Appendix D. Functional enrichment analysis.

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| Module | Terms | Description |
| Module 1 | OMIM:616078 | mental retardation, autosomal dominant 29; mrd29 |
| Module 1 | OMIM:612446 | complement component 6 deficiency; c6d; c6 deficiencycomplement component 6 deficiency, subtotal, included; c6 deficiency, subtotal, included |
| Module 1 | OMIM:269150 | schinzel-giedion midface retraction syndrome; sgs |
| Module 2 | GO:0051239 | regulation of multicellular organismal process |
| Module 2 | GO:0032502 | developmental process |
| Module 2 | GO:0048856 | anatomical structure development |
| Module 2 | GO:0009653 | anatomical structure morphogenesis |
| Module 2 | GO:0044767 | single-organism developmental process |
| Module 2 | GO:0044707 | single-multicellular organism process |
| Module 2 | GO:0007275 | multicellular organism development |
| Module 2 | GO:0048731 | system development |
| Module 2 | GO:0007399 | nervous system development |
| Module 2 | CORUM:2073 | tnfrsf11a-traf6-src complex |
| Module 2 | CORUM:2958 | smad1-cbp complex |
| Module 2 | HPA:005010\_10 | bronchus; respiratory epithelial cells |
| Module 2 | HPA:007010\_10 | cerebral cortex; endothelial cells |
| Module 2 | HPA:027010\_10 | pancreas; exocrine glandular cells |
| Module 2 | HPA:006020\_10 | cerebellum; cells in granular layer |
| Module 2 | HPA:021020\_10 | liver; hepatocytes |
| Module 2 | HPA:001010\_10 | adrenal gland; glandular cells |
| Module 2 | HPA:018010\_10 | hippocampus; glial cells |
| Module 2 | HPA:022020\_10 | lung; pneumocytes |
| Module 2 | HPA:007030\_10 | cerebral cortex; neuronal cells |
| Module 2 | HPA:025010\_10 | oral mucosa; squamous epithelial cells |
| Module 2 | HPA:035030\_10 | skin 1; keratinocytes |
| Module 2 | HPA:012010\_10 | endometrium 2; cells in endometrial stroma |
| Module 2 | HPA:039030\_10 | soft tissue 1; fibroblasts |
| Module 2 | HPA:010010\_10 | duodenum; glandular cells |
| Module 2 | HPA:037010\_10 | small intestine; glandular cells |
| Module 2 | HPA:004010\_10 | breast; adipocytes |
| Module 2 | HPA:004020\_10 | breast; glandular cells |
| Module 2 | HPA:032010\_10 | salivary gland; glandular cells |
| Module 2 | HPA:029020\_10 | placenta; trophoblastic cells |
| Module 2 | HPA:048010\_10 | vagina; squamous epithelial cells |
| Module 2 | HPA:042010\_10 | stomach 1; glandular cells |
| Module 2 | HPA:045010\_10 | thyroid gland; glandular cells |
| Module 2 | HPA:003010\_10 | bone marrow; hematopoietic cells |
| Module 2 | HPA:044010\_10 | testis; leydig cells |
| Module 2 | HPA:035010\_10 | skin 1; langerhans |
| Module 2 | HPA:007020\_10 | cerebral cortex; glial cells |
| Module 2 | HPA:029010\_10 | placenta; decidual cells |
| Module 2 | HPA:021010\_10 | liver; bile duct cells |
| Module 2 | HPA:034010\_10 | skeletal muscle; myocytes |
| Module 2 | HPA:018020\_10 | hippocampus; neuronal cells |
| Module 2 | HPA:002010\_10 | appendix; glandular cells |
| Module 2 | HPA:035020\_10 | skin 1; fibroblasts |
| Module 2 | HPA:006010\_10 | cerebellum; purkinje cells |
| Module 2 | HPA:026020\_10 | ovary; ovarian stroma cells |
| Module 2 | HPA:023010\_10 | lymph node; germinal center cells |
| Module 2 | HPA:022010\_10 | lung; macrophages |
| Module 2 | HPA:041010\_10 | spleen; cells in red pulp |
| Module 2 | HPA:040040\_10 | soft tissue 2; peripheral nerve |
| Module 2 | HPA:039010\_10 | soft tissue 1; adipocytes |
| Module 2 | HPA:020010\_10 | lateral ventricle; glial cells |
| Module 2 | HPA:009020\_10 | colon; glandular cells |
| Module 2 | HPA:046010\_10 | tonsil; germinal center cells |
| Module 2 | HPA:047010\_10 | urinary bladder; urothelial cells |
| Module 2 | HPA:011010\_10 | endometrium 1; cells in endometrial stroma |
| Module 2 | HPA:014010\_10 | esophagus; squamous epithelial cells |
| Module 2 | HPA:031010\_10 | rectum; glandular cells |
| Module 2 | HPA:012020\_10 | endometrium 2; glandular cells |
| Module 2 | HPA:017010\_10 | heart muscle; myocytes |
| Module 2 | HPA:006030\_10 | cerebellum; cells in molecular layer |
| Module 2 | HPA:011020\_10 | endometrium 1; glandular cells |
| Module 2 | HPA:041020\_10 | spleen; cells in white pulp |
| Module 2 | HPA:019020\_10 | kidney; cells in tubules |
| Module 2 | HPA:009010\_10 | colon; endothelial cells |
| Module 2 | HPA:038010\_10 | smooth muscle; smooth muscle cells |
| Module 2 | HPA:019010\_10 | kidney; cells in glomeruli |
| Module 2 | HPA:040010\_10 | soft tissue 2; adipocytes |
| Module 2 | HPA:004030\_10 | breast; myoepithelial cells |
| Module 2 | HPA:043010\_10 | stomach 2; glandular cells |
| Module 2 | HPA:007040\_10 | cerebral cortex; neuropil |
| Module 2 | HPA:035040\_10 | skin 1; melanocytes |
| Module 2 | HPA:016010\_10 | gallbladder; glandular cells |
| Module 2 | HPA:023020\_10 | lymph node; non-germinal center cells |
| Module 2 | HPA:044020\_10 | testis; cells in seminiferous ducts |
| Module 2 | HPA:030010\_10 | prostate; glandular cells |
| Module 2 | HPA:015010\_10 | fallopian tube; glandular cells |
| Module 2 | HPA:013010\_10 | epididymis; glandular cells |
| Module 2 | HPA:046020\_10 | tonsil; non-germinal center cells |
| Module 2 | KEGG:05200 | pathways in cancer |
| Module 3 | - | - |
| Module 4 | MI:hsa-miR-614 | mi:hsa-mir-614 |
| Module 5 | CORUM:1149 | histone h3.1 complex |
| Module 5 | OMIM:226900 | epiphyseal dysplasia, multiple, 4; edm4; multiple epiphyseal dysplasia, autosomal recessive; multiple epiphyseal dysplasia with clubfoot; multiple epiphyseal dysplasia with bilayered patellae |
| Module 5 | OMIM:222600 | diastrophic dysplasia; dtd; dddiastrophic dysplasia, broad bone-platyspondylic variant, included |
| Module 5 | OMIM:256050 | atelosteogenesis, type ii; ao2; aoii; neonatal osseous dysplasia ide la chapelle dysplasia, included; dlcd, included |
| Module 5 | OMIM:600972 | achondrogenesis, type ib; acg1b; achondrogenesis, fraccaro type |
| Module 6 | - | - |
| Module 7 | GO:0046035 | cmp metabolic process |
| Module 7 | GO:0009224 | cmp biosynthetic process |
| Module 7 | GO:0006238 | cmp salvage |
| Module 8 | - | - |
| Module 9 | - | - |
| Module 10 | GO:0044267 | cellular protein metabolic process |
| Module 10 | OMIM:142946 | holoprosencephaly 4; hpe4 |
| Module 10 | OMIM:608957 | cd8 deficiency, familial |
| Module 10 | OMIM:613953 | candidiasis, familial, 5; candf5; candidiasis, familial chronic mucocutaneous, autosomal recessive |
| Module 10 | OMIM:611092 | mental retardation, autosomal recessive 6; mrt6 |
| Module 10 | OMIM:615598 | palmoplantar keratoderma, nagashima type; ppkn |
| Module 10 | OMIM:308700 | hypogonadotropic hypogonadism 1 with or without anosmia; hh1; kallmann syndrome 1; kal1; kms; hypogonadotropic hypogonadism and anosmia; hha; dysplasia olfactogenitalis of de morsier; anosmic hypogonadism |
| Module 10 | OMIM:614714 | porokeratosis 7, multiple types; porok7 |
| Module 11 | GO:0032994 | protein-lipid complex |
| Module 11 | GO:1990777 | lipoprotein particle |
| Module 11 | GO:0034358 | plasma lipoprotein particle |
| Module 11 | OMIM:614028 | apolipoprotein c-iii deficiency; hyperalphalipoproteinemia 2; halp2 |
| Module 11 | REAC:174824 | lipoprotein metabolism |
| Module 12 | - | - |
| Module 13 | CORUM:2578 | sam68-p120gap complex |
| Module 13 | CORUM:2581 | rasgap-aurka/aurkb-survivin complex |
| Module 13 | OMIM:613784 | macular degeneration, age-related, 12; armd12 |
| Module 13 | OMIM:607339 | coronary heart disease, susceptibility to, 1; chds1 |
| Module 13 | OMIM:608354 | capillary malformation-arteriovenous malformation; cmavmcapillary malformation without arteriovenous malformation, included |
| Module 13 | OMIM:608355 | parkes weber syndrome; pkws |
| Module 14 | - | - |
| Module 15 | - | - |
| Module 16 | OMIM:237500 | dubin-johnson syndrome; djs; hyperbilirubinemia, dubin-johnson type; hblrdj; hyperbilirubinemia ii |
| Module 16 | OMIM:616171 | microcephaly and chorioretinopathy, autosomal recessive, 2; mccrp2 |
| Module 16 | OMIM:607499 | bulimia nervosa, susceptibility to, 1; buln1; bn |
| Module 16 | OMIM:610269 | bulimia nervosa, susceptibility to, 2; buln2anorexia nervosa, susceptibility to, 2, included; anon2, included |
| Module 17 | GO:0001890 | placenta development |
| Module 17 | HPA:018010\_03 | hippocampus; glial cells |
| Module 17 | OMIM:613068 | neurodegeneration due to cerebral folate transport deficiency |
| Module 17 | OMIM:178110 | arthrogryposis, distal, type 8; da8; multiple pterygium syndrome, autosomal dominant; pterygium syndrome, multiple, autosomal dominant |
| Module 17 | OMIM:193700 | arthrogryposis, distal, type 2a; da2a; freeman-sheldon syndrome; fss; whistling face-windmill vane hand syndrome; craniocarpotarsal dystrophy; craniocarpotarsal dysplasia |
| Module 18 | HPA:046010\_03 | tonsil; germinal center cells |
| Module 19 | - | - |
| Module 20 | - | - |
| Module 21 | GO:0004092 | carnitine o-acetyltransferase activity |
| Module 22 | GO:0070429 | negative regulation of nucleotide-binding oligomerization domain containing 1 signaling pathway |
| Module 22 | GO:0034147 | regulation of toll-like receptor 5 signaling pathway |
| Module 22 | GO:0034148 | negative regulation of toll-like receptor 5 signaling pathway |
| Module 23 | OMIM:304340 | pettigrew syndrome; pgs; mental retardation, x-linked, syndromic 5; mrxs5; mental retardation, x-linked, with dandy-walker malformation, basalganglia disease, and seizures; mental retardation, x-linked, syndromic, fried type; mrxsf; mental retardation, x-linked 59; mrx59; mental retardation, x-linked, syndromic 21; mrxs21 |
| Module 23 | OMIM:615752 | polymicrogyria, bilateral perisylvian, autosomal recessive; bppr; pmgr |
| Module 23 | OMIM:606854 | polymicrogyria, bilateral frontoparietal; bfpp; cerebellar ataxia with neuronal migration defect |
| Module 24 | GO:0050794 | regulation of cellular process |
| Module 24 | GO:0070106 | interleukin-27-mediated signaling pathway |
| Module 24 | GO:0045509 | interleukin-27 receptor activity |
| Module 25 | OMIM:614075 | hermansky-pudlak syndrome 6; hps6 |
| Module 25 | OMIM:604364 | epilepsy, familial focal, with variable foci; ffevf; epilepsy, partial, with variable foci; fpevf |
| Module 26 | GO:0031616 | spindle pole centrosome |
| Module 26 | GO:0032133 | chromosome passenger complex |
| Module 26 | GO:0035174 | histone serine kinase activity |
| Module 26 | OMIM:243060 | spermatogenic failure 5; spgf5; male infertility with large-headed, multiflagellar, polyploid spermatozoa; infertility associated with multi-tailed spermatozoa and excessivedna |
| Module 26 | OMIM:613463 | fasting plasma glucose level quantitative trait locus 5; fgqtl5 |
| Module 26 | OMIM:259710 | osteopetrosis, autosomal recessive 2; optb2; osteopetrosis, osteoclast-poor; osteopetrosis, mild autosomal recessive form |
| Module 27 | CORUM:2029 | bnip2-arhgap8 complex |
| Module 28 | GO:0008150 | biological\_process |
| Module 28 | GO:0065007 | biological regulation |
| Module 28 | GO:0065008 | regulation of biological quality |
| Module 28 | GO:0044699 | single-organism process |
| Module 28 | GO:0009987 | cellular process |
| Module 28 | GO:0044763 | single-organism cellular process |
| Module 28 | GO:0007154 | cell communication |
| Module 28 | GO:0023052 | signaling |
| Module 28 | GO:0044700 | single organism signaling |
| Module 28 | GO:0032501 | multicellular organismal process |
| Module 28 | GO:0044707 | single-multicellular organism process |
| Module 28 | GO:0002376 | immune system process |
| Module 28 | GO:0050896 | response to stimulus |
| Module 28 | GO:0006950 | response to stress |
| Module 28 | GO:0006952 | defense response |
| Module 28 | GO:0006955 | immune response |
| Module 28 | GO:0051716 | cellular response to stimulus |
| Module 28 | GO:0050789 | regulation of biological process |
| Module 28 | GO:0048583 | regulation of response to stimulus |
| Module 28 | GO:0050794 | regulation of cellular process |
| Module 28 | GO:0007165 | signal transduction |
| Module 28 | GO:0007166 | cell surface receptor signaling pathway |
| Module 28 | GO:0048518 | positive regulation of biological process |
| Module 28 | GO:0048584 | positive regulation of response to stimulus |
| Module 28 | GO:0048522 | positive regulation of cellular process |
| Module 28 | GO:0070887 | cellular response to chemical stimulus |
| Module 28 | GO:0010033 | response to organic substance |
| Module 28 | GO:0071310 | cellular response to organic substance |
| Module 28 | GO:0005575 | cellular\_component |
| Module 28 | GO:0005623 | cell |
| Module 28 | GO:0044464 | cell part |
| Module 28 | GO:0005829 | cytosol |
| Module 28 | GO:0005488 | binding |
| Module 28 | GO:0005515 | protein binding |
| Module 28 | HPA:025010\_10 | oral mucosa; squamous epithelial cells |
| Module 28 | HPA:007030\_10 | cerebral cortex; neuronal cells |
| Module 28 | HPA:010010\_10 | duodenum; glandular cells |
| Module 28 | HPA:032010\_10 | salivary gland; glandular cells |
| Module 28 | HPA:039030\_10 | soft tissue 1; fibroblasts |
| Module 28 | HPA:039010 | soft tissue 1; adipocytes |
| Module 28 | HPA:039010\_10 | soft tissue 1; adipocytes |
| Module 28 | HPA:006030\_10 | cerebellum; cells in molecular layer |
| Module 28 | HPA:042010\_10 | stomach 1; glandular cells |
| Module 28 | HPA:019010\_10 | kidney; cells in glomeruli |
| Module 28 | HPA:041010\_10 | spleen; cells in red pulp |
| Module 28 | HPA:035040\_10 | skin 1; melanocytes |
| Module 28 | HPA:026020\_10 | ovary; ovarian stroma cells |
| Module 28 | HPA:021010\_10 | liver; bile duct cells |
| Module 28 | HPA:029020\_10 | placenta; trophoblastic cells |
| Module 28 | HPA:046020\_10 | tonsil; non-germinal center cells |
| Module 28 | HPA:004020\_10 | breast; glandular cells |
| Module 28 | HPA:013010\_10 | epididymis; glandular cells |
| Module 28 | HPA:040040\_10 | soft tissue 2; peripheral nerve |
| Module 28 | HPA:023010\_10 | lymph node; germinal center cells |
| Module 28 | HPA:041010\_12 | spleen; cells in red pulp |
| Module 28 | HPA:033010\_10 | seminal vesicle; glandular cells |
| Module 28 | HPA:040040\_12 | soft tissue 2; peripheral nerve |
| Module 28 | HPA:040030\_10 | soft tissue 2; fibroblasts |
| Module 28 | HPA:037010\_10 | small intestine; glandular cells |
| Module 28 | HPA:046010\_10 | tonsil; germinal center cells |
| Module 28 | HPA:046010\_11 | tonsil; germinal center cells |
| Module 28 | HPA:012020\_10 | endometrium 2; glandular cells |
| Module 28 | HPA:029010\_10 | placenta; decidual cells |
| Module 28 | HPA:022020\_10 | lung; pneumocytes |
| Module 28 | HPA:014010\_10 | esophagus; squamous epithelial cells |
| Module 28 | HPA:035010\_10 | skin 1; langerhans |
| Module 28 | HPA:007010\_10 | cerebral cortex; endothelial cells |
| Module 28 | HPA:044020\_10 | testis; cells in seminiferous ducts |
| Module 28 | HPA:007040\_10 | cerebral cortex; neuropil |
| Module 28 | HPA:048010\_10 | vagina; squamous epithelial cells |
| Module 28 | HPA:047010\_10 | urinary bladder; urothelial cells |
| Module 28 | HPA:008010\_10 | cervix, uterine; glandular cells |
| Module 28 | HPA:002010\_10 | appendix; glandular cells |
| Module 28 | HPA:039040\_10 | soft tissue 1; peripheral nerve |
| Module 28 | HPA:009010\_10 | colon; endothelial cells |
| Module 28 | HPA:011010\_10 | endometrium 1; cells in endometrial stroma |
| Module 28 | HPA:006010\_10 | cerebellum; purkinje cells |
| Module 28 | HPA:041020\_10 | spleen; cells in white pulp |
| Module 28 | HPA:036010\_10 | skin 2; epidermal cells |
| Module 28 | HPA:038010\_10 | smooth muscle; smooth muscle cells |
| Module 28 | HPA:015010\_10 | fallopian tube; glandular cells |
| Module 28 | HPA:046030\_10 | tonsil; squamous epithelial cells |
| Module 28 | HPA:004010\_10 | breast; adipocytes |
| Module 28 | HPA:044010\_10 | testis; leydig cells |
| Module 28 | HPA:018010\_10 | hippocampus; glial cells |
| Module 28 | HPA:004030\_10 | breast; myoepithelial cells |
| Module 28 | HPA:031010\_10 | rectum; glandular cells |
| Module 28 | HPA:020020\_10 | lateral ventricle; neuronal cells |
| Module 28 | HPA:011020\_10 | endometrium 1; glandular cells |
| Module 28 | HPA:022010\_10 | lung; macrophages |
| Module 28 | HPA:035020\_10 | skin 1; fibroblasts |
| Module 28 | HPA:040010\_10 | soft tissue 2; adipocytes |
| Module 28 | HPA:019020\_10 | kidney; cells in tubules |
| Module 28 | HPA:019020\_11 | kidney; cells in tubules |
