Supplemental Legends

Supplemental Fig. 1 - Replicate GeneChips cluster faithfully with each other using GO distributions. Depicted are dendrograms prepared by clustering expression profiles in terms of GO distribution as for Figs. 1 & 2. Each expression profile in this case was derived by comparing a single Affymetrix GeneChip to a baseline comprising all the replicates of the opposite differentiation state. For example, the first GeneChip from the lateral ventricle brain from Ramalho-Santos et al. (2002) was referenced to both Neural SC chips from the same study, and the first Neural SC chip was referenced to both brain chips. Note how in almost all cases expression profiles prepared from individual GeneChips cluster with their replicates, and all SC expression profiles still cluster separately from those of differentiated expression profiles. The most divergent replicates are the intestinal polyp GeneChips, each of which, according to the authors, was prepared from a different polyp; thus, these profiles may diverge due to biological differences and not due to technical problems inherent to GO distribution-based clustering. A) and B) were generated identically, because the experiments from Goodell and co-workers comprised so many replicate GeneChips, they were separated for clarity of presentation.

Supplemental Fig. 2 – Plots of GO terms used for one-way ANOVA with Bonferroni correction on expression profiles performed in replicates. Lists of preferentially expressed genes in each cell population were generated from individual GeneChips in experiments where replicate GeneChips had been performed. Variance between levels of GO term representation in replicate gene lists were used as the basis for one-way ANOVAs comparing the variance among replicates in each cell population with the replicates and variance of all other cell populations, with no a priori designation of whether each population was SC-specific or DC-specific. Mean (±SD) fractional representations of each GO term within each cell population are plotted. Red: profiles presumed to be DCs; Blue: presumed SC populations. The tables under each plot show statistically significant different populations as determined by Bonferroni multiple comparison post-test with cutoff for significance set as $p<0.05$. Note how with the distinguishing GO terms “nucleus” (A), “integral to membrane” (B), and “RNA binding” (C), SCs tend to be similar to every other SC profile and statistically different from the differentiated populations. The non-distinguishing term “protein binding” (D) shows that most individual populations are similar to most other populations, regardless of whether they are biologically likely to be SCs or DCs. For those sporadic individual population-by-population comparisons that do show significant differences in “protein binding”, just as many differ within each category (*e.g.*, SC vs. SC) as across categories (SC vs. Differentiated). Note also that the bone marrow profile (8) behaves more like an intermediate population, perhaps because it contains a large reservoir of progenitor cells of intermediate differentiation as well as DCs.

Supplemental Table 1. Sources of primary data for initial profiles. Data sources for the initial dataset (used in Figs. 1 and 2) are given grouped by tissue type. Sources are indicated by investigator and citation.

Supplemental Table 2. Sources of primary data for prospectively analyzed profiles. Sources described as for Supplemental Table 1. Note that the colonic dividing crypt cell profile was generated *de novo* for the current manuscript.

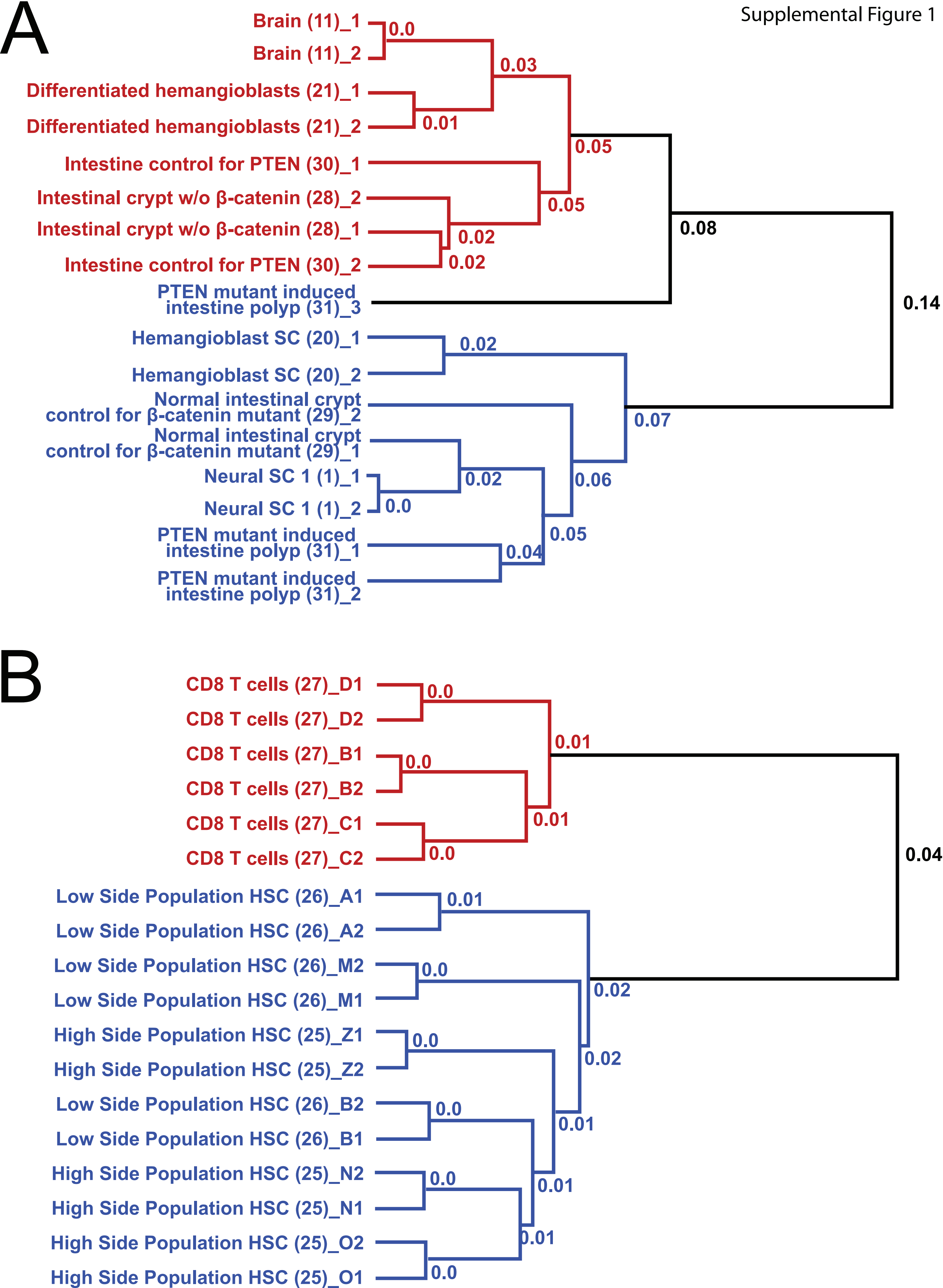
Supplemental Table 3. Algorithm for deriving lists of genes preferentially expressed in each cell population. For each cell population, the algorithm used to determine the genes preferentially expressed in that cell population is shown. Note that the list of preferentially expressed genes was the input for the GOurmet software, which subsequently re-expressed each gene list in terms of the GO terms associated with the genes. These GO term distributions were then used to represent each cell population gene expression profile in all the figures in the current manuscript. For example, the Neural SC 1 expression profile was determined by identifying the genes whose expression was significantly enriched in duplicate Neural SC GeneChips from

Melton and co-workers relative to duplicate brain GeneChips in the same study. In most cases, results from all replicates in a given study were averaged and, wherever possible, samples of one differentiation state were referenced to samples of the opposite differentiation state in the same study.

Supplemental Table 4. GO terms significantly increased in TAs. Those GO terms changed with $p<0.05$ by pairwise T-tests between TA and SC populations are depicted. Note that all but one of these also differs in independent T-tests between TA and DC populations. The list does not include: 1) GO terms changed by less than 0.7-fold on a log2 scale (*i.e.* increased by only ~1.6-fold or decreased by only 0.62-fold); 2) GO terms whose fractional representation on average in the TA population was less than 1%.

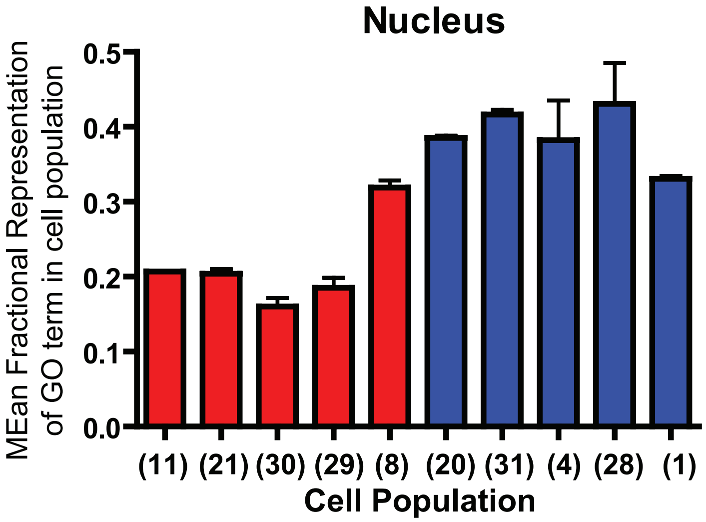
Supplemental Workbook. Excel Workbook showing how a single expression profile (colonic transit amplifying cell population) was re-expressed as a function of the fractional representation of its associated GO terms. "Summary" worksheet shows: the number of genes that constitute the colon transit amplifying cell expression profile; the number of GO terms associated with those genes; the percentage of genes that had been annotated well enough to have associated GO terms; and the breakdown of the GO terms into each of the principal GO term categories. "Gene→GO" worksheet shows each gene in the colonic TA expression profile in the first column, followed by all the GO terms associated with that gene (note most genes are associated with multiple GO terms). "GO→gene" worksheet shows the GO term in the first column, followed by all the genes associated with that GO term. "Fract Rep" worksheet shows the fractional representation of each GO term within the list of genes, followed by the averages fractional representation of that GO term among all the expression profiles of the three major categories of expression profile for reference. Thus, for "nucleus", 47% of the genes with GO terms in the colon transit amplifying profile were associated with the GO term "nucleus", compared to 46% for TA cells on average, 35% for SC and 22% for DC.

Supplemental Figure 1



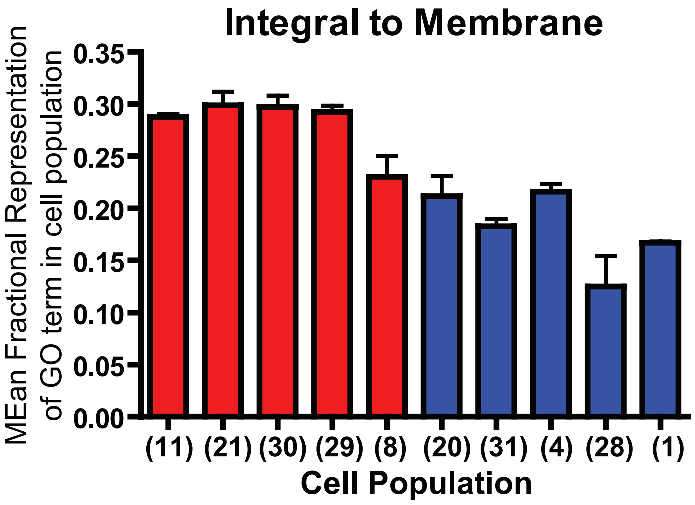
Supplemental Figure 2

A



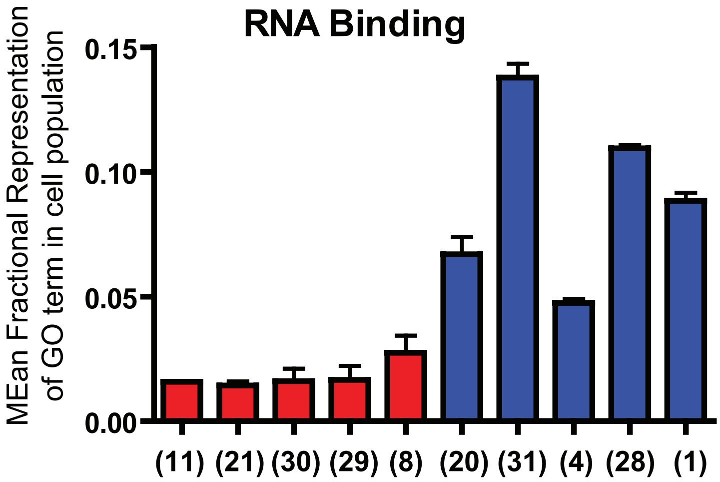
Population	Significantly Different Populations	Similar Populations
(1)	(11) (21) (29) (30)	(4) (20) (28) (31) (8)
(4)	(11) (21) (29) (30)	(1) (20) (28) (31) (8)
(20)	(11) (21) (29) (30)	(1) (4) (28) (31) (8)
(28)	(11) (21) (29) (30)	(1) (4) (20) (31) (8)
(31)	(11) (21) (29) (30)	(1) (4) (20) (28) (8)
(8)		(11) (21) (29) (30) (1) (4) (20) (28) (31)
(11)	(1) (20) (28) (31)	(8) (21) (29) (30) (4)
(21)	(1) (4) (20) (28) (31)	(8) (11) (29) (30)
(29)	(1) (20) (28) (31)	(8) (11) (21) (30) (4)
(30)	(1) (4) (20) (28) (31)	(8) (11) (21) (29)

B



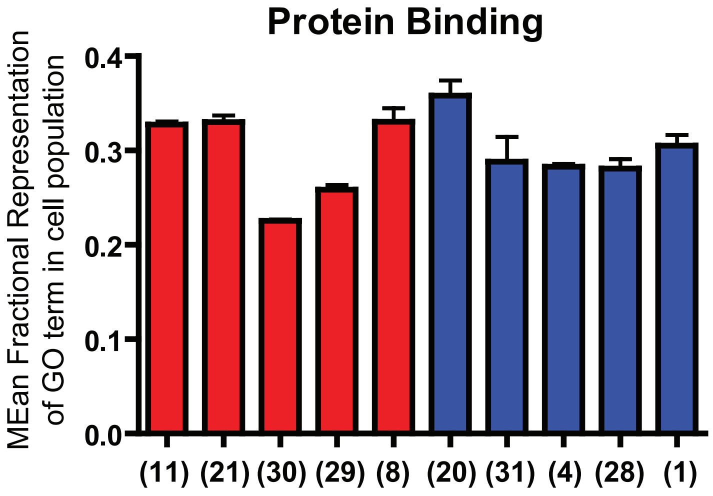
Population	Significantly Different Populations	Similar Populations
(1)	(11) (21) (29) (30)	(4) (20) (28) (31) (8)
(4)		(1) (20) (28) (31) (8) (11) (21) (29) (30)
(20)		(1) (4) (28) (31) (8) (11) (21) (29) (30)
(28)	(8) (11) (21) (29) (30)	(1) (4) (20) (31)
(31)	(11) (21) (29) (30)	(1) (4) (20) (28) (8)
(8)	(28)	(11) (21) (29) (30) (1) (4) (20) (31)
(11)	(1) (28) (31)	(8) (21) (29) (30) (4) (20)
(21)	(1) (28) (31)	(8) (11) (29) (30) (4) (20)
(29)	(1) (28) (31)	(8) (11) (21) (30) (4) (20)
(30)	(1) (28) (31)	(8) (11) (21) (29) (4) (20)

C



Population	Significantly Different Populations	Similar Populations
(1)	(8) (11) (21) (29) (30) (4) (31)	(20) (28)
(4)	(8) (11) (21) (29) (30) (1) (28) (31)	(20)
(20)	(8) (11) (21) (29) (30) (28) (31)	(1) (4)
(28)	(8) (11) (21) (29) (30) (4) (20)	(1) (31)
(31)	(8) (11) (21) (29) (30) (1) (4) (20)	(28) (31)
(8)	(1) (20) (28) (31)	(11) (21) (29) (30) (4)
(11)	(1) (4) (20) (28) (31)	(8) (21) (29) (30)
(21)	(1) (4) (20) (28) (31)	(8) (11) (29) (30)
(29)	(1) (4) (20) (28) (31)	(8) (11) (21) (30)
(30)	(1) (4) (20) (28) (31)	(8) (11) (21) (29)

D



Population	Significantly Different Populations	Similar Populations
(1)		
(4)		(1) (20) (28) (31) (8) (11) (21) (29) (30)
(20)	(29) (30)	(1) (4) (28) (31) (8) (11) (21)
(28)		(1) (4) (20) (31) (8) (11) (21) (29) (30)
(31)		(1) (4) (20) (28) (8) (11) (21) (29) (30)
(8)		(11) (21) (29) (30) (1) (4) (20) (28) (31)
(11)	(30)	(8) (21) (29) (1) (4) (20) (28) (31)
(21)	(30)	(8) (11) (29) (1) (4) (20) (28) (31)
(29)	(20)	(8) (11) (21) (30) (1) (4) (28) (31)
(30)	(1) (20) (8) (11) (21)	(29) (4) (28) (31)

Supplemental Table 1

ID	Sample	Data Type	Source
(1)	Neural SC 1	Affymetrix mgU74	Douglas A. Melton (Ramalho-Santos et al., 2002) --http://mcb.harvard.edu/melton/index.html --http://www.ebi.ac.uk/arrayexpress/ Accession: E-MEXP-1158
(2)	Neural SC 2	Affymetrix mgU74	Ihor R. Lemischka (Ivanova et al., 2002) --http://www.cbil.upenn.edu/RAD3/php/displayStudy.php?study_id=270
(3)	Neural SC 3	Affymetrix mgU74	Fred H. Gage (D'Amour and Gage, 2003) --available upon request of F.H. Gage
(4)	Hematopoietic SC 1	Affymetrix mgU74	Douglas A. Melton (Ramalho-Santos et al., 2002) --http://mcb.harvard.edu/melton/index.html --http://www.ebi.ac.uk/arrayexpress/ Accession: E-MEXP-1158
(5)	Hematopoietic SC 2	Affymetrix mgU74	Ihor R. Lemischka (Ivanova et al., 2002) --http://www.cbil.upenn.edu/RAD3/php/displayStudy.php?study_id=270
(6)	Hematopoietic SC (EST)	subtracted ESTs	Ihor R. Lemischka --Unigene Library 11946
(7)	Skin SC	Affymetrix mgU74	Elaine Fuchs (Tumbar et al., 2004) --http://www.rockefeller.edu/labheads/fuchs/database.php
(8)	Bone Marrow 1	Affymetrix mgU74	Douglas A. Melton (Ramalho-Santos et al., 2002) --http://mcb.harvard.edu/melton/index.html --http://www.ebi.ac.uk/arrayexpress/ Accession: E-MEXP-1158
(9)	Bone Marrow 2	Affymetrix mgU74	Ihor R. Lemischka (Ivanova et al., 2002) --http://www.cbil.upenn.edu/RAD3/php/displayStudy.php?study_id=270
(10)	Small Intestine	Affymetrix mu11K	Lora V. Hooper (Hooper et al., 2001) --available upon request of L.V. Hooper
(11)	Brain	Affymetrix mgU74	Douglas A. Melton (Ramalho-Santos et al., 2002) --http://mcb.harvard.edu/melton/index.html --http://www.ebi.ac.uk/arrayexpress/ Accession: E-MEXP-1158
(12)	Stomach Chief Cells	Affymetrix MOE430v2	Jason C. Mills (Ramsey et al., 2007) --GEO: GSM113347
(13)	Stomach Surface Cells	Affymetrix MOE430v2	Jason C. Mills (Ramsey et al., 2007) --GEO: GSM113348
(14)	Small Intestine SC	Affymetrix mu11K	Thaddeus S. Stappenbeck (Stappenbeck et al., 2003) --http://gutsc.wustl.edu/supplement
(15)	Mesenchymal SC (EST)	subtracted ESTs	Akihiro Umezawa (Sharov et al., 2003) --Unigene Library 10031
(16)	Gastric SC	Affymetrix mu11K	Jason C. Mills (Mills et al., 2002) --http://gutsc.wustl.edu/supplement
(17)	Gastric SC (EST)	subtracted ESTs	Jason C. Mills --Unigene Library 14504
(18)	Retina	Affymetrix mgU74	N. O. Fortunel (Fortunel et al., 2003) --http://giscompute.gis.a-star.edu.sg/suppdata_stemness/
(19)	Skin	Affymetrix mgU74	D. W. Mozingo (Feezor et al., 2004) --GEO: GSM7478,GSM7479,GSM7480; Raw chip data available upon request of R.J. Feezor

