription initiation from RNA polymerase II promoter	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	transcription from RNA polymerase II promoter	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Basal transcription factors	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	RNA polymerase II transcriptional preinitiation complex assembly	RT	
Annotation Cluster 51		Enrichment Score: 0.21	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	DNA repair	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	DNA repair	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	DNA damage	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	cellular response to DNA damage stimulus	RT	
Annotation Cluster 52		Enrichment Score: 0.2	G	
<input type="checkbox"/>	GOTERM_CC_DIRECT	Golgi membrane	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Golgi apparatus	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	Golgi apparatus	RT	
Annotation Cluster 53		Enrichment Score: 0.19	G	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Mitochondrion	RT	
<input type="checkbox"/>	UP_KW_DOMAIN	Transit peptide	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	TRANSIT:Mitochondrion	RT	
Annotation Cluster 54		Enrichment Score: 0.18	G	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	DNA replication	RT	

Annotation Cluster 1		Enrichment Score: 2.91	G	
<input type="checkbox"/>	INTERPRO	Zinc finger C2H2-type/integrase DNA-binding domain	RT	
Annotation Cluster 60		Enrichment Score: 0.05	G	
<input type="checkbox"/>	GOTERM_BP_DIRECT	chromosome segregation	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Mitosis	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromosome	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Kinetochores	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Chromosome	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	kinetochores	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	chromosome, centromeric region	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Centromere	RT	
Annotation Cluster 61		Enrichment Score: 0.03	G	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 4	RT	
<input type="checkbox"/>	INTERPRO	WD40-repeat-containing domain	RT	
<input type="checkbox"/>	SMART	WD40	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 3	RT	
<input type="checkbox"/>	UP_KW_DOMAIN	WD repeat	RT	
<input type="checkbox"/>	INTERPRO	WD40 repeat	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 1	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 2	RT	
<input type="checkbox"/>	INTERPRO	WD40 repeat, conserved site	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 6	RT	
<input type="checkbox"/>	INTERPRO	WD40/YVTN repeat-like-containing domain	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:WD 5	RT	
Annotation Cluster 62		Enrichment Score: 0.01	G	
<input type="checkbox"/>	GOTERM_MF_DIRECT	peptidase activity	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	proteolysis	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Protease	RT	
Annotation Cluster 63		Enrichment Score: 0	G	
<input type="checkbox"/>	UP_KW_LIGAND	S-adenosyl-L-methionine	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	methyltransferase activity	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Methyltransferase	RT	
<input type="checkbox"/>	GOTERM_BP_DIRECT	methylation	RT	
Annotation Cluster 64		Enrichment Score: 0	G	
<input type="checkbox"/>	KEGG_PATHWAY	Ribosome	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Ribosomal protein	RT	
<input type="checkbox"/>	GOTERM_MF_DIRECT	structural constituent of ribosome	RT	
<input type="checkbox"/>	GOTERM_CC_DIRECT	ribosome	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Ribonucleoprotein	RT	

363 terms

 were not clustered.