| Module 28 | HPA:001010\_10 | adrenal gland; glandular cells |
| Module 28 | HPA:037010\_12 | small intestine; glandular cells |
| Module 28 | HPA:006020\_10 | cerebellum; cells in granular layer |
| Module 28 | HPA:043010\_10 | stomach 2; glandular cells |
| Module 28 | HPA:024010\_10 | nasopharynx; respiratory epithelial cells |
| Module 28 | HPA:028010\_10 | parathyroid gland; glandular cells |
| Module 28 | HPA:005010\_10 | bronchus; respiratory epithelial cells |
| Module 28 | HPA:009030\_10 | colon; peripheral nerve/ganglion |
| Module 28 | HPA:002020\_10 | appendix; lymphoid tissue |
| Module 28 | HPA:008020\_10 | cervix, uterine; squamous epithelial cells |
| Module 28 | HPA:027020\_10 | pancreas; islets of langerhans |
| Module 28 | HPA:007020\_10 | cerebral cortex; glial cells |
| Module 28 | HPA:018020\_10 | hippocampus; neuronal cells |
| Module 28 | HPA:021020\_10 | liver; hepatocytes |
| Module 28 | HPA:009020\_10 | colon; glandular cells |
| Module 28 | HPA:023020\_10 | lymph node; non-germinal center cells |
| Module 28 | HPA:003010\_10 | bone marrow; hematopoietic cells |
| Module 28 | HPA:012010\_10 | endometrium 2; cells in endometrial stroma |
| Module 28 | HPA:017010\_10 | heart muscle; myocytes |
| Module 28 | HPA:030010\_10 | prostate; glandular cells |
| Module 28 | HPA:034010\_10 | skeletal muscle; myocytes |
| Module 28 | HPA:016010\_10 | gallbladder; glandular cells |
| Module 28 | HPA:045010\_10 | thyroid gland; glandular cells |
| Module 28 | HPA:027010\_10 | pancreas; exocrine glandular cells |
| Module 28 | HPA:035030\_10 | skin 1; keratinocytes |
| Module 28 | HPA:020010\_10 | lateral ventricle; glial cells |
| Module 29 | HP:0001639 | hypertrophic cardiomyopathy |
| Module 29 | OMIM:616295 | peeling skin with leukonychia, acral punctate keratoses, cheilitis,and knuckle pads; plack |
| Module 29 | OMIM:203800 | alstrom syndrome; alms; alss |
| Module 29 | OMIM:201450 | acyl-coa dehydrogenase, medium-chain, deficiency of; acadmd; acadm deficiency; mcad deficiency; mcadh deficiency; carnitine deficiency secondary to medium-chain acyl-coa dehydrogenasedeficiency |
| Module 29 | OMIM:614885 | peroxisome biogenesis disorder 11b; pbd11b |
| Module 29 | OMIM:609241 | schindler disease, type i; neuroaxonal dystrophy, schindler type; alpha-n-acetylgalactosaminidase deficiency, type i; naga deficiency, type ialpha-n-acetylgalactosaminidase deficiency, type iii, included; naga deficiency, type iii, included; schindler disease, type iii, included |
| Module 29 | OMIM:609242 | kanzaki disease; alpha-n-acetylgalactosaminidase deficiency, type ii; alpha-n-acetylgalactosaminidase deficiency, adult-onset; naga deficiency, type ii; schindler disease, type ii |
| Module 29 | OMIM:614883 | peroxisome biogenesis disorder 11a (zellweger); pbd11aperoxisome biogenesis disorder, complementation group 13, included;cg13, included; peroxisome biogenesis disorder, complementation group h, included;cgh, included |
| Module 29 | OMIM:609909 | cardiomyopathy, dilated, 1p; cmd1p |
| Module 29 | OMIM:613874 | cardiomyopathy, familial hypertrophic, 18; cmh18 |
| Module 30 | CORUM:5530 | homodimeric complex ltbr |
| Module 31 | OMIM:615841 | spermatogenic failure 13; spgf13 |
| Module 31 | TF:M00772\_1 | factor: irf; motif: bncrstttcanttyy; match class: 1 |
| Module 32 | - | - |
| Module 33 | OMIM:615422 | inclusion body myopathy with early-onset paget disease with or withoutfrontotemporal dementia 2; ibmpfd2; multisystem proteinopathy 2; msp2 |
| Module 34 | - | - |
| Module 35 | - | - |
| Module 36 | - | - |
| Module 37 | - | - |
| Module 38 | CORUM:2439 | itga8-itgb1 complex |
| Module 38 | OMIM:216550 | cohen syndrome; coh1; coh; hypotonia, obesity, and prominent incisors; pepper syndrome; chs1, formerly |
| Module 39 | MI:hsa-miR-577 | mi:hsa-mir-577 |
| Module 39 | OMIM:251880 | mitochondrial dna depletion syndrome 3 (hepatocerebral type); mtdps3 |
| Module 39 | OMIM:213980 | craniofacial dysmorphism, skeletal anomalies, and mental retardationsyndrome; cfsmr; cerebrofaciothoracic dysplasia |
| Module 40 | OMIM:260300 | parkinson disease 15, autosomal recessive early-onset; park15; parkinsonian-pyramidal syndrome; pkps; pallidopyramidal syndrome; pallido-pyramidal syndrome |
| Module 41 | - | - |
| Module 42 | GO:0045292 | mrna cis splicing, via spliceosome |
| Module 42 | OMIM:613507 | glycogen storage disease xv; gsd15; gsd xv; glycogenin deficiency; gyg1 deficiency |
| Module 42 | OMIM:112240 | cole-carpenter syndrome |
| Module 42 | OMIM:616199 | polyglucosan body myopathy 2; pgbm2 |
| Module 42 | TF:M02066\_0 | factor: pea3; motif: rccggaagyn; match class: 0 |
| Module 42 | TF:M02063\_0 | factor: c-ets-1; motif: accggawgtn; match class: 0 |
| Module 43 | OMIM:300844 | mental retardation, x-linked 19; mrx19 |
| Module 43 | OMIM:308700 | hypogonadotropic hypogonadism 1 with or without anosmia; hh1; kallmann syndrome 1; kal1; kms; hypogonadotropic hypogonadism and anosmia; hha; dysplasia olfactogenitalis of de morsier; anosmic hypogonadism |
| Module 43 | OMIM:275350 | transcobalamin ii deficiency; tc ii deficiency; tcn2 deficiency |
| Module 43 | OMIM:303600 | coffin-lowry syndrome; cls |
| Module 43 | OMIM:610297 | parkinson disease 13, autosomal dominant, susceptibility to; park13 |
| Module 43 | OMIM:211800 | calcification of joints and arteries; calja; arterial calcification due to deficiency of cd73; acdc |
| Module 44 | - | - |
| Module 45 | - | - |
| Module 46 | GO:0005773 | vacuole |
| Module 46 | GO:0000323 | lytic vacuole |
| Module 46 | GO:0005764 | lysosome |
| Module 46 | OMIM:254600 | myeloperoxidase deficiency; mpod; mpo deficiency |
| Module 46 | OMIM:614320 | pancreatic cancer, susceptibility to, 4; pnca4 |
| Module 46 | OMIM:166600 | osteopetrosis, autosomal dominant 2; opta2; osteopetrosis, autosomal dominant, type ii; marble bones, autosomal dominant; osteosclerosis fragilis generalisata; albers-schonberg disease, autosomal dominant |
| Module 46 | OMIM:611490 | osteopetrosis, autosomal recessive 4; optb4; osteopetrosis, infantile malignant 2 |
| Module 46 | OMIM:604370 | breast-ovarian cancer, familial, susceptibility to, 1; brovca1breast cancer, familial, susceptibility to, 1, included; ovarian cancer, familial, susceptibility to, 1, included |
| Module 46 | REAC:6796648 | tp53 regulates transcription of dna repair genes |
| Module 47 | - | - |
| Module 48 | GO:0008150 | biological\_process |
| Module 48 | GO:0065007 | biological regulation |
| Module 48 | GO:0065008 | regulation of biological quality |
| Module 48 | GO:0050878 | regulation of body fluid levels |
| Module 48 | GO:0007599 | hemostasis |
| Module 48 | GO:0042592 | homeostatic process |
| Module 48 | GO:0048878 | chemical homeostasis |
| Module 48 | GO:0050801 | ion homeostasis |
| Module 48 | GO:0065009 | regulation of molecular function |
| Module 48 | GO:0044093 | positive regulation of molecular function |
| Module 48 | GO:0002376 | immune system process |
| Module 48 | GO:0050896 | response to stimulus |
| Module 48 | GO:0042221 | response to chemical |
| Module 48 | GO:1901698 | response to nitrogen compound |
| Module 48 | GO:1901700 | response to oxygen-containing compound |
| Module 48 | GO:0010033 | response to organic substance |
| Module 48 | GO:0014070 | response to organic cyclic compound |
| Module 48 | GO:0033993 | response to lipid |
| Module 48 | GO:0070848 | response to growth factor |
| Module 48 | GO:0010035 | response to inorganic substance |
| Module 48 | GO:0042493 | response to drug |
| Module 48 | GO:0009719 | response to endogenous stimulus |
| Module 48 | GO:0071495 | cellular response to endogenous stimulus |
| Module 48 | GO:0009725 | response to hormone |
| Module 48 | GO:0010243 | response to organonitrogen compound |
| Module 48 | GO:1901652 | response to peptide |
| Module 48 | GO:0043434 | response to peptide hormone |
| Module 48 | GO:0032868 | response to insulin |
| Module 48 | GO:0006950 | response to stress |
| Module 48 | GO:0006952 | defense response |
| Module 48 | GO:0009611 | response to wounding |
| Module 48 | GO:0042060 | wound healing |
| Module 48 | GO:0009628 | response to abiotic stimulus |
| Module 48 | GO:0009605 | response to external stimulus |
| Module 48 | GO:0051179 | localization |
| Module 48 | GO:0051674 | localization of cell |
| Module 48 | GO:0033036 | macromolecule localization |
| Module 48 | GO:0008104 | protein localization |
| Module 48 | GO:0051234 | establishment of localization |
| Module 48 | GO:0006810 | transport |
| Module 48 | GO:0071702 | organic substance transport |
| Module 48 | GO:0016192 | vesicle-mediated transport |
| Module 48 | GO:0006897 | endocytosis |
| Module 48 | GO:0045184 | establishment of protein localization |
| Module 48 | GO:0015031 | protein transport |
| Module 48 | GO:0051641 | cellular localization |
| Module 48 | GO:0070727 | cellular macromolecule localization |
| Module 48 | GO:0034613 | cellular protein localization |
| Module 48 | GO:0051649 | establishment of localization in cell |
| Module 48 | GO:0046907 | intracellular transport |
| Module 48 | GO:0016482 | cytosolic transport |
| Module 48 | GO:0071840 | cellular component organization or biogenesis |
| Module 48 | GO:0008152 | metabolic process |
| Module 48 | GO:0044238 | primary metabolic process |
| Module 48 | GO:0071704 | organic substance metabolic process |
| Module 48 | GO:0043170 | macromolecule metabolic process |
| Module 48 | GO:0043412 | macromolecule modification |
| Module 48 | GO:0019538 | protein metabolic process |
| Module 48 | GO:0006508 | proteolysis |
| Module 48 | GO:0036211 | protein modification process |
| Module 48 | GO:0044267 | cellular protein metabolic process |
| Module 48 | GO:0006464 | cellular protein modification process |
| Module 48 | GO:0018193 | peptidyl-amino acid modification |
| Module 48 | GO:0005975 | carbohydrate metabolic process |
| Module 48 | GO:0009056 | catabolic process |
| Module 48 | GO:0023052 | signaling |
| Module 48 | GO:0044699 | single-organism process |
| Module 48 | GO:0044710 | single-organism metabolic process |
| Module 48 | GO:0044712 | single-organism catabolic process |
| Module 48 | GO:0044281 | small molecule metabolic process |
| Module 48 | GO:0008283 | cell proliferation |
| Module 48 | GO:1902578 | single-organism localization |
| Module 48 | GO:0044765 | single-organism transport |
| Module 48 | GO:1902582 | single-organism intracellular transport |
| Module 48 | GO:0006811 | ion transport |
| Module 48 | GO:1902580 | single-organism cellular localization |
| Module 48 | GO:0044700 | single organism signaling |
| Module 48 | GO:0040011 | locomotion |
| Module 48 | GO:0042330 | taxis |
| Module 48 | GO:0006935 | chemotaxis |
| Module 48 | GO:0009987 | cellular process |
| Module 48 | GO:0044763 | single-organism cellular process |
| Module 48 | GO:0006928 | movement of cell or subcellular component |
| Module 48 | GO:0048870 | cell motility |
| Module 48 | GO:0016477 | cell migration |
| Module 48 | GO:0008219 | cell death |
| Module 48 | GO:0012501 | programmed cell death |
| Module 48 | GO:0006915 | apoptotic process |
| Module 48 | GO:0007154 | cell communication |
| Module 48 | GO:0007267 | cell-cell signaling |
| Module 48 | GO:0051716 | cellular response to stimulus |
| Module 48 | GO:0070887 | cellular response to chemical stimulus |
| Module 48 | GO:1901699 | cellular response to nitrogen compound |
| Module 48 | GO:1901701 | cellular response to oxygen-containing compound |
| Module 48 | GO:0071310 | cellular response to organic substance |
| Module 48 | GO:0071407 | cellular response to organic cyclic compound |
| Module 48 | GO:0071396 | cellular response to lipid |
| Module 48 | GO:0032870 | cellular response to hormone stimulus |
| Module 48 | GO:0071417 | cellular response to organonitrogen compound |
| Module 48 | GO:1901653 | cellular response to peptide |
| Module 48 | GO:0071375 | cellular response to peptide hormone stimulus |
| Module 48 | GO:0044237 | cellular metabolic process |
| Module 48 | GO:0006793 | phosphorus metabolic process |
| Module 48 | GO:0006796 | phosphate-containing compound metabolic process |
| Module 48 | GO:0016310 | phosphorylation |
| Module 48 | GO:0006468 | protein phosphorylation |
| Module 48 | GO:0018105 | peptidyl-serine phosphorylation |
| Module 48 | GO:0016043 | cellular component organization |
| Module 48 | GO:0032501 | multicellular organismal process |
| Module 48 | GO:0044707 | single-multicellular organism process |
| Module 48 | GO:0050817 | coagulation |
| Module 48 | GO:0007596 | blood coagulation |
| Module 48 | GO:0032502 | developmental process |
| Module 48 | GO:0048856 | anatomical structure development |
| Module 48 | GO:0009888 | tissue development |
| Module 48 | GO:0044767 | single-organism developmental process |
| Module 48 | GO:0048869 | cellular developmental process |
| Module 48 | GO:0030154 | cell differentiation |
| Module 48 | GO:0048468 | cell development |
| Module 48 | GO:0007275 | multicellular organism development |
| Module 48 | GO:0048731 | system development |
| Module 48 | GO:0048513 | animal organ development |
| Module 48 | GO:0007399 | nervous system development |
| Module 48 | GO:0022008 | neurogenesis |
| Module 48 | GO:0048699 | generation of neurons |
| Module 48 | GO:0030182 | neuron differentiation |
| Module 48 | GO:0009653 | anatomical structure morphogenesis |
| Module 48 | GO:0048646 | anatomical structure formation involved in morphogenesis |
| Module 48 | GO:0050789 | regulation of biological process |
| Module 48 | GO:0048583 | regulation of response to stimulus |
| Module 48 | GO:0080134 | regulation of response to stress |
| Module 48 | GO:0032101 | regulation of response to external stimulus |
| Module 48 | GO:0048518 | positive regulation of biological process |
| Module 48 | GO:0048584 | positive regulation of response to stimulus |
| Module 48 | GO:0048519 | negative regulation of biological process |
| Module 48 | GO:0032879 | regulation of localization |
| Module 48 | GO:0051049 | regulation of transport |
| Module 48 | GO:0050794 | regulation of cellular process |
| Module 48 | GO:0080135 | regulation of cellular response to stress |
| Module 48 | GO:0048522 | positive regulation of cellular process |
| Module 48 | GO:0048523 | negative regulation of cellular process |
| Module 48 | GO:0051128 | regulation of cellular component organization |
| Module 48 | GO:0010646 | regulation of cell communication |
| Module 48 | GO:0060341 | regulation of cellular localization |
| Module 48 | GO:0032386 | regulation of intracellular transport |
| Module 48 | GO:1903649 | regulation of cytoplasmic transport |
| Module 48 | GO:1903827 | regulation of cellular protein localization |
| Module 48 | GO:0051270 | regulation of cellular component movement |
| Module 48 | GO:0007165 | signal transduction |
| Module 48 | GO:0007166 | cell surface receptor signaling pathway |
| Module 48 | GO:0007167 | enzyme linked receptor protein signaling pathway |
| Module 48 | GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway |
| Module 48 | GO:0019222 | regulation of metabolic process |
| Module 48 | GO:0050790 | regulation of catalytic activity |
| Module 48 | GO:0051336 | regulation of hydrolase activity |
| Module 48 | GO:0009893 | positive regulation of metabolic process |
| Module 48 | GO:0010604 | positive regulation of macromolecule metabolic process |
| Module 48 | GO:0043085 | positive regulation of catalytic activity |
| Module 48 | GO:0051347 | positive regulation of transferase activity |
| Module 48 | GO:0023051 | regulation of signaling |
| Module 48 | GO:0009966 | regulation of signal transduction |
| Module 48 | GO:0051174 | regulation of phosphorus metabolic process |
| Module 48 | GO:0019220 | regulation of phosphate metabolic process |
| Module 48 | GO:0042325 | regulation of phosphorylation |
| Module 48 | GO:0051246 | regulation of protein metabolic process |
| Module 48 | GO:0051247 | positive regulation of protein metabolic process |
| Module 48 | GO:0031325 | positive regulation of cellular metabolic process |
| Module 48 | GO:0010562 | positive regulation of phosphorus metabolic process |
| Module 48 | GO:0045937 | positive regulation of phosphate metabolic process |
| Module 48 | GO:0032268 | regulation of cellular protein metabolic process |