Supplemental Table 2

ID	Sample	Data Type	Source
(20)	Hemangioblast	Affymetrix mgU74	Kyunghee Choi (Lugus et al., 2007) --GEO:GSM157405-157406
(21)	Differentiated hemangioblasts	Affymetrix mgU74	Kyunghee Choi (Lugus et al., 2007) --GEO:GSM157407-157408
(22)	Differentiated fibroblasts	Affymetrix hgU133v2	George Q. Daly (Park et al., 2007) --GEO:GSM248201-248202, GSM248204
(23)	Induced pluripotent SCs	Affymetrix hgU133v2	George Q. Daly (Park et al., 2007) --GEO:GSM248205-248208
(24)	Embryonic SC	Affymetrix hgU133v2	George Q. Daley (Park et al., 2007) --GEO:GSM248200
(25)	High SP hematopoietic SCs	Affymetrix mgU74	Margaret A. Goodell (Ramos et al., 2006) --GEO:GSM48321-48326
(26)	Low SP hematopoietic SCs	Affymetrix mgU74	Margaret A. Goodell (Ramos et al., 2006) --GEO:GSM48315-48320
(27)	CD8 T cells	Affymetrix mgU74	Margaret A. Goodell (Ramos et al., 2006) --GEO:GSM48327-48332
(28)	Catenin crypt mutant	Affymetrix MOE430v2	Joerg Huelsken (Fevr et al., 2007) --GEO:GSM219116-219117
(29)	Catenin crypt control	Affymetrix MOE430v2	Joerg Huelsken (Fevr et al., 2007) --GEO:GSM219114-219115
(30)	PTEN control	Affymetrix MOE430v2	Linheng Li (He et al., 2007) --GEO:GSM140792, GSM140816
(31)	PTEN mutant (polyp)	Affymetrix MOE430v2	Linheng Li (He et al., 2007) --GEO:GSM140813, GSM140817-140818
(32)	Retinal epithelial progenitor	Affymetrix mgU74	N. O. Fortunel (Fortunel et al., 2003) --http://giscompute.gis.a-star.edu.sg/suppdata_stemness/
(33)	Human colonic crypt cells	cDNA microarray	Xin Chen (Kosinski et al., 2007) --GEO:GSE6894
(34)	Dividing colonic crypt cells	Affymetrix MOE430	Thaddeus Stappenbeck (current manuscript) --GEO:Pending
	Myoblast series for Fig. 2C	Affymetrix hgU133A,B	Michael A. Rudnicki (unpublished) --GEO:GSM86678-GSM86737 Stembase experiment ID E210 (Perez-Iratxeta et al., 2005)

Genes	455
Go Terms	1129
% of Genes with Go Terms:	0.905495
cellular component %	0.159433
molecular function %	0.318866
biological process %	0.521701

1190002H23Rik	cytoplasm	cell cycle
1200016G03Rik		
1500010J02Rik		
1600029D21Rik		
1700022L09Rik	nucleus	
1700097N02Rik		
1810003N24Rik	nucleic acid binding	RNA binding
2010012C16Rik	sex determination	nucleus
2210407C18Rik	extracellular space	
2210411K19Rik		
2310008M10Rik		
2310035K24Rik		
2600005C20Rik		
2610039C10Rik		
2610528M18Rik		
2810026P18Rik		
2810028N01Rik	exonuclease activity	RNA binding
2810417H13Rik	nucleus	mitochondrion
2810421I24Rik		
2810430M08Rik		
3110048L19Rik		
5730507H05Rik	biological process unknown	cellular component unknown
6330416L07Rik	zinc ion binding	nucleus
6330527O06Rik	integral to membrane	membrane
9030408N13Rik		
9830147J24Rik		
A030007L17Rik		
AI132487	transport	integral to membrane
AU020206		
AU021838	magnesium ion binding	ribose phosphate diphosphokinase activity
Aaas	cellular component unknown	biological process unknown
Abce1	nucleoside-triphosphatase activity	ATPase activity
Acsl5	lipid metabolism	peroxisome
Acsm2	cellular component unknown	biological process unknown
Acta2	biological process unknown	protein binding
Actl6a	nucleus	transcription

Ada	methylated-DNA-[protein]-cysteine S-methy	regulation of transcription, DNA-dependent
Agr2	extracellular space	
Aldh18a1	cytoplasm	catalytic activity
Amd1	purine nucleotide metabolism	cytoplasm
Amdhd1	imidazolonepropionase activity	
Amot	ruffle	regulation of cell migration
Anapc1	mitosis	nucleus
Anp32e	phosphatase inhibitor activity	biological process unknown
Ap3m1	transport	protein transport
Apex1	protein binding	cell redox homeostasis
Api5	transport	anti-apoptosis
Apobec3	hydrolase activity, acting on carbon-nitroger	zinc ion binding
Aqp1	transport	integral to membrane
Arfgap1	transport	zinc ion binding
Asf1b	chromatin	nucleosome assembly
Asns	soluble fraction	glutamine metabolism
Aspm	calmodulin binding	biological process unknown
Atp4a	cation transport	integral to membrane
Atp6ap2	hydrogen ion transporter activity	hydrolase activity
Atrn	development	sugar binding
Aurka	protein-tyrosine kinase activity	cell cycle
Aurkb	protein-tyrosine kinase activity	protein binding
B230120H23Rik	protein-tyrosine kinase activity	nucleus
BC023814	transferase activity	methyltransferase activity
BC027231		
BC027344	zinc ion binding	nucleus
BC053440		
Bcl11a	cytoplasm	transcription corepressor activity
Bclaf1	nucleus	protein binding
Birc5	protein binding	nucleus
Blmh	nucleus	proteolysis
Boc	primary spermatocyte growth	protein binding
Brca2	DNA recombination	nucleus
Brrn1	cell division	mitosis
Bub1b	nucleus	kinetochore
Bxdc1	cellular component unknown	biological process unknown
Bysl	cellular component unknown	molecular function unknown

Bzw1	transcription regulator activity	G1/S-specific transcription in mitotic cell cyc
C1qbp	mitochondrial matrix	complement component C1q binding
C79407	nucleus	
C80913	protein folding	prefoldin complex
Car12	integral to membrane	zinc ion binding
Car8	cytoplasm	zinc ion binding
Cbx5	nucleus	protein binding
Ccdc5	mitosis	biological process unknown
Ccdc80		
Ccl9	calcium ion homeostasis	signal transduction
Ccna2	mitosis	cytoplasm
Ccnb1	oocyte maturation	nucleus
Ccnb1-rs1	mitosis	nucleus
Ccnb2	mitosis	cell cycle
Ccnd1	protein binding	nucleus
Ccne2	cell division	regulation of progression through cell cycle
Cct3	protein binding	nucleus
Cd24a	synaptic vesicle endocytosis	neuromuscular synaptic transmission
Cd44	protein binding	integral to membrane
Cdc25b	protein tyrosine phosphatase activity	mitosis
Cdc2a	protein-tyrosine kinase activity	protein binding
Cdc6	nucleoside-triphosphatase activity	protein binding
Cdc7	spindle pole body	protein binding
Cdca5	cell division	mitosis
Cdk2ap1	cell cycle	negative regulation of progression through c
Cdk4	positive regulation of progression through ce	protein binding
Cdk5rap2	biological process unknown	regulation of neuron differentiation
Cdkn2c	cell cycle	cyclin-dependent protein kinase inhibitor act
Cdo1	cytosol	taurine metabolism
Cdt1	regulation of DNA replication initiation	pre-replicative complex
Cebpz	transcription	nucleus
Cenpf	spindle pole	regulation of striated muscle development
Cep55	cell division	mitosis
Cep70	binding	
Chac1		
Chek1	protein-tyrosine kinase activity	DNA damage checkpoint
Chek2	protein-tyrosine kinase activity	protein binding

Ckap4	biological process unknown	cell surface
Cks1b	cell division	cell cycle
Cldn2	extracellular space	integral to membrane
Clns1a	auxiliary transport protein activity	transport
Cnn1	calmodulin binding	actomyosin structure organization and bioge
Cnn3	calmodulin binding	actomyosin structure organization and bioge
Cnot6	transcription	nucleus
Cpsf2	biological process unknown	mRNA cleavage and polyadenylation specif
Cstf2	nucleus	nucleic acid binding
Ctnnal1	Rho protein signal transduction	cytosol
Ctps	ligase activity	catalytic activity
Cxcl10	protein secretion	chemotaxis
Cxcl11	cytokine activity	inflammatory response
Cxcl9	cytokine activity	inflammatory response
D17H6S56E-5	viral envelope	
Dbf4	nucleus	zinc ion binding
Ddx39	protein binding	nucleus
Dek	nucleus	SRP-dependent cotranslational protein targ
Diap2	development	actin filament polymerization
Dnajc10	protein folding	unfolded protein binding
Dnajc2	nucleus	protein binding
Dnajc9	protein folding	heat shock protein binding
Dnmt1	transcription factor binding	zinc ion binding
Dynlt1	Golgi apparatus	axonemal dynein complex
E2f8	transcription	cell cycle
Ect2	cytoplasm	protein binding
Eftud2	protein biosynthesis	nucleus
Eif1a	protein biosynthesis	transport
Eif4e2	protein biosynthesis	regulation of protein biosynthesis
Eif4ebp2	regulation of protein biosynthesis	eukaryotic initiation factor 4E binding
Eif4g1	protein biosynthesis	regulation of protein biosynthesis
Eif5a	protein biosynthesis	cytoplasm
Elovl5	integral to membrane	fatty acid elongase activity
Entpd4	integral to membrane	hydrolase activity
Epb4.1l5	cytoskeleton	axial mesoderm development
Ephb2	protein-tyrosine kinase activity	integral to membrane
Ephb3	protein-tyrosine kinase activity	integral to membrane

Ercc6l	helicase activity	
F730047E07Rik		
Fads1	fatty acid desaturation	iron ion binding
Fancl	ubiquitin-protein ligase activity	regulation of cell proliferation
Fancm	DNA metabolism	nucleus
Fen1	protein binding	double-stranded DNA specific exodeoxyribo
Ffar2	signal transduction	integral to membrane
Fignl1	nucleotide binding	membrane
Fkbp3	nucleus	protein folding
Fzd1	development	integral to membrane
Fzd7	development	integral to membrane
Galk1	carbohydrate metabolism	galactokinase activity
Gart	phosphoribosylformylglycinamidine cyclo-lig	phosphoribosylglycinamide formyltransferas
Gas5	biological process unknown	cell wall (sensu Fungi)
Gbp2	nucleus	nucleotide binding
Gbp4	GTP binding	cytosol
Gemin6	spliceosome assembly	protein binding
Gins4	cytoplasm	protein binding
Gjb2	protein binding	integral to membrane
Gkn1	digestion	cell proliferation
Gmnn	regulation of progression through cell cycle	molecular function unknown
Gnl3	regulation of cell proliferation	biological process unknown
Gp1ba	extracellular matrix (sensu Metazoa)	integral to membrane
Gpatc4	nucleic acid binding	intracellular
Gpiap1	membrane	integral to plasma membrane
Grem1	development	protein binding
Grwd1	nucleus	
Gtf2h2	regulation of transcription	RNA polymerase II transcription factor activi
Gtl2		
Gtpbp4	nucleotide binding	nucleus
H1f0	development	DNA binding
H2-T22	defense response	
H2afz	development	nucleus
Hdgf	cytoplasm	heparin binding
Heatr1	binding	
Hells	anti-apoptosis	nucleus
Hmga2	transcription	chromosome organization and biogenesis (s

Hmgb1	structural constituent of chromatin	protein binding
Hmgn1	response to UV-C	nucleus
Hmmr	cytoskeleton organization and biogenesis	cell motility
Hnrpa1	transport	RNA metabolism
Hnrpab	nucleus	nucleic acid binding
Hnrpdl	nucleus	ribonucleoprotein complex
Hod	development	regulation of transcription
Hoxa11	development	nucleus
Hoxa9	development	protein binding
Hrasls	Ras protein signal transduction	cytoplasm
Hspd1	protein binding	response to heat
Hspe1	mitochondrial matrix	ATP binding
Id4	transcription corepressor activity	regulation of transcription
Idh1	isocitrate dehydrogenase (NAD+) activity	cytosol
Ifitm2	protein binding	response to biotic stimulus
Ifitm3	response to biotic stimulus	integral to membrane
Igfbp5	signal transduction	regulation of cell growth
Igtp	cytosol	GTPase activity
Iigp1	nucleotide binding	cellular component unknown
Iigp2	biological process unknown	cellular component unknown
Impdh2	GMP biosynthesis	catalytic activity
Incenp	protein binding	nucleus
Indo	tryptophan metabolism	cytosol
Ins1	positive regulation of vasodilation	negative regulation of protein catabolism
Irgm	defense response	endoplasmic reticulum
Isg20l1	exonuclease activity	nucleus
Itga6	integrin-mediated signaling pathway	filopodium formation
Itpka	calmodulin binding	signal transduction
Kap	extracellular space	
Kcnk3	ion channel activity	transport
Kcnn4	calmodulin binding	ion channel activity
Kif11	kinesin complex	microtubule motor activity
Kif22	mitosis	nucleus
Kif2c	nucleus	microtubule motor activity
Kpnb1	nuclear localization sequence binding	protein binding
Krtap15		
Krtcap2	extracellular space	integral to membrane

LOC622757		
LOC623809		
LOC630539		
LOC636537		
LOC640611		
LOC672274		
LOC676501		
LOC677159		
Lap3	prolyl aminopeptidase activity	zinc ion binding
Lats2	oxidoreductase activity, acting on iron-sulfur	cell division
Lgals2	galactoside binding	sugar binding
Lgr5	signal transduction	extracellular matrix (sensu Metazoa)
Lig1	DNA recombination	nucleus
Lin9	DNA binding	regulation of transcription
Lman1	Golgi apparatus	mannose binding
Lrg1	cell wall biosynthesis (sensu Fungi)	cytoplasm
Lrig1	extracellular space	integral to membrane
Lrrc56		
Lrrc59	integral to membrane	membrane
Luzp5	protein binding	inner cell mass cell proliferation
Lyar	zinc ion binding	nucleus
Mad2l1	mitosis	spindle pole body
Mcm10	pre-replicative complex	nucleus
Mcm2	DNA unwinding during replication	protein binding
Mcm3	ATP-dependent DNA helicase activity	nucleoside-triphosphatase activity
Mcm5	nucleoside-triphosphatase activity	negative regulation of apoptosis
Mcm6	protein binding	DNA unwinding during replication
Mcm7	nucleoside-triphosphatase activity	pre-replicative complex
Melk	protein-tyrosine kinase activity	cytoplasm
Mgat2	Golgi apparatus	protein amino acid terminal N-glycosylation
Mia1	extracellular space	extracellular matrix organization and biogen
Mki67	cytoplasm	nucleus
Mki67ip	cytoplasm	biological process unknown
Moap1	protein binding	nucleus
Mod1	enoyl-[acyl-carrier protein] reductase activity	NAD binding
Mpa2l		
Mtap	S-methyl-5-thioadenosine phosphorylase ac	transferase activity, transferring pentosyl gr

Mthfd2	methylenetetrahydrofolate dehydrogenase (	catalytic activity
Mtm1	transporter activity	hydrolase activity
Nap1l1	protein binding	nucleus
Narg1	development	cytoplasm
Ncl	nucleotide binding	DNA binding
Nedd4	ubiquitin-protein ligase activity	protein binding
Nek2	spindle pole	protein binding
Neto1	integral to membrane	membrane
Neurog3	development	regulation of transcription
Nhp2l1	nucleus	ribosome biogenesis and assembly
Nme1	pyrimidine ribonucleoside triphosphate bios	ribonuclease MRP complex
Nol5	rRNA methyltransferase activity	small nucleolar ribonucleoprotein complex
Nol5a	rRNA processing	nucleus
Nola1	dense fibrillar component	biological process unknown
Nola2	protein biosynthesis	nucleus
Nolc1	nucleus	protein binding
Nono	DNA recombination	transcription
Nras	protein binding	small GTPase mediated signal transduction
Nucb2	calcium ion homeostasis	cytoplasm
Nucks1	nucleus	
Nudcd2	cellular component unknown	biological process unknown
Nup107	integral to membrane	protein binding
Nup155	transport	nucleus
Nup37	transport	integral to membrane
Nup62	negative regulation of apoptosis	protein binding
Nusap1	biological process unknown	spindle microtubule
Odz4	gastrulation (sensu Mammalia)	
Olfr157	integral to membrane	rhodopsin-like receptor activity
Omd	extracellular space	extracellular matrix (sensu Metazoa)
Orc2l	DNA replication origin binding	protein binding
P4hb	protein disulfide oxidoreductase activity	extracellular space
Pa2g4	nucleus	protein binding
Pap	transcription	sugar binding
Park2	ubiquitin-protein ligase activity	regulation of neurotransmitter secretion
Pbk	protein-tyrosine kinase activity	protein binding
Pck2	cell wall biosynthesis (sensu Fungi)	zinc ion binding
Pcna	protein binding	nucleus

Perq1	cellular component unknown	protein binding
Phgdh	NAD binding	L-serine biosynthesis
Pitpnm2	transport	soluble fraction
Plk4	protein-tyrosine kinase activity	protein binding
Pnmt	S-adenosylmethionine-dependent methyltra	catecholamine biosynthesis
Pnpt1	carbohydrate metabolism	nucleic acid binding
Pola1	zinc ion binding	nucleus
Pold3	delta DNA polymerase activity	nucleus
Pole	nucleus	zinc ion binding
Pole2	epsilon DNA polymerase activity	nucleus
Polr2a	nucleus	zinc ion binding
Polr3f	nucleus	transcription
Polr3h	tricarboxylic acid cycle	nucleus
Pomt1	development	integral to membrane
Ppap2a	integral to membrane	integral to plasma membrane
Ppp1r14b	phosphatase inhibitor activity	protein phosphatase inhibitor activity
Ppp2r2b	protein phosphatase type 2A complex	signal transduction
Ppp3cb	calmodulin binding	calcium-dependent protein serine/threonine
Ppp4r2		
Pprc1	RNA binding	receptor activity
Prc1	cytoplasm	vacuole (sensu Fungi)
Prim1	DNA primase activity	zinc ion binding
Prkrip1	protein binding	nucleolus
Proc	negative regulation of apoptosis	serine-type endopeptidase activity
Prps2	nucleoside metabolism	ribonucleoside monophosphate biosynthesi
Psat1	metabolism	transaminase activity
Psip1	DNA binding	transcription
Psmc6	nucleoside-triphosphatase activity	cytoplasm
Ptpro	protein tyrosine phosphatase activity	transmembrane receptor protein tyrosine ph
Pycr1	pyrroline-5-carboxylate reductase activity	electron transport
Racgap1	nucleus	zinc ion binding
Rad51	nucleoside-triphosphatase activity	DNA recombination
Rad51ap1	DNA recombination	nucleus
Rad54l	DNA-dependent ATPase activity	nucleus
Ran	protein binding	nucleocytoplasmic transport
Rangap1	cell plate	cytoplasm
Rbbp4	nucleus	protein binding

Rbmx	nucleotide binding	nucleic acid binding
Rbmxrt	nucleotide binding	nucleus
Rcl1	RNA-3'-phosphate cyclase activity	molecular function unknown
Rcn1	protein phosphatase type 2A complex	regulation of stomatal movement
Recc1	nucleoside-triphosphatase activity	protein binding
Reg3g	extracellular space	sugar binding
Rem2	two-component signal transduction system (	regulation of transcription, DNA-dependent
Retnlb	extracellular space	cytokine activity
Rexo2	nucleus	nucleotide metabolism
Rfc2	nucleoside-triphosphatase activity	nucleus
Rfc4	nucleoside-triphosphatase activity	nucleus
Rfc5	nucleoside-triphosphatase activity	nucleus
Rg9mtd2	transferase activity	methyltransferase activity
Rif1	telomeric 3' overhang formation	nucleus
Rnf157	zinc ion binding	metal ion binding
Rpa1	DNA recombination	protein binding
Rpa2	nucleotide-excision repair	protein binding
Rpe	carbohydrate metabolism	biological process unknown
Rpl7l1	protein biosynthesis	ribonucleoprotein complex
Rpo1-4	protein binding	nucleus
Rpp14	nucleus	cellular component unknown
Rps6	protein biosynthesis	small nucleolar ribonucleoprotein complex
Rrm1	catalytic activity	ribonucleoside-diphosphate reductase activi
Rrm2	protein binding	deoxyribonucleoside diphosphate metabolis
Rrs1	nucleus	rRNA processing
Rsnl2		
Rtp3	integral to membrane	membrane
Scd1	protein binding	cellular morphogenesis
Sec23b	COPII vesicle coat	transport
Serpina10	extracellular space	serine-type endopeptidase inhibitor activity
Set	phosphatase inhibitor activity	nucleus
Sf3b3	biological process unknown	nucleus
Sfpq	protein binding	nucleus
Sfrs2	protein binding	nucleus
Sgol1	mitosis	cell cycle
Shcbp1	biological process unknown	cellular component unknown
Shmt1	cytoplasm	glycine metabolism

Shmt2	glycine metabolism	transferase activity
Siva	cytoplasm	protein binding
Skp2	G1/S transition of mitotic cell cycle	regulation of progression through cell cycle
Slc12a2	gamma-aminobutyric acid signaling pathwa	protein binding
Slc1a4	transport	integral to membrane
Slc39a8	metal ion transport	integral to membrane
Slc5a4b	transporter activity	sodium ion transport
Slco3a1	biological process unknown	transport
Smarcad1	nucleus	nucleic acid binding
Smarcc1	nucleus	regulation of transcription, DNA-dependent
Smc1l1		
Smc2l1		
Smc4l1	chromosome organization and biogenesis (	nucleus
Smpdl3b	extracellular space	carbohydrate metabolism
Snord22	protein binding	nucleus
Snrpa1	nucleus	RNA binding
Snrpd3	cytoplasm	small nucleolar ribonucleoprotein complex
Snrpg	small nucleolar ribonucleoprotein complex	nucleus
Snx10	phosphoinositide binding	transport
Snx6	transport	protein binding
Socs3	regulation of protein amino acid phosphoryl	anti-apoptosis
Spats2	biological process unknown	cytoplasm
Spbc25		
Spdef	DNA binding	nucleus
Ssrp1	protein binding	transcription
Stat1	protein binding	nucleus
Statip1	regulation of JAK-STAT cascade	protein binding
Steap1	integral to membrane	electron transport
Stmn1	cytoplasm	protein binding
Strap	protein binding	negative regulation of transcription from RN
Suz12	zinc ion binding	nucleus
Syncrip	cytoplasm	RNA splicing
Sypl	transport	integral to membrane
Syt9	transport	protein binding
T2bp	cellular component unknown	protein binding
Tacc3	biological process unknown	cytoplasm
Taf9	general RNA polymerase II transcription fac	G1-specific transcription in mitotic cell cycle

Tceal8	transcription	nucleus
Tcf19	nucleus	transcription factor complex
Tdg	transcription factor binding	carbohydrate metabolism
Terf1	nucleus	protein binding
Tfam	nucleus	transcription factor complex
Tgm2	proteolysis	histone phosphorylation
Tgtp	cellular component unknown	GTP binding
Thoc3	biological process unknown	transport
Timeless	development	protein binding
Tipin	biological process unknown	cytoplasm
Tk1	cytoplasm	thymidine kinase activity
Tmed5	transport	integral to membrane
Tmem33	biological process unknown	molecular function unknown
Tmem87a	integral to membrane	
Tmpo	protein binding	integral to membrane
Tnfrsf1b	protein binding	integral to membrane
Top2a	embryonic cleavage	DNA unwinding during replication
Topbp1	nucleus	meiotic recombination
Tpm3	cytoskeleton	muscle thin filament tropomyosin
Tpx2	nucleus	aster
Trip13	nucleoside-triphosphatase activity	biological process unknown
Trip6	zinc ion binding	nucleus
Tubb5	protein complex	structural molecule activity
Txndc5	protein disulfide oxidoreductase activity	electron transport
Ubap2		
Ube2c	ubiquitin-protein ligase activity	mitosis
Uble1a	nucleus	protein binding
Uble1b	transcription factor binding	catalytic activity
Uchl5	protein binding	cytosol
Ufm1	nucleus	ubiquitin cycle
Usp1	cellular component unknown	ubiquitin thiolesterase activity
Usp39	nucleus	zinc ion binding
Utrn	protein binding	neuromuscular junction
Vav3	integrin-mediated signaling pathway	positive regulation of phosphoinositide 3-kin
Vip	extracellular space	vasodilation
Wars	protein biosynthesis	cytoplasm
Wbp5	biological process unknown	cellular component unknown

Wdr4	extracellular space	biological process unknown
Wipi2	biological process unknown	cellular component unknown
Wiz	zinc ion binding	nucleus
Wnk1	protein binding	circadian rhythm
Wwp1	ubiquitin-protein ligase activity	protein binding
Xpo1	protein binding	nucleus
Xpo4	cellular component unknown	biological process unknown
Zfp142	DNA binding	zinc ion binding
Zfp703		
Zipro1	development	oogenesis
Zwint	protein binding	nucleus

protein kinase activator activity	protein binding	nucleus
ribonuclease activity		
molecular function unknown		
nucleic acid binding	regulation of transcription, DNA-dependent	intracellular
serine-type endopeptidase activity	hydrolase activity	peptidase activity
transferase activity	metal ion binding	kinase activity
molecular function unknown	nucleocytoplasmic transport	nuclear pore
chemotaxis	nucleotide binding	cellular component unknown
integral to membrane	long-chain-fatty-acid-CoA ligase activity	catalytic activity
molecular function unknown		
structural constituent of cytoskeleton	structural molecule activity	ATP binding
protein binding	regulation of cell growth	structural constituent of cytoskeleton

deaminase activity	regulation of circadian sleep/wake cycle, sle	cellular component unknown
transferase activity	kinase activity	oxidoreductase activity
spermidine biosynthesis	embryonic development (sensu Mammalia)	polyamine metabolism
endocytic vesicle	chemotaxis	lamellipodium
protein binding	cell cycle	ubiquitin cycle
cytoplasm	nucleus	cytoplasmic membrane-bound vesicle
Golgi stack	intracellular protein transport	lysosome
lyase activity	perinuclear region	transcription regulator activity
nucleus	apoptosis	binding
hydrolase activity	nucleus	metal ion binding
porin activity	basolateral plasma membrane	water transport
ER to Golgi vesicle-mediated transport	metal ion binding	protein transport
histone binding		
asparagine synthase (glutamine-hydrolyzing	ligase activity	cellular component unknown
mitosis	cell cycle	nucleus
catalytic activity	integral to plasma membrane	hydrogen:potassium-exchanging ATPase a
integral to membrane	membrane	proton transport
integral to membrane	protein binding	integral to plasma membrane
transferase activity	kinase activity	ATP binding
nucleus	DNA methylation	midbody
nucleotide binding	cytoskeleton organization and biogenesis	protein serine/threonine kinase activity
metal ion binding		
transcription	zinc ion binding	nucleus
transcription	regulation of transcription, DNA-dependent	positive regulation of apoptosis
zinc ion binding	midbody	spindle microtubule
cellular component unknown	hydrolase activity	cysteine-type endopeptidase activity
integral to membrane	regulation of striated muscle development	integral to plasma membrane
protein binding	nucleic acid binding	double-strand break repair via homologous
nucleus	cell cycle	mitotic cell cycle
nucleotide binding	cell division	outer kinetochore of condensed chromosom
molecular function unknown	nucleus	
protein binding	cell adhesion	

regulation of translational initiation	translation initiation factor activity	
protein binding	complement activation	plasma membrane
metal ion binding	one-carbon compound metabolism	lyase activity
protein binding	phosphoinositide-mediated signaling	metal ion binding
kinetochore	nuclear heterochromatin	chromatin binding
mitotic metaphase/anaphase transition	cell cycle	spindle stabilization
cell-cell signaling	cytokine activity	chemoattractant activity
nucleus	protein binding	cell cycle
protein binding	regulation of cell cycle	cell division
cell cycle	protein targeting	regulation of progression through cell cycle
nucleus	protein binding	cell division
cytosol	G1/S transition of mitotic cell cycle	cell division
nucleus	cell cycle	DNA replication initiation
cytosol	negative regulation of retinal programmed c	chaperonin-containing T-complex
external side of plasma membrane	membrane	GPI anchor binding
external side of plasma membrane	hyaluronic acid binding	ureteric bud branching
cell cycle	M phase of mitotic cell cycle	phosphoprotein phosphatase activity
nucleus	mitotic G2 checkpoint	nucleotide binding
DNA-directed DNA polymerase activity	DNA clamp loader activity	pre-replicative complex formation and maint
septation initiation signaling	nucleus	nucleotide binding
nucleus	cell cycle	
cell cycle		
receptor signaling protein serine/threonine k	G1/S transition of mitotic cell cycle	cell growth
cytoskeleton	brain development	cellular component unknown
regulation of transcription, DNA-dependent	kinase activity	oligodendrocyte differentiation
cysteine dioxygenase activity	electron transport	L-cysteine catabolism to taurine
regulation of S phase of mitotic cell cycle	nucleus	cell cycle
regulation of transcription, DNA-dependent	binding	
protein heterodimerization activity	kinetochore	protein homodimerization activity
cell cycle		
nucleus	protein binding	nucleotide binding
nucleus	DNA damage checkpoint	nucleotide binding

protein binding	endoplasmic reticulum	
kinase activity	cyclin-dependent protein kinase regulator activity	
membrane	structural molecule activity	tight junction
nucleus	visual perception	cytosol
nucleus	actin binding	kinetochore
protein binding	protein binding, bridging	microtubule
nuclease activity	regulation of transcription, DNA-dependent	metal ion binding
nucleus	mRNA cleavage	cellular component unknown
nucleotide binding	cellular component unknown	mRNA cleavage
cadherin binding	structural molecule activity	cell adhesion
pyrimidine nucleotide biosynthesis	glutamine metabolism	CTP synthase activity
extracellular space	positive regulation of cell migration	muscle development
chemotaxis	extracellular space	chemokine receptor binding
induction of positive chemotaxis	extracellular space	CXCR3 chemokine receptor binding
nucleic acid binding	nucleoplasm	DNA replication initiation
nucleic acid binding	ATP binding	nuclear mRNA splicing, via spliceosome
DNA binding	RNA binding	GTP binding
oogenesis	Rho GTPase binding	transferase activity
endoplasmic reticulum		
negative regulation of cell growth	G2 phase of mitotic cell cycle	DNA binding
unfolded protein binding		
protein binding	nucleus	catalytic activity
protein binding	microtubule	motor activity
nucleus	regulation of transcription, DNA-dependent	cell proliferation
nucleus	guanyl-nucleotide exchange factor activity	intracellular signaling cascade
protein binding	RNA splicing	ribonucleoprotein complex
nucleic acid binding	ribosome	transporter activity
cytoplasm	translational initiation	RNA binding
protein binding	regulation of translational initiation	cAMP-mediated signaling
cytoplasm	regulation of translational initiation	RNA binding
nucleus	nucleic acid binding	translational initiation
fatty acid elongation, unsaturated fatty acid	integral to plasma membrane	fatty acid elongation
magnesium ion binding	nucleoside-diphosphatase activity	vacuole
paraxial mesoderm development		
protein binding	learning	integral to plasma membrane
integral to plasma membrane	nucleotide binding	extracellular space

linoleoyl-CoA desaturase activity	metal ion binding	long-chain fatty acid biosynthesis
nucleus	zinc ion binding	protein binding
nuclease activity	nucleic acid binding	ATP binding
endoplasmic reticulum membrane	hydrolase activity	flap endonuclease activity
rhodopsin-like receptor activity	receptor activity	extracellular space
ATP binding		
isomerase activity	peptidyl-prolyl cis-trans isomerase activity	
protein binding	cell-cell signaling	cell surface receptor linked signal transducti
cell surface receptor linked signal transducti	extracellular space	metabolism
cytoplasm	transferase activity	carbohydrate phosphorylation
phosphoribosylamine-glycine ligase activity	catalytic activity	nucleotide binding
rRNA processing	1,3-beta-glucanosyltransferase activity	
cellular component unknown	poly(A)+ mRNA export from nucleus	RNA binding
GTPase activity	immune response	
nucleus	mRNA processing	spliceosome complex
nucleus		
cell-cell signaling	lateral plasma membrane	membrane
growth factor activity	positive regulation of cell proliferation	extracellular space
nucleus	cell cycle	organ morphogenesis
protein binding	nucleus	nucleolus
cellular morphogenesis	integral to plasma membrane	cell adhesion
GPI anchor binding		
embryonic limb morphogenesis	cell-cell signaling	proximal/distal pattern formation
nucleus	zinc ion binding	nucleic acid binding
ribosome biogenesis	GTP binding	small GTPase mediated signal transduction
nucleus	chromosome	
chromosome organization and biogenesis (	nucleosome assembly	nucleosome
nucleus	signal transduction	growth factor activity
DNA methylation	nucleic acid binding	urogenital system development
nucleus	DNA packaging	regulation of transcription, DNA-dependent

nucleus	heparin binding	cellular morphogenesis
positive transcription elongation factor activi	transcription-coupled nucleotide-excision re	pyrimidine dimer repair via nucleotide-excisi
cell-cell signaling	hyaluronic acid binding	receptor activity
nucleus	ribonucleoprotein complex	nucleic acid binding
RNA helicase activity	regulation of transcription, DNA-dependent	mRNA binding
nucleic acid binding	DNA binding	nucleotide binding
protein binding	nucleus	transcription
metanephros development	transcription factor complex	skeletal development
nucleus	transcription factor complex	regulation of transcription, DNA-dependent
molecular function unknown	regulation of cell growth	nuclear envelope lumen
nucleotide binding	chaperone binding	protein folding
ATPase activity, coupled	response to unfolded protein	protein folding
nucleus	negative regulation of astrocyte differentiati	regulation of transcription from RNA polyme
isocitrate dehydrogenase (NADP+) activity	glutamate biosynthesis	metabolism
integral to membrane	immune response	
negative regulation of cell proliferation	cytoplasmic membrane-bound vesicle	
intracellular signaling cascade	skeletal muscle growth	extracellular space
identical protein binding	hydrolase activity	GTP binding
GTPase activity		
metal ion binding	purine nucleotide biosynthesis	oxidoreductase activity
midbody	histone phosphorylation	cell division
heme binding	metal ion binding	indoleamine-pyrrole 2,3-dioxygenase activit
alpha-beta T cell activation	protein binding	cell surface receptor linked signal transducti
hydrolase activity		
protein binding	integral to membrane	cell adhesion
calcium- and calmodulin-dependent protein	transferase activity	inositol or phosphatidylinositol kinase activit
integral to membrane	voltage-gated ion channel activity	integral to plasma membrane
integral to membrane	voltage-gated potassium channel activity	integral to plasma membrane
microtubule	mitotic centrosome separation	ATP binding
kinesin complex	microtubule motor activity	spindle
protein binding	meiosis	motor activity
nucleus	zinc ion binding	protein import into nucleus, docking
membrane		

leucyl aminopeptidase activity	nucleic acid binding	proteolysis
nucleotide binding	electron transport	protein amino acid phosphorylation
soluble fraction		
integral to membrane	rhodopsin-like receptor activity	receptor activity
morphogenesis	nucleotide binding	cell division
biological process unknown	cellular component unknown	molecular function unknown
integral to membrane	ER to Golgi vesicle-mediated transport	protein transport
integral to membrane	small GTPase mediated signal transduction	extracellular space
membrane		
metal ion binding		
negative regulation of mitotic metaphase/an	cell cycle	nucleus
chromatin silencing at telomere	female meiosis chromosome segregation	chromatin binding
nuclear origin of replication recognition com	regulation of transcription, DNA-dependent	pre-replicative complex formation and maint
MCM complex	pre-replicative complex	DNA unwinding during replication
protein binding	regulation of transcription, DNA-dependent	pre-replicative complex formation and maint
regulation of transcription, DNA-dependent	pre-replicative complex formation and maint	DNA replication initiation
MCM complex	DNA unwinding during replication	protein binding
transferase activity	kinase activity	ATP binding
integral to membrane	transferase activity, transferring glycosyl grc	membrane
cell-matrix adhesion	cell proliferation	extracellular region
nucleolus	cell proliferation	meiosis
protein binding	nucleus	nucleic acid binding
regulation of apoptosis	apoptosis	
fatty acid synthase complex	soluble fraction	malic enzyme activity
nucleobase, nucleoside, nucleotide and nuc	transferase activity	transferase activity, transferring glycosyl grc

methenyltetrahydrofolate cyclohydrolase ac	methylenetetrahydrofolate dehydrogenase (	one-carbon compound metabolism
muscle development	protein amino acid dephosphorylation	phospholipid dephosphorylation
nucleosome assembly	chromatin assembly complex	positive regulation of cell proliferation
nucleus	transcription	protein binding
nucleus	nucleic acid binding	RNA binding
cytosol	ubiquitin cycle	proteolysis
midbody	intracellular signaling cascade	receptor signaling protein serine/threonine k
protein targeting	receptor activity	
nucleus	transcription	regulation of transcription, DNA-dependent
ribonucleoprotein complex	fertilization (sensu Metazoa)	nucleolus
ribonuclease MRP activity	CTP biosynthesis	cytoplasm
nucleus	rRNA processing	nucleic acid binding
RNA binding	ribosome biogenesis	nucleolus
small nucleolar ribonucleoprotein complex	nucleus	rRNA processing
rRNA processing	ribonucleoprotein complex	ribosome biogenesis and assembly
nucleolus	ATP binding	nucleotide binding
nucleus	nucleic acid binding	regulation of transcription, DNA-dependent
protein transport	nucleotide binding	cellular physiological process
nucleus	cytosol	DNA binding
molecular function unknown		
nucleus	cytosol	porin activity
integral to membrane	porin activity	nucleocytoplasmic transport
nucleus	outer membrane	porin activity
cell surface receptor linked signal transducti	nucleocytoplasmic transport	hormone-mediated signaling
nucleolus	positive regulation of mitosis	cytokinesis after mitosis
integral to plasma membrane	receptor activity	sensory perception of smell
protein binding	extracellular matrix structural constituent	regulation of bone mineralization
nucleus	nuclear origin of replication recognition com	origin recognition complex
cell surface	membrane	protein folding
regulation of transcription, DNA-dependent	hydrolase activity	ribosome assembly
nucleic acid binding	inflammatory response	extracellular space
protein binding	neuron projection	proteolysis
transferase activity	kinase activity	peptidyl-serine phosphorylation
intracellular signaling cascade	gluconeogenesis	phosphoenolpyruvate carboxykinase activity
DNA replication factor C complex	lagging strand elongation	DNA polymerase processivity factor activity

insulin-like growth factor receptor signaling pathway		
electron carrier activity	oxidoreductase activity	brain development
phospholipid binding	metal ion binding	oxidoreductase activity
transferase activity	kinase activity	ATP binding
S-adenosylhomocysteine metabolism	transferase activity	phenylethanolamine N-methyltransferase ac
hydrolase activity, hydrolyzing O-glycosyl c	transferase activity	nucleotidyltransferase activity
alpha DNA polymerase activity	DNA-directed DNA polymerase activity	nucleotidyltransferase activity
mismatch repair	DNA-directed DNA polymerase activity	nucleotidyltransferase activity
DNA-directed DNA polymerase activity	nucleotidyltransferase activity	nucleotide binding
nucleic acid binding	DNA-directed DNA polymerase activity	transferase activity
protein binding	transcription	nucleotidyltransferase activity
nucleotidyltransferase activity	transferase activity	regulation of transcription, DNA-dependent
transcription	nucleic acid binding	nucleotidyltransferase activity
mannosyltransferase activity	extracellular matrix organization and biogen	transferase activity, transferring glycosyl gr
diacylglycerol biosynthesis	ceramide metabolism	hydrolase activity
protein phosphatase type 1 regulator activity		
protein phosphatase type 2A regulator activ	spermatid development	
zinc ion binding	protein binding	protein heterodimerization activity

cell cycle	nucleus	spindle
nucleotidyltransferase activity	transferase activity	metal ion binding
double-stranded RNA binding	negative regulation of protein kinase activity	negative regulation of phosphorylation
anti-inflammatory response	negative regulation of blood coagulation	proteolysis
transferase activity	metal ion binding	kinase activity
transferase activity	L-serine biosynthesis	amino acid biosynthesis
nucleus	regulation of transcription, DNA-dependent	
nucleus	nucleic acid binding	protein complex
integral to membrane	integral to plasma membrane	transmembrane receptor protein tyrosine ph
amino acid biosynthesis	proline biosynthesis	oxidoreductase activity
intracellular signaling cascade	cell division	electron transport
response to methylmercury	protein binding	telomere maintenance via recombination
DNA binding	response to DNA damage stimulus	molecular function unknown
nucleic acid binding	ATP binding	helicase activity
regulation of cell shape	small GTPase mediated signal transduction	spermatid development
Ran GTPase activator activity	M phase specific microtubule process	signal transduction
cell cycle	transcription	chromatin modification

ribonucleoprotein complex	RNA binding	
nucleic acid binding	RNA binding	ribonucleoprotein complex
35S primary transcript processing	nucleus	nucleolus
calcium-mediated signaling	extracellular space	calcium-dependent protein serine/threonine
nucleus	zinc ion binding	DNA replication factor C complex
acute-phase response	inflammatory response	
small GTPase mediated signal transduction	nucleotide binding	DNA binding
hormone activity	extracellular region	
nuclease activity	exonuclease activity	hydrolase activity
cytosol	DNA replication factor C complex	Ctf18 RFC-like complex
protein complex	cytosol	DNA replication factor C complex
protein complex	cytosol	DNA replication factor C complex
protein binding	nuclear telomeric heterochromatin	female pronucleus
nucleus	zinc ion binding	nucleic acid binding
nucleus	zinc ion binding	nucleic acid binding
cytoplasm	secretory pathway	cellular component unknown
ribosome	large ribosomal subunit	transcription regulator activity
transcription	zinc ion binding	nucleotidyltransferase activity
molecular function unknown	hydrolase activity	tRNA processing
nucleic acid binding	ribosome	cytosolic small ribosomal subunit (sensu Eu
ATP binding	oxidoreductase activity	nucleotide binding
ribonucleoside-diphosphate reductase activi	metal ion binding	oxidoreductase activity
ribosome biogenesis and assembly	molecular function unknown	ribosome biogenesis
intracellular signaling cascade	integral to endoplasmic reticulum membrane	microtubule cytoskeleton organization and b
zinc ion binding	protein binding	ER to Golgi vesicle-mediated transport
endopeptidase inhibitor activity	tissue regeneration	
nucleosome assembly	spermatogenesis	DNA binding
protein binding	RNA splicing	nucleic acid binding
nucleic acid binding	regulation of transcription, DNA-dependent	nucleotide binding
nucleic acid binding	nucleotide binding	cellular component unknown
nucleus	meiotic chromosome segregation	cell division
SH2 domain binding	molecular function unknown	protein binding
cytosol	transferase activity	one-carbon compound metabolism