| Module 48 | GO:0048015 | phosphatidylinositol-mediated signaling |
| Module 48 | GO:0005575 | cellular\_component |
| Module 48 | GO:0005623 | cell |
| Module 48 | GO:0005576 | extracellular region |
| Module 48 | GO:0043226 | organelle |
| Module 48 | GO:0043227 | membrane-bounded organelle |
| Module 48 | GO:0031982 | vesicle |
| Module 48 | GO:0044421 | extracellular region part |
| Module 48 | GO:0043230 | extracellular organelle |
| Module 48 | GO:1903561 | extracellular vesicle |
| Module 48 | GO:0070062 | extracellular exosome |
| Module 48 | GO:0044464 | cell part |
| Module 48 | GO:0044463 | cell projection part |
| Module 48 | GO:0044459 | plasma membrane part |
| Module 48 | GO:0005622 | intracellular |
| Module 48 | GO:0044424 | intracellular part |
| Module 48 | GO:0005737 | cytoplasm |
| Module 48 | GO:0044444 | cytoplasmic part |
| Module 48 | GO:0005829 | cytosol |
| Module 48 | GO:0043229 | intracellular organelle |
| Module 48 | GO:0043231 | intracellular membrane-bounded organelle |
| Module 48 | GO:0012505 | endomembrane system |
| Module 48 | GO:0044422 | organelle part |
| Module 48 | GO:0044446 | intracellular organelle part |
| Module 48 | GO:0098805 | whole membrane |
| Module 48 | GO:0098589 | membrane region |
| Module 48 | GO:0098590 | plasma membrane region |
| Module 48 | GO:0030554 | adenyl nucleotide binding |
| Module 48 | GO:0032559 | adenyl ribonucleotide binding |
| Module 48 | GO:0003674 | molecular\_function |
| Module 48 | GO:0003824 | catalytic activity |
| Module 48 | GO:0005488 | binding |
| Module 48 | GO:0097367 | carbohydrate derivative binding |
| Module 48 | GO:0036094 | small molecule binding |
| Module 48 | GO:0043167 | ion binding |
| Module 48 | GO:0043168 | anion binding |
| Module 48 | GO:0005515 | protein binding |
| Module 48 | GO:0005102 | receptor binding |
| Module 48 | GO:0019899 | enzyme binding |
| Module 48 | GO:0016772 | transferase activity, transferring phosphorus-containing groups |
| Module 48 | GO:0016773 | phosphotransferase activity, alcohol group as acceptor |
| Module 48 | GO:0016301 | kinase activity |
| Module 48 | GO:0004672 | protein kinase activity |
| Module 48 | GO:0004674 | protein serine/threonine kinase activity |
| Module 48 | CORUM:2582 | chromosomal passenger complex cpc (cdca8, aurkb, birc5) |
| Module 48 | HPA:041010\_10 | spleen; cells in red pulp |
| Module 48 | HPA:042010\_10 | stomach 1; glandular cells |
| Module 48 | HPA:045010\_10 | thyroid gland; glandular cells |
| Module 48 | HPA:018010\_10 | hippocampus; glial cells |
| Module 48 | HPA:035020\_10 | skin 1; fibroblasts |
| Module 48 | HPA:019020\_10 | kidney; cells in tubules |
| Module 48 | HPA:035040\_10 | skin 1; melanocytes |
| Module 48 | HPA:007040\_10 | cerebral cortex; neuropil |
| Module 48 | HPA:036010\_10 | skin 2; epidermal cells |
| Module 48 | HPA:010010\_10 | duodenum; glandular cells |
| Module 48 | HPA:006010\_10 | cerebellum; purkinje cells |
| Module 48 | HPA:001010\_10 | adrenal gland; glandular cells |
| Module 48 | HPA:038010\_10 | smooth muscle; smooth muscle cells |
| Module 48 | HPA:035010\_10 | skin 1; langerhans |
| Module 48 | HPA:046030\_10 | tonsil; squamous epithelial cells |
| Module 48 | HPA:011010\_10 | endometrium 1; cells in endometrial stroma |
| Module 48 | HPA:046020\_10 | tonsil; non-germinal center cells |
| Module 48 | HPA:040030\_10 | soft tissue 2; fibroblasts |
| Module 48 | HPA:018020\_10 | hippocampus; neuronal cells |
| Module 48 | HPA:027010\_10 | pancreas; exocrine glandular cells |
| Module 48 | HPA:008020\_10 | cervix, uterine; squamous epithelial cells |
| Module 48 | HPA:030010\_10 | prostate; glandular cells |
| Module 48 | HPA:017010\_10 | heart muscle; myocytes |
| Module 48 | HPA:044010\_10 | testis; leydig cells |
| Module 48 | HPA:037010\_10 | small intestine; glandular cells |
| Module 48 | HPA:021010\_10 | liver; bile duct cells |
| Module 48 | HPA:015010\_10 | fallopian tube; glandular cells |
| Module 48 | HPA:026020\_10 | ovary; ovarian stroma cells |
| Module 48 | HPA:022010\_10 | lung; macrophages |
| Module 48 | HPA:016010\_10 | gallbladder; glandular cells |
| Module 48 | HPA:029020\_10 | placenta; trophoblastic cells |
| Module 48 | HPA:013010\_10 | epididymis; glandular cells |
| Module 48 | HPA:009030\_10 | colon; peripheral nerve/ganglion |
| Module 48 | HPA:046010\_10 | tonsil; germinal center cells |
| Module 48 | HPA:007020\_10 | cerebral cortex; glial cells |
| Module 48 | HPA:025010\_10 | oral mucosa; squamous epithelial cells |
| Module 48 | HPA:012010\_10 | endometrium 2; cells in endometrial stroma |
| Module 48 | HPA:034010\_10 | skeletal muscle; myocytes |
| Module 48 | HPA:006020\_10 | cerebellum; cells in granular layer |
| Module 48 | HPA:043010\_10 | stomach 2; glandular cells |
| Module 48 | HPA:032010\_10 | salivary gland; glandular cells |
| Module 48 | HPA:011020\_10 | endometrium 1; glandular cells |
| Module 48 | HPA:048010\_10 | vagina; squamous epithelial cells |
| Module 48 | HPA:019010\_10 | kidney; cells in glomeruli |
| Module 48 | HPA:022020\_10 | lung; pneumocytes |
| Module 48 | HPA:008010\_10 | cervix, uterine; glandular cells |
| Module 48 | HPA:021020\_10 | liver; hepatocytes |
| Module 48 | HPA:029010\_10 | placenta; decidual cells |
| Module 48 | HPA:040000 | soft tissue 2 |
| Module 48 | HPA:031010\_10 | rectum; glandular cells |
| Module 48 | HPA:014010\_10 | esophagus; squamous epithelial cells |
| Module 48 | HPA:007010\_10 | cerebral cortex; endothelial cells |
| Module 48 | HPA:009020\_10 | colon; glandular cells |
| Module 48 | HPA:047010\_10 | urinary bladder; urothelial cells |
| Module 48 | HPA:009010\_10 | colon; endothelial cells |
| Module 48 | HPA:035030\_10 | skin 1; keratinocytes |
| Module 48 | HPA:012020\_10 | endometrium 2; glandular cells |
| Module 48 | HPA:044020\_10 | testis; cells in seminiferous ducts |
| Module 48 | HPA:006030\_10 | cerebellum; cells in molecular layer |
| Module 48 | HPA:041020\_10 | spleen; cells in white pulp |
| Module 48 | HPA:027020\_10 | pancreas; islets of langerhans |
| Module 48 | KEGG:04510 | focal adhesion |
| Module 48 | MI:hsa-miR-150 | mi:hsa-mir-150 |
| Module 48 | MI:hsa-miR-554 | mi:hsa-mir-554 |
| Module 48 | REAC:382551 | transmembrane transport of small molecules |
| Module 48 | REAC:425407 | slc-mediated transmembrane transport |
| Module 48 | REAC:109582 | hemostasis |
| Module 48 | TF:M02036\_0 | factor: wt1; motif: cgcccccncn; match class: 0 |
| Module 48 | TF:M00196\_0 | factor: sp1; motif: ngggggcggggyn; match class: 0 |
| Module 48 | TF:M00196\_1 | factor: sp1; motif: ngggggcggggyn; match class: 1 |
| Module 48 | TF:M00378\_1 | factor: pax-4; motif: nnnnnycacccb; match class: 1 |
| Module 48 | TF:M01240\_1 | factor: ben; motif: cagcgrnv; match class: 1 |
| Module 48 | TF:M07344\_0 | factor: zic1; motif: vggggags; match class: 0 |
| Module 48 | TF:M01778\_0 | factor: plag1; motif: grggcnnhnnnrrggg; match class: 0 |
| Module 48 | TF:M00933\_0 | factor: sp1; motif: ccccgccccn; match class: 0 |
| Module 48 | TF:M00933\_1 | factor: sp1; motif: ccccgccccn; match class: 1 |
| Module 48 | TF:M07289\_0 | factor: gklf; motif: nnnrggngnggsn; match class: 0 |
| Module 48 | TF:M07289\_1 | factor: gklf; motif: nnnrggngnggsn; match class: 1 |
| Module 48 | TF:M01118\_0 | factor: wt1; motif: smcnccnsc; match class: 0 |
| Module 48 | TF:M01118\_1 | factor: wt1; motif: smcnccnsc; match class: 1 |
| Module 48 | TF:M04863\_0 | factor: tf3c-beta; motif: ccnggagggcttcctggaggag; match class: 0 |
| Module 48 | TF:M04863\_1 | factor: tf3c-beta; motif: ccnggagggcttcctggaggag; match class: 1 |
| Module 48 | TF:M07277\_0 | factor: bteb2; motif: rgggngkggn; match class: 0 |
| Module 48 | TF:M07277\_1 | factor: bteb2; motif: rgggngkggn; match class: 1 |
| Module 48 | TF:M07226\_0 | factor: sp1; motif: ncccckccccc; match class: 0 |
| Module 48 | TF:M04760\_0 | factor: gr; motif: tctcgcgag; match class: 0 |
| Module 48 | TF:M05386\_0 | factor: klf17; motif: ngggcgg; match class: 0 |
| Module 48 | TF:M05386\_1 | factor: klf17; motif: ngggcgg; match class: 1 |
| Module 48 | TF:M01199\_0 | factor: rnf96; motif: bcccgcrgcc; match class: 0 |
| Module 48 | TF:M01199\_1 | factor: rnf96; motif: bcccgcrgcc; match class: 1 |
| Module 48 | TF:M04687\_0 | factor: brca1; motif: tmtcgcgag; match class: 0 |
| Module 48 | TF:M04687\_1 | factor: brca1; motif: tmtcgcgag; match class: 1 |
| Module 48 | TF:M07062\_0 | factor: rreb1; motif: grsdsgggktgggkgg; match class: 0 |
| Module 48 | TF:M00695\_0 | factor: etf; motif: gvggmgg; match class: 0 |
| Module 48 | TF:M00695\_1 | factor: etf; motif: gvggmgg; match class: 1 |
| Module 48 | TF:M03893\_0 | factor: wt1; motif: gngggggcgggg; match class: 0 |
| Module 48 | TF:M03893\_1 | factor: wt1; motif: gngggggcgggg; match class: 1 |
| Module 48 | TF:M01104\_0 | factor: movo-b; motif: gnggggg; match class: 0 |
| Module 48 | TF:M01104\_1 | factor: movo-b; motif: gnggggg; match class: 1 |
| Module 48 | TF:M00931\_0 | factor: sp1; motif: ggggcggggc; match class: 0 |
| Module 48 | TF:M00931\_1 | factor: sp1; motif: ggggcggggc; match class: 1 |
| Module 48 | TF:M02089\_0 | factor: e2f-3; motif: ggcgggn; match class: 0 |
| Module 48 | TF:M02089\_1 | factor: e2f-3; motif: ggcgggn; match class: 1 |
| Module 48 | TF:M05439\_0 | factor: rreb-1; motif: gggwcsa; match class: 0 |
| Module 48 | TF:M05439\_1 | factor: rreb-1; motif: gggwcsa; match class: 1 |
| Module 48 | TF:M07208\_0 | factor: egr1; motif: ncnccgcccccgcn; match class: 0 |
| Module 48 | TF:M07039\_0 | factor: etf; motif: ccccgccccyn; match class: 0 |
| Module 48 | TF:M07039\_1 | factor: etf; motif: ccccgccccyn; match class: 1 |
| Module 48 | TF:M00333\_0 | factor: zf5; motif: nrngngcgcgcwn; match class: 0 |
| Module 48 | TF:M00333\_1 | factor: zf5; motif: nrngngcgcgcwn; match class: 1 |
| Module 48 | TF:M00986\_0 | factor: churchill; motif: cgggnn; match class: 0 |
| Module 48 | TF:M00986\_1 | factor: churchill; motif: cgggnn; match class: 1 |
| Module 48 | TF:M05499\_0 | factor: lklf; motif: ngggcgg; match class: 0 |
| Module 48 | TF:M05499\_1 | factor: lklf; motif: ngggcgg; match class: 1 |
| Module 48 | TF:M02023\_0 | factor: maz; motif: nkgggaggggrggr; match class: 0 |
| Module 48 | TF:M07129\_0 | factor: sp2; motif: gycccgccycynnnn; match class: 0 |
| Module 48 | TF:M07129\_1 | factor: sp2; motif: gycccgccycynnnn; match class: 1 |
| Module 48 | TF:M00800\_0 | factor: ap-2; motif: gsccscrggcnrnrnn; match class: 0 |
| Module 48 | TF:M01721\_0 | factor: pur1; motif: gggncagnn; match class: 0 |
| Module 48 | TF:M01858\_0 | factor: ap-2beta; motif: gcnnnggscngvgggn; match class: 0 |
| Module 48 | TF:M01858\_1 | factor: ap-2beta; motif: gcnnnggscngvgggn; match class: 1 |
| Module 48 | TF:M00649\_0 | factor: maz; motif: ggggaggg; match class: 0 |
| Module 48 | TF:M00649\_1 | factor: maz; motif: ggggaggg; match class: 1 |
| Module 48 | TF:M00008\_0 | factor: sp1; motif: ggggcggggt; match class: 0 |
| Module 48 | TF:M00008\_1 | factor: sp1; motif: ggggcggggt; match class: 1 |
| Module 48 | TF:M00189\_0 | factor: ap-2; motif: mkcccscnggcg; match class: 0 |
| Module 48 | TF:M00189\_1 | factor: ap-2; motif: mkcccscnggcg; match class: 1 |
| Module 48 | TF:M07250\_0 | factor: e2f1; motif: nnnsscgcsaann; match class: 0 |
| Module 48 | TF:M07250\_1 | factor: e2f1; motif: nnnsscgcsaann; match class: 1 |
| Module 48 | TF:M04595\_1 | factor: sall2; motif: gggtggg; match class: 1 |
| Module 48 | TF:M01857\_0 | factor: ap-2alpha; motif: ngccysnngsn; match class: 0 |
| Module 48 | TF:M01857\_1 | factor: ap-2alpha; motif: ngccysnngsn; match class: 1 |
| Module 48 | TF:M07348\_0 | factor: ap-2alpha; motif: nsccncrggsn; match class: 0 |
| Module 48 | TF:M07348\_1 | factor: ap-2alpha; motif: nsccncrggsn; match class: 1 |
| Module 48 | TF:M03807\_0 | factor: sp2; motif: gnngggggcggggsn; match class: 0 |
| Module 48 | TF:M03807\_1 | factor: sp2; motif: gnngggggcggggsn; match class: 1 |
| Module 48 | TF:M01100\_1 | factor: lrf; motif: vnnrmcccc; match class: 1 |
| Module 48 | TF:M05332\_0 | factor: sp2; motif: wgggcgg; match class: 0 |
| Module 48 | TF:M05361\_0 | factor: sp6; motif: wgggcgg; match class: 0 |
| Module 48 | TF:M00932\_0 | factor: sp1; motif: nnggggcggggnn; match class: 0 |
| Module 48 | TF:M00932\_1 | factor: sp1; motif: nnggggcggggnn; match class: 1 |
| Module 48 | TF:M07354\_0 | factor: egr-1; motif: gcgggggcgg; match class: 0 |
| Module 48 | TF:M07354\_1 | factor: egr-1; motif: gcgggggcgg; match class: 1 |
| Module 48 | TF:M03567\_0 | factor: sp2; motif: nysgccccgcccccy; match class: 0 |
| Module 48 | TF:M03567\_1 | factor: sp2; motif: nysgccccgcccccy; match class: 1 |
| Module 48 | TF:M05444\_0 | factor: cpbp; motif: ngggcgg; match class: 0 |
| Module 48 | TF:M07040\_0 | factor: gklf; motif: nnrrgrrngnsnnn; match class: 0 |
| Module 48 | TF:M07040\_1 | factor: gklf; motif: nnrrgrrngnsnnn; match class: 1 |
| Module 48 | TF:M00915\_0 | factor: ap-2; motif: snnnccncaggcn; match class: 0 |
| Module 48 | TF:M07329\_0 | factor: osx; motif: ccncccccnnn; match class: 0 |
| Module 48 | TF:M07329\_1 | factor: osx; motif: ccncccccnnn; match class: 1 |
| Module 48 | TF:M00982\_0 | factor: krox; motif: cccgcccccrcccc; match class: 0 |
| Module 48 | TF:M00982\_1 | factor: krox; motif: cccgcccccrcccc; match class: 1 |
| Module 48 | TF:M03814\_0 | factor: bteb2; motif: gnagggggngggssnn; match class: 0 |
| Module 48 | TF:M01873\_0 | factor: egr-1; motif: gcgggggcgg; match class: 0 |
| Module 48 | TF:M00430\_0 | factor: e2f-1; motif: nttsgcgg; match class: 0 |
| Module 48 | TF:M03920\_0 | factor: sp1; motif: rccmcrcccmc; match class: 0 |
| Module 48 | TF:M00803\_0 | factor: e2f; motif: ggcgsg; match class: 0 |
| Module 48 | TF:M00803\_1 | factor: e2f; motif: ggcgsg; match class: 1 |
| Module 48 | TF:M01175\_0 | factor: ckrox; motif: sccctcccc; match class: 0 |
| Module 48 | TF:M01175\_1 | factor: ckrox; motif: sccctcccc; match class: 1 |
| Module 48 | TF:M02281\_0 | factor: sp1; motif: cccckccccc; match class: 0 |
| Module 48 | TF:M02281\_1 | factor: sp1; motif: cccckccccc; match class: 1 |
| Module 48 | TF:M07063\_0 | factor: sp1; motif: ggggcggggc; match class: 0 |
| Module 48 | TF:M07063\_1 | factor: sp1; motif: ggggcggggc; match class: 1 |
| Module 48 | TF:M00716\_0 | factor: zf5; motif: gsgcgcgr; match class: 0 |
| Module 48 | TF:M00716\_1 | factor: zf5; motif: gsgcgcgr; match class: 1 |
| Module 48 | TF:M07395\_0 | factor: sp1; motif: nggggcggggn; match class: 0 |
| Module 48 | TF:M07395\_1 | factor: sp1; motif: nggggcggggn; match class: 1 |
| Module 49 | - | - |
| Module 50 | MI:hsa-miR-449b | mi:hsa-mir-449b |
| Module 50 | OMIM:277180 | vas deferens, congenital bilateral aplasia of; cbavd; cavd |
| Module 51 | MI:hsa-miR-629\* | mi:hsa-mir-629\* |
| Module 51 | MI:hsa-miR-25\* | mi:hsa-mir-25\* |
| Module 51 | MI:hsa-miR-32\* | mi:hsa-mir-32\* |
| Module 51 | MI:hsa-miR-377\* | mi:hsa-mir-377\* |
| Module 52 | GO:0072347 | response to anesthetic |
| Module 52 | GO:1903927 | response to cyanide |
| Module 52 | GO:1903928 | cellular response to cyanide |
| Module 52 | GO:0021502 | neural fold elevation formation |
| Module 52 | CORUM:5382 | arnt-hif1a complex |
| Module 52 | HPA:007040\_13 | cerebral cortex; neuropil |
| Module 52 | REAC:8849473 | ptk6 expression |
| Module 52 | REAC:1234162 | oxygen-dependent asparagine hydroxylation of hypoxia-inducible factor alpha |
| Module 53 | HP:0004607 | anterior beaking of lower thoracic vertebrae |
| Module 53 | KEGG:00531 | glycosaminoglycan degradation |
| Module 53 | OMIM:253220 | mucopolysaccharidosis, type vii; mps7; mps vii; sly syndrome; beta-glucuronidase deficiency; gusb deficiency |
| Module 53 | TF:M00237\_0 | factor: ahr:arnt; motif: grgkatygcgtgmcwnscc; match class: 0 |
| Module 54 | GO:0030154 | cell differentiation |
| Module 54 | GO:0030510 | regulation of bmp signaling pathway |
| Module 54 | GO:0030514 | negative regulation of bmp signaling pathway |
| Module 54 | GO:0008150 | biological\_process |
| Module 54 | GO:0023052 | signaling |
| Module 54 | GO:0022610 | biological adhesion |
| Module 54 | GO:0007155 | cell adhesion |
| Module 54 | GO:0002376 | immune system process |
| Module 54 | GO:0044700 | single organism signaling |
| Module 54 | GO:0007154 | cell communication |
| Module 54 | GO:0007165 | signal transduction |
| Module 54 | GO:0007166 | cell surface receptor signaling pathway |
| Module 54 | GO:0007167 | enzyme linked receptor protein signaling pathway |
| Module 54 | GO:0042325 | regulation of phosphorylation |
| Module 54 | GO:0006468 | protein phosphorylation |
| Module 54 | GO:0001932 | regulation of protein phosphorylation |
| Module 54 | GO:0043549 | regulation of kinase activity |
| Module 54 | GO:0045859 | regulation of protein kinase activity |
| Module 54 | GO:0071900 | regulation of protein serine/threonine kinase activity |
| Module 54 | GO:0023014 | signal transduction by protein phosphorylation |
| Module 54 | GO:0000165 | mapk cascade |
| Module 54 | GO:0043408 | regulation of mapk cascade |
| Module 54 | GO:0006952 | defense response |
| Module 54 | GO:0070887 | cellular response to chemical stimulus |
| Module 54 | GO:0010033 | response to organic substance |
| Module 54 | GO:0070848 | response to growth factor |
| Module 54 | GO:0071772 | response to bmp |
| Module 54 | GO:0071310 | cellular response to organic substance |
| Module 54 | GO:0071363 | cellular response to growth factor stimulus |
| Module 54 | GO:0071773 | cellular response to bmp stimulus |
| Module 54 | GO:0043062 | extracellular structure organization |
| Module 54 | GO:0030198 | extracellular matrix organization |
| Module 54 | GO:0005615 | extracellular space |
| Module 54 | KEGG:05145 | toxoplasmosis |
| Module 54 | KEGG:04670 | leukocyte transendothelial migration |
| Module 54 | REAC:1280215 | cytokine signaling in immune system |
| Module 54 | REAC:449147 | signaling by interleukins |
| Module 55 | OMIM:312600 | retinitis pigmentosa 2; rp2 |
| Module 56 | GO:0051702 | interaction with symbiont |
| Module 56 | GO:0051851 | modification by host of symbiont morphology or physiology |
| Module 56 | OMIM:614608 | mental retardation, autosomal dominant 15; mrd15 |
| Module 56 | OMIM:609322 | rhabdoid tumor predisposition syndrome 1; rtps1; brain tumor, posterior fossa, of infancy, familialmalignant rhabdoid tumor, somatic, included; rhabdoid tumor, included; rdt, included; teratoid tumor, atypical, included; at/rt, included |
| Module 57 | - | - |
| Module 58 | OMIM:219500 | cystathioninuria; cystathionase deficiency |
| Module 59 | - | - |
| Module 60 | OMIM:616559 | noonan syndrome 9; ns9 |
| Module 61 | GO:0003014 | renal system process |
| Module 61 | OMIM:614131 | focal segmental glomerulosclerosis 6; fsgs6; glomerulosclerosis, focal segmental, 6 |
| Module 61 | OMIM:262850 | alpha-2-plasmin inhibitor deficiency; antiplasmin deficiency; plasmin inhibitor deficiency |
| Module 62 | OMIM:215140 | greenberg dysplasia; grbgd; hydrops-ectopic calcification-moth-eaten skeletal dysplasia; hem skeletal dysplasia; moth-eaten skeletal dysplasia; chondrodystrophy, hydropic and prenatally lethal type |
| Module 62 | OMIM:169400 | pelger-huet anomaly; pha |
| Module 62 | OMIM:613862 | retinitis pigmentosa 38; rp38; rod-cone dystrophy, childhood-onset |
| Module 62 | OMIM:614701 | cornelia de lange syndrome 4; cdls4 |
| Module 62 | OMIM:616517 | achromatopsia 7; achm7 |
| Module 62 | OMIM:109720 | primary biliary cirrhosis |
| Module 62 | OMIM:613471 | reynolds syndrome; primary biliary cirrhosis, scleroderma, raynaud disease, and telangiectasia |
| Module 62 | OMIM:615160 | mitochondrial complex iii deficiency, nuclear type 5; mc3dn5 |
| Module 63 | HP:0006642 | large sternal ossification centers |
| Module 63 | HP:0006048 | distal widening of metacarpals |
| Module 63 | HP:0009845 | bullet-shaped middle phalanges of the hand |
| Module 63 | OMIM:614753 | sotos syndrome 2; sotos2 |
| Module 63 | OMIM:602535 | marshall-smith syndrome; mrshss |
| Module 64 | GO:1990426 | homologous recombination-dependent replication fork processing |
| Module 64 | GO:1902521 | response to etoposide |
| Module 64 | GO:1990414 | replication-born double-strand break repair via sister chromatid exchange |
| Module 64 | CORUM:2824 | brca1-rad51 complex |
| Module 64 | CORUM:5683 | hrad51c-hxrcc3 complex |
| Module 64 | OMIM:614508 | mirror movements 2; mrmv2 |
| Module 65 | MI:hsa-miR-553 | mi:hsa-mir-553 |
| Module 65 | OMIM:615758 | immunodeficiency 22; imd22 |
| Module 65 | OMIM:608688 | aicar transformylase/imp cyclohydrolase deficiency; atic deficiency; aica-ribosuria due to atic deficiency |
| Module 65 | OMIM:300953 | trichothiodystrophy 5, nonphotosensitive; ttd5 |
| Module 65 | OMIM:138900 | serum uric acid concentration quantitative trait loci |
| Module 65 | OMIM:128100 | dystonia 1, torsion, autosomal dominant; dyt1; dystonia musculorum deformans 1; early-onset torsion dystonia; eotd |
| Module 65 | OMIM:614490 | blood group, junior system; jr |
| Module 66 | GO:0002223 | stimulatory c-type lectin receptor signaling pathway |
| Module 66 | GO:0007167 | enzyme linked receptor protein signaling pathway |
| Module 66 | GO:0033365 | protein localization to organelle |
| Module 66 | GO:0072594 | establishment of protein localization to organelle |
| Module 66 | GO:0002474 | antigen processing and presentation of peptide antigen via mhc class i |
| Module 66 | GO:0007264 | small gtpase mediated signal transduction |
| Module 66 | GO:0051437 | positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition |
| Module 66 | GO:0051649 | establishment of localization in cell |
| Module 66 | GO:0046907 | intracellular transport |
| Module 66 | GO:1902582 | single-organism intracellular transport |
| Module 66 | GO:0006886 | intracellular protein transport |
| Module 66 | GO:0006605 | protein targeting |
| Module 66 | GO:0038061 | nik/nf-kappab signaling |
| Module 66 | GO:0071156 | regulation of cell cycle arrest |
| Module 66 | GO:0070987 | error-free translesion synthesis |
| Module 66 | GO:0000209 | protein polyubiquitination |
| Module 66 | GO:0006367 | transcription initiation from rna polymerase ii promoter |
| Module 66 | GO:0070647 | protein modification by small protein conjugation or removal |
| Module 66 | GO:1903320 | regulation of protein modification by small protein conjugation or removal |
| Module 66 | GO:1903322 | positive regulation of protein modification by small protein conjugation or removal |
| Module 66 | GO:0032446 | protein modification by small protein conjugation |
| Module 66 | GO:0051704 | multi-organism process |
| Module 66 | GO:0044419 | interspecies interaction between organisms |
| Module 66 | GO:0044403 | symbiosis, encompassing mutualism through parasitism |
| Module 66 | GO:0065008 | regulation of biological quality |
| Module 66 | GO:0071840 | cellular component organization or biogenesis |
| Module 66 | GO:0009987 | cellular process |
| Module 66 | GO:0044764 | multi-organism cellular process |
| Module 66 | GO:0016032 | viral process |
| Module 66 | GO:0016043 | cellular component organization |
| Module 66 | GO:0051716 | cellular response to stimulus |
| Module 66 | GO:0033554 | cellular response to stress |
| Module 66 | GO:0006974 | cellular response to dna damage stimulus |
| Module 66 | GO:0051340 | regulation of ligase activity |
| Module 66 | GO:0042221 | response to chemical |
| Module 66 | GO:0070887 | cellular response to chemical stimulus |
| Module 66 | GO:0010033 | response to organic substance |
| Module 66 | GO:0071310 | cellular response to organic substance |
| Module 66 | GO:0044699 | single-organism process |
| Module 66 | GO:0044763 | single-organism cellular process |
| Module 66 | GO:0008219 | cell death |
| Module 66 | GO:0012501 | programmed cell death |
| Module 66 | GO:0010941 | regulation of cell death |
| Module 66 | GO:0043067 | regulation of programmed cell death |
| Module 66 | GO:0042981 | regulation of apoptotic process |
| Module 66 | GO:0007049 | cell cycle |
| Module 66 | GO:0000278 | mitotic cell cycle |
| Module 66 | GO:0022402 | cell cycle process |
| Module 66 | GO:0044770 | cell cycle phase transition |
| Module 66 | GO:0044843 | cell cycle g1/s phase transition |
| Module 66 | GO:1903047 | mitotic cell cycle process |
| Module 66 | GO:0044772 | mitotic cell cycle phase transition |
| Module 66 | GO:0000082 | g1/s transition of mitotic cell cycle |
| Module 66 | GO:0009719 | response to endogenous stimulus |
| Module 66 | GO:0071495 | cellular response to endogenous stimulus |
| Module 66 | GO:0009725 | response to hormone |
| Module 66 | GO:0032870 | cellular response to hormone stimulus |
| Module 66 | GO:0008152 | metabolic process |
| Module 66 | GO:0044238 | primary metabolic process |
| Module 66 | GO:0009058 | biosynthetic process |
| Module 66 | GO:0009056 | catabolic process |
| Module 66 | GO:0071704 | organic substance metabolic process |
| Module 66 | GO:0043170 | macromolecule metabolic process |
| Module 66 | GO:0010467 | gene expression |
| Module 66 | GO:0019538 | protein metabolic process |
| Module 66 | GO:1901575 | organic substance catabolic process |
| Module 66 | GO:0009057 | macromolecule catabolic process |
| Module 66 | GO:0030163 | protein catabolic process |
| Module 66 | GO:1901576 | organic substance biosynthetic process |
| Module 66 | GO:0009059 | macromolecule biosynthetic process |
| Module 66 | GO:1901360 | organic cyclic compound metabolic process |
| Module 66 | GO:1901362 | organic cyclic compound biosynthetic process |
| Module 66 | GO:0006807 | nitrogen compound metabolic process |
| Module 66 | GO:1901564 | organonitrogen compound metabolic process |
| Module 66 | GO:1901566 | organonitrogen compound biosynthetic process |
| Module 66 | GO:0044237 | cellular metabolic process |
| Module 66 | GO:0044248 | cellular catabolic process |
| Module 66 | GO:0044260 | cellular macromolecule metabolic process |
| Module 66 | GO:0044267 | cellular protein metabolic process |
| Module 66 | GO:0044265 | cellular macromolecule catabolic process |
| Module 66 | GO:0043632 | modification-dependent macromolecule catabolic process |
| Module 66 | GO:0044257 | cellular protein catabolic process |
| Module 66 | GO:0006259 | dna metabolic process |
| Module 66 | GO:0022616 | dna strand elongation |
| Module 66 | GO:0006725 | cellular aromatic compound metabolic process |
| Module 66 | GO:0046483 | heterocycle metabolic process |
| Module 66 | GO:0034641 | cellular nitrogen compound metabolic process |
| Module 66 | GO:0006139 | nucleobase-containing compound metabolic process |
| Module 66 | GO:0044249 | cellular biosynthetic process |
| Module 66 | GO:0019438 | aromatic compound biosynthetic process |
| Module 66 | GO:0018130 | heterocycle biosynthetic process |
| Module 66 | GO:0044271 | cellular nitrogen compound biosynthetic process |
| Module 66 | GO:0034654 | nucleobase-containing compound biosynthetic process |
| Module 66 | GO:0034645 | cellular macromolecule biosynthetic process |
| Module 66 | GO:0006260 | dna replication |
| Module 66 | GO:0006261 | dna-dependent dna replication |
| Module 66 | GO:0006271 | dna strand elongation involved in dna replication |
| Module 66 | GO:0048519 | negative regulation of biological process |
| Module 66 | GO:0051352 | negative regulation of ligase activity |
| Module 66 | GO:0048518 | positive regulation of biological process |
| Module 66 | GO:0048522 | positive regulation of cellular process |
| Module 66 | GO:0019222 | regulation of metabolic process |
| Module 66 | GO:0060255 | regulation of macromolecule metabolic process |
| Module 66 | GO:0010468 | regulation of gene expression |
| Module 66 | GO:0010608 | posttranscriptional regulation of gene expression |
| Module 66 | GO:0043487 | regulation of rna stability |
| Module 66 | GO:0043488 | regulation of mrna stability |
| Module 66 | GO:0080090 | regulation of primary metabolic process |
| Module 66 | GO:0051246 | regulation of protein metabolic process |
| Module 66 | GO:0030162 | regulation of proteolysis |
| Module 66 | GO:0009889 | regulation of biosynthetic process |
| Module 66 | GO:0051171 | regulation of nitrogen compound metabolic process |
| Module 66 | GO:0009894 | regulation of catabolic process |
| Module 66 | GO:0042176 | regulation of protein catabolic process |
| Module 66 | GO:0045732 | positive regulation of protein catabolic process |
| Module 66 | GO:0009893 | positive regulation of metabolic process |
| Module 66 | GO:0051173 | positive regulation of nitrogen compound metabolic process |
| Module 66 | GO:0010604 | positive regulation of macromolecule metabolic process |
| Module 66 | GO:0009891 | positive regulation of biosynthetic process |
| Module 66 | GO:0051276 | chromosome organization |
| Module 66 | GO:0032200 | telomere organization |
| Module 66 | GO:0000723 | telomere maintenance |
| Module 66 | GO:0000722 | telomere maintenance via recombination |
| Module 66 | GO:0048523 | negative regulation of cellular process |
| Module 66 | GO:0031323 | regulation of cellular metabolic process |
| Module 66 | GO:0031326 | regulation of cellular biosynthetic process |
| Module 66 | GO:0031329 | regulation of cellular catabolic process |
| Module 66 | GO:0031325 | positive regulation of cellular metabolic process |
| Module 66 | GO:0045935 | positive regulation of nucleobase-containing compound metabolic process |
| Module 66 | GO:0031331 | positive regulation of cellular catabolic process |
| Module 66 | GO:0031328 | positive regulation of cellular biosynthetic process |
| Module 66 | GO:0032268 | regulation of cellular protein metabolic process |
| Module 66 | GO:1903362 | regulation of cellular protein catabolic process |
| Module 66 | GO:1903364 | positive regulation of cellular protein catabolic process |
| Module 66 | GO:0006518 | peptide metabolic process |
| Module 66 | GO:0043043 | peptide biosynthetic process |
| Module 66 | GO:0006412 | translation |
| Module 66 | GO:0006413 | translational initiation |
| Module 66 | GO:0043434 | response to peptide hormone |
| Module 66 | GO:0032868 | response to insulin |
| Module 66 | GO:0072331 | signal transduction by p53 class mediator |
| Module 66 | GO:0030330 | dna damage response, signal transduction by p53 class mediator |
| Module 66 | GO:0010948 | negative regulation of cell cycle process |
| Module 66 | GO:1901988 | negative regulation of cell cycle phase transition |
| Module 66 | GO:1901991 | negative regulation of mitotic cell cycle phase transition |
| Module 66 | GO:0044783 | g1 dna damage checkpoint |
| Module 66 | GO:1902806 | regulation of cell cycle g1/s phase transition |
| Module 66 | GO:1902807 | negative regulation of cell cycle g1/s phase transition |
| Module 66 | GO:2000134 | negative regulation of g1/s transition of mitotic cell cycle |
| Module 66 | GO:1901653 | cellular response to peptide |
| Module 66 | GO:0071375 | cellular response to peptide hormone stimulus |
| Module 66 | GO:0032869 | cellular response to insulin stimulus |
| Module 66 | GO:0008286 | insulin receptor signaling pathway |
| Module 66 | GO:0051603 | proteolysis involved in cellular protein catabolic process |
| Module 66 | GO:1903050 | regulation of proteolysis involved in cellular protein catabolic process |
| Module 66 | GO:0010498 | proteasomal protein catabolic process |
| Module 66 | GO:0061136 | regulation of proteasomal protein catabolic process |
| Module 66 | GO:0019941 | modification-dependent protein catabolic process |
| Module 66 | GO:0006511 | ubiquitin-dependent protein catabolic process |
| Module 66 | GO:0043161 | proteasome-mediated ubiquitin-dependent protein catabolic process |
| Module 66 | GO:0031145 | anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process |
| Module 66 | GO:1903052 | positive regulation of proteolysis involved in cellular protein catabolic process |
| Module 66 | GO:0007093 | mitotic cell cycle checkpoint |
| Module 66 | GO:0044774 | mitotic dna integrity checkpoint |
| Module 66 | GO:0044773 | mitotic dna damage checkpoint |
| Module 66 | GO:0044819 | mitotic g1/s transition checkpoint |
| Module 66 | GO:0031571 | mitotic g1 dna damage checkpoint |
| Module 66 | GO:0006281 | dna repair |
| Module 66 | GO:0006289 | nucleotide-excision repair |
| Module 66 | GO:0070911 | global genome nucleotide-excision repair |
| Module 66 | GO:0006302 | double-strand break repair |
| Module 66 | GO:0006284 | base-excision repair |
| Module 66 | GO:0072395 | signal transduction involved in cell cycle checkpoint |
| Module 66 | GO:0072401 | signal transduction involved in dna integrity checkpoint |
| Module 66 | GO:0072422 | signal transduction involved in dna damage checkpoint |
| Module 66 | GO:1902400 | intracellular signal transduction involved in g1 dna damage checkpoint |