L-serine metabolism	pyridoxal phosphate binding	mitochondrial inner membrane
apoptosis	CD27 receptor binding	induction of apoptosis
ubiquitin cycle	ubiquitin-dependent protein catabolism	ubiquitin ligase complex
integral to membrane	integral to plasma membrane	sodium:potassium:chloride symporter activit
L-serine transport	L-serine transporter activity	dicarboxylic acid transport
zinc ion transporter activity	extracellular space	zinc ion transport
transport	integral to membrane	ion transport
integral to membrane	prostaglandin transport	transporter activity
ATP binding	helicase activity	DNA binding
chromatin binding	chromatin assembly or disassembly	intracellular
protein heterodimerization activity	condensin complex	ATP binding
hydrolase activity	hydrolase activity, acting on glycosyl bonds	
ribonucleoprotein complex		
nucleus	ribonucleoprotein complex	nuclear mRNA splicing, via spliceosome
ribonucleoprotein complex	nuclear mRNA splicing, via spliceosome	RNA splicing factor activity, transesterificati
protein binding	intracellular signaling cascade	protein transport
intracellular signaling cascade	protein transport	phosphoinositide binding
protein binding	signal transduction	regulation of cell growth
molecular function unknown		
transcription	sequence-specific DNA binding	regulation of transcription, DNA-dependent
nucleus	regulation of transcription, DNA-dependent	DNA binding
regulation of transcription, DNA-dependent	intracellular signaling cascade	I-kappaB kinase/NF-kappaB cascade
transcription elongation factor complex	protein kinase binding	
iron ion binding	membrane	FAD binding
tubulin binding	microtubule	intracellular signaling cascade
receptor binding	kinase activity	negative regulation of transforming growth f
nucleic acid binding	histone methyltransferase activity	regulation of transcription, DNA-dependent
nucleus	ribonucleoprotein complex	nucleic acid binding
vesicle-mediated transport	transporter activity	synaptic vesicle
integral to membrane	metal ion binding	synapse
I-kappaB kinase/NF-kappaB cascade		
protein binding	response to stress	hemopoiesis
regulation of transcription, DNA-dependent	transcription coactivator activity	SLIK (SAGA-like) complex

regulation of transcription, DNA-dependent		
regulation of transcription, DNA-dependent	transcription factor activity	
nucleus	protein domain specific binding	base-excision repair
cell division	chromosome, telomeric region	mitosis
regulation of transcription, DNA-dependent	positive regulation of transcription, DNA-dep	apoptosis
peptide cross-linking	elevation of cytosolic calcium ion concentrat	calcium ion binding
nucleus	nuclear mRNA splicing, via spliceosome	mRNA export from nucleus
nucleus	circadian rhythm	regulation of transcription, DNA-dependent
protein binding	nucleus	
transferase activity	kinase activity	ATP binding
membrane	ER-Golgi intermediate compartment	endoplasmic reticulum
protein binding	integral to membrane	membrane
nucleus	mitotic nuclear envelope reassembly	chromatin binding
cell surface receptor linked signal transducti	extracellular space	membrane
nucleus	nucleotide binding	positive regulation of transcription from RNA
DNA binding	response to DNA damage stimulus	condensed nuclear chromosome
regulation of muscle contraction	actin binding	
spindle microtubule	protein kinase binding	mitotic spindle assembly
nucleus	protein binding	transcription cofactor activity
heme binding	regulation of transcription, DNA-dependent	metal ion binding
nucleotide binding	GTP binding	microtubule-based movement
isomerase activity	electron carrier activity	endoplasmic reticulum
cell cycle	ubiquitin cycle	positive regulation of cell proliferation
catalytic activity	ubiquitin activating enzyme activity	ubiquitin cycle
ubiquitin activating enzyme activity	ubiquitin cycle	ATP binding
protein complex	cysteine-type peptidase activity	ubiquitin cycle
cysteine-type endopeptidase activity	ubiquitin-dependent protein catabolism	peptidase activity
nucleic acid binding	metal ion binding	nuclear mRNA splicing, via spliceosome
structural molecule activity	adult somatic muscle development	chemotaxis
guanyl-nucleotide exchange factor activity	zinc ion binding	intracellular signaling cascade
hormone activity	extracellular region	
soluble fraction	tryptophan-tRNA ligase activity	aminoacyl-tRNA ligase activity
WW domain binding		

cellular component unknown	tRNA processing	molecular function unknown
cytoplasm	molecular function unknown	autophagy
nucleic acid binding	metal ion binding	
nucleotide binding	cellular component unknown	protein serine/threonine kinase activity
chloroplast	cellular component unknown	protein ubiquitination
protein import into nucleus, docking	nuclear export	binding
transport	nucleus	binding
transcription	nucleus	regulation of transcription, DNA-dependent
nucleus	zinc ion binding	nucleic acid binding
exocytosis		

metal ion binding		
nucleotide biosynthesis		
plastid	electron transport	membrane
ligase activity	metabolism	magnesium ion binding
nucleotide binding	cytoskeleton	cytoskeleton organization and biogenesis
chromatin modification	regulation of transcription, DNA-dependent	ATP binding

transcription regulator activity

membrane
spermine biosynthesis

embryonic development (sensu Mammalia)
cell division

intracellular transport
transcription coactivator activity
spliceosome complex

integral to plasma membrane
Golgi stack

metabolism
binding
nucleotide binding
receptor activity
inflammatory response
nucleotide binding
cell division
protein amino acid phosphorylation

nucleic acid binding
DNA binding
microtubule cytoskeleton organization and b
response to toxin
cell adhesion
extracellular space
mitotic chromosome condensation
protein serine/threonine kinase activity

hydrolase activity

glutamate 5-kinase activity
AMP deaminase activity

external side of plasma membrane
regulation of progression through cell cycle

clathrin vesicle coat
cytoplasm

microvillus
regulation of GTPase activity

amino acid metabolism
cell division
metabolism

receptor activity
mitotic cell cycle
nucleotide binding
cytoplasm

regulation of transcription, DNA-dependent
negative regulation of transcription
caspase inhibitor activity
cytoplasm
membrane
DNA repair

protein amino acid phosphorylation

DNA repair

amino acid biosynthesis
lyase activity

receptor activity

protein targeting to lysosome
metal ion binding

transporter activity
GTPase activator activity

amino acid biosynthesis
cellular component unknown
hydrolase activity

extracellular space
protein amino acid phosphorylation
protein serine/threonine kinase activity
cell cycle

T cell differentiation
transcriptional repressor activity
cell division
response to drug
smoothened signaling pathway
chromatin remodeling

mitosis

mitochondrion	immune response	
membrane	carbonate dehydratase activity	
one-carbon compound metabolism	carbonate dehydratase activity	
chromatin	chromatin assembly or disassembly	
microtubule	cell division	cellular component unknown
chemotaxis	extracellular space	chemokine activity
cell division	regulation of progression through cell cycle	cyclin-dependent protein kinase regulator ac
protein amino acid phosphorylation	G2/M transition of mitotic cell cycle	cyclin-dependent protein kinase regulator ac
cytokinesis	cyclin-dependent protein kinase regulator activity	
regulation of progression through cell cycle	cyclin-dependent protein kinase regulator activity	
protein amino acid phosphorylation	cyclin-dependent protein kinase regulator ac	eye morphogenesis (sensu Vertebrata)
cyclin-dependent protein kinase regulator activity		
tubulin folding	nucleotide binding	centrosome
cell adhesion	receptor activity	membrane
cell division	phosphoric monoester hydrolase activity	hydrolase activity
cell division	G1 phase of mitotic cell cycle	protein amino acid phosphorylation
mitosis	cytoplasm	spindle
cell division	cellular component unknown	DNA replication initiation
cyclin-dependent protein kinase activity	protein serine/threonine kinase activity	mitosis
molecular function unknown	neuronal Cdc2-like kinase binding	protein kinase binding
DNA binding	transcription factor activity	
taurine biosynthesis	sulfur amino acid biosynthesis	L-cysteine metabolism
DNA binding	S phase of mitotic cell cycle	DNA replication initiation
cytoplasm	response to drug	nuclear matrix
condensed nuclear chromosome	DNA repair	protein amino acid phosphorylation
protein serine/threonine kinase activity	protein amino acid phosphorylation	cell cycle

circulation	plasma membrane	chloride transport
actin cytoskeleton organization and biogene	chromosome segregation	molecular function unknown
actin binding	smooth muscle contraction	actin filament
exonuclease activity	hydrolase activity	magnesium ion binding
molecular function unknown	RNA binding	mRNA processing
RNA binding	mRNA processing	mRNA polyadenylylation
actin cytoskeleton	cytoskeleton	molecular function unknown
sensory perception	electron transport	immune response
chemokine activity	immune response	extracellular region
chemokine activity	immune response	extracellular region
protein amino acid phosphorylation	protein serine/threonine kinase activity	DNA replication
helicase activity	mRNA export from nucleus	nucleotide binding
membrane	mRNA processing	
kinase activity	actin binding	nucleotide binding
protein folding	unfolded protein binding	heat shock protein binding
DNA methylation	regulation of transcription, DNA-dependent	heterochromatin
cytoplasmic dynein complex	microtubule-based process	dynein complex
DNA binding	protein homodimerization activity	
regulation of Rho protein signal transductio	regulation of progression through cell cycle	cellular physiological process
nuclear mRNA splicing, via spliceosome	nucleotide binding	GTP binding
translational initiation	RNA binding	membrane
regulation of translation	translation initiation factor activity	
cellular component unknown	insulin receptor signaling pathway	negative regulation of translational initiation
translation initiation factor activity	regulation of translation	
apoptosis	translation initiation factor activity	
very-long-chain fatty acid biosynthesis	long-chain fatty acid biosynthesis	
lysosome	membrane	calcium ion binding
nucleotide binding	membrane	positive regulation of long-term neuronal sy
membrane	transmembrane receptor protein tyrosine ki	protein serine/threonine kinase activity

oxidoreductase activity		
ubiquitin cycle	metal ion binding	gametogenesis
helicase activity	nucleotide binding	DNA binding
5'-flap endonuclease activity	fatty acid elongase activity	exonuclease activity
G-protein coupled receptor protein signaling	membrane	purinergic nucleotide receptor activity, G-pr
epithelial cell differentiation	metabolism	membrane
membrane	G-protein coupled receptor activity	signal transducer activity
phosphotransferase activity, alcohol group a	phosphorylation	kinase activity
purine base biosynthesis	cytoplasm	transferase activity
membrane	GTP binding	GTPase activity
nuclear mRNA splicing, via spliceosome		
plasma membrane	gap-junction forming channel activity	connexon channel activity
cell growth	regulation of progression through cell cycle	secretory granule
negative regulation of DNA replication		
cell proliferation	nucleotide binding	regulation of progression through cell cycle
membrane fraction	hemostasis	plasma membrane
cytokine activity	negative regulation of cell growth	extracellular space
DNA repair		
Barr body	DNA binding	chromosome
cell proliferation	extracellular space	cellular physiological process
helicase activity	DNA binding	ATP-dependent helicase activity
DNA binding	nuclear chromosome	chromatin

regulation of transcription, DNA-dependent	extracellular space	chromatin binding
DNA binding	RNA polymerase II transcription factor activi	response to UV-B
RNA processing	mRNA export from nucleus	nucleotide binding
nucleotide binding	DNA replication origin binding	transcription
RNA binding	mRNA metabolism	
heart development	regulation of transcription, DNA-dependent	DNA binding
regulation of transcription, DNA-dependent	regulation of transcription	transcription
cytoplasm	regulation of transcription	transcription
cellular protein metabolism	mitochondrion	cytoplasm
unfolded protein binding	mitochondrion	
positive regulation of cell proliferation	negative regulation of transcription	neuroblast proliferation (sensu Vertebrata)
isocitrate metabolism	mitochondrial nucleoid	glyoxylate cycle
insulin-like growth factor binding protein con	insulin-like growth factor binding	growth factor binding
membrane	cytokine and chemokine mediated signaling	GTPase activity
potassium ion binding	lymphocyte proliferation	IMP dehydrogenase activity
protein localization	central element	synaptonemal complex
oxidoreductase activity, acting on single dor	oxidoreductase activity	defense response
cell-cell signaling	extracellular space	membrane
odontogenesis (sensu Vertebrata)	membrane	calcium ion binding
myo-inositol metabolism	kinase activity	ATP binding
potassium ion transport	extracellular space	potassium ion binding
membrane	transport	voltage-gated potassium channel complex
motor activity	nucleotide binding	microtubule associated complex
microtubule	kinetochore	ATP binding
nucleotide binding	microtubule associated complex	microtubule-based movement
binding	protein transport	protein import into nucleus, translocation

transcription regulator activity	hydrolase activity	protein metabolism
protein serine/threonine kinase activity	mitosis	cell cycle
extracellular space	G-protein coupled receptor protein signaling	protein-hormone receptor activity
RNA ligase (ATP) activity	DNA repair	DNA replication
receptor activity		
endoplasmic reticulum membrane	membrane	protein folding
membrane	Rho GTPase activator activity	bud neck
kinetochore	cell division	molecular function unknown
DNA strand elongation	pre-replicative complex formation and maint	DNA replication initiation
DNA replication initiation	DNA helicase activity	DNA-dependent ATPase activity
nucleus	cytosol	nucleic acid binding
mitotic cell cycle	DNA replication initiation	DNA helicase activity
DNA helicase activity	DNA-dependent ATPase activity	cytoplasm
nucleus	nucleic acid binding	regulation of transcription, DNA-dependent
nucleotide binding	protein serine/threonine kinase activity	protein amino acid phosphorylation
protein amino acid N-linked glycosylation via	alpha-1,6-mannosylglycoprotein 2-beta-N-a	acetylglucosaminyltransferase activity
growth factor activity		
chromosome, pericentric region	condensed chromosome	
nucleolus	nucleotide binding	RNA binding
malate metabolism	metal ion binding	oxidoreductase activity

oups

oxidoreductase activity	extracellular space	cellular component unknown
muscle maintenance	protein serine/threonine phosphatase activit	mitochondrion
DNA replication		
regulation of transcription, DNA-dependent	binding	receptor activity
nucleolus		
ubiquitin ligase complex	ligase activity	protein ubiquitination
centrosome cycle	condensed nuclear chromosome	protein serine/threonine kinase activity
epithelial cell differentiation	DNA binding	positive regulation of transcription from RNA
nuclear mRNA splicing, via spliceosome	regulation of progression through cell cycle	RNA binding
rRNA processing	transferase activity	microsome
nucleolus	cell growth	snoRNP binding
ribonucleoprotein complex	rRNA binding	snoRNA binding
ribosome	ribosome biogenesis	RNA binding
regulation of protein import into nucleus	GTP binding	nucleoplasm
nuclear mRNA splicing, via spliceosome	DNA binding	nucleotide binding
membrane	GTP binding	intracellular
extracellular space	Golgi medial cisterna	ER-Golgi intermediate compartment
Nup107-160 complex	nucleocytoplasmic transport	protein transport
transporter activity	structural constituent of nuclear pore	nucleocytoplasmic transporter activity
protein transport		
transcription regulator activity	nucleocytoplasmic shuttling complex	outer membrane
establishment of mitotic spindle localization	microtubule binding	mitotic chromosome condensation
G-protein coupled receptor protein signaling	olfactory receptor activity	
cell adhesion		
inner kinetochore of condensed chromosom	chromatin	DNA replication initiation
ER-Golgi intermediate compartment	endoplasmic reticulum	microsome
regulation of translation	cell cycle arrest	regulation of protein biosynthesis
acute-phase response	polynucleotide adenylyltransferase activity	
regulation of synaptic transmission	synaptic transmission, dopaminergic	dopamine uptake
ATP binding	peptidyl-threonine phosphorylation	nucleotide binding
protein kinase C activity	regulation of cell shape	lyase activity
DNA repair	DNA replication	leading strand elongation

metabolism	phosphoglycerate dehydrogenase activity	amino acid biosynthesis
electron transport	membrane	calcium ion binding
nucleotide binding	protein amino acid phosphorylation	protein serine/threonine kinase activity
S-adenosylmethionine metabolism	methyltransferase activity	epinephrine biosynthesis
RNA processing	3'-5'-exoribonuclease activity	RNA binding
lagging strand elongation	protein heterodimerization activity	nucleotide binding
transferase activity	DNA binding	DNA synthesis during DNA repair
hydrolase activity	DNA repair	DNA replication
nucleotidyltransferase activity	epsilon DNA polymerase complex	DNA-dependent DNA replication
transferase activity	nucleolus	metal ion binding
DNA binding	DNA-directed RNA polymerase activity	
transferase activity	citrate metabolism	iron ion binding
protein amino acid O-linked glycosylation	endoplasmic reticulum membrane	neuron migration
membrane	phospholipid dephosphorylation	protein amino acid dephosphorylation
hydrolase activity	insoluble fraction	protein amino acid dephosphorylation
microtubule	vacuolar lumen (sensu Fungi)	cell division
alpha DNA polymerase:primase complex	DNA replication, synthesis of RNA primer	DNA-directed RNA polymerase activity
protein kinase binding	protein kinase inhibitor activity	
extracellular space	hydrolase activity	amino acid metabolism
nucleotide biosynthesis	magnesium ion binding	lipoate-protein ligase B activity
phosphoserine transaminase activity		
cytosol	ATP binding	nucleotide binding
receptor activity	hydrolase activity	nervous system development
intracellular	diacylglycerol binding	transport
condensed nuclear chromosome	intracellular	DNA-dependent ATPase activity
RNA binding	DNA repair	
DNA binding	nucleotide binding	response to DNA damage stimulus
microtubule cytoskeleton organization and b	cell adhesion	intracellular protein transport
soluble fraction	perinuclear region	nuclear envelope
regulation of transcription, DNA-dependent	chromatin remodeling	NuRD complex