| Module 66 | GO:0072413 | signal transduction involved in mitotic cell cycle checkpoint |
| Module 66 | GO:1902403 | signal transduction involved in mitotic dna integrity checkpoint |
| Module 66 | GO:1902402 | signal transduction involved in mitotic dna damage checkpoint |
| Module 66 | GO:0072431 | signal transduction involved in mitotic g1 dna damage checkpoint |
| Module 66 | GO:0006977 | dna damage response, signal transduction by p53 class mediator resulting in cell cycle arrest |
| Module 66 | GO:0031396 | regulation of protein ubiquitination |
| Module 66 | GO:0051438 | regulation of ubiquitin-protein transferase activity |
| Module 66 | GO:0051439 | regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle |
| Module 66 | GO:0051444 | negative regulation of ubiquitin-protein transferase activity |
| Module 66 | GO:0051436 | negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle |
| Module 66 | GO:2000058 | regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process |
| Module 66 | GO:0006521 | regulation of cellular amino acid metabolic process |
| Module 66 | GO:0031398 | positive regulation of protein ubiquitination |
| Module 66 | GO:0032201 | telomere maintenance via semi-conservative replication |
| Module 66 | GO:0032991 | macromolecular complex |
| Module 66 | GO:0043234 | protein complex |
| Module 66 | GO:0031974 | membrane-enclosed lumen |
| Module 66 | GO:0005576 | extracellular region |
| Module 66 | GO:0043226 | organelle |
| Module 66 | GO:0043228 | non-membrane-bounded organelle |
| Module 66 | GO:0043227 | membrane-bounded organelle |
| Module 66 | GO:0031982 | vesicle |
| Module 66 | GO:0044422 | organelle part |
| Module 66 | GO:0043233 | organelle lumen |
| Module 66 | GO:0044421 | extracellular region part |
| Module 66 | GO:0043230 | extracellular organelle |
| Module 66 | GO:1903561 | extracellular vesicle |
| Module 66 | GO:0070062 | extracellular exosome |
| Module 66 | GO:0005622 | intracellular |
| Module 66 | GO:0044424 | intracellular part |
| Module 66 | GO:0005737 | cytoplasm |
| Module 66 | GO:0044444 | cytoplasmic part |
| Module 66 | GO:0005829 | cytosol |
| Module 66 | GO:0043229 | intracellular organelle |
| Module 66 | GO:0043232 | intracellular non-membrane-bounded organelle |
| Module 66 | GO:0005694 | chromosome |
| Module 66 | GO:0044446 | intracellular organelle part |
| Module 66 | GO:0070013 | intracellular organelle lumen |
| Module 66 | GO:0044427 | chromosomal part |
| Module 66 | GO:0098687 | chromosomal region |
| Module 66 | GO:0000781 | chromosome, telomeric region |
| Module 66 | GO:0005657 | replication fork |
| Module 66 | GO:0043231 | intracellular membrane-bounded organelle |
| Module 66 | GO:0005634 | nucleus |
| Module 66 | GO:0044428 | nuclear part |
| Module 66 | GO:0031981 | nuclear lumen |
| Module 66 | GO:0005654 | nucleoplasm |
| Module 66 | GO:0000228 | nuclear chromosome |
| Module 66 | GO:0044454 | nuclear chromosome part |
| Module 66 | GO:0000784 | nuclear chromosome, telomeric region |
| Module 66 | GO:0000502 | proteasome complex |
| Module 66 | GO:0048770 | pigment granule |
| Module 66 | GO:0042470 | melanosome |
| Module 66 | GO:1901363 | heterocyclic compound binding |
| Module 66 | GO:0097159 | organic cyclic compound binding |
| Module 66 | GO:0003676 | nucleic acid binding |
| Module 66 | GO:0003723 | rna binding |
| Module 66 | GO:0044822 | poly(a) rna binding |
| Module 66 | GO:0005515 | protein binding |
| Module 66 | GO:0019899 | enzyme binding |
| Module 66 | GO:0044877 | macromolecular complex binding |
| Module 66 | GO:0044769 | atpase activity, coupled to transmembrane movement of ions, rotational mechanism |
| Module 66 | GO:0046933 | proton-transporting atp synthase activity, rotational mechanism |
| Module 66 | GO:0003684 | damaged dna binding |
| Module 66 | GO:0016817 | hydrolase activity, acting on acid anhydrides |
| Module 66 | GO:0016818 | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides |
| Module 66 | GO:0016462 | pyrophosphatase activity |
| Module 66 | GO:0017111 | nucleoside-triphosphatase activity |
| Module 66 | GO:0016887 | atpase activity |
| Module 66 | GO:0042623 | atpase activity, coupled |
| Module 66 | CORUM:5235 | wrn-ku70-ku80-parp1 complex |
| Module 66 | CORUM:1193 | rap1 complex |
| Module 66 | CORUM:4081 | ku70/ku86 complex |
| Module 66 | CORUM:328 | ku antigen complex |
| Module 66 | CORUM:5231 | 53bp1-containing complex |
| Module 66 | CORUM:5179 | ncoa6-dna-pk-ku-parp1 complex |
| Module 66 | CORUM:5183 | dna-pk-ku-eif2-nf90-nf45 complex |
| Module 66 | CORUM:1092 | pcna-ku antigen complex |
| Module 66 | HPA:011010 | endometrium 1; cells in endometrial stroma |
| Module 66 | HPA:011010\_10 | endometrium 1; cells in endometrial stroma |
| Module 66 | HPA:011010\_01 | endometrium 1; cells in endometrial stroma |
| Module 66 | HPA:011010\_02 | endometrium 1; cells in endometrial stroma |
| Module 66 | HPA:011010\_11 | endometrium 1; cells in endometrial stroma |
| Module 66 | HPA:011010\_12 | endometrium 1; cells in endometrial stroma |
| Module 66 | HPA:020020 | lateral ventricle; neuronal cells |
| Module 66 | HPA:020020\_01 | lateral ventricle; neuronal cells |
| Module 66 | HPA:020020\_02 | lateral ventricle; neuronal cells |
| Module 66 | HPA:020020\_10 | lateral ventricle; neuronal cells |
| Module 66 | HPA:020020\_11 | lateral ventricle; neuronal cells |
| Module 66 | HPA:020020\_12 | lateral ventricle; neuronal cells |
| Module 66 | HPA:039040 | soft tissue 1; peripheral nerve |
| Module 66 | HPA:039040\_10 | soft tissue 1; peripheral nerve |
| Module 66 | HPA:039040\_11 | soft tissue 1; peripheral nerve |
| Module 66 | HPA:039040\_12 | soft tissue 1; peripheral nerve |
| Module 66 | HPA:028010\_01 | parathyroid gland; glandular cells |
| Module 66 | HPA:028010\_10 | parathyroid gland; glandular cells |
| Module 66 | HPA:028010\_11 | parathyroid gland; glandular cells |
| Module 66 | HPA:028010\_12 | parathyroid gland; glandular cells |
| Module 66 | HPA:005010\_10 | bronchus; respiratory epithelial cells |
| Module 66 | HPA:005010\_11 | bronchus; respiratory epithelial cells |
| Module 66 | HPA:005010\_12 | bronchus; respiratory epithelial cells |
| Module 66 | HPA:005010\_13 | bronchus; respiratory epithelial cells |
| Module 66 | HPA:025010\_10 | oral mucosa; squamous epithelial cells |
| Module 66 | HPA:025010\_11 | oral mucosa; squamous epithelial cells |
| Module 66 | HPA:025010\_12 | oral mucosa; squamous epithelial cells |
| Module 66 | HPA:025010\_13 | oral mucosa; squamous epithelial cells |
| Module 66 | HPA:012010 | endometrium 2; cells in endometrial stroma |
| Module 66 | HPA:012010\_10 | endometrium 2; cells in endometrial stroma |
| Module 66 | HPA:012010\_01 | endometrium 2; cells in endometrial stroma |
| Module 66 | HPA:012010\_02 | endometrium 2; cells in endometrial stroma |
| Module 66 | HPA:012010\_11 | endometrium 2; cells in endometrial stroma |
| Module 66 | HPA:012010\_12 | endometrium 2; cells in endometrial stroma |
| Module 66 | HPA:041020 | spleen; cells in white pulp |
| Module 66 | HPA:041020\_01 | spleen; cells in white pulp |
| Module 66 | HPA:041020\_02 | spleen; cells in white pulp |
| Module 66 | HPA:041020\_10 | spleen; cells in white pulp |
| Module 66 | HPA:041020\_11 | spleen; cells in white pulp |
| Module 66 | HPA:041020\_12 | spleen; cells in white pulp |
| Module 66 | HPA:041020\_13 | spleen; cells in white pulp |
| Module 66 | HPA:036010\_10 | skin 2; epidermal cells |
| Module 66 | HPA:036010\_11 | skin 2; epidermal cells |
| Module 66 | HPA:036010\_02 | skin 2; epidermal cells |
| Module 66 | HPA:036010\_12 | skin 2; epidermal cells |
| Module 66 | HPA:037010\_10 | small intestine; glandular cells |
| Module 66 | HPA:037010\_11 | small intestine; glandular cells |
| Module 66 | HPA:037010\_02 | small intestine; glandular cells |
| Module 66 | HPA:037010\_12 | small intestine; glandular cells |
| Module 66 | HPA:037010\_13 | small intestine; glandular cells |
| Module 66 | HPA:040030\_10 | soft tissue 2; fibroblasts |
| Module 66 | HPA:040030\_11 | soft tissue 2; fibroblasts |
| Module 66 | HPA:040030\_12 | soft tissue 2; fibroblasts |
| Module 66 | HPA:029010\_10 | placenta; decidual cells |
| Module 66 | HPA:029010\_11 | placenta; decidual cells |
| Module 66 | HPA:029010\_12 | placenta; decidual cells |
| Module 66 | HPA:029010\_13 | placenta; decidual cells |
| Module 66 | HPA:022020 | lung; pneumocytes |
| Module 66 | HPA:022020\_10 | lung; pneumocytes |
| Module 66 | HPA:022020\_11 | lung; pneumocytes |
| Module 66 | HPA:022020\_12 | lung; pneumocytes |
| Module 66 | HPA:047010\_10 | urinary bladder; urothelial cells |
| Module 66 | HPA:047010\_02 | urinary bladder; urothelial cells |
| Module 66 | HPA:047010\_11 | urinary bladder; urothelial cells |
| Module 66 | HPA:047010\_12 | urinary bladder; urothelial cells |
| Module 66 | HPA:047010\_13 | urinary bladder; urothelial cells |
| Module 66 | HPA:048010\_10 | vagina; squamous epithelial cells |
| Module 66 | HPA:048010\_11 | vagina; squamous epithelial cells |
| Module 66 | HPA:048010\_12 | vagina; squamous epithelial cells |
| Module 66 | HPA:048010\_13 | vagina; squamous epithelial cells |
| Module 66 | HPA:008020\_10 | cervix, uterine; squamous epithelial cells |
| Module 66 | HPA:008020\_11 | cervix, uterine; squamous epithelial cells |
| Module 66 | HPA:008020\_12 | cervix, uterine; squamous epithelial cells |
| Module 66 | HPA:032010\_10 | salivary gland; glandular cells |
| Module 66 | HPA:032010\_11 | salivary gland; glandular cells |
| Module 66 | HPA:032010\_12 | salivary gland; glandular cells |
| Module 66 | HPA:032010\_13 | salivary gland; glandular cells |
| Module 66 | HPA:007010\_10 | cerebral cortex; endothelial cells |
| Module 66 | HPA:007010\_11 | cerebral cortex; endothelial cells |
| Module 66 | HPA:007010\_12 | cerebral cortex; endothelial cells |
| Module 66 | HPA:009030\_10 | colon; peripheral nerve/ganglion |
| Module 66 | HPA:009030\_11 | colon; peripheral nerve/ganglion |
| Module 66 | HPA:009030\_12 | colon; peripheral nerve/ganglion |
| Module 66 | HPA:009030\_13 | colon; peripheral nerve/ganglion |
| Module 66 | HPA:034010\_10 | skeletal muscle; myocytes |
| Module 66 | HPA:034010\_11 | skeletal muscle; myocytes |
| Module 66 | HPA:007040\_10 | cerebral cortex; neuropil |
| Module 66 | HPA:007040\_11 | cerebral cortex; neuropil |
| Module 66 | HPA:009020\_10 | colon; glandular cells |
| Module 66 | HPA:009020\_11 | colon; glandular cells |
| Module 66 | HPA:009020\_12 | colon; glandular cells |
| Module 66 | HPA:009020\_13 | colon; glandular cells |
| Module 66 | HPA:021020\_10 | liver; hepatocytes |
| Module 66 | HPA:021020\_11 | liver; hepatocytes |
| Module 66 | HPA:040040\_10 | soft tissue 2; peripheral nerve |
| Module 66 | HPA:040040\_11 | soft tissue 2; peripheral nerve |
| Module 66 | HPA:040040\_12 | soft tissue 2; peripheral nerve |
| Module 66 | HPA:023010\_10 | lymph node; germinal center cells |
| Module 66 | HPA:023010\_01 | lymph node; germinal center cells |
| Module 66 | HPA:023010\_02 | lymph node; germinal center cells |
| Module 66 | HPA:023010\_11 | lymph node; germinal center cells |
| Module 66 | HPA:023010\_12 | lymph node; germinal center cells |
| Module 66 | HPA:023010\_13 | lymph node; germinal center cells |
| Module 66 | HPA:033010\_10 | seminal vesicle; glandular cells |
| Module 66 | HPA:033010\_11 | seminal vesicle; glandular cells |
| Module 66 | HPA:033010\_12 | seminal vesicle; glandular cells |
| Module 66 | HPA:033010\_13 | seminal vesicle; glandular cells |
| Module 66 | HPA:001010\_10 | adrenal gland; glandular cells |
| Module 66 | HPA:001010\_11 | adrenal gland; glandular cells |
| Module 66 | HPA:001010\_12 | adrenal gland; glandular cells |
| Module 66 | HPA:001010\_13 | adrenal gland; glandular cells |
| Module 66 | HPA:041010\_10 | spleen; cells in red pulp |
| Module 66 | HPA:041010\_11 | spleen; cells in red pulp |
| Module 66 | HPA:041010\_12 | spleen; cells in red pulp |
| Module 66 | HPA:003010\_10 | bone marrow; hematopoietic cells |
| Module 66 | HPA:003010\_01 | bone marrow; hematopoietic cells |
| Module 66 | HPA:003010\_11 | bone marrow; hematopoietic cells |
| Module 66 | HPA:003010\_12 | bone marrow; hematopoietic cells |
| Module 66 | HPA:003010\_03 | bone marrow; hematopoietic cells |
| Module 66 | HPA:003010\_13 | bone marrow; hematopoietic cells |
| Module 66 | HPA:029020\_10 | placenta; trophoblastic cells |
| Module 66 | HPA:029020\_11 | placenta; trophoblastic cells |
| Module 66 | HPA:029020\_12 | placenta; trophoblastic cells |
| Module 66 | HPA:029020\_13 | placenta; trophoblastic cells |
| Module 66 | HPA:009010\_10 | colon; endothelial cells |
| Module 66 | HPA:009010\_11 | colon; endothelial cells |
| Module 66 | HPA:009010\_12 | colon; endothelial cells |
| Module 66 | HPA:019020\_10 | kidney; cells in tubules |
| Module 66 | HPA:019020\_11 | kidney; cells in tubules |
| Module 66 | HPA:019020\_12 | kidney; cells in tubules |
| Module 66 | HPA:019020\_13 | kidney; cells in tubules |
| Module 66 | HPA:039010 | soft tissue 1; adipocytes |
| Module 66 | HPA:039010\_10 | soft tissue 1; adipocytes |
| Module 66 | HPA:039010\_11 | soft tissue 1; adipocytes |
| Module 66 | HPA:039010\_12 | soft tissue 1; adipocytes |
| Module 66 | HPA:012020\_01 | endometrium 2; glandular cells |
| Module 66 | HPA:012020\_02 | endometrium 2; glandular cells |
| Module 66 | HPA:012020\_10 | endometrium 2; glandular cells |
| Module 66 | HPA:012020\_11 | endometrium 2; glandular cells |
| Module 66 | HPA:012020\_12 | endometrium 2; glandular cells |
| Module 66 | HPA:012020\_13 | endometrium 2; glandular cells |
| Module 66 | HPA:013010\_01 | epididymis; glandular cells |
| Module 66 | HPA:013010\_10 | epididymis; glandular cells |
| Module 66 | HPA:013010\_11 | epididymis; glandular cells |
| Module 66 | HPA:013010\_12 | epididymis; glandular cells |
| Module 66 | HPA:013010\_13 | epididymis; glandular cells |
| Module 66 | HPA:035010\_10 | skin 1; langerhans |
| Module 66 | HPA:035010\_01 | skin 1; langerhans |
| Module 66 | HPA:035010\_02 | skin 1; langerhans |
| Module 66 | HPA:035010\_11 | skin 1; langerhans |
| Module 66 | HPA:035010\_12 | skin 1; langerhans |
| Module 66 | HPA:035010\_13 | skin 1; langerhans |
| Module 66 | HPA:002010\_10 | appendix; glandular cells |
| Module 66 | HPA:002010\_11 | appendix; glandular cells |
| Module 66 | HPA:002010\_02 | appendix; glandular cells |
| Module 66 | HPA:002010\_12 | appendix; glandular cells |
| Module 66 | HPA:002010\_13 | appendix; glandular cells |
| Module 66 | HPA:004010 | breast; adipocytes |
| Module 66 | HPA:004010\_10 | breast; adipocytes |
| Module 66 | HPA:004010\_11 | breast; adipocytes |
| Module 66 | HPA:004010\_12 | breast; adipocytes |
| Module 66 | HPA:035040\_01 | skin 1; melanocytes |
| Module 66 | HPA:035040\_10 | skin 1; melanocytes |
| Module 66 | HPA:035040\_11 | skin 1; melanocytes |
| Module 66 | HPA:035040\_12 | skin 1; melanocytes |
| Module 66 | HPA:035040\_13 | skin 1; melanocytes |
| Module 66 | HPA:043010\_10 | stomach 2; glandular cells |
| Module 66 | HPA:043010\_11 | stomach 2; glandular cells |
| Module 66 | HPA:043010\_12 | stomach 2; glandular cells |
| Module 66 | HPA:043010\_13 | stomach 2; glandular cells |
| Module 66 | HPA:046030\_10 | tonsil; squamous epithelial cells |
| Module 66 | HPA:046030\_11 | tonsil; squamous epithelial cells |
| Module 66 | HPA:046030\_12 | tonsil; squamous epithelial cells |
| Module 66 | HPA:046030\_13 | tonsil; squamous epithelial cells |
| Module 66 | HPA:016010\_10 | gallbladder; glandular cells |
| Module 66 | HPA:016010\_11 | gallbladder; glandular cells |
| Module 66 | HPA:016010\_12 | gallbladder; glandular cells |
| Module 66 | HPA:007030\_10 | cerebral cortex; neuronal cells |
| Module 66 | HPA:007030\_11 | cerebral cortex; neuronal cells |
| Module 66 | HPA:007030\_12 | cerebral cortex; neuronal cells |
| Module 66 | HPA:007030\_13 | cerebral cortex; neuronal cells |
| Module 66 | HPA:035030\_01 | skin 1; keratinocytes |
| Module 66 | HPA:035030\_02 | skin 1; keratinocytes |
| Module 66 | HPA:035030\_03 | skin 1; keratinocytes |
| Module 66 | HPA:035030\_10 | skin 1; keratinocytes |
| Module 66 | HPA:035030\_11 | skin 1; keratinocytes |
| Module 66 | HPA:035030\_12 | skin 1; keratinocytes |
| Module 66 | HPA:035030\_13 | skin 1; keratinocytes |
| Module 66 | HPA:017010\_10 | heart muscle; myocytes |
| Module 66 | HPA:017010\_11 | heart muscle; myocytes |
| Module 66 | HPA:046010 | tonsil; germinal center cells |
| Module 66 | HPA:046010\_10 | tonsil; germinal center cells |
| Module 66 | HPA:046010\_01 | tonsil; germinal center cells |
| Module 66 | HPA:046010\_02 | tonsil; germinal center cells |
| Module 66 | HPA:046010\_03 | tonsil; germinal center cells |
| Module 66 | HPA:046010\_11 | tonsil; germinal center cells |
| Module 66 | HPA:046010\_12 | tonsil; germinal center cells |
| Module 66 | HPA:046010\_13 | tonsil; germinal center cells |
| Module 66 | HPA:022010\_10 | lung; macrophages |
| Module 66 | HPA:022010\_11 | lung; macrophages |
| Module 66 | HPA:022010\_12 | lung; macrophages |
| Module 66 | HPA:022010\_13 | lung; macrophages |
| Module 66 | HPA:011020\_01 | endometrium 1; glandular cells |
| Module 66 | HPA:011020\_02 | endometrium 1; glandular cells |
| Module 66 | HPA:011020\_10 | endometrium 1; glandular cells |
| Module 66 | HPA:011020\_11 | endometrium 1; glandular cells |
| Module 66 | HPA:011020\_12 | endometrium 1; glandular cells |
| Module 66 | HPA:011020\_13 | endometrium 1; glandular cells |
| Module 66 | HPA:035020\_10 | skin 1; fibroblasts |
| Module 66 | HPA:035020\_03 | skin 1; fibroblasts |
| Module 66 | HPA:035020\_11 | skin 1; fibroblasts |
| Module 66 | HPA:035020\_12 | skin 1; fibroblasts |
| Module 66 | HPA:035020\_13 | skin 1; fibroblasts |
| Module 66 | HPA:038010\_10 | smooth muscle; smooth muscle cells |
| Module 66 | HPA:038010\_11 | smooth muscle; smooth muscle cells |
| Module 66 | HPA:006030 | cerebellum; cells in molecular layer |
| Module 66 | HPA:006030\_01 | cerebellum; cells in molecular layer |
| Module 66 | HPA:006030\_10 | cerebellum; cells in molecular layer |
| Module 66 | HPA:006030\_11 | cerebellum; cells in molecular layer |
| Module 66 | HPA:006030\_12 | cerebellum; cells in molecular layer |
| Module 66 | HPA:002020 | appendix; lymphoid tissue |
| Module 66 | HPA:002020\_01 | appendix; lymphoid tissue |
| Module 66 | HPA:002020\_02 | appendix; lymphoid tissue |
| Module 66 | HPA:002020\_10 | appendix; lymphoid tissue |
| Module 66 | HPA:002020\_11 | appendix; lymphoid tissue |
| Module 66 | HPA:002020\_12 | appendix; lymphoid tissue |
| Module 66 | HPA:002020\_13 | appendix; lymphoid tissue |
| Module 66 | HPA:019010\_10 | kidney; cells in glomeruli |
| Module 66 | HPA:019010\_11 | kidney; cells in glomeruli |
| Module 66 | HPA:019010\_12 | kidney; cells in glomeruli |
| Module 66 | HPA:018020 | hippocampus; neuronal cells |
| Module 66 | HPA:018020\_10 | hippocampus; neuronal cells |
| Module 66 | HPA:018020\_01 | hippocampus; neuronal cells |
| Module 66 | HPA:018020\_02 | hippocampus; neuronal cells |
| Module 66 | HPA:018020\_11 | hippocampus; neuronal cells |
| Module 66 | HPA:018020\_12 | hippocampus; neuronal cells |
| Module 66 | HPA:026020 | ovary; ovarian stroma cells |
| Module 66 | HPA:026020\_10 | ovary; ovarian stroma cells |
| Module 66 | HPA:026020\_01 | ovary; ovarian stroma cells |
| Module 66 | HPA:026020\_02 | ovary; ovarian stroma cells |
| Module 66 | HPA:026020\_11 | ovary; ovarian stroma cells |
| Module 66 | HPA:026020\_12 | ovary; ovarian stroma cells |
| Module 66 | HPA:026020\_13 | ovary; ovarian stroma cells |
| Module 66 | HPA:027010\_10 | pancreas; exocrine glandular cells |
| Module 66 | HPA:027010\_11 | pancreas; exocrine glandular cells |
| Module 66 | HPA:027010\_12 | pancreas; exocrine glandular cells |
| Module 66 | HPA:023020\_10 | lymph node; non-germinal center cells |
| Module 66 | HPA:023020\_01 | lymph node; non-germinal center cells |
| Module 66 | HPA:023020\_02 | lymph node; non-germinal center cells |
| Module 66 | HPA:023020\_03 | lymph node; non-germinal center cells |
| Module 66 | HPA:023020\_11 | lymph node; non-germinal center cells |
| Module 66 | HPA:023020\_12 | lymph node; non-germinal center cells |
| Module 66 | HPA:023020\_13 | lymph node; non-germinal center cells |
| Module 66 | HPA:018010 | hippocampus; glial cells |
| Module 66 | HPA:018010\_01 | hippocampus; glial cells |
| Module 66 | HPA:018010\_10 | hippocampus; glial cells |
| Module 66 | HPA:018010\_11 | hippocampus; glial cells |
| Module 66 | HPA:018010\_12 | hippocampus; glial cells |
| Module 66 | HPA:014010\_02 | esophagus; squamous epithelial cells |
| Module 66 | HPA:014010\_03 | esophagus; squamous epithelial cells |
| Module 66 | HPA:014010\_10 | esophagus; squamous epithelial cells |
| Module 66 | HPA:014010\_11 | esophagus; squamous epithelial cells |
| Module 66 | HPA:014010\_12 | esophagus; squamous epithelial cells |
| Module 66 | HPA:014010\_13 | esophagus; squamous epithelial cells |
| Module 66 | HPA:044020\_10 | testis; cells in seminiferous ducts |
| Module 66 | HPA:044020\_11 | testis; cells in seminiferous ducts |
| Module 66 | HPA:044020\_12 | testis; cells in seminiferous ducts |
| Module 66 | HPA:044020\_13 | testis; cells in seminiferous ducts |
| Module 66 | HPA:010010\_10 | duodenum; glandular cells |
| Module 66 | HPA:010010\_11 | duodenum; glandular cells |
| Module 66 | HPA:010010\_12 | duodenum; glandular cells |
| Module 66 | HPA:010010\_13 | duodenum; glandular cells |
| Module 66 | HPA:006010\_02 | cerebellum; purkinje cells |
| Module 66 | HPA:006010\_10 | cerebellum; purkinje cells |
| Module 66 | HPA:006010\_11 | cerebellum; purkinje cells |
| Module 66 | HPA:006010\_12 | cerebellum; purkinje cells |
| Module 66 | HPA:006010\_13 | cerebellum; purkinje cells |
| Module 66 | HPA:027020\_10 | pancreas; islets of langerhans |
| Module 66 | HPA:027020\_11 | pancreas; islets of langerhans |
| Module 66 | HPA:027020\_02 | pancreas; islets of langerhans |
| Module 66 | HPA:027020\_12 | pancreas; islets of langerhans |
| Module 66 | HPA:024010\_10 | nasopharynx; respiratory epithelial cells |
| Module 66 | HPA:024010\_11 | nasopharynx; respiratory epithelial cells |
| Module 66 | HPA:024010\_12 | nasopharynx; respiratory epithelial cells |
| Module 66 | HPA:024010\_13 | nasopharynx; respiratory epithelial cells |
| Module 66 | HPA:020010\_13 | lateral ventricle; glial cells |
| Module 66 | HPA:039020\_10 | soft tissue 1; chondrocytes |
| Module 66 | HPA:039020\_11 | soft tissue 1; chondrocytes |
| Module 66 | HPA:039020\_12 | soft tissue 1; chondrocytes |
| Module 66 | HPA:042010\_10 | stomach 1; glandular cells |
| Module 66 | HPA:042010\_11 | stomach 1; glandular cells |
| Module 66 | HPA:042010\_12 | stomach 1; glandular cells |
| Module 66 | HPA:042010\_13 | stomach 1; glandular cells |
| Module 66 | HPA:026010\_11 | ovary; follicle cells |
| Module 66 | HPA:026010\_12 | ovary; follicle cells |
| Module 66 | HPA:046020\_10 | tonsil; non-germinal center cells |
| Module 66 | HPA:046020\_01 | tonsil; non-germinal center cells |
| Module 66 | HPA:046020\_11 | tonsil; non-germinal center cells |
| Module 66 | HPA:046020\_12 | tonsil; non-germinal center cells |
| Module 66 | HPA:046020\_13 | tonsil; non-germinal center cells |
| Module 66 | HPA:004020\_01 | breast; glandular cells |
| Module 66 | HPA:004020\_02 | breast; glandular cells |
| Module 66 | HPA:004020\_10 | breast; glandular cells |
| Module 66 | HPA:004020\_11 | breast; glandular cells |
| Module 66 | HPA:004020\_12 | breast; glandular cells |
| Module 66 | HPA:004020\_13 | breast; glandular cells |
| Module 66 | HPA:030010\_10 | prostate; glandular cells |
| Module 66 | HPA:030010\_11 | prostate; glandular cells |
| Module 66 | HPA:030010\_12 | prostate; glandular cells |
| Module 66 | HPA:006020\_10 | cerebellum; cells in granular layer |
| Module 66 | HPA:006020\_11 | cerebellum; cells in granular layer |
| Module 66 | HPA:006020\_12 | cerebellum; cells in granular layer |
| Module 66 | HPA:006020\_13 | cerebellum; cells in granular layer |
| Module 66 | HPA:040010 | soft tissue 2; adipocytes |
| Module 66 | HPA:040010\_10 | soft tissue 2; adipocytes |
| Module 66 | HPA:040010\_11 | soft tissue 2; adipocytes |
| Module 66 | HPA:040010\_12 | soft tissue 2; adipocytes |
| Module 66 | HPA:039030\_01 | soft tissue 1; fibroblasts |
| Module 66 | HPA:039030\_10 | soft tissue 1; fibroblasts |
| Module 66 | HPA:039030\_11 | soft tissue 1; fibroblasts |
| Module 66 | HPA:039030\_12 | soft tissue 1; fibroblasts |
| Module 66 | HPA:004030\_10 | breast; myoepithelial cells |
| Module 66 | HPA:004030\_11 | breast; myoepithelial cells |
| Module 66 | HPA:004030\_12 | breast; myoepithelial cells |
| Module 66 | HPA:015010\_02 | fallopian tube; glandular cells |
| Module 66 | HPA:015010\_10 | fallopian tube; glandular cells |
| Module 66 | HPA:015010\_11 | fallopian tube; glandular cells |
| Module 66 | HPA:015010\_12 | fallopian tube; glandular cells |
| Module 66 | HPA:007020 | cerebral cortex; glial cells |
| Module 66 | HPA:007020\_10 | cerebral cortex; glial cells |
| Module 66 | HPA:007020\_01 | cerebral cortex; glial cells |
| Module 66 | HPA:007020\_11 | cerebral cortex; glial cells |
| Module 66 | HPA:007020\_12 | cerebral cortex; glial cells |
| Module 66 | HPA:021010\_10 | liver; bile duct cells |
| Module 66 | HPA:021010\_11 | liver; bile duct cells |
| Module 66 | HPA:021010\_12 | liver; bile duct cells |
| Module 66 | HPA:045010\_10 | thyroid gland; glandular cells |
| Module 66 | HPA:045010\_11 | thyroid gland; glandular cells |
| Module 66 | HPA:045010\_02 | thyroid gland; glandular cells |
| Module 66 | HPA:045010\_12 | thyroid gland; glandular cells |
| Module 66 | HPA:045010\_13 | thyroid gland; glandular cells |
| Module 66 | HPA:017010\_13 | heart muscle; myocytes |
| Module 66 | HPA:044010\_10 | testis; leydig cells |
| Module 66 | HPA:044010\_11 | testis; leydig cells |
| Module 66 | HPA:044010\_12 | testis; leydig cells |
| Module 66 | HPA:044010\_13 | testis; leydig cells |
| Module 66 | HPA:020010 | lateral ventricle; glial cells |
| Module 66 | HPA:020010\_01 | lateral ventricle; glial cells |
| Module 66 | HPA:020010\_10 | lateral ventricle; glial cells |
| Module 66 | HPA:020010\_11 | lateral ventricle; glial cells |
| Module 66 | HPA:031010\_10 | rectum; glandular cells |
| Module 66 | HPA:031010\_11 | rectum; glandular cells |
| Module 66 | HPA:031010\_12 | rectum; glandular cells |
| Module 66 | HPA:031010\_13 | rectum; glandular cells |
| Module 66 | HPA:008010\_10 | cervix, uterine; glandular cells |
| Module 66 | HPA:008010\_11 | cervix, uterine; glandular cells |
| Module 66 | HPA:008010\_12 | cervix, uterine; glandular cells |
| Module 66 | KEGG:03050 | proteasome |
| Module 66 | KEGG:04110 | cell cycle |
| Module 66 | KEGG:05169 | epstein-barr virus infection |
| Module 66 | KEGG:03450 | non-homologous end-joining |
| Module 66 | KEGG:03030 | dna replication |
| Module 66 | KEGG:04114 | oocyte meiosis |
| Module 66 | REAC:5610785 | gli3 is processed to gli3r by the proteasome |
| Module 66 | REAC:445355 | smooth muscle contraction |
| Module 66 | REAC:5676590 | nik-->noncanonical nf-kb signaling |
| Module 66 | REAC:1169091 | activation of nf-kappab in b cells |
| Module 66 | REAC:350562 | regulation of ornithine decarboxylase (odc) |
| Module 66 | REAC:73894 | dna repair |
| Module 66 | REAC:73884 | base excision repair |
| Module 66 | REAC:73933 | resolution of abasic sites (ap sites) |
| Module 66 | REAC:110373 | resolution of ap sites via the multiple-nucleotide patch replacement pathway |
| Module 66 | REAC:5651801 | pcna-dependent long patch base excision repair |
| Module 66 | REAC:5696398 | nucleotide excision repair |
| Module 66 | REAC:5696399 | global genome nucleotide excision repair (gg-ner) |
| Module 66 | REAC:5693532 | dna double-strand break repair |
| Module 66 | REAC:1236978 | cross-presentation of soluble exogenous antigens (endosomes) |
| Module 66 | REAC:5610783 | degradation of gli2 by the proteasome |
| Module 66 | REAC:4641257 | degradation of axin |
| Module 66 | REAC:1643685 | disease |
| Module 66 | REAC:5663205 | infectious disease |
| Module 66 | REAC:162906 | hiv infection |
| Module 66 | REAC:162909 | host interactions of hiv factors |
| Module 66 | REAC:180585 | vif-mediated degradation of apobec3g |
| Module 66 | REAC:180534 | vpu mediated degradation of cd4 |
| Module 66 | REAC:162587 | hiv life cycle |
| Module 66 | REAC:162594 | early phase of hiv life cycle |
| Module 66 | REAC:8852276 | the role of gtse1 in g2/m progression after g2 checkpoint |
| Module 66 | REAC:202424 | downstream tcr signaling |
| Module 66 | REAC:69166 | removal of the flap intermediate |
| Module 66 | REAC:4608870 | asymmetric localization of pcp proteins |
| Module 66 | REAC:5387390 | hh mutants abrogate ligand secretion |
| Module 66 | REAC:5362768 | hh mutants that don't undergo autocatalytic processing are degraded by erad |
| Module 66 | REAC:75035 | chk1/chk2(cds1) mediated inactivation of cyclin b:cdk1 complex |
| Module 66 | REAC:180786 | extension of telomeres |
| Module 66 | REAC:174417 | telomere c-strand (lagging strand) synthesis |
| Module 66 | REAC:174414 | processive synthesis on the c-strand of the telomere |
| Module 66 | REAC:174437 | removal of the flap intermediate from the c-strand |
| Module 66 | REAC:5357801 | programmed cell death |
| Module 66 | REAC:109581 | apoptosis |
| Module 66 | REAC:169911 | regulation of apoptosis |
| Module 66 | REAC:211733 | regulation of activated pak-2p34 by proteasome mediated degradation |
| Module 66 | REAC:5607764 | clec7a (dectin-1) signaling |
| Module 66 | REAC:5607761 | dectin-1 mediated noncanonical nf-kb signaling |
| Module 66 | REAC:1236974 | er-phagosome pathway |
| Module 66 | REAC:5610780 | degradation of gli1 by the proteasome |
| Module 66 | REAC:5358346 | hedgehog ligand biogenesis |
| Module 66 | REAC:450531 | regulation of mrna stability by proteins that bind au-rich elements |
| Module 66 | REAC:450408 | auf1 (hnrnp d0) binds and destabilizes mrna |
| Module 66 | REAC:4641258 | degradation of dvl |
| Module 66 | REAC:5687128 | mapk6/mapk4 signaling |
| Module 66 | REAC:1640170 | cell cycle |
| Module 66 | REAC:69620 | cell cycle checkpoints |
| Module 66 | REAC:69615 | g1/s dna damage checkpoints |
| Module 66 | REAC:69613 | p53-independent g1/s dna damage checkpoint |
| Module 66 | REAC:69610 | p53-independent dna damage response |
| Module 66 | REAC:69601 | ubiquitin mediated degradation of phosphorylated cdc25a |
| Module 66 | REAC:69580 | p53-dependent g1/s dna damage checkpoint |
| Module 66 | REAC:69563 | p53-dependent g1 dna damage response |
| Module 66 | REAC:69541 | stabilization of p53 |
| Module 66 | REAC:349425 | autodegradation of the e3 ubiquitin ligase cop1 |
| Module 66 | REAC:69481 | g2/m checkpoints |
| Module 66 | REAC:69278 | cell cycle, mitotic |
| Module 66 | REAC:69242 | s phase |
| Module 66 | REAC:75815 | ubiquitin-dependent degradation of cyclin d |
| Module 66 | REAC:69229 | ubiquitin-dependent degradation of cyclin d1 |
| Module 66 | REAC:453279 | mitotic g1-g1/s phases |
| Module 66 | REAC:69206 | g1/s transition |
| Module 66 | REAC:69202 | cyclin e associated events during g1/s transition |
| Module 66 | REAC:453276 | regulation of mitotic cell cycle |
| Module 66 | REAC:174143 | apc/c-mediated degradation of cell cycle proteins |
| Module 66 | REAC:176814 | activation of apc/c and apc/c:cdc20 mediated degradation of mitotic proteins |
| Module 66 | REAC:176409 | apc/c:cdc20 mediated degradation of mitotic proteins |
| Module 66 | REAC:174154 | apc/c:cdc20 mediated degradation of securin |
| Module 66 | REAC:179419 | apc:cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint |
| Module 66 | REAC:174184 | cdc20:phospho-apc/c mediated degradation of cyclin a |
| Module 66 | REAC:174084 | autodegradation of cdh1 by cdh1:apc/c |
| Module 66 | REAC:176408 | regulation of apc/c activators between g1/s and early anaphase |
| Module 66 | REAC:174113 | scf-beta-trcp mediated degradation of emi1 |
| Module 66 | REAC:69306 | dna replication |
| Module 66 | REAC:68874 | m/g1 transition |
| Module 66 | REAC:69002 | dna replication pre-initiation |
| Module 66 | REAC:68867 | assembly of the pre-replicative complex |
| Module 66 | REAC:68827 | cdt1 association with the cdc6:orc:origin complex |
| Module 66 | REAC:69239 | synthesis of dna |
| Module 66 | REAC:69190 | dna strand elongation |
| Module 66 | REAC:69186 | lagging strand synthesis |
| Module 66 | REAC:69052 | switching of origins to a post-replicative state |
| Module 66 | REAC:69304 | regulation of dna replication |