RNA processing		
protein phosphatase type 2A regulator activ	auxin polar transport	calcineurin complex
regulation of transcription, DNA-dependent	nucleotide binding	DNA repair
membrane	GTP binding	GTPase activity
3'-5' exonuclease activity	manganese ion binding	nucleobase, nucleoside, nucleotide and nuc
nucleotide binding	DNA replication checkpoint	DNA clamp loader activity
Ctf18 RFC-like complex	nucleotide binding	DNA clamp loader activity
Ctf18 RFC-like complex	ATPase activity	nucleotide binding
chromosome, telomeric region	nuclear telomere cap complex	male pronucleus
meiosis	chromatin binding	DNA repair
base-excision repair	gene silencing	plastid
generation of precursor metabolites and ene	molecular function unknown	pentose-phosphate shunt
intracellular	structural constituent of ribosome	
transferase activity	metal ion binding	DNA binding
RNA binding	ribonuclease activity	response to pathogenic fungi
ribosome biogenesis	intracellular	regulation of translation
ribonucleoside-diphosphate reductase comp	DNA replication	
iron ion binding	deoxyribonucleotide metabolism	DNA replication
defense response to pathogenic bacteria, in	transcription factor activity	
copper, zinc superoxide dismutase activity	oxidoreductase activity, acting on paired do	membrane
protein transport	perinuclear region	intracellular protein transport
cyclin binding	DNA replication	endoplasmic reticulum
protein complex assembly	RNA splicing factor activity, transesterificatio	small nuclear ribonucleoprotein complex
cellular component unknown	DNA repair	mRNA processing
mRNA processing	spliceosome complex	transcription corepressor activity
chromosome segregation	chromosome, pericentric region	
L-serine metabolism	pyridoxal phosphate binding	L-serine catabolism

methyltransferase activity	mitochondrion	glycine hydroxymethyltransferase activity
positive regulation of apoptosis		
kinase activity		
transporter activity	positive regulation of cell volume	membrane
sodium:dicarboxylate symporter activity	membrane	symporter activity
membrane	metal ion transporter activity	
membrane		
ion transport	molecular function unknown	membrane
nucleotide binding	hydrolase activity	ATP-dependent helicase activity
regulation of transcription	transcription	DNA packaging
chromosome segregation	mitotic chromosome condensation	
molecular function unknown	mRNA processing	mRNA metabolism
RNA binding	mRNA processing	mRNA metabolism
intracellular protein transport	protein transporter activity	
negative regulation of signal transduction	intracellular signaling cascade	negative regulation of insulin receptor signa
transcription factor activity		
transcription regulator activity	response to DNA damage stimulus	chromatin
caspase activation	tyrosine phosphorylation of STAT protein	transcription from RNA polymerase II promo
oxidoreductase activity		
negative regulation of microtubule polymeriz	positive regulation of cell motility	microtubule depolymerization
receptor activity		
chromatin binding	ESC/E(Z) complex	intracellular
nuclear mRNA splicing, via spliceosome	nucleotide binding	RNA binding
membrane	secretory granule	
transporter activity	synaptic vesicle	membrane
cellular component unknown	centrosome	regulation of progression through cell cycle
TATA-binding protein binding	chromatin modification	transferase activity

uracil DNA N-glycosylase activity	response to DNA damage stimulus	hydrolase activity
regulation of transcription	cell cycle	chromosome organization and biogenesis (
mitochondrion	regulation of transcription	transcription
protein serine/threonine kinase activity	enzyme binding	cytoplasm
cellular component unknown	molecular function unknown	RNA binding
regulation of circadian rhythm	protein heterodimerization activity	rhythmic process
nucleotide binding	cellular component unknown	nucleobase, nucleoside, nucleotide and nuc
membrane	nuclear inner membrane	hormone activity
tumor necrosis factor receptor activity	immune response	negative regulation of inflammatory respons
DNA topoisomerase complex (ATP-hydroly	DNA topoisomerase (ATP-hydrolyzing) acti	DNA metabolism
DNA repair	intracellular	
ATP binding	nucleotide binding	cellular component unknown
electron carrier activity	receptor activity	DNA binding
protein polymerization	microtubule-based process	cytoplasm
cell division	ligase activity	cytokinesis
protein heterodimerization activity	ligase activity	cellular component unknown
electron carrier activity	ligase activity	nucleotide binding
hydrolase activity	ubiquitin thiolesterase activity	intracellular
DNA binding	cysteine-type endopeptidase activity	ubiquitin thiolesterase activity
actin filament binding	growth cone	muscle development
small GTPase mediated signal transduction	Rac guanyl-nucleotide exchange factor acti	regulation of GTPase activity
tRNA aminoacylation for protein translation	ATP binding	ligase activity

protein amino acid phosphorylation intracellular protein transport protein transport metal ion binding	protein kinase inhibitor activity protein modification protein export from nucleus	vesicular fraction biological process unknown nucleoplasm
regulation of transcription, DNA-dependent	cell differentiation	intracellular

protein folding
membrane

mitochondrion
fatty acid metabolism

transport
mitochondrial inner membrane

actin filament
chromatin binding

muscle contraction
actin filament

chromatin remodeling

purine base metabolism	purine ribonucleoside monophosphate biosy	adenosine deaminase activity
glutamate-5-semialdehyde dehydrogenase	proline biosynthesis	mitochondrion
adenosylmethionine decarboxylase activity	cellular component unknown	carboxy-lyase activity
positive regulation of embryonic developme	vasculogenesis	cell migration during gastrulation
oxidoreductase activity	nucleus	nuclease activity
extracellular space	membrane	outer membrane
Golgi membrane		
asparagine biosynthesis		
molecular function unknown		
hydrogen ion transporter activity	membrane	gastric acid secretion
membrane	plasma membrane	regulation of body size
protein serine/threonine kinase activity	protein kinase activity	ubiquitin protein ligase binding
protein amino acid phosphorylation	N-methyltransferase activity	mitosis
MAP kinase kinase kinase activity	transferase activity	metal ion binding
metal ion binding	hemopoiesis	B cell differentiation
negative regulation of neuron apoptosis	apoptosis	intracellular
bleomycin hydrolase activity	cysteine-type peptidase activity	soluble fraction
axon guidance		
regulation of transcription	cytoplasm	mitotic checkpoint
cell cycle	transferase activity	kinase activity

molecular function unknown		
antimicrobial humoral response (sensu Vert	immune response	extracellular region
ctivity		
mitosis	cell cycle	kinase activity
cell cycle	kinase activity	regulation of progression through cell cycle
cytoskeleton organization and biogenesis	protein folding	cellular protein metabolism
protein amino acid dephosphorylation	intracellular	
protein serine/threonine kinase activity	mitosis	cell cycle
S phase of mitotic cell cycle	pre-replicative complex	nucleus
nucleoplasm	protein amino acid phosphorylation	protein serine/threonine kinase activity
regulation of cell growth	transferase activity	kinase activity
inflammatory response	electron carrier activity	oxidoreductase activity
DNA replication	mitochondrion	
molecular function unknown	chromosome, pericentric region	development
protein serine/threonine kinase activity	G2/M transition of mitotic cell cycle	cell cycle checkpoint
transferase activity	metal ion binding	kinase activity

regulation of cell volume		
smooth muscle contraction	regulation of smooth muscle contraction	
microtubule binding	troponin C binding	tropomyosin binding
RNA binding		
mRNA polyadenylylation		
signal transduction	cell motility	cytokine activity
cell cycle	regulation of S phase of mitotic cell cycle	kinase activity
ATP-dependent helicase activity	hydrolase activity	mRNA processing
actin cytoskeleton organization and biogene	cell differentiation	cell organization and biogenesis
DNA replication		
site-specific DNA-methyltransferase (cytosi	DNA (cytosine-5-)-methyltransferase activit	negative regulation of transcription from RN
intracellular	GTPase activator activity	Rho guanyl-nucleotide exchange factor acti
translation elongation factor activity	GTPase activity	mRNA processing
translation initiation factor activity		
negative regulation of protein biosynthesis	regulation of translation	translation initiation factor activity
transmembrane receptor protein tyrosine ki	protein serine/threonine kinase activity	protein amino acid phosphorylation
protein amino acid phosphorylation	transmembrane-ephrin receptor activity	transferase activity

ligase activity	response to DNA damage stimulus	nuclear envelope
response to DNA damage stimulus	ATP-dependent helicase activity	hydrolase activity
nucleus	nuclease activity	nucleic acid binding
G-protein coupled receptor activity	lipid binding	signal transducer activity
regulation of osteoblast differentiation	G-protein coupled receptor activity	signal transducer activity
signal transduction	non-G-protein coupled 7TM receptor activity	receptor activity
ATP binding	nucleotide binding	metabolism
purine nucleotide biosynthesis	ATP binding	hydroxymethyl-, formyl- and related transfer
telomeric DNA binding	telomere maintenance	immune response
transport	male genitalia development	gap junction
molecular function unknown	GTP binding	intracellular
nervous system development	organ morphogenesis	apoptosis
chromatin binding	chromatin silencing	lymphocyte differentiation
chromosome		

chromatin assembly or disassembly	transport	nitric oxide biosynthesis
chromatin binding	chromatin	establishment and/or maintenance of chrom
RNA binding	single-stranded DNA binding	mRNA processing
ribonucleoprotein complex	RNA processing	mRNA editing
sequence-specific DNA binding	negative regulation of transcription from RN	transcription factor activity
pattern specification	DNA binding	organ morphogenesis
pattern specification	transcriptional activator activity	DNA binding
regulation of apoptosis	protein import into mitochondrial matrix	ATP binding
transcription regulator activity	negative regulation of neuron differentiation	
carbohydrate metabolism	main pathways of carbohydrate metabolism	tricarboxylic acid cycle
extracellular region		
GDP binding	endoplasmic reticulum	
mitosis	cell cycle	microtubule
iron ion binding	tryptophan catabolism to kynurenine	immune response
carbohydrate metabolism	physiological process	positive regulation of nitric-oxide synthase a
plasma membrane	integrin complex	basolateral plasma membrane
inositol trisphosphate 3-kinase activity	nucleotide binding	cellular component unknown
ion transport	membrane	synaptic transmission
defense response	potassium ion transport	ion transport
microtubule-based movement	microtubule-based process	mitochondrion
motor activity	nucleotide binding	chromatin
centromeric DNA binding	mitosis	kinesin complex
protein import into nucleus	nuclear pore	biological process unknown

intracellular	mitochondrion	cytoplasm
transferase activity	metal ion binding	kinase activity
membrane	G-protein coupled receptor activity	signal transducer activity
cell cycle	ATP binding	DNA ligase (ATP) activity
ER-Golgi intermediate compartment	calcium ion binding	endoplasmic reticulum
extracellular region	mitochondrion	
chromosome, pericentric region	mitotic spindle checkpoint	mitotic sister chromatid segregation
chromatin silencing at silent mating-type cas	DNA replication	chromosome condensation
cytoplasm	nucleosome assembly	metal ion binding
regulation of transcription, DNA-dependent	nucleotide binding	chromatin binding
DNA-dependent ATPase activity	cytoplasm	S phase of mitotic cell cycle
oogenesis (sensu Insecta)	S phase of mitotic cell cycle	single-stranded DNA binding
nucleotide binding	chromatin binding	pre-replicative complex formation and maint
protein kinase activity		
transferase activity	Golgi stack	protein amino acid N-linked glycosylation
condensed chromosome		
fatty acid biosynthesis	malate dehydrogenase (decarboxylating) ac	malate dehydrogenase (oxaloacetate-decar

hydrolase activity	magnesium ion binding	folic acid and derivative biosynthesis
protein tyrosine phosphatase activity	inositol or phosphatidylinositol phosphatase	transport
angiogenesis	cell differentiation	N-acetyltransferase activity
intracellular	axon guidance	protein modification
regulation of mitosis	mitosis	cytoplasm
transcription regulator activity	cell differentiation	nervous system development
mRNA processing	plasma membrane	spliceosome complex
metal ion binding	kinase activity	lactation
unfolded protein binding	snRNP protein import into nucleus	rRNA modification
ribosome biogenesis	RNA binding	
structural constituent of ribosome		
nucleolus organization and biogenesis	small nuclear ribonucleoprotein complex	Cajal body
response to DNA damage stimulus	RNA binding	DNA repair
Ras protein signal transduction	regulation of progression through cell cycle	Golgi stack
calcium ion binding	plasma membrane	nuclear outer membrane
rRNA export from nucleus	outer membrane	nuclear pore
outer membrane	nuclear pore	
negative regulation of non-apoptotic progra	protein serine/threonine kinase activity	transport
mitotic sister chromatid segregation		
negative regulation of transcription from RN	DNA replication	
electron carrier activity	peptidyl-proline hydroxylation to 4-hydroxy-	protein disulfide isomerase activity
transcription	rRNA processing	ribonucleoprotein complex
intracellular	dopamine metabolism	ubiquitin cycle
cellular component unknown	protein amino acid phosphorylation	protein serine/threonine kinase activity
nucleotide binding	GTP binding	protein amino acid phosphorylation
phosphoinositide-mediated signaling	base-excision repair, gap-filling	PCNA complex

oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor		
intracellular	lipid binding	
protein kinase activity		
polyribonucleotide nucleotidyltransferase activity		
plastid	DNA replication initiation	purine nucleotide binding
delta DNA polymerase complex	DNA replication	
transferase activity	metal ion binding	DNA binding
DNA binding	DNA repair	DNA replication
DNA binding	DNA-directed RNA polymerase II, core com	transcription from RNA polymerase II prom
DNA-directed RNA polymerase activity	mitochondrion	
membrane	dolichyl-phosphate-mannose-protein mann	endoplasmic reticulum
protein kinase C activation	plasma membrane	signal transduction
muscle maintenance	protein serine/threonine phosphatase activit	soluble fraction
vacuolar protein catabolism	cytokinesis	carboxypeptidase C activity
DNA replication		
calcium ion binding	negative regulation of actin filament polyme	receptor binding
ribose phosphate diphosphokinase activity		
hydrolase activity	protein catabolism	peptidase activity
membrane	protein amino acid dephosphorylation	plasma membrane
cell cycle	signal transduction	metal ion binding
meiotic recombination	meiotic joint molecule formation	nuclear chromosome
ATP-dependent helicase activity	hydrolase activity	DNA repair
cellular physiological process	intracellular	cytoplasm
protein import into nucleus	GTPase activator activity	nuclear pore
DNA replication		

calcium ion binding	response to ethylene stimulus	positive regulation of abscisic acid mediatec
intracellular	DNA replication	transcription
intracellular	mitochondrion	
DNA replication initiation	Rad17 RFC-like complex	purine nucleotide binding
Rad17 RFC-like complex	purine nucleotide binding	DNA replication
DNA clamp loader activity	DNA replication initiation	DNA repair
cell cycle	chromatin silencing at telomere	nucleolus
DNA replication	transcription	DNA-dependent DNA replication
DNA repair	mitochondrion	DNA replication
plastid	isomerase activity	ribulose-phosphate 3-epimerase activity
DNA-directed RNA polymerase I complex	DNA-directed RNA polymerase activity	
ribonuclease P activity		
cytosolic ribosome (sensu Eukaryota)	immune response	cytoplasm
endocytosis	cell tip	spindle
endoplasmic reticulum		
spliceosome complex		
biological process unknown	RNA splicing	transcription
RNA splicing	nuclear mRNA splicing, via spliceosome	nuclear speck
methyltransferase activity	mitochondrion	glycine hydroxymethyltransferase activity

symporter activity	chloride transport	amino acid transport
neutral amino acid transporter activity		
chromatin modification	DNA binding	SWI/SNF complex
spliceosome complex		
protein kinase cascade	JAK-STAT cascade	protein kinase inhibitor activity
DNA repair	chromosome	DNA replication
calcium ion binding	JAK-STAT cascade	signal transducer activity
mitotic spindle organization and biogenesis	axonogenesis	
negative regulation of transcription from RN	biological process unknown	histone ubiquitination
mRNA processing	poly(A) binding	
calcium ion binding		
molecular function unknown	cytoplasmic sequestering of transcription factor	
kinase activity	establishment and/or maintenance of chrom	SAGA complex

DNA repair	negative regulation of transcription from RN	transcriptional repressor activity
double-stranded telomeric DNA binding	DNA binding	chromosome
transcription from mitochondrial promoter	p53 binding	embryonic development (sensu Mammalia)
transferase activity	protein oligomerization	metal ion binding
mRNA processing		
negative regulation of transcription	lung development	protein homodimerization activity
DNA replication		
nuclear envelope reassembly	regulation of transcription	nuclear envelope-endoplasmic reticulum ne
inflammatory response	cell proliferation	receptor activity
DNA topological change	nucleolus	ATP binding
identical protein binding	transcription from RNA polymerase II promoter	
electron transport		
microtubule	tubulin	structural constituent of cytoskeleton
cyclin catabolism	ubiquitin-dependent protein catabolism	protein modification
protein ubiquitination	protein C-terminus binding	protein modification
electron transport	protein modification	
ubiquitin-dependent protein catabolism	peptidase activity	
intracellular	ubiquitin-dependent protein catabolism	mRNA processing
membrane	calcium ion binding	plasma membrane
epidermal growth factor receptor binding	plasma membrane	intracellular
nucleotide binding	negative regulation of cell proliferation	tryptophanyl-tRNA aminoacylation

soluble fraction
signal transduction
mRNA processing

transferase activity
ubiquitin cycle
nuclear pore

kinase activity
central nervous system development
cytoplasm

transcription

spermatogenesis

transcriptional activator activity

ATP binding
mitochondrion

electron carrier activity

viral capsid assembly

chromatin remodeling complex

immune response	cytoplasm	purine nucleotide metabolism
negative regulation of angiogenesis	gastrulation (sensu Mammalia)	
base-excision repair	ribosome	cellular component unknown
water channel activity		
proton transport	transport	hydrolase activity, acting on acid anhydrides
cell cycle kinase activity	spindle ATP binding	transferase activity magnesium ion binding
intracellular		
G2/M transition of mitotic cell cycle carboxypeptidase activity	mitosis aminopeptidase activity	cytoplasm peptidase activity
regulation of S phase of mitotic cell cycle	transcriptional activator activity	regulation of progression through cell cycle
ATP binding	protein kinase activity	

regulation of progression through cell cycle	cytokinesis	tissue regeneration
re-entry into mitotic cell cycle	cyclin-dependent protein kinase holoenzym	fat cell differentiation
cytoplasm	ATP binding	embryonic eye morphogenesis
transferase activity zinc ion binding cell cycle	Hsp70 protein binding ATPase activity M phase of mitotic cell cycle	kinase activity nucleotide binding transferase activity
cyclin-dependent protein kinase holoenzym	protein kinase activity	regulation of cell proliferation
oxidoreductase activity, acting on single dor	iron ion binding	cysteine metabolism
transcription factor binding	nucleus	dynein binding
cell cycle ATP binding	meiotic recombination response to DNA damage stimulus	regulation of cyclin-dependent protein kinas magnesium ion binding

inflammatory response	electron carrier activity	positive regulation of cell proliferation
metal ion binding	traversing start control point of mitotic cell cy	regulation of DNA replication
transcriptional repressor activity	S-adenosylmethionine-dependent methyltra	maintenance of DNA methylation
vity		
spliceosome complex		
receptor binding	transmembrane-ephrin receptor activity	regulation of axonogenesis
kinase activity	receptor activity	ATP binding

DNA repair		
DNA repair		
UV protection	fatty acid elongation	exodeoxyribonuclease activity
signal transduction	non-G-protein coupled 7TM receptor activity	Wnt receptor signaling pathway
Wnt receptor signaling pathway	oxidoreductase activity	G-protein coupled receptor protein signaling
galactose metabolism		
ligase activity	'de novo' IMP biosynthesis	biosynthesis
cell communication	connexon complex	sensory perception of sound

DNA packaging	DNA binding	chromatin
atin architecture		
DNA binding	RNA binding	negative regulation of transcription, DNA-de
transcriptional repressor activity		
induction of an organ	sequence-specific DNA binding	transcription factor activity
organ morphogenesis	sequence-specific DNA binding	transcription factor activity
response to unfolded protein	fin regeneration	tissue regeneration
cytoplasm	mitochondrial matrix	soluble fraction
chromosome, pericentric region	microtubule binding	metaphase plate congression
cell death	positive regulation of nitric oxide biosynthes	extracellular region
receptor activity	cell-substrate junction assembly	cell-matrix adhesion
potassium channel activity		
membrane fraction	calcium-activated potassium channel activit	positive regulation of protein secretion
microtubule-based process		
microtubule	ATP binding	cell proliferation
transport	cytoplasm	ribosomal protein import into nucleus

cysteine-type peptidase activity ATP binding	metal ion binding magnesium ion binding	aminopeptidase activity negative regulation of progression through c
tRNA splicing	DNA ligase activity	DNA binding
transport	blood coagulation	sugar binding
S phase of mitotic cell cycle pre-replicative complex formation and maint chromosome condensation ATP-dependent DNA helicase activity DNA replication initiation	chromosome condensation DNA replication initiation MCM complex pre-replicative complex DNA replication	ATP-dependent DNA helicase activity DNA replication pre-replicative complex MCM complex DNA-dependent ATPase activity
membrane fraction	oligosaccharide biosynthesis	
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor		

mitochondrion metallochaperone activity	phosphoprotein phosphatase activity	mitochondrial inner membrane
transferase activity	metal ion binding	kinase activity
transcription factor activity		
nucleoside diphosphate kinase activity	negative regulation of cell proliferation	GTP biosynthesis
mRNA processing membrane fraction endoplasmic reticulum	GTPase activity	
nuclear membrane	transport	mRNA export from nucleus
cytoplasm	regulation of signal transduction	nucleocytoplasmic transporter activity
isomerase activity cobalt ion binding	unfolded protein binding cell proliferation	extracellular region DNA binding
metal ion binding protein kinase activity	locomotory behavior	ubiquitin-dependent protein catabolism
alpha-glucan biosynthesis cell proliferation	mitochondrion DNA binding	cell tip regulation of progression through cell cycle

DNA replication	pyrimidine nucleotide binding	transferase activity
response to DNA damage stimulus	3'-5' exonuclease activity	
DNA-directed RNA polymerase activity		
carbohydrate metabolism	transferase activity	metal ion binding
sphingosine metabolism	phosphatidate phosphatase activity	regulation of lipid metabolism
phosphoprotein phosphatase activity	heart development	metal ion binding
endoplasmic reticulum		
proline biosynthesis	negative regulation of inflammatory respons	blood coagulation
electron carrier activity	iron ion binding	GTPase activator activity
nucleus	double-strand break repair via single-strand	double-strand break repair via homologous
transport	GTPase activity	nucleus

endoplasmic reticulum DNA-dependent DNA replication	enzyme activator activity	metal ion binding
DNA replication leading strand elongation Rad17 RFC-like complex	cell cycle checkpoint sister chromatid cohesion DNA replication	leading strand elongation mismatch repair leading strand elongation
response to DNA damage stimulus	protection from non-homologous end joining	chromosome
metal ion binding protein N-terminus binding cytoplasmic membrane-bound vesicle	mRNA export from nucleus transcription	DNA binding DNA-dependent DNA replication
ribonucleoprotein complex	RNA binding	structural constituent of ribosome
microsome	metal ion binding	oxidoreductase activity
nuclear mRNA splicing, via spliceosome mRNA splice site selection	DNA binding RNA binding	response to DNA damage stimulus

hyperosmotic response	sodium ion transport	transport
chromatin	organ morphogenesis	
cytoplasm	transcription	signal transduction
transcription	sex chromatin	chromatin modification
histone acetylation	nucleus	adenylate kinase activity

hydrolase activity, acting on glycosyl bonds		
telomere maintenance via telomerase	telomere maintenance	
mitochondrion organization and biogenesis	regulation of transcription from RNA polyme	DNA binding
molecular function unknown	positive regulation of smooth muscle cell pr	histone acetylation
biological process unknown	transcription	morphogenesis of an epithelium
lamin binding	DNA binding	nuclear envelope
cell death	cytokine and chemokine mediated signaling	RNA destabilization
DNA binding	chromosome segregation	chromosome
cytoskeleton	GTPase activity	mitotic spindle assembly
cortical actin cytoskeleton	cell junction	transmembrane receptor activity
diacylglycerol binding	Rho guanyl-nucleotide exchange factor acti	vesicle fusion

ATP binding
ubiquitin ligase complex
transport

metal ion binding

protein kinase activity
ligase activity
mRNA export from nucleus

DNA binding

molecular function unknown
nuclear envelope

transcription factor activity

iron ion binding

unfolded protein binding

DNA metabolism	nucleotide metabolism	metal ion binding
DNA repair	endoplasmic reticulum	regulation of cell redox homeostasis
monovalent inorganic cation transporter acti	metal ion binding	ATPase activity, coupled to transmembrane
kinase activity protein kinase activity	ATP binding	DNA binding
anti-apoptosis	cell cycle	endopeptidase inhibitor activity
response to DNA damage stimulus	establishment and/or maintenance of chrom	single-stranded DNA binding

protein kinase activity		
cytoskeleton	unfolded protein binding	chaperonin-mediated tubulin folding
ATP binding cell division kinase activity	protein kinase activity chromatin binding ATP binding	DNA strand elongation protein kinase activity
nucleus	transcription factor complex	cell division
pronucleus	G2 phase of mitotic cell cycle	cell division
transferase activity protein kinase activity	kinase activity	ATP binding

chemokine activity

extracellular region

transcription

protein domain specific binding

transferase activity

transferase activity
ephrin receptor activity

kinase activity
axon guidance

receptor activity
axon guidance receptor activity

DNA repair

DNA replication

endoplasmic reticulum

receptor activity
pathway

G-protein coupled receptor protein signaling pathway

nervous system development	chromosome	nitric-oxide synthase regulator activity
pendent		
unfolded protein binding	mitochondrial inner membrane	
oxidoreductase activity	oxidoreductase activity, acting on NADH or	RNA binding
condensed chromosome		
insulin receptor binding	regulation of protein secretion	sterol metabolism
NLS-bearing substrate import into nucleus	molecular function unknown	protein transporter activity

magnesium ion binding protein kinase activity	manganese ion binding	response to antibiotic
ligase activity	response to DNA damage stimulus	
Golgi stack	unfolded protein binding	Golgi membrane
pre-replicative complex DNA-dependent ATPase activity nucleus nucleus DNA helicase activity	MCM complex DNA helicase activity nucleic acid binding chorion gene amplification DNA replication origin binding	nucleus cytoplasm cytosol nucleic acid binding cell cycle

manganese ion transport		
protein kinase activity	mitotic sister chromatid segregation	protein-tyrosine kinase activity
nucleoside triphosphate biosynthesis	nucleus	deoxyribonuclease activity
nucleocytoplasmic transporter activity	poly(A)+ mRNA export from nucleus	
cell death	negative regulation of cell proliferation	positive regulation of transcription
procollagen-proline 4-dioxygenase activity		
RNA binding	negative regulation of transcription, DNA-de	transcription factor activity
norepinephrine metabolism	zinc ion binding	learning
diacylglycerol binding	barrier septum	kinase activity
nuclear lamina	cyclin-dependent protein kinase holoenzym	replication fork

alpha DNA polymerase:primase complex	metal ion binding	DNA replication, synthesis of RNA primer
magnesium ion binding membrane fraction	negative regulation of cell proliferation	androgen receptor signaling pathway
T cell differentiation	iron ion binding	response to amphetamine
actin nucleation	protein domain specific binding	phospholipid binding
strand invasion	double-strand break repair via synthesis-de	meiosis
RNA localization	protein targeting	protein transport

ATP binding	DNA binding	specific transcriptional repressor activity
sister chromatid cohesion	mismatch repair	ATP binding
ATP binding	DNA binding	Elg1 RFC-like complex
sister chromatid cohesion	mismatch repair	ATP binding
telomere maintenance via telomerase	telomeric DNA binding	telomere cap complex
transcription from RNA polymerase I promo	DNA-directed RNA polymerase I complex	single-stranded DNA binding
nucleolus	DNA binding	transcription from RNA polymerase I promo
iron ion binding	regulation of Cdc42 GTPase activity	GTPase activator activity
RNA binding		

basolateral plasma membrane	amino acid-polyamine transporter activity	potassium ion transport
hematopoietin/interferon-class (D200-domai	DNA binding	regulation of progression through cell cycle
metal ion binding	positive regulation of cell proliferation	histone methylation
cytosol	nucleotide binding	transcription from RNA polymerase II promo

mitochondrial DNA replication	transcription initiation from mitochondrial pr	transcription factor activity
protein-glutamine gamma-glutamyltransfera	blood vessel remodeling	acyltransferase activity
DNA binding	branching morphogenesis of a tube	
chromosome	condensed chromosome	
DNA topoisomerase activity	isomerase activity	condensed chromosome
signal transduction	synapse	actin binding
lamellipodium biogenesis	cell migration	cytoplasm

entry of virus into host cell
response to virus

RNA binding

protein transporter activity

adenosine metabolism	antimicrobial humoral response (sensu Vertebrata)	
ribonuclease H activity	phosphodiesterase I activity	endonuclease activity
ATP binding	potassium ion transport	potassium ion binding
chromosome, pericentric region	cytokinesis	chromosome
metal ion binding	embryonic development	cysteine protease inhibitor activity
secretory granule		

DNA replication regulation of DNA replication	cell cycle	ATP binding
nucleotide binding	tracheal system development (sensu Insect	protein amino acid phosphorylation
negative regulation of transcription	outer kinetochore of condensed chromosom	chromatin binding
gametogenesis	response to DNA damage stimulus	negative regulation of cell proliferation

metal ion binding	DNA binding	negative regulation of transcription, DNA-de
ATP binding protein kinase activity	ephrin receptor activity	organ morphogenesis

ribonuclease H activity

5'-3' exonuclease activity

vesicle-mediated transport

glutathione metabolism

response to oxidative stress

generation of precursor metabolites and ene

glucose transport

insulin-like growth factor binding

peptidase activity

sarcomere

zinc ion binding
DNA replication origin binding
ATPase activity
cytosol
transcription

nucleic acid binding
cell cycle
nucleotide binding
nucleotide binding
cell proliferation

cytosol
transcription
cell division
chromatin binding
ATP binding

nucleus	meiosis	cell division
nucleotide binding	centrosome	mammary gland development
integral to membrane	nucleus	porin activity
cysteine-type endopeptidase activity	protein metabolism	protein modification
ATP binding	establishment and/or maintenance of cell pc	cell septum
regulation of DNA replication		

DNA binding	double-stranded DNA binding	3'-5' exonuclease activity
actin cytoskeleton	actin binding	pyrroline-5-carboxylate reductase activity
nucleotide binding	heteroduplex formation	DNA repair
nucleotide binding	protein export from nucleus	GTP binding

DNA ligase (NAD+) activity	telomere maintenance via telomerase	
DNA binding	Elg1 RFC-like complex	nuclear chromatin
nuclear chromatin	S phase of mitotic cell cycle	
DNA binding	Elg1 RFC-like complex	nuclear chromatin
telomere maintenance		
nucleolus organization and biogenesis	DNA replication factor A complex	DNA-directed RNA polymerase activity
DNA-directed RNA polymerase I complex	single-stranded DNA binding	DNA replication factor A complex
superoxide metabolism	integral to membrane	nucleus

cation:chloride symporter activity

potassium ion binding

membrane fraction

STAT protein nuclear translocation

transcription factor activity

protein C-terminus binding

chromatin remodeling

transcription initiation

cellular component unknown

GTP binding

cysteine-type endopeptidase activity

chromosome condensation

cytoskeleton
metal ion binding

membrane fraction
cell projection biogenesis

neuromuscular junction development
regulation of Rho protein signal transductior

DNA-(apurinic or apyrimidinic site) lyase act	DNA binding	response to DNA damage stimulus
monovalent inorganic cation transport	magnesium ion binding	ion transport
protein kinase activity		
chromosome, pericentric region	microtubule binding	chromosome

DNA binding

JAK-STAT cascade

mitotic spindle checkpoint

protein kinase activity

DNA synthesis during DNA repair

signal transduction

protein C-terminus binding

replication fork

delta DNA polymerase complex

cell cycle

cell proliferation

methyltransferase activity

replication fork

axon guidance

protein kinase activity

axon guidance receptor activity

endonuclease activity

phosphoinositide-mediated signaling

sphingolipid biosynthesis

hormone activity

endoplasmic reticulum

glucose metabolism

nucleotide binding
ATP binding
chromatin binding
DNA replication
DNA binding

chromatin binding
DNA binding
DNA replication
DNA replication origin binding
S phase of mitotic cell cycle

DNA replication
S phase of mitotic cell cycle
DNA replication origin binding
transcription
single-stranded DNA binding

nucleotide binding	centrosome	protein amino acid phosphorylation
nucleotide metabolism	regulation of apoptosis	soluble fraction
ubiquitin binding	protein targeting	SH2 domain binding
endoplasmic reticulum	synaptic transmission, glutamatergic	central nervous system development
phosphoenolpyruvate carboxykinase (GTP)	manganese ion binding	carboxy-lyase activity

protein C (activated) activity	negative regulation of coagulation	peptidase activity
response to cadmium ion	DNA metabolism	ATP binding
protein import into nucleus	cell cycle	regulation of progression through cell cycle

S phase of mitotic cell cycle

S phase of mitotic cell cycle

condensed chromosome
DNA-directed RNA polymerase activity

cytosol	fatty acid biosynthesis	signal transduction during conjugation with

ion transport

sodium ion binding

apical plasma membrane

transcription initiation from RNA polymerase

negative regulation of transcription from RN

nucleotide kinase activity

plasma membrane activation of NF-kappaB transcription factor protein homooligomerization

muscle contraction
positive regulation of cell adhesion

magnesium ion binding	3'-5' exonuclease activity

3'-5' exonuclease activity

replication fork

mitochondrion organization and biogenesis

ATP binding

cell proliferation

chromatin

nuclear envelope

kinetochore assembly

regulation of neuronal synaptic plasticity double-strand break repair DNA binding double-stranded DNA binding negative regulation of vasodilation positive regulation of cytokine secretion acute-phase response

DNA replication origin binding	cell cycle	transcription
transcription	ATP binding	DNA binding
cell cycle	ATP binding	DNA binding

regulation of progression through mitotic cel	cell cycle	ATP binding
ATP binding	DNA binding	UTP biosynthesis
chromatin binding	regulation of Ras protein signal transductior	thyroid hormone receptor binding
ligase activity	response to unfolded protein	startle response

extracellular region

DNA binding

actin filament organization

response to DNA damage stimulus

exosome (RNase complex)

recombinase activity

spindle organization and biogenesis

cytokinesis by cell plate formation

multidimensional cell growth

carrier activity

transcription

transcription factor TFIID complex

ATP binding

mitochondrion	G-protein signaling, coupled to IP3 second	release of cytoplasmic sequestered NF-kap

regulation of progression through cell cycle cyclin binding blastoderm segmentation

metaphase plate congression

magnesium ion binding

damaged DNA binding

manganese ion binding

ATP binding
cell proliferation
DNA binding

regulation of progression through cell cycle
nuclear chromatin

regulation of progression through cell cycle	magnesium ion binding	
magnesium ion binding		
nuclear pore	receptor signaling complex scaffold activity	structural constituent of nuclear pore
Golgi membrane		

damaged DNA binding

condensed chromosome

endoplasmic reticulum	Rho guanyl-nucleotide exchange factor acti	barrier septum

protein amino acid acetylation	DNA binding	chromatin

induction of apoptosis	protein domain specific binding	positive regulation of I-kappaB kinase/NF-ka

positive regulation of I-kappaB kinase/NF-ka positive regulation of epidermal growth factor receptor signaling pathway

lipid biosynthesis

mating projection tip

site of polarized growth

positive regulation of inflammatory response	isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine

regulation of Rho protein signal transductior	barrier septum formation	establishment and/or maintenance of cell pc

guard mother cell cytokinesis

stearoyl-CoA 9-desaturase activity

guard cell differentiation

nucleus	GO:GO:0005634	1190002H	1700022L	2010012C	2810417H	6330416L	Actl6a	Anapc1
protein binding	GO:GO:0005515	1190002H	Acta2	Actl6a	Anapc1	Apex1	Atrn	Aurkb
nucleotide binding	GO:GO:0000166	Abce1	Acta2	Atp4a	Aurka	Aurkb	B230120H	Bub1b
DNA binding	GO:GO:0003677	Apex1	Aurkb	Bclaf1	Cdc6	Cdkn2c	Cdt1	Dek
cytoplasm	GO:GO:0005737	1190002H	Ada	Aldh18a1	Amd1	Anp32e	Apex1	B230120H
membrane	GO:GO:0016020	6330527O	Abce1	Acsl5	Aldh18a1	Aqp1	Atp4a	Atp6ap2
ATP binding	GO:GO:0005524	Abce1	Acta2	Actl6a	Atp4a	Aurka	Aurkb	B230120H
integral to membrane	GO:GO:0016021	6330527O	AI132487	Acsl5	Aqp1	Atp4a	Atp6ap2	Atrn
metal ion binding	GO:GO:0046872	6330416L	AU021838	Ada	Apex1	Apobec3	Arfgap1	Atp4a
cell cycle	GO:GO:0007049	1190002H	Anapc1	Aspm	Aurka	Aurkb	B230120H	Birc5
transferase activity	GO:GO:0016740	AU021838	Aldh18a1	Aurka	Aurkb	B230120H	BC023814	Bub1b
nucleic acid binding	GO:GO:0003676	1810003N	6330416L	Bcl11a	Brca2	Cstf2	Dbf4	Ddx39
cellular component unknown	GO:GO:0008372	5730507H	Aaas	Abce1	Acsm2	Ada	Amd1	Apex1
regulation of transcription, DNA-dependent	GO:GO:0006355	6330416L	Actl6a	Ada	Bcl11a	Bclaf1	Cdkn2c	Cebpz
transcription	GO:GO:0006350	Actl6a	Bcl11a	Bclaf1	Cebpz	Cnot6	Dnmt1	E2f8
extracellular space	GO:GO:0005615	2210407C	Agr2	Aqp1	Atrn	Brca2	Ccl9	Cldn2
biological process unknown	GO:GO:0000004	5730507H	Aaas	Acsm2	Acta2	Anp32e	Aspm	Bxdc1
zinc ion binding	GO:GO:0008270	6330416L	Apobec3	Arfgap1	BC027344	Bcl11a	Birc5	Car12
transport	GO:GO:0006810	AI132487	Abce1	Ap3m1	Api5	Aqp1	Arfgap1	Atp4a
RNA binding	GO:GO:0003723	1810003N	2810028N	Cnot6	Cpsf2	Cstf2	Dek	Eif1a
molecular function unknown	GO:GO:0005554	5730507H	Aaas	Acsm2	Aspm	Bxdc1	Bysl	Ccdc5
kinase activity	GO:GO:0016301	AU021838	Aldh18a1	Aurka	Aurkb	B230120H	Bub1b	Ccnb1
cell division	GO:GO:0051301	Anapc1	Aspm	Aurkb	Birc5	Brrn1	Bub1b	Ccdc5
DNA replication	GO:GO:0006260	Cdc6	Cdt1	Dbf4	Dnajc2	Fen1	Lig1	Mcm10
hydrolase activity	GO:GO:0016787	AI132487	Ada	Apobec3	Atp4a	Atp6ap2	Blmh	Cdc25b
intracellular	GO:GO:0005622	6330416L	Bcl11a	Birc5	Cdc25b	Ect2	Gnl3	Gpatc4
mitosis	GO:GO:0007067	Anapc1	Aspm	Aurkb	Birc5	Brrn1	Bub1b	Ccdc5
DNA repair	GO:GO:0006281	Ada	Apex1	Brca2	Chek1	Fancl	Fancm	Fen1
cytosol	GO:GO:0005829	Ccnd1	Cct3	Cdo1	Clns1a	Ctnnal1	Gbp4	Idh1
regulation of progression through cell cycle	GO:GO:0000074	Anapc1	Brca2	Ccna2	Ccnb1	Ccnb1-rs1	Ccnb2	Ccnd1
receptor activity	GO:GO:0004872	Amot	Atp6ap2	Atrn	Cd44	Ephb2	Ephb3	Ffar2
mitochondrion	GO:GO:0005739	2810417H	Abce1	Acsl5	Aldh18a1	C1qbp	Cdt1	Hspd1
protein amino acid phosphorylation	GO:GO:0006468	Aurka	Aurkb	B230120H	Bub1b	Ccnb1	Ccnd1	Cdc2a
protein serine/threonine kinase activity	GO:GO:0004674	Aurka	Aurkb	B230120H	Bub1b	Cdc2a	Cdc7	Cdk4
endoplasmic reticulum	GO:GO:0005783	Apex1	Ckap4	Dnajc10	Fen1	Iigp1	Ins1	Irgm
signal transduction	GO:GO:0007165	Ccl9	Cdk4	Cxcl10	Ffar2	Fzd1	Fzd7	Hdgf
chromatin binding	GO:GO:0003682	Actl6a	Cbx5	Cdc6	Cenpf	Hells	Hmgb1	Hmgn1