| Module 66 | REAC:69300 | removal of licensing factors from origins |
| Module 66 | REAC:68949 | orc1 removal from chromatin |
| Module 66 | REAC:69017 | cdk-mediated phosphorylation and removal of cdc6 |
| Module 66 | REAC:187577 | scf(skp2)-mediated degradation of p27/p21 |
| Module 66 | REAC:5658442 | regulation of ras by gaps |
| Module 66 | REAC:110313 | translesion synthesis by y family dna polymerases bypasses lesions on dna template |
| Module 66 | REAC:110320 | translesion synthesis by polh |
| Module 66 | TF:M02102\_1 | factor: nrf-1; motif: ygcgcmtgcgc; match class: 1 |
| Module 66 | TF:M01258\_0 | factor: gabp; motif: cacttccggnnn; match class: 0 |
| Module 66 | TF:M02065\_1 | factor: er81; motif: rccggaaryn; match class: 1 |
| Module 66 | TF:M00803\_1 | factor: e2f; motif: ggcgsg; match class: 1 |
| Module 67 | TF:M07090\_1 | factor: c-fos; motif: nntgastcatn; match class: 1 |
| Module 68 | - | - |
| Module 69 | - | - |
| Module 70 | GO:0003017 | lymph circulation |
| Module 71 | MI:hsa-miR-619 | mi:hsa-mir-619 |
| Module 72 | REAC:390247 | beta-oxidation of very long chain fatty acids |
| Module 72 | TF:M01588\_0 | factor: gklf; motif: gccmcrcccnnn; match class: 0 |
| Module 73 | - | - |
| Module 74 | GO:0051240 | positive regulation of multicellular organismal process |
| Module 74 | GO:0032717 | negative regulation of interleukin-8 production |
| Module 74 | GO:0032879 | regulation of localization |
| Module 74 | GO:0014068 | positive regulation of phosphatidylinositol 3-kinase signaling |
| Module 74 | KEGG:05323 | rheumatoid arthritis |
| Module 75 | - | - |
| Module 76 | HPA:046030\_13 | tonsil; squamous epithelial cells |
| Module 76 | HPA:046010\_03 | tonsil; germinal center cells |
| Module 76 | HPA:046010\_11 | tonsil; germinal center cells |
| Module 76 | HPA:046010\_12 | tonsil; germinal center cells |
| Module 76 | HPA:046010\_13 | tonsil; germinal center cells |
| Module 76 | HPA:044020\_13 | testis; cells in seminiferous ducts |
| Module 76 | HPA:023020\_03 | lymph node; non-germinal center cells |
| Module 76 | HPA:023020\_13 | lymph node; non-germinal center cells |
| Module 76 | HPA:026020\_11 | ovary; ovarian stroma cells |
| Module 76 | HPA:048010\_11 | vagina; squamous epithelial cells |
| Module 76 | HPA:002010\_13 | appendix; glandular cells |
| Module 76 | HPA:025010\_13 | oral mucosa; squamous epithelial cells |
| Module 76 | HPA:007020\_03 | cerebral cortex; glial cells |
| Module 76 | HPA:007020\_12 | cerebral cortex; glial cells |
| Module 76 | HPA:007020\_13 | cerebral cortex; glial cells |
| Module 76 | HPA:043010\_13 | stomach 2; glandular cells |
| Module 76 | HPA:009020\_13 | colon; glandular cells |
| Module 76 | HPA:039010\_02 | soft tissue 1; adipocytes |
| Module 76 | HPA:035040\_12 | skin 1; melanocytes |
| Module 76 | HPA:023010\_12 | lymph node; germinal center cells |
| Module 76 | HPA:023010\_13 | lymph node; germinal center cells |
| Module 76 | HPA:002020\_12 | appendix; lymphoid tissue |
| Module 76 | HPA:042010\_12 | stomach 1; glandular cells |
| Module 76 | HPA:035030\_12 | skin 1; keratinocytes |
| Module 76 | HPA:006020\_12 | cerebellum; cells in granular layer |
| Module 76 | KEGG:03040 | spliceosome |
| Module 77 | OMIM:615575 | neuronopathy, distal hereditary motor, type iid; hmn2d; hmn iid; neuropathy, distal hereditary motor, type iid; dhmn2d; spinal muscular atrophy, distal, autosomal dominant, calf-predominant |
| Module 78 | - | - |
| Module 79 | MI:hsa-miR-744\* | mi:hsa-mir-744\* |
| Module 79 | MI:hsa-miR-432\* | mi:hsa-mir-432\* |
| Module 80 | GO:0032812 | positive regulation of epinephrine secretion |
| Module 81 | GO:0032502 | developmental process |
| Module 81 | GO:0048856 | anatomical structure development |
| Module 81 | GO:0050793 | regulation of developmental process |
| Module 81 | GO:0044699 | single-organism process |
| Module 81 | GO:0044763 | single-organism cellular process |
| Module 81 | GO:0044767 | single-organism developmental process |
| Module 81 | GO:0048869 | cellular developmental process |
| Module 81 | GO:0030154 | cell differentiation |
| Module 81 | GO:0032501 | multicellular organismal process |
| Module 81 | GO:0044707 | single-multicellular organism process |
| Module 81 | GO:0007275 | multicellular organism development |
| Module 81 | GO:0051239 | regulation of multicellular organismal process |
| Module 81 | GO:0048519 | negative regulation of biological process |
| Module 81 | GO:0071944 | cell periphery |
| Module 81 | GO:0005886 | plasma membrane |
| Module 81 | GO:0009986 | cell surface |
| Module 82 | KEGG:00290 | valine, leucine and isoleucine biosynthesis |
| Module 83 | KEGG:00983 | drug metabolism - other enzymes |
| Module 83 | KEGG:00140 | steroid hormone biosynthesis |
| Module 83 | OMIM:217300 | cornea plana 2; cna2 |
| Module 83 | OMIM:180105 | retinitis pigmentosa 10; rp10 |
| Module 83 | OMIM:607060 | parkinson disease 8, autosomal dominant; park8 |
| Module 83 | OMIM:300910 | bone mineral density quantitative trait locus 18; bmnd18; osteoporosis and osteoporotic fractures, susceptibility to |
| Module 83 | OMIM:280000 | coloboma, congenital heart disease, ichthyosiform dermatosis, mentalretardation, and ear anomalies syndrome; chime; chime syndrome; zunich neuroectodermal syndrome |
| Module 83 | OMIM:610478 | retinal cone dystrophy 4; rcd4 |
| Module 83 | OMIM:202110 | adrenal hyperplasia, congenital, due to 17-alpha-hydroxylase deficiency; adrenal hyperplasia v; 17-@alpha-hydroxylase deficiency17,20-@lyase deficiency, isolated, included; 17-@alpha-hydroxylase/17,20-lyase deficiency, combined complete, included; 17-@alpha-hydroxylase/17,20-lyase deficiency, combined partial, included |
| Module 83 | OMIM:609040 | arrhythmogenic right ventricular dysplasia, familial, 9; arvd9; arrhythmogenic right ventricular cardiomyopathy 9; arvc9 |
| Module 83 | OMIM:613837 | leber congenital amaurosis 11; lca11 |
| Module 84 | GO:0043227 | membrane-bounded organelle |
| Module 84 | KEGG:00524 | butirosin and neomycin biosynthesis |
| Module 85 | - | - |
| Module 86 | GO:0032502 | developmental process |
| Module 86 | GO:0048856 | anatomical structure development |
| Module 86 | GO:0044767 | single-organism developmental process |
| Module 86 | GO:0023052 | signaling |
| Module 86 | GO:0009987 | cellular process |
| Module 86 | GO:0065007 | biological regulation |
| Module 86 | GO:0050789 | regulation of biological process |
| Module 86 | GO:0050794 | regulation of cellular process |
| Module 86 | GO:0023051 | regulation of signaling |
| Module 86 | GO:0032501 | multicellular organismal process |
| Module 86 | GO:0051239 | regulation of multicellular organismal process |
| Module 86 | GO:0044700 | single organism signaling |
| Module 86 | GO:0044707 | single-multicellular organism process |
| Module 86 | GO:0051240 | positive regulation of multicellular organismal process |
| Module 86 | GO:0007154 | cell communication |
| Module 86 | GO:0010646 | regulation of cell communication |
| Module 86 | GO:0007165 | signal transduction |
| Module 86 | GO:0070848 | response to growth factor |
| Module 86 | GO:1900006 | positive regulation of dendrite development |
| Module 86 | GO:0006629 | lipid metabolic process |
| Module 86 | GO:0044255 | cellular lipid metabolic process |
| Module 86 | GO:0005575 | cellular\_component |
| Module 86 | GO:0043226 | organelle |
| Module 86 | GO:0043227 | membrane-bounded organelle |
| Module 86 | GO:0005623 | cell |
| Module 86 | GO:0044464 | cell part |
| Module 86 | GO:0005622 | intracellular |
| Module 86 | GO:0044424 | intracellular part |
| Module 86 | TF:M07039\_1 | factor: etf; motif: ccccgccccyn; match class: 1 |
| Module 86 | TF:M00932\_1 | factor: sp1; motif: nnggggcggggnn; match class: 1 |
| Module 86 | TF:M00933\_1 | factor: sp1; motif: ccccgccccn; match class: 1 |
| Module 86 | TF:M03567\_1 | factor: sp2; motif: nysgccccgcccccy; match class: 1 |
| Module 87 | GO:0009987 | cellular process |
| Module 87 | GO:0044238 | primary metabolic process |
| Module 87 | GO:0006807 | nitrogen compound metabolic process |
| Module 87 | GO:0071704 | organic substance metabolic process |
| Module 87 | GO:1901360 | organic cyclic compound metabolic process |
| Module 87 | GO:0044237 | cellular metabolic process |
| Module 87 | GO:0046483 | heterocycle metabolic process |
| Module 87 | GO:0006725 | cellular aromatic compound metabolic process |
| Module 87 | GO:0034641 | cellular nitrogen compound metabolic process |
| Module 87 | GO:0006139 | nucleobase-containing compound metabolic process |
| Module 87 | GO:0031974 | membrane-enclosed lumen |
| Module 87 | GO:0043228 | non-membrane-bounded organelle |
| Module 87 | GO:0043227 | membrane-bounded organelle |
| Module 87 | GO:0044422 | organelle part |
| Module 87 | GO:0043233 | organelle lumen |
| Module 87 | GO:0005622 | intracellular |
| Module 87 | GO:0044424 | intracellular part |
| Module 87 | GO:0005737 | cytoplasm |
| Module 87 | GO:0044444 | cytoplasmic part |
| Module 87 | GO:0043229 | intracellular organelle |
| Module 87 | GO:0043232 | intracellular non-membrane-bounded organelle |
| Module 87 | GO:0044446 | intracellular organelle part |
| Module 87 | GO:0070013 | intracellular organelle lumen |
| Module 87 | GO:0044428 | nuclear part |
| Module 87 | GO:0031981 | nuclear lumen |
| Module 87 | GO:0043231 | intracellular membrane-bounded organelle |
| Module 87 | GO:0005739 | mitochondrion |
| Module 87 | GO:1990204 | oxidoreductase complex |
| Module 87 | GO:0032991 | macromolecular complex |
| Module 87 | GO:0043234 | protein complex |
| Module 87 | GO:0003723 | rna binding |
| Module 87 | GO:0097159 | organic cyclic compound binding |
| Module 87 | GO:1901363 | heterocyclic compound binding |
| Module 87 | HPA:039040\_10 | soft tissue 1; peripheral nerve |
| Module 87 | HPA:029010 | placenta; decidual cells |
| Module 87 | HPA:029010\_10 | placenta; decidual cells |
| Module 87 | HPA:029010\_01 | placenta; decidual cells |
| Module 87 | HPA:029010\_11 | placenta; decidual cells |
| Module 87 | HPA:029010\_12 | placenta; decidual cells |
| Module 87 | HPA:029010\_13 | placenta; decidual cells |
| Module 87 | HPA:040010\_10 | soft tissue 2; adipocytes |
| Module 87 | HPA:040010\_11 | soft tissue 2; adipocytes |
| Module 87 | HPA:040010\_12 | soft tissue 2; adipocytes |
| Module 87 | HPA:048010\_10 | vagina; squamous epithelial cells |
| Module 87 | HPA:048010\_01 | vagina; squamous epithelial cells |
| Module 87 | HPA:048010\_11 | vagina; squamous epithelial cells |
| Module 87 | HPA:048010\_12 | vagina; squamous epithelial cells |
| Module 87 | HPA:018020 | hippocampus; neuronal cells |
| Module 87 | HPA:018020\_01 | hippocampus; neuronal cells |
| Module 87 | HPA:018020\_02 | hippocampus; neuronal cells |
| Module 87 | HPA:018020\_10 | hippocampus; neuronal cells |
| Module 87 | HPA:018020\_11 | hippocampus; neuronal cells |
| Module 87 | HPA:018020\_12 | hippocampus; neuronal cells |
| Module 87 | HPA:017010\_10 | heart muscle; myocytes |
| Module 87 | HPA:017010\_11 | heart muscle; myocytes |
| Module 87 | HPA:017010\_12 | heart muscle; myocytes |
| Module 87 | HPA:017010\_13 | heart muscle; myocytes |
| Module 87 | HPA:009030\_10 | colon; peripheral nerve/ganglion |
| Module 87 | HPA:009030\_11 | colon; peripheral nerve/ganglion |
| Module 87 | HPA:009030\_12 | colon; peripheral nerve/ganglion |
| Module 87 | HPA:033010\_10 | seminal vesicle; glandular cells |
| Module 87 | HPA:033010\_11 | seminal vesicle; glandular cells |
| Module 87 | HPA:033010\_12 | seminal vesicle; glandular cells |
| Module 87 | HPA:033010\_13 | seminal vesicle; glandular cells |
| Module 87 | HPA:021020\_10 | liver; hepatocytes |
| Module 87 | HPA:021020\_11 | liver; hepatocytes |
| Module 87 | HPA:021020\_12 | liver; hepatocytes |
| Module 87 | HPA:007020\_10 | cerebral cortex; glial cells |
| Module 87 | HPA:007020\_11 | cerebral cortex; glial cells |
| Module 87 | HPA:007020\_12 | cerebral cortex; glial cells |
| Module 87 | HPA:037010\_10 | small intestine; glandular cells |
| Module 87 | HPA:037010\_11 | small intestine; glandular cells |
| Module 87 | HPA:037010\_12 | small intestine; glandular cells |
| Module 87 | HPA:020010 | lateral ventricle; glial cells |
| Module 87 | HPA:020010\_10 | lateral ventricle; glial cells |
| Module 87 | HPA:020010\_11 | lateral ventricle; glial cells |
| Module 87 | HPA:020010\_12 | lateral ventricle; glial cells |
| Module 87 | HPA:035020\_10 | skin 1; fibroblasts |
| Module 87 | HPA:035020\_11 | skin 1; fibroblasts |
| Module 87 | HPA:035020\_12 | skin 1; fibroblasts |
| Module 87 | HPA:030010\_10 | prostate; glandular cells |
| Module 87 | HPA:030010\_11 | prostate; glandular cells |
| Module 87 | HPA:030010\_12 | prostate; glandular cells |
| Module 87 | HPA:009010\_10 | colon; endothelial cells |
| Module 87 | HPA:009010\_11 | colon; endothelial cells |
| Module 87 | HPA:003010\_02 | bone marrow; hematopoietic cells |
| Module 87 | HPA:003010\_10 | bone marrow; hematopoietic cells |
| Module 87 | HPA:003010\_11 | bone marrow; hematopoietic cells |
| Module 87 | HPA:003010\_12 | bone marrow; hematopoietic cells |
| Module 87 | HPA:025010\_02 | oral mucosa; squamous epithelial cells |
| Module 87 | HPA:025010\_10 | oral mucosa; squamous epithelial cells |
| Module 87 | HPA:025010\_11 | oral mucosa; squamous epithelial cells |
| Module 87 | HPA:025010\_12 | oral mucosa; squamous epithelial cells |
| Module 87 | HPA:012000 | endometrium 2 |
| Module 87 | HPA:012010 | endometrium 2; cells in endometrial stroma |
| Module 87 | HPA:012010\_10 | endometrium 2; cells in endometrial stroma |
| Module 87 | HPA:012010\_01 | endometrium 2; cells in endometrial stroma |
| Module 87 | HPA:012010\_02 | endometrium 2; cells in endometrial stroma |
| Module 87 | HPA:012010\_11 | endometrium 2; cells in endometrial stroma |
| Module 87 | HPA:012010\_12 | endometrium 2; cells in endometrial stroma |
| Module 87 | HPA:012020 | endometrium 2; glandular cells |
| Module 87 | HPA:012020\_01 | endometrium 2; glandular cells |
| Module 87 | HPA:012020\_10 | endometrium 2; glandular cells |
| Module 87 | HPA:012020\_11 | endometrium 2; glandular cells |
| Module 87 | HPA:012020\_12 | endometrium 2; glandular cells |
| Module 87 | HPA:039030\_10 | soft tissue 1; fibroblasts |
| Module 87 | HPA:039030\_11 | soft tissue 1; fibroblasts |
| Module 87 | HPA:039030\_12 | soft tissue 1; fibroblasts |
| Module 87 | HPA:023000 | lymph node |
| Module 87 | HPA:023020 | lymph node; non-germinal center cells |
| Module 87 | HPA:023020\_01 | lymph node; non-germinal center cells |
| Module 87 | HPA:023020\_02 | lymph node; non-germinal center cells |
| Module 87 | HPA:023020\_10 | lymph node; non-germinal center cells |
| Module 87 | HPA:023020\_11 | lymph node; non-germinal center cells |
| Module 87 | HPA:023020\_12 | lymph node; non-germinal center cells |
| Module 87 | HPA:023020\_13 | lymph node; non-germinal center cells |
| Module 87 | HPA:006020\_10 | cerebellum; cells in granular layer |
| Module 87 | HPA:006020\_11 | cerebellum; cells in granular layer |
| Module 87 | HPA:006020\_12 | cerebellum; cells in granular layer |
| Module 87 | HPA:029020\_10 | placenta; trophoblastic cells |
| Module 87 | HPA:029020\_02 | placenta; trophoblastic cells |
| Module 87 | HPA:029020\_11 | placenta; trophoblastic cells |
| Module 87 | HPA:029020\_12 | placenta; trophoblastic cells |
| Module 87 | HPA:027020\_10 | pancreas; islets of langerhans |
| Module 87 | HPA:027020\_11 | pancreas; islets of langerhans |
| Module 87 | HPA:027020\_12 | pancreas; islets of langerhans |
| Module 87 | HPA:005010\_10 | bronchus; respiratory epithelial cells |
| Module 87 | HPA:005010\_11 | bronchus; respiratory epithelial cells |
| Module 87 | HPA:005010\_12 | bronchus; respiratory epithelial cells |
| Module 87 | HPA:005010\_13 | bronchus; respiratory epithelial cells |
| Module 87 | HPA:043010\_10 | stomach 2; glandular cells |
| Module 87 | HPA:043010\_11 | stomach 2; glandular cells |
| Module 87 | HPA:043010\_12 | stomach 2; glandular cells |
| Module 87 | HPA:004010 | breast; adipocytes |
| Module 87 | HPA:004010\_10 | breast; adipocytes |
| Module 87 | HPA:004010\_11 | breast; adipocytes |
| Module 87 | HPA:004010\_12 | breast; adipocytes |
| Module 87 | HPA:002020\_10 | appendix; lymphoid tissue |
| Module 87 | HPA:002020\_11 | appendix; lymphoid tissue |
| Module 87 | HPA:002020\_12 | appendix; lymphoid tissue |
| Module 87 | HPA:002020\_13 | appendix; lymphoid tissue |
| Module 87 | HPA:018010 | hippocampus; glial cells |
| Module 87 | HPA:018010\_10 | hippocampus; glial cells |
| Module 87 | HPA:018010\_11 | hippocampus; glial cells |
| Module 87 | HPA:018010\_12 | hippocampus; glial cells |
| Module 87 | HPA:040030\_10 | soft tissue 2; fibroblasts |
| Module 87 | HPA:040030\_11 | soft tissue 2; fibroblasts |
| Module 87 | HPA:040030\_12 | soft tissue 2; fibroblasts |
| Module 87 | HPA:008020\_02 | cervix, uterine; squamous epithelial cells |
| Module 87 | HPA:008020\_10 | cervix, uterine; squamous epithelial cells |
| Module 87 | HPA:008020\_11 | cervix, uterine; squamous epithelial cells |
| Module 87 | HPA:008020\_12 | cervix, uterine; squamous epithelial cells |
| Module 87 | HPA:013010\_02 | epididymis; glandular cells |
| Module 87 | HPA:013010\_03 | epididymis; glandular cells |
| Module 87 | HPA:013010\_10 | epididymis; glandular cells |
| Module 87 | HPA:013010\_11 | epididymis; glandular cells |
| Module 87 | HPA:013010\_12 | epididymis; glandular cells |
| Module 87 | HPA:013010\_13 | epididymis; glandular cells |
| Module 87 | HPA:010010\_10 | duodenum; glandular cells |
| Module 87 | HPA:010010\_11 | duodenum; glandular cells |
| Module 87 | HPA:010010\_12 | duodenum; glandular cells |
| Module 87 | HPA:010010\_13 | duodenum; glandular cells |
| Module 87 | HPA:026010\_11 | ovary; follicle cells |
| Module 87 | HPA:023010\_02 | lymph node; germinal center cells |
| Module 87 | HPA:023010\_03 | lymph node; germinal center cells |
| Module 87 | HPA:023010\_10 | lymph node; germinal center cells |
| Module 87 | HPA:023010\_11 | lymph node; germinal center cells |
| Module 87 | HPA:023010\_12 | lymph node; germinal center cells |
| Module 87 | HPA:023010\_13 | lymph node; germinal center cells |
| Module 87 | HPA:020020\_10 | lateral ventricle; neuronal cells |
| Module 87 | HPA:020020\_11 | lateral ventricle; neuronal cells |
| Module 87 | HPA:020020\_12 | lateral ventricle; neuronal cells |
| Module 87 | HPA:042010\_10 | stomach 1; glandular cells |
| Module 87 | HPA:042010\_11 | stomach 1; glandular cells |
| Module 87 | HPA:042010\_12 | stomach 1; glandular cells |
| Module 87 | HPA:042010\_13 | stomach 1; glandular cells |
| Module 87 | HPA:045000 | thyroid gland |
| Module 87 | HPA:045010 | thyroid gland; glandular cells |
| Module 87 | HPA:045010\_10 | thyroid gland; glandular cells |
| Module 87 | HPA:045010\_11 | thyroid gland; glandular cells |
| Module 87 | HPA:045010\_12 | thyroid gland; glandular cells |
| Module 87 | HPA:045010\_13 | thyroid gland; glandular cells |
| Module 87 | HPA:019010 | kidney; cells in glomeruli |
| Module 87 | HPA:019010\_10 | kidney; cells in glomeruli |
| Module 87 | HPA:019010\_11 | kidney; cells in glomeruli |
| Module 87 | HPA:019010\_12 | kidney; cells in glomeruli |
| Module 87 | HPA:041010\_10 | spleen; cells in red pulp |
| Module 87 | HPA:041010\_11 | spleen; cells in red pulp |
| Module 87 | HPA:041010\_12 | spleen; cells in red pulp |
| Module 87 | HPA:027010\_10 | pancreas; exocrine glandular cells |
| Module 87 | HPA:027010\_11 | pancreas; exocrine glandular cells |
| Module 87 | HPA:027010\_12 | pancreas; exocrine glandular cells |
| Module 87 | HPA:026020 | ovary; ovarian stroma cells |
| Module 87 | HPA:026020\_01 | ovary; ovarian stroma cells |
| Module 87 | HPA:026020\_10 | ovary; ovarian stroma cells |
| Module 87 | HPA:026020\_11 | ovary; ovarian stroma cells |
| Module 87 | HPA:026020\_12 | ovary; ovarian stroma cells |
| Module 87 | HPA:008010\_10 | cervix, uterine; glandular cells |
| Module 87 | HPA:008010\_11 | cervix, uterine; glandular cells |
| Module 87 | HPA:008010\_12 | cervix, uterine; glandular cells |
| Module 87 | HPA:007010\_10 | cerebral cortex; endothelial cells |
| Module 87 | HPA:007010\_11 | cerebral cortex; endothelial cells |
| Module 87 | HPA:007010\_12 | cerebral cortex; endothelial cells |
| Module 87 | HPA:032010\_10 | salivary gland; glandular cells |
| Module 87 | HPA:032010\_11 | salivary gland; glandular cells |
| Module 87 | HPA:032010\_12 | salivary gland; glandular cells |
| Module 87 | HPA:032010\_13 | salivary gland; glandular cells |
| Module 87 | HPA:035010 | skin 1; langerhans |
| Module 87 | HPA:035010\_10 | skin 1; langerhans |
| Module 87 | HPA:035010\_11 | skin 1; langerhans |
| Module 87 | HPA:035010\_12 | skin 1; langerhans |
| Module 87 | HPA:046010\_01 | tonsil; germinal center cells |
| Module 87 | HPA:046010\_10 | tonsil; germinal center cells |
| Module 87 | HPA:046010\_11 | tonsil; germinal center cells |
| Module 87 | HPA:046010\_12 | tonsil; germinal center cells |
| Module 87 | HPA:046010\_13 | tonsil; germinal center cells |
| Module 87 | HPA:041020\_10 | spleen; cells in white pulp |
| Module 87 | HPA:041020\_11 | spleen; cells in white pulp |
| Module 87 | HPA:041020\_12 | spleen; cells in white pulp |
| Module 87 | HPA:024000 | nasopharynx |
| Module 87 | HPA:024010 | nasopharynx; respiratory epithelial cells |
| Module 87 | HPA:024010\_10 | nasopharynx; respiratory epithelial cells |
| Module 87 | HPA:024010\_11 | nasopharynx; respiratory epithelial cells |
| Module 87 | HPA:024010\_12 | nasopharynx; respiratory epithelial cells |
| Module 87 | HPA:024010\_13 | nasopharynx; respiratory epithelial cells |
| Module 87 | HPA:014010\_10 | esophagus; squamous epithelial cells |
| Module 87 | HPA:014010\_11 | esophagus; squamous epithelial cells |
| Module 87 | HPA:014010\_12 | esophagus; squamous epithelial cells |
| Module 87 | HPA:007040\_10 | cerebral cortex; neuropil |
| Module 87 | HPA:007040\_11 | cerebral cortex; neuropil |
| Module 87 | HPA:046030\_10 | tonsil; squamous epithelial cells |
| Module 87 | HPA:046030\_01 | tonsil; squamous epithelial cells |
| Module 87 | HPA:046030\_02 | tonsil; squamous epithelial cells |
| Module 87 | HPA:046030\_11 | tonsil; squamous epithelial cells |
| Module 87 | HPA:046030\_12 | tonsil; squamous epithelial cells |
| Module 87 | HPA:035030 | skin 1; keratinocytes |
| Module 87 | HPA:035030\_10 | skin 1; keratinocytes |
| Module 87 | HPA:035030\_11 | skin 1; keratinocytes |
| Module 87 | HPA:035030\_12 | skin 1; keratinocytes |
| Module 87 | HPA:021010 | liver; bile duct cells |
| Module 87 | HPA:021010\_01 | liver; bile duct cells |
| Module 87 | HPA:021010\_10 | liver; bile duct cells |
| Module 87 | HPA:021010\_11 | liver; bile duct cells |
| Module 87 | HPA:021010\_12 | liver; bile duct cells |
| Module 87 | HPA:039010\_10 | soft tissue 1; adipocytes |
| Module 87 | HPA:039010\_11 | soft tissue 1; adipocytes |
| Module 87 | HPA:039010\_12 | soft tissue 1; adipocytes |
| Module 87 | HPA:031010\_10 | rectum; glandular cells |
| Module 87 | HPA:031010\_11 | rectum; glandular cells |
| Module 87 | HPA:031010\_12 | rectum; glandular cells |
| Module 87 | HPA:031010\_13 | rectum; glandular cells |
| Module 87 | HPA:004030\_10 | breast; myoepithelial cells |
| Module 87 | HPA:004030\_11 | breast; myoepithelial cells |
| Module 87 | HPA:004030\_12 | breast; myoepithelial cells |
| Module 87 | HPA:034010\_10 | skeletal muscle; myocytes |
| Module 87 | HPA:034010\_11 | skeletal muscle; myocytes |
| Module 87 | HPA:034010\_12 | skeletal muscle; myocytes |
| Module 87 | HPA:046020\_10 | tonsil; non-germinal center cells |
| Module 87 | HPA:046020\_11 | tonsil; non-germinal center cells |
| Module 87 | HPA:046020\_12 | tonsil; non-germinal center cells |
| Module 87 | HPA:046020\_13 | tonsil; non-germinal center cells |
| Module 87 | HPA:022010\_10 | lung; macrophages |
| Module 87 | HPA:022010\_11 | lung; macrophages |
| Module 87 | HPA:022010\_12 | lung; macrophages |
| Module 87 | HPA:022010\_13 | lung; macrophages |
| Module 87 | HPA:022020\_10 | lung; pneumocytes |
| Module 87 | HPA:022020\_11 | lung; pneumocytes |
| Module 87 | HPA:022020\_12 | lung; pneumocytes |
| Module 87 | HPA:047010\_10 | urinary bladder; urothelial cells |
| Module 87 | HPA:047010\_11 | urinary bladder; urothelial cells |
| Module 87 | HPA:047010\_12 | urinary bladder; urothelial cells |
| Module 87 | HPA:047010\_13 | urinary bladder; urothelial cells |
| Module 87 | HPA:044020\_10 | testis; cells in seminiferous ducts |
| Module 87 | HPA:044020\_11 | testis; cells in seminiferous ducts |
| Module 87 | HPA:044020\_12 | testis; cells in seminiferous ducts |
| Module 87 | HPA:036010\_01 | skin 2; epidermal cells |
| Module 87 | HPA:036010\_02 | skin 2; epidermal cells |
| Module 87 | HPA:036010\_10 | skin 2; epidermal cells |
| Module 87 | HPA:036010\_11 | skin 2; epidermal cells |
| Module 87 | HPA:036010\_12 | skin 2; epidermal cells |
| Module 87 | HPA:011000 | endometrium 1 |
| Module 87 | HPA:011010 | endometrium 1; cells in endometrial stroma |
| Module 87 | HPA:011010\_10 | endometrium 1; cells in endometrial stroma |
| Module 87 | HPA:011010\_11 | endometrium 1; cells in endometrial stroma |
| Module 87 | HPA:011010\_12 | endometrium 1; cells in endometrial stroma |
| Module 87 | HPA:004020 | breast; glandular cells |
| Module 87 | HPA:004020\_10 | breast; glandular cells |
| Module 87 | HPA:004020\_01 | breast; glandular cells |
| Module 87 | HPA:004020\_11 | breast; glandular cells |
| Module 87 | HPA:004020\_12 | breast; glandular cells |
| Module 87 | HPA:004020\_13 | breast; glandular cells |
| Module 87 | HPA:035040\_10 | skin 1; melanocytes |
| Module 87 | HPA:035040\_11 | skin 1; melanocytes |
| Module 87 | HPA:035040\_12 | skin 1; melanocytes |
| Module 87 | HPA:002010\_10 | appendix; glandular cells |
| Module 87 | HPA:002010\_11 | appendix; glandular cells |
| Module 87 | HPA:002010\_12 | appendix; glandular cells |
| Module 87 | HPA:015010\_10 | fallopian tube; glandular cells |
| Module 87 | HPA:015010\_11 | fallopian tube; glandular cells |
| Module 87 | HPA:015010\_12 | fallopian tube; glandular cells |
| Module 87 | HPA:015010\_13 | fallopian tube; glandular cells |
| Module 87 | HPA:009020\_10 | colon; glandular cells |
| Module 87 | HPA:009020\_11 | colon; glandular cells |
| Module 87 | HPA:009020\_12 | colon; glandular cells |
| Module 87 | HPA:009020\_13 | colon; glandular cells |
| Module 87 | HPA:007030\_10 | cerebral cortex; neuronal cells |
| Module 87 | HPA:007030\_11 | cerebral cortex; neuronal cells |
| Module 87 | HPA:007030\_12 | cerebral cortex; neuronal cells |
| Module 87 | HPA:007030\_13 | cerebral cortex; neuronal cells |
| Module 87 | HPA:006010\_10 | cerebellum; purkinje cells |
| Module 87 | HPA:006010\_11 | cerebellum; purkinje cells |
| Module 87 | HPA:006010\_12 | cerebellum; purkinje cells |
| Module 87 | HPA:006010\_13 | cerebellum; purkinje cells |
| Module 87 | HPA:016010\_10 | gallbladder; glandular cells |
| Module 87 | HPA:016010\_11 | gallbladder; glandular cells |
| Module 87 | HPA:016010\_12 | gallbladder; glandular cells |
| Module 87 | HPA:016010\_13 | gallbladder; glandular cells |
| Module 87 | HPA:040040\_10 | soft tissue 2; peripheral nerve |
| Module 87 | HPA:040040\_11 | soft tissue 2; peripheral nerve |
| Module 87 | HPA:006030 | cerebellum; cells in molecular layer |
| Module 87 | HPA:006030\_10 | cerebellum; cells in molecular layer |
| Module 87 | HPA:006030\_11 | cerebellum; cells in molecular layer |
| Module 87 | HPA:006030\_12 | cerebellum; cells in molecular layer |
| Module 87 | HPA:011020\_10 | endometrium 1; glandular cells |
| Module 87 | HPA:011020\_11 | endometrium 1; glandular cells |
| Module 87 | HPA:011020\_12 | endometrium 1; glandular cells |
| Module 87 | HPA:011020\_13 | endometrium 1; glandular cells |
| Module 87 | HPA:039020 | soft tissue 1; chondrocytes |
| Module 87 | HPA:039020\_01 | soft tissue 1; chondrocytes |
| Module 87 | HPA:039020\_02 | soft tissue 1; chondrocytes |
| Module 87 | HPA:039020\_10 | soft tissue 1; chondrocytes |
| Module 87 | HPA:039020\_11 | soft tissue 1; chondrocytes |
| Module 87 | HPA:039020\_12 | soft tissue 1; chondrocytes |
| Module 87 | HPA:039020\_13 | soft tissue 1; chondrocytes |
| Module 87 | HPA:019020\_10 | kidney; cells in tubules |
| Module 87 | HPA:019020\_11 | kidney; cells in tubules |
| Module 87 | HPA:019020\_12 | kidney; cells in tubules |
| Module 87 | HPA:019020\_13 | kidney; cells in tubules |
| Module 87 | HPA:028000 | parathyroid gland |
| Module 87 | HPA:028010 | parathyroid gland; glandular cells |
| Module 87 | HPA:028010\_10 | parathyroid gland; glandular cells |
| Module 87 | HPA:028010\_01 | parathyroid gland; glandular cells |
| Module 87 | HPA:028010\_02 | parathyroid gland; glandular cells |
| Module 87 | HPA:028010\_11 | parathyroid gland; glandular cells |
| Module 87 | HPA:028010\_12 | parathyroid gland; glandular cells |
| Module 87 | HPA:028010\_13 | parathyroid gland; glandular cells |
| Module 87 | HPA:001010\_10 | adrenal gland; glandular cells |
| Module 87 | HPA:001010\_11 | adrenal gland; glandular cells |
| Module 87 | HPA:001010\_12 | adrenal gland; glandular cells |
| Module 87 | HPA:038000 | smooth muscle |
| Module 87 | HPA:038010 | smooth muscle; smooth muscle cells |
| Module 87 | HPA:038010\_01 | smooth muscle; smooth muscle cells |
| Module 87 | HPA:038010\_10 | smooth muscle; smooth muscle cells |
| Module 87 | HPA:038010\_11 | smooth muscle; smooth muscle cells |
| Module 87 | HPA:038010\_12 | smooth muscle; smooth muscle cells |
| Module 87 | HPA:044010\_10 | testis; leydig cells |
| Module 87 | HPA:044010\_11 | testis; leydig cells |
| Module 87 | HPA:044010\_12 | testis; leydig cells |
| Module 87 | KEGG:05010 | alzheimer's disease |
| Module 87 | KEGG:05012 | parkinson's disease |
| Module 87 | KEGG:04932 | non-alcoholic fatty liver disease (nafld) |
| Module 87 | KEGG:00670 | one carbon pool by folate |
| Module 88 | OMIM:613794 | retinitis pigmentosa 20; rp20 |
| Module 88 | OMIM:204100 | leber congenital amaurosis 2; lca2; amaurosis congenita of leber ii |
| Module 89 | CORUM:3066 | rna polymerase ii complex, chromatin structure modifying |
| Module 89 | HPA:011010\_12 | endometrium 1; cells in endometrial stroma |
| Module 89 | OMIM:615637 | mental retardation, autosomal recessive 41; mrt41 |
| Module 89 | OMIM:610048 | corneal dystrophy, congenital stromal; cscd; congenital stromal corneal dystrophy |
| Module 89 | OMIM:261500 | eosinophil peroxidase deficiency; epxd; eosinophil peroxidase deficiency, partial; peroxidase and phospholipid deficiency in eosinophils; presentey anomaly |
| Module 89 | OMIM:607626 | ichthyosis, leukocyte vacuoles, alopecia, and sclerosing cholangitis; ilvasc; ichthyosis-sclerosing cholangitis syndrome; neonatal ichthyosis-sclerosing cholangitis syndrome; nisch syndrome |
| Module 89 | OMIM:601358 | nicolaides-baraitser syndrome; ncbrs; sparse hair and mental retardation; nbs |
| Module 89 | OMIM:180849 | rubinstein-taybi syndrome |
| Module 90 | - | - |
| Module 91 | TF:M00953\_1 | factor: ar; motif: nnngnrrgnacanngtgttctnnnnnn; match class: 1 |
| Module 92 | OMIM:616216 | thrombocytopenia 5; thc5; thrombocytopenia 5 with increased susceptibility to malignancy; thrombocytopenia, autosomal dominant, 5 |
| Module 92 | TF:M06650\_1 | factor: znf670; motif: nntgtracccgn; match class: 1 |
| Module 93 | - | - |
| Module 94 | GO:0012505 | endomembrane system |
| Module 94 | OMIM:615530 | parkinson disease 20, early-onset; park20 |
| Module 94 | OMIM:146800 | ichthyosis bullosa of siemens; ibs; ichthyosis, bullous typeichthyosis exfoliativa, included |
| Module 94 | OMIM:300868 | multiple congenital anomalies-hypotonia-seizures syndrome 2; mcahs2; epileptic encephalopathy, early infantile, 20; eiee20 |
| Module 94 | OMIM:613751 | heterotaxy, visceral, 4, autosomal; htx4 |
| Module 94 | OMIM:616511 | maturity-onset diabetes of the young, type 14; mody14 |
| Module 94 | OMIM:601110 | congenital disorder of glycosylation, type id; cdg1d; cdg id; cdgid; carbohydrate-deficient glycoprotein syndrome, type iv, formerly; cdgs4,formerly; cdgs, type iv, formerly |
| Module 94 | OMIM:310400 | myopathy, centronuclear, x-linked; cnmx; myotubular myopathy, x-linked; mtmx; xlmtm; myotubular myopathy 1; mtm1 |
| Module 94 | OMIM:614886 | peroxisome biogenesis disorder 12a (zellweger); pbd12aperoxisome biogenesis disorder, complementation group 14, included; cg14, included; peroxisome biogenesis disorder, complementation group j, included; cgj, included |
| Module 95 | - | - |

Note: Annotations were omitted if unknown