protein kinase activity	GO:GO:0004672	Aurka	Aurkb	B230120H	Bub1b	Ccnd1	Cdc2a	Cdc7
oxidoreductase activity	GO:GO:0016491	Aldh18a1	Apex1	Cdo1	Fads1	Fzd7	Idh1	Impdh2
mRNA processing	GO:GO:0006397	Cpsf2	Cstf2	Ddx39	Dek	Eftud2	Gemin6	Hnrpa1
response to DNA damage stimulus	GO:GO:0006974	Apex1	Brca2	Chek1	Chek2	Fancl	Fancm	Lig1
development	GO:GO:0007275	Atrn	Cenpf	Diap2	Fzd1	Fzd7	Grem1	H1f0
ribonucleoprotein complex	GO:GO:0030529	Eftud2	Hnrpa1	Hnrpab	Hnrpdl	Nhp2l1	Nola1	Nola2
magnesium ion binding	GO:GO:0000287	AU021838	Acsl5	Apex1	Atp4a	B230120H	Chek2	Cnot6
nucleolus	GO:GO:0005730	Gnl3	Mki67	Mki67ip	Ncl	Nhp2l1	Nol5	Nol5a
GTP binding	GO:GO:0005525	Dek	Eftud2	Gbp2	Gbp4	Gnl3	Gtpbp4	Iigp1
integral to plasma membrane	GO:GO:0005887	Aqp1	Atp4a	Atrn	Boc	Elovl5	Ephb2	Ephb3
DNA replication initiation	GO:GO:0006270	Ccne2	Cdc7	Cdt1	Dbf4	Mcm10	Mcm2	Mcm3
cell proliferation	GO:GO:0008283	Cdk4	Cenpf	E2f8	Gkn1	Gnl3	Hdgf	Kif2c
plasma membrane	GO:GO:0005886	Atrn	C1qbp	Clns1a	Gjb2	Gp1ba	Itga6	Nhp2l1
protein transport	GO:GO:0015031	Ap3m1	Arfgap1	Kpnb1	Lman1	Nras	Nup107	Nup37
ligase activity	GO:GO:0016874	Acsl5	Asns	Ctps	Fancl	Gart	Lig1	Nedd4
protein-tyrosine kinase activity	GO:GO:0004713	Aurka	Aurkb	B230120H	Cdc2a	Chek1	Chek2	Ephb2
immune response	GO:GO:0006955	Ada	C1qbp	Ccl9	Cxcl10	Cxcl11	Cxcl9	Gbp2
transcription factor activity	GO:GO:0003700	Cdkn2c	Hod	Hoxa11	Hoxa9	Neurog3	Pa2g4	Rrs1
nuclear mRNA splicing, via spliceosome	GO:GO:0000398	Ddx39	Eftud2	Gemin6	Nhp2l1	Nono	Sfpq	Sfrs2
regulation of transcription	GO:GO:0045449	Brca2	Gtf2h2	Hod	Hoxa11	Hoxa9	Id4	Lin9
extracellular region	GO:GO:0005576	Ccl9	Cxcl10	Cxcl11	Cxcl9	Igfbp5	Ins1	Lrg1
intracellular signaling cascade	GO:GO:0007242	Ect2	Igfbp5	Nek2	Pck2	Racgap1	Scd1	Snx10
nucleoside-triphosphatase activity	GO:GO:0017111	Abce1	Cdc6	Mcm3	Mcm5	Mcm7	Psmc6	Rad51
chromatin	GO:GO:0000785	Asf1b	Cbx5	Cenpf	Hmga2	Hmgb1	Hmgn1	Kif22
soluble fraction	GO:GO:0005625	Asns	Blmh	Idh1	Lgals2	Mod1	Nme1	Pitpnm2
ubiquitin cycle	GO:GO:0006512	Anapc1	Fancl	Nedd4	Park2	Skp2	Ube2c	Uble1a
protein folding	GO:GO:0006457	Abce1	C80913	Cct3	Dnajc10	Dnajc2	Dnajc9	Fkbp3
calcium ion binding	GO:GO:0005509	Entpd4	Itga6	Lman1	Nucb2	Pitpnm2	Proc	Rcn1
electron transport	GO:GO:0006118	Abce1	Cdo1	Cxcl10	Lats2	Pitpnm2	Pycr1	Racgap1
chromosome	GO:GO:0005694	Aurkb	Birc5	H1f0	H2afz	Hmga2	Hmgb1	Rif1
catalytic activity	GO:GO:0003824	Acsl5	Aldh18a1	Atp4a	Ctps	Dnmt1	Gart	Impdh2
nucleotidyltransferase activity	GO:GO:0016779	Pnpt1	Pola1	Pold3	Pole	Pole2	Polr2a	Polr3f
unfolded protein binding	GO:GO:0051082	Abce1	Cct3	Dnajc10	Dnajc2	Dnajc9	Hspd1	Hspe1
GTPase activity	GO:GO:0003924	Eftud2	Gbp2	Gbp4	Igtp	Iigp1	Iigp2	Nras
S phase of mitotic cell cycle	GO:GO:0000084	Cdc6	Cdt1	Mcm2	Mcm3	Mcm5	Mcm6	Mcm7
microtubule	GO:GO:0005874	Ccdc5	Cnn3	Dynlt1	Incenp	Kif11	Kif22	Kif2c
iron ion binding	GO:GO:0005506	Abce1	Cdo1	Fads1	Indo	Polr3h	Ppp3cb	Racgap1

protein biosynthesis	GO:GO:0006412	Eftud2	Eif1a	Eif4e2	Eif4g1	Eif5a	Nola2	Rpl7l1
transporter activity	GO:GO:0005215	Aqp1	Eif1a	Mtm1	Nup155	Slc12a2	Slc5a4b	Slco3a1
electron carrier activity	GO:GO:0009055	Abce1	Cdo1	Cxcl10	P4hb	Phgdh	Racgap1	Trip6
transcription regulator activity	GO:GO:0030528	Ada	Apex1	Bzw1	Id4	Lap3	Neurog3	Nup62
binding	GO:GO:0005488	Api5	Aspm	Cebpz	Cep70	Heatr1	Kpnb1	Narg1
metabolism	GO:GO:0008152	Acsl5	Asns	Atp4a	Fzd1	Fzd7	Galk1	Idh1
cytoskeleton	GO:GO:0005856	Acta2	Cct3	Cdk5rap2	Ctnnal1	Epb4.1l5	Tpm3	Tubb5
carbohydrate metabolism	GO:GO:0005975	Galk1	Idh1	Ins1	Pnpt1	Pomt1	Rpe	Smpdl3b
rRNA processing	GO:GO:0006364	Gas5	Nme1	Nol5	Nol5a	Nola1	Nola2	Pa2g4
inflammatory response	GO:GO:0006954	Atrn	Cdo1	Cxcl10	Cxcl11	Cxcl9	Pap	Reg3g
cell adhesion	GO:GO:0007155	Boc	Bysl	Cd44	Ctnnal1	Gp1ba	Itga6	Omd
pre-replicative complex	GO:GO:0005656	Cdc6	Cdt1	Mcm10	Mcm2	Mcm3	Mcm5	Mcm6
DNA-directed RNA polymerase activity	GO:GO:0003899	Polr2a	Polr3f	Polr3h	Prim1	Rpa1	Rpa2	Rpo1-4
apoptosis	GO:GO:0006915	Api5	Birc5	Eif5a	Grem1	Moap1	Siva	Tfam
DNA replication origin binding	GO:GO:0003688	Hnrpab	Mcm2	Mcm3	Mcm5	Mcm6	Mcm7	Orc2l
DNA-dependent ATPase activity	GO:GO:0008094	Mcm2	Mcm3	Mcm5	Mcm6	Mcm7	Rad51	Rad54l
cyclin-dependent protein kinase regulator activity	GO:GO:0016538	Ccna2	Ccnb1	Ccnb1-rs1	Ccnb2	Ccnd1	Ccne2	Cks1b
condensed chromosome	GO:GO:0000793	Incenp	Mki67	Mki67ip	Rad51	Rpa1	Tmpo	Top2a
chromosome, pericentric region	GO:GO:0000775	Aurkb	Birc5	Cenpf	Incenp	Mad2l1	Mki67	Sgol1
negative regulation of transcription from RNA polymerase II promoter	GO:GO:0000122	Dnmt1	Hod	Orc2l	Strap	Suz12	Taf9	Tdg
spliceosome complex	GO:GO:0005681	Api5	Eftud2	Gemin6	Nhp2l1	Sf3b3	Sfrs2	Snrpg
nuclear pore	GO:GO:0005643	Aaas	Kpnb1	Nup107	Nup155	Nup62	Rangap1	Xpo1
peptidase activity	GO:GO:0008233	AI132487	Blmh	Lap3	Proc	Psmc6	Uchl5	Usp1
membrane fraction	GO:GO:0005624	Gp1ba	Kcnn4	Mgat2	Nras	Ppap2a	Slc12a2	Utrn
pre-replicative complex formation and maintenance	GO:GO:0006267	Cdc6	Mcm10	Mcm2	Mcm3	Mcm5	Mcm6	Mcm7
proteolysis	GO:GO:0006508	Blmh	Lap3	Nedd4	Park2	Proc	Tgm2	
negative regulation of cell proliferation	GO:GO:0008285	Chek1	Ifitm3	Nme1	Nup62	Ppap2a	Wars	
chemotaxis	GO:GO:0006935	Abce1	Amot	Ccl9	Cxcl10	Cxcl11	Utrn	
protein heterodimerization activity	GO:GO:0046982	Cenpf	Pola1	Ppp3cb	Smc4l1	Timeless	Uble1a	
protein modification	GO:GO:0006464	Nedd4	Park2	Ube2c	Uble1a	Uble1b	Wwp1	
organ morphogenesis	GO:GO:0009887	Ephb2	Gmnn	Grem1	Hoxa11	Hoxa9	Smarcc1	
positive regulation of cell proliferation	GO:GO:0008284	Cxcl10	Gkn1	Id4	Nap1l1	Suz12	Ube2c	
ion transport	GO:GO:0006811	Atp4a	Kcnk3	Kcnn4	Slc12a2	Slc5a4b	Slco3a1	
ribosome biogenesis	GO:GO:0007046	Gtpbp4	Nol5a	Nola1	Nola2	Rps6	Rrs1	

helicase activity	GO:GO:0004386	Ddx39	Ercc6l	Fancm	Hells	Rad54l	Smarcad1
mRNA export from nucleus	GO:GO:0006406	Ddx39	Hnrpa1	Nup107	Rpa1	Thoc3	Xpo1
ubiquitin-dependent protein catabolism	GO:GO:0006511	Park2	Skp2	Ube2c	Uchl5	Usp1	Usp39
calmodulin binding	GO:GO:0005516	Aspm	Cnn1	Cnn3	Itpka	Kcnn4	Ppp3cb
methyltransferase activity	GO:GO:0008168	BC023814	Dnmt1	Pnmt	Rg9mtd2	Shmt1	Shmt2
cytokine activity	GO:GO:0005125	Ccl9	Cxcl10	Cxcl11	Cxcl9	Grem1	Retnlb
translation initiation factor activity	GO:GO:0003743	Bzw1	Eif1a	Eif4e2	Eif4ebp2	Eif4g1	Eif5a
small GTPase mediated signal transduction	GO:GO:0007264	Gtpbp4	Lrg1	Nras	Ran	Rem2	Vav3
actin binding	GO:GO:0003779	Cnn1	Cnn3	Diap2	Proc	Tpm3	Utrn
DNA recombination	GO:GO:0006310	Brca2	Lig1	Nono	Rad51	Rad51ap1	Rpa1
single-stranded DNA binding	GO:GO:0003697	Brca2	Hnrpa1	Mcm6	Mcm7	Rpa1	Rpa2
kinetochore	GO:GO:0000776	Bub1b	Cbx5	Cenpf	Cnn1	Kif22	Mad2l1
cell-cell signaling	GO:GO:0007267	Ccl9	Fzd1	Gjb2	Grem1	Hmmr	Ins1
amino acid biosynthesis	GO:GO:0008652	Aldh18a1	Asns	Phgdh	Psat1	Pycr1	
regulation of cell growth	GO:GO:0001558	Actl6a	Cdk4	Hrasls	Igfbp5	Socs3	
ribosome	GO:GO:0005840	Apex1	Eif1a	Nola2	Rpl7l1	Rps6	
nucleosome assembly	GO:GO:0006334	Asf1b	H2afz	Mcm2	Nap1l1	Set	
transcription factor complex	GO:GO:0005667	Cdk4	Hoxa11	Hoxa9	Tcf19	Tfam	
cell surface receptor linked signal transduction	GO:GO:0007166	Fzd1	Fzd7	Ins1	Nup62	Tnfrsf1b	
isomerase activity	GO:GO:0016853	Fkbp3	P4hb	Rpe	Top2a	Txndc5	
G-protein coupled receptor protein signaling pathway	GO:GO:0007186	Ffar2	Fzd1	Fzd7	Lgr5	Olfr157	
ATP-dependent helicase activity	GO:GO:0008026	Ddx39	Fancm	Hells	Rad54l	Smarcad1	
nucleocytoplasmic transport	GO:GO:0006913	Aaas	Nup107	Nup155	Nup62	Ran	
cytokinesis	GO:GO:0000910	Aurkb	Ccnb1	Ccnb1-rs1	Prc1	Ube2c	
nuclease activity	GO:GO:0004518	Apex1	Cnot6	Fancm	Fen1	Rexo2	
porin activity	GO:GO:0015288	Aqp1	Nup107	Nup155	Nup37	Nup62	
cysteine-type endopeptidase activity	GO:GO:0004197	Blmh	Park2	Tgm2	Usp1	Usp39	
small nucleolar ribonucleoprotein complex	GO:GO:0005732	Nol5	Nola1	Rps6	Snrpd3	Snrpg	
sugar binding	GO:GO:0005529	Atrn	Lgals2	Lman1	Pap	Reg3g	
ubiquitin-protein ligase activity	GO:GO:0004842	Fancl	Nedd4	Park2	Ube2c	Wwp1	
chromatin modification	GO:GO:0016568	Actl6a	Rbbp4	Smarcc1	Suz12	Taf9	
outer membrane	GO:GO:0019867	Aqp1	Nup107	Nup155	Nup37	Nup62	
DNA-directed DNA polymerase activity	GO:GO:0003887	Cdc6	Pola1	Pold3	Pole	Pole2	
MCM complex	GO:GO:0042555	Mcm2	Mcm3	Mcm5	Mcm6	Mcm7	

DNA helicase activity	GO:GO:0003678	Mcm2	Mcm3	Mcm5	Mcm6	Mcm7
protein amino acid dephosphorylation	GO:GO:0006470	Cdc25b	Mtm1	Ppap2a	Ppp3cb	Ptpro
3'-5' exonuclease activity	GO:GO:0008408	Apex1	Cdc6	Pola1	Pole	Rexo2
DNA unwinding during replication	GO:GO:0006268	Mcm2	Mcm3	Mcm6	Mcm7	Top2a
structural molecule activity	GO:GO:0005198	Acta2	Cldn2	Ctnnal1	Tubb5	Utrn
GTPase activator activity	GO:GO:0005096	Arfgap1	Ect2	Racgap1	Rangap1	Scd1
meiosis	GO:GO:0007126	Kif2c	Mki67	Nek2	Rad51	Rpa1
protein complex	GO:GO:0043234	Psmc6	Rfc4	Rfc5	Tubb5	Uchl5
regulation of translation	GO:GO:0006445	Eif4e2	Eif4ebp2	Eif4g1	Pa2g4	Rps6
Golgi stack	GO:GO:0005795	Ap3m1	Arfgap1	Lman1	Mgat2	Nras
nuclear envelope	GO:GO:0005635	Cenpf	Fancl	Rangap1	Tmpo	Xpo1
exonuclease activity	GO:GO:0004527	2810028N	Cnot6	Fen1	Isg20l1	Rexo2
signal transducer activity	GO:GO:0004871	Ffar2	Fzd1	Fzd7	Lgr5	Stat1
RNA splicing	GO:GO:0008380	Eftud2	Sf3b3	Sfpq	Sfrs2	Syncrip
spindle	GO:GO:0005819	Aurkb	Cdc6	Kif22	Prc1	Scd1
DNA replication factor C complex	GO:GO:0005663	Pcna	Recc1	Rfc2	Rfc4	Rfc5
chromosome segregation	GO:GO:0007059	Cnn1	Sgol1	Smc4l1	Top2a	
replication fork	GO:GO:0005657	Cdc6	Chek1	Dnmt1	Pcna	
negative regulation of transcription	GO:GO:0016481	Bclaf1	Cenpf	Id4	Timeless	
chromatin remodeling	GO:GO:0006338	Actl6a	Brca2	Rbbp4	Taf9	
microtubule binding	GO:GO:0008017	Birc5	Cnn3	Incenp	Nusap1	
cellular physiological process	GO:GO:0050875	Ect2	Hdgf	Nras	Ran	
microtubule-based process	GO:GO:0007017	Dynlt1	Kif11	Kif22	Tubb5	
nervous system development	GO:GO:0007399	Grem1	Hmgb1	Neurog3	Ptpro	
transcription factor binding	GO:GO:0008134	Cenpf	Dnmt1	Tdg	Uble1b	
DNA-dependent DNA replication	GO:GO:0006261	Pole2	Recc1	Rpa1	Rpa2	
protein targeting	GO:GO:0006605	Ccnb1-rs1	Neto1	Nup62	Ran	
defense response	GO:GO:0006952	H2-T22	Indo	Irgm	Kcnn4	
chemokine activity	GO:GO:0008009	Ccl9	Cxcl10	Cxcl11	Cxcl9	
condensed nuclear chromosome	GO:GO:0000794	Chek1	Nek2	Rad51	Topbp1	
midbody	GO:GO:0030496	Aurkb	Birc5	Incenp	Nek2	
cell differentiation	GO:GO:0030154	Diap2	Narg1	Neurog3	Zipro1	
cytoskeleton organization and biogenesis	GO:GO:0007010	Acta2	B230120H	Cct3	Hmmr	
RNA processing	GO:GO:0006396	Hnrpa1	Hnrpab	Pnpt1	Rbmxrt	
ER-Golgi intermediate compartment	GO:GO:0005793	Lman1	Nucb2	P4hb	Tmed5	
chromosome organization and biogenesis (sensu Eukaryota)	GO:GO:0007001	H2afz	Hmga2	Smc4l1	Terf1	

centrosome	GO:GO:0005813	Cct3	Nek2	Nme1	Tacc3
potassium ion binding	GO:GO:0030955	Atp4a	Impdh2	Kcnk3	Slc12a2
nucleoplasm	GO:GO:0005654	Cdc7	Dbf4	Nolc1	Xpo1
axon guidance	GO:GO:0007411	Boc	Ephb2	Ephb3	Nedd4
lyase activity	GO:GO:0016829	Amd1	Apex1	Car12	Pck2
one-carbon compound metabolism	GO:GO:0006730	Car12	Car8	Mthfd2	Shmt1
chromosome condensation	GO:GO:0030261	Mcm10	Mcm2	Mcm5	Top2a
DNA metabolism	GO:GO:0006259	Ada	Fancm	Rad51	Top2a
DNA clamp loader activity	GO:GO:0003689	Cdc6	Rfc2	Rfc4	Rfc5
transcriptional repressor activity	GO:GO:0016564	Bclaf1	Dnmt1	Hod	Tdg
intracellular protein transport	GO:GO:0006886	Ap3m1	Ran	Sec23b	Snx6
sequence-specific DNA binding	GO:GO:0043565	Hod	Hoxa11	Hoxa9	Spdef
protein domain specific binding	GO:GO:0019904	Dnmt1	Proc	Tdg	Tgm2
ATPase activity	GO:GO:0016887	Abce1	Cdc6	Mcm5	Rfc5
plastid	GO:GO:0009536	Abce1	Pola1	Rpa2	Rpe
G-protein coupled receptor activity	GO:GO:0004930	Ffar2	Fzd1	Fzd7	Lgr5
motor activity	GO:GO:0003774	Dynlt1	Kif11	Kif22	Kif2c
manganese ion binding	GO:GO:0030145	Fen1	Lap3	Pck2	Rexo2
nuclear chromatin	GO:GO:0000790	Mcm6	Rfc2	Rfc4	Rfc5
transcription from RNA polymerase II promoter	GO:GO:0006366	Polr2a	Stat1	Taf9	Trip13
potassium ion transport	GO:GO:0006813	Atp4a	Kcnk3	Kcnn4	Slc12a2
regulation of protein biosynthesis	GO:GO:0006417	Eif4e2	Eif4ebp2	Eif4g1	Pa2g4
protein kinase binding	GO:GO:0019901	Cdk5rap2	Prkrip1	Statip1	Tpx2
mitochondrial inner membrane	GO:GO:0005743	Acsl5	Hspd1	Mtm1	Shmt2
leading strand elongation	GO:GO:0006272	Pcna	Rfc2	Rfc4	Rfc5
anti-apoptosis	GO:GO:0006916	Api5	Birc5	Hells	Socs3
hormone activity	GO:GO:0005179	Ins1	Retnlb	Tmpo	Vip
mismatch repair	GO:GO:0006298	Pold3	Rfc2	Rfc4	Rfc5
sister chromatid cohesion	GO:GO:0007062	Rfc2	Rfc4	Rfc5	
cysteine-type peptidase activity	GO:GO:0008234	Blmh	Lap3	Uchl5	
G2/M transition of mitotic cell cycle	GO:GO:0000086	Birc5	Ccnb1	Chek1	
microsome	GO:GO:0005792	Nme1	P4hb	Scd1	
Rho guanyl-nucleotide exchange factor activity	GO:GO:0005089	Ect2	Scd1	Vav3	
embryonic development (sensu Mammalia)	GO:GO:0001701	Amd1	Amot	Tfam	
spindle microtubule	GO:GO:0005876	Birc5	Nusap1	Tpx2	

G1/S transition of mitotic cell cycle	GO:GO:0000082	Ccnd1	Cdk4	Skp2
Elg1 RFC-like complex	GO:GO:0031391	Rfc2	Rfc4	Rfc5
cell death	GO:GO:0008219	Ins1	Nup62	Tnfrsf1b
receptor binding	GO:GO:0005102	Ephb2	Proc	Strap
negative regulation of apoptosis	GO:GO:0043066	Mcm5	Nup62	Proc
purine nucleotide binding	GO:GO:0017076	Pola1	Rfc2	Rfc4
mitotic chromosome condensation	GO:GO:0007076	Brrn1	Nusap1	Smc4l1
perinuclear region	GO:GO:0048471	Apex1	Rangap1	Sec23b

regulation of Rho protein signal transduction	GO:GO:0035023	Ect2	Scd1	Vav3
protein C-terminus binding	GO:GO:0008022	Cenpf	Taf9	Uble1a
regulation of S phase of mitotic cell cycle	GO:GO:0007090	Brca2	Cdt1	Dbf4
rhodopsin-like receptor activity	GO:GO:0001584	Ffar2	Lgr5	Olfr157
response to unfolded protein	GO:GO:0006986	Hspd1	Hspe1	Park2
protein kinase inhibitor activity	GO:GO:0004860	Prkrip1	Socs3	Wnk1
regulation of apoptosis	GO:GO:0042981	Hspd1	Moap1	Nme1
Rad17 RFC-like complex	GO:GO:0031389	Rfc2	Rfc4	Rfc5
tissue regeneration	GO:GO:0042246	Ccnb1	Hspd1	Serpina10
structural constituent of ribosome	GO:GO:0003735	Nola2	Rpl7l1	Rps6
Ctf18 RFC-like complex	GO:GO:0031390	Rfc2	Rfc4	Rfc5
mitotic cell cycle	GO:GO:0000278	Aurka	Brrn1	Mcm5
external side of plasma membrane	GO:GO:0009897	Amot	Cd24a	Cd44
structural constituent of cytoskeleton	GO:GO:0005200	Acta2	Actl6a	Tubb5
ATP-dependent DNA helicase activity	GO:GO:0004003	Mcm2	Mcm3	Mcm6
JAK-STAT cascade	GO:GO:0007259	Cdk4	Socs3	Stat1
diacylglycerol binding	GO:GO:0019992	Pck2	Racgap1	Vav3
cell growth	GO:GO:0016049	Cdk4	Gkn1	Nol5
microtubule motor activity	GO:GO:0003777	Kif11	Kif22	Kif2c
transferase activity, transferring glycosyl groups	GO:GO:0016757	Mgat2	Mtap	Pomt1
microtubule-based movement	GO:GO:0007018	Kif11	Kif2c	Tubb5
kinesin complex	GO:GO:0005871	Kif11	Kif22	Kif2c
meiotic recombination	GO:GO:0007131	Chek1	Rad51	Topbp1
muscle development	GO:GO:0007517	Cxcl10	Mtm1	Utrn
phosphoinositide-mediated signaling	GO:GO:0048015	Car8	Fen1	Pcna
DNA packaging	GO:GO:0006323	Hmga2	Hmgb1	Smarcc1
phosphoprotein phosphatase activity	GO:GO:0004721	Cdc25b	Mtm1	Ppp3cb

protein import into nucleus	GO:GO:0006606	Kpnb1	Ran	Rangap1
cytoplasmic membrane-bound vesicle	GO:GO:0016023	Anp32e	Ifitm3	Rpe
mitochondrial matrix	GO:GO:0005759	C1qbp	Hspe1	Idh1
ubiquitin ligase complex	GO:GO:0000151	Nedd4	Skp2	Wwp1
protein tyrosine phosphatase activity	GO:GO:0004725	Cdc25b	Mtm1	Ptpro
transcription corepressor activity	GO:GO:0003714	Bcl11a	Id4	Sfrs2
regulation of translational initiation	GO:GO:0006446	Bzw1	Eif4ebp2	Eif4g1
DNA-directed RNA polymerase I complex	GO:GO:0005736	Rpa1	Rpa2	Rpo1-4
telomere maintenance via telomerase	GO:GO:0007004	Recc1	Rif1	Terf1
cellular morphogenesis	GO:GO:0000902	Gp1ba	Hmgb1	Scd1
microtubule cytoskeleton organization and biogenesis	GO:GO:0000226	Birc5	Ran	Scd1
actin filament	GO:GO:0005884	Acta2	Actl6a	Cnn3
Golgi apparatus	GO:GO:0005794	Dynlt1	Lman1	Mgat2
DNA methylation	GO:GO:0006306	Aurkb	Dnmt1	Hells
proline biosynthesis	GO:GO:0006561	Aldh18a1	Proc	Pycr1
growth factor activity	GO:GO:0008083	Gkn1	Hdgf	Mia1
secretory granule	GO:GO:0030141	Brca2	Gkn1	Sypl
acute-phase response	GO:GO:0006953	Ins1	Pap	Reg3g
protein homodimerization activity	GO:GO:0042803	Cenpf	E2f8	Timeless
extracellular matrix (sensu Metazoa)	GO:GO:0005578	Gp1ba	Lgr5	Omd
ribosome biogenesis and assembly	GO:GO:0042254	Nhp2l1	Nola2	Rrs1
cyclin-dependent protein kinase holoenzyme complex	GO:GO:0000307	Ccnd1	Cdk4	Pcna
nucleobase, nucleoside, nucleotide and nucleic acid metabolism	GO:GO:0006139	Mtap	Rexo2	Tk1
base-excision repair	GO:GO:0006284	Apex1	Rpa2	Tdg
Golgi membrane	GO:GO:0000139	Arfgap1	Lman1	Park2
negative regulation of transcription, DNA-dependent	GO:GO:0045892	Dnmt1	Hnrpab	Pa2g4
transcriptional activator activity	GO:GO:0016563	Brca2	Hoxa9	Zipro1
endoplasmic reticulum membrane	GO:GO:0005789	Fen1	Lman1	Pomt1
chromatin assembly or disassembly	GO:GO:0006333	Cbx5	Hmgb1	Smarcc1
ubiquitin thiolesterase activity	GO:GO:0004221	Uchl5	Usp1	Usp39
protein transporter activity	GO:GO:0008565	Kpnb1	Snx6	Xpo1
mitotic sister chromatid segregation	GO:GO:0000070	Mad2l1	Nek2	Nusap1
regulation of cell proliferation	GO:GO:0042127	Cdk4	Fancl	Gnl3

protein ubiquitination	GO:GO:0016567	Nedd4	Uble1a	Wwp1
basolateral plasma membrane	GO:GO:0016323	Aqp1	Itga6	Slc12a2
phosphatase inhibitor activity	GO:GO:0019212	Anp32e	Ppp1r14b	Set
mRNA metabolism	GO:GO:0016071	Hnrpdl	Snrpd3	Snrpg
nucleotide metabolism	GO:GO:0009117	Ada	Nme1	Rexo2
establishment and/or maintenance of chromatin architecture	GO:GO:0006325	Brca2	Hmgn1	Taf9
telomere maintenance	GO:GO:0000723	Gbp2	Rif1	Terf1
nucleocytoplasmic transporter activity	GO:GO:0005487	Nup107	Nup155	Nup62
ER to Golgi vesicle-mediated transport	GO:GO:0006888	Arfgap1	Lman1	Sec23b
translational initiation	GO:GO:0006413	Eif1a	Eif4e2	Eif5a
regulation of DNA replication	GO:GO:0006275	Cdc7	Dbf4	Pcna
amino acid metabolism	GO:GO:0006520	Asns	Proc	
symporter activity	GO:GO:0015293	Slc12a2	Slc1a4	
fatty acid elongation	GO:GO:0030497	Elovl5	Fen1	
cell cycle checkpoint	GO:GO:0000075	Chek1	Rfc2	
aminopeptidase activity	GO:GO:0004177	Blmh	Lap3	
antimicrobial humoral response (sensu Vertebrata)	GO:GO:0019735	Ada	Ccl9	
lipid binding	GO:GO:0008289	Ffar2	Pitpnm2	
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:GO:0016616	Mod1	Phgdh	
glutamine metabolism	GO:GO:0006541	Asns	Ctps	
nuclear chromosome	GO:GO:0000228	Hmga2	Rad51	
heat shock protein binding	GO:GO:0031072	Dnajc2	Dnajc9	
histone phosphorylation	GO:GO:0016572	Incenp	Tgm2	
hemopoiesis	GO:GO:0030097	Bcl11a	Tacc3	
identical protein binding	GO:GO:0042802	Iigp1	Trip13	
response to biotic stimulus	GO:GO:0009607	Ifitm2	Ifitm3	
non-G-protein coupled 7TM receptor activity	GO:GO:0004926	Fzd1	Fzd7	
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	GO:GO:0016702	Cdo1	Indo	
brain development	GO:GO:0007420	Cdk5rap2	Phgdh	

smooth muscle contraction	GO:GO:0006939	Cnn1	Cnn3
sodium ion transport	GO:GO:0006814	Slc12a2	Slc5a4b
protein export from nucleus	GO:GO:0006611	Ran	Xpo1
generation of precursor metabolites and energy	GO:GO:0006091	Ins1	Rpe
mRNA polyadenylylation	GO:GO:0006378	Cpsf2	Cstf2
heart development	GO:GO:0007507	Hod	Ppp3cb
purine nucleotide biosynthesis	GO:GO:0006164	Gart	Impdh2
ribose phosphate diphosphokinase activity	GO:GO:0004749	AU021838	Prps2
guanyl-nucleotide exchange factor activity	GO:GO:0005085	Ect2	Vav3
carbonate dehydratase activity	GO:GO:0004089	Car12	Car8
small nuclear ribonucleoprotein complex	GO:GO:0030532	Nolc1	Sf3b3
metaphase plate congression	GO:GO:0051310	Cenpf	Incenp
positive regulation of apoptosis	GO:GO:0043065	Bclaf1	Siva
L-serine metabolism	GO:GO:0006563	Shmt1	Shmt2
glycine hydroxymethyltransferase activity	GO:GO:0004372	Shmt1	Shmt2
RNA splicing factor activity, transesterification mechanism	GO:GO:0031202	Sf3b3	Snrpg
GPI anchor binding	GO:GO:0048503	Cd24a	Gpiap1
nuclear origin of replication recognition complex	GO:GO:0005664	Mcm2	Orc2l
cellular protein metabolism	GO:GO:0044267	Cct3	Hspd1
circadian rhythm	GO:GO:0007623	Timeless	Wnk1
chloride transport	GO:GO:0006821	Clns1a	Slc12a2
pyridoxal phosphate binding	GO:GO:0030170	Shmt1	Shmt2
protein serine/threonine phosphatase activity	GO:GO:0004722	Mtm1	Ppp3cb
cell tip	GO:GO:0051286	Pck2	Scd1
phospholipid binding	GO:GO:0005543	Pitpnm2	Proc
DNA strand elongation	GO:GO:0006271	Cdc6	Mcm10
pattern specification	GO:GO:0007389	Hoxa11	Hoxa9
tricarboxylic acid cycle	GO:GO:0006099	Idh1	Polr3h
alpha DNA polymerase:primase complex	GO:GO:0005658	Pola1	Prim1
mitotic spindle assembly	GO:GO:0051227	Tpx2	Tubb5
insulin-like growth factor binding	GO:GO:0005520	Igfbp5	Ins1
ubiquitin activating enzyme activity	GO:GO:0004839	Uble1a	Uble1b

protein phosphatase type 2A regulator activity	GO:GO:0008601	Ppp2r2b	Rcn1
ribonuclease activity	GO:GO:0004540	2810028N	Rpp14
mitochondrion organization and biogenesis	GO:GO:0007005	Cdk4	Tfam
histone acetylation	GO:GO:0016573	Taf9	Tgm2
G2 phase of mitotic cell cycle	GO:GO:0000085	Cenpf	Dnajc2
blood coagulation	GO:GO:0007596	Lman1	Proc
cell motility	GO:GO:0006928	Cxcl10	Hmmr
heme binding	GO:GO:0020037	Indo	Trip6
pyrroline-5-carboxylate reductase activity	GO:GO:0004735	Proc	Pycr1
nucleotide biosynthesis	GO:GO:0009165	AU021838	Prps2
transmembrane receptor protein tyrosine kinase signaling pathway	GO:GO:0007169	Ephb2	Ephb3
microtubule associated complex	GO:GO:0005875	Kif11	Kif2c
transmembrane-ephrin receptor activity	GO:GO:0005005	Ephb2	Ephb3
actin cytoskeleton organization and biogenesis	GO:GO:0030036	Cnn1	Diap2
negative regulation of inflammatory response	GO:GO:0050728	Proc	Tnfrsf1b
chromosome, telomeric region	GO:GO:0000781	Rif1	Terf1
vesicle-mediated transport	GO:GO:0016192	Fen1	Sypl
DNA replication, synthesis of RNA primer	GO:GO:0006269	Pola1	Prim1
receptor signaling protein serine/threonine kinase activity	GO:GO:0004702	Cdk4	Nek2
response to drug	GO:GO:0042493	Blmh	Cenpf
nucleolus organization and biogenesis	GO:GO:0007000	Nolc1	Rpa1
serine-type endopeptidase activity	GO:GO:0004252	AI132487	Proc
regulation of transcription from RNA polymerase II promoter	GO:GO:0006357	Id4	Tfam
Ras protein signal transduction	GO:GO:0007265	Hrasls	Nras
structural constituent of nuclear pore	GO:GO:0017056	Nup155	Nup62
DNA synthesis during DNA repair	GO:GO:0000731	Cdc6	Pold3
spindle pole	GO:GO:0000922	Cenpf	Nek2
ion channel activity	GO:GO:0005216	Kcnk3	Kcnn4
S-adenosylmethionine-dependent methyltransferase activity	GO:GO:0008757	Dnmt1	Pnmt
phosphoinositide binding	GO:GO:0035091	Snx10	Snx6

calcium ion homeostasis	GO:GO:0006874	Ccl9	Nucb2
endonuclease activity	GO:GO:0004519	Apex1	Fen1
axon guidance receptor activity	GO:GO:0008046	Ephb2	Ephb3
oogenesis	GO:GO:0048477	Diap2	Zipro1
regulation of cell shape	GO:GO:0008360	Pck2	Ran
protein phosphatase type 2A complex	GO:GO:0000159	Ppp2r2b	Rcn1
NAD binding	GO:GO:0051287	Mod1	Phgdh
synapse	GO:GO:0045202	Syt9	Utrn
DNA damage checkpoint	GO:GO:0000077	Chek1	Chek2
Wnt receptor signaling pathway	GO:GO:0016055	Fzd1	Fzd7
heparin binding	GO:GO:0008201	Hdgf	Hmgb1
learning	GO:GO:0007612	Ephb2	Park2
spindle pole body	GO:GO:0005816	Cdc7	Mad2l1
glycine metabolism	GO:GO:0006544	Shmt1	Shmt2
double-stranded DNA binding	GO:GO:0003690	Fen1	Pola1
delta DNA polymerase complex	GO:GO:0043625	Cdc6	Pold3
long-chain fatty acid biosynthesis	GO:GO:0042759	Elovl5	Fads1
outer kinetochore of condensed chromosome	GO:GO:0000940	Bub1b	Cenpf
tRNA processing	GO:GO:0008033	Rpp14	Wdr4
cell surface	GO:GO:0009986	Ckap4	P4hb
L-serine biosynthesis	GO:GO:0006564	Phgdh	Psat1
epithelial cell differentiation	GO:GO:0030855	Fzd1	Neurog3
fatty acid elongase activity	GO:GO:0009922	Elovl5	Fen1
hydrolase activity, acting on glycosyl bonds	GO:GO:0016798	Smpdl3b	Tdg
positive regulation of I-kappaB kinase/NF-kappaB cascade	GO:GO:0043123	Nup62	Tgm2
purine nucleotide metabolism	GO:GO:0006163	Ada	Amd1
transcription from RNA polymerase I promoter	GO:GO:0006360	Rpa1	Rpa2
double-strand break repair via homologous recombination	GO:GO:0000724	Brca2	Rad51
protein disulfide oxidoreductase activity	GO:GO:0015035	P4hb	Txndc5
integrin-mediated signaling pathway	GO:GO:0007229	Itga6	Vav3
RNA polymerase II transcription factor activity	GO:GO:0003702	Gtf2h2	Hmgn1

lagging strand elongation	GO:GO:0006273	Pcna	Pola1
mitotic spindle checkpoint	GO:GO:0007094	Cenpf	Mad2l1
induction of apoptosis	GO:GO:0006917	Siva	Tgm2
establishment and/or maintenance of cell polarity (sensu Fungi)	GO:GO:0030467	Pck2	Scd1
cytokine and chemokine mediated signaling pathway	GO:GO:0019221	Iigp1	Tnfrsf1b
endopeptidase inhibitor activity	GO:GO:0004866	Birc5	Serpina10
protein import into nucleus, docking	GO:GO:0000059	Kpnb1	Xpo1
I-kappaB kinase/NF-kappaB cascade	GO:GO:0007249	Stat1	T2bp
SH2 domain binding	GO:GO:0042169	Nup62	Shcbp1
protein metabolism	GO:GO:0019538	Lap3	Park2
DNA replication factor A complex	GO:GO:0005662	Rpa1	Rpa2
actin cytoskeleton	GO:GO:0015629	Ctnnal1	Proc
ephrin receptor activity	GO:GO:0005003	Ephb2	Ephb3
transcription coactivator activity	GO:GO:0003713	Apex1	Taf9
spermatogenesis	GO:GO:0007283	Set	Zipro1
poly(A)+ mRNA export from nucleus	GO:GO:0016973	Gbp2	Nup107
M phase of mitotic cell cycle	GO:GO:0000087	Cdc25b	Cdc7
chromatin silencing at telomere	GO:GO:0006348	Mcm10	Rif1
mRNA cleavage	GO:GO:0006379	Cpsf2	Cstf2
fatty acid biosynthesis	GO:GO:0006633	Mod1	Scd1
central nervous system development	GO:GO:0007417	Park2	Wwp1
lysosome	GO:GO:0005764	Ap3m1	Entpd4
negative regulation of progression through cell cycle	GO:GO:0045786	Cdk2ap1	Lats2
telomeric DNA binding	GO:GO:0042162	Gbp2	Rif1
cell wall biosynthesis (sensu Fungi)	GO:GO:0009272	Lrg1	Pck2
extracellular matrix organization and biogenesis	GO:GO:0030198	Mia1	Pomt1
gametogenesis	GO:GO:0007276	Chek1	Fancl
gastrulation (sensu Mammalia)	GO:GO:0010003	Amot	Odz4
proton transport	GO:GO:0015992	Atp4a	Atp6ap2
damaged DNA binding	GO:GO:0003684	Fen1	Rad51
muscle contraction	GO:GO:0006936	Acta2	Utrn
regulation of striated muscle development	GO:GO:0016202	Boc	Cenpf
phospholipid dephosphorylation	GO:GO:0046839	Mtm1	Ppap2a

carboxy-lyase activity	GO:GO:0016831	Amd1	Pck2
cell-matrix adhesion	GO:GO:0007160	Itga6	Mia1
T cell differentiation	GO:GO:0030217	Bcl11a	Ppp3cb
cyclin binding	GO:GO:0030332	Cdk4	Set
muscle maintenance	GO:GO:0046716	Mtm1	Ppp3cb
ribonuclease H activity	GO:GO:0004523	Apex1	Fen1
spermatid development	GO:GO:0007286	Ppp2r2b	Ran
hydrogen ion transporter activity	GO:GO:0015078	Atp4a	Atp6ap2
regulation of GTPase activity	GO:GO:0043087	Arfgap1	Vav3
actomyosin structure organization and biogenesis	GO:GO:0031032	Cnn1	Cnn3
negative regulation of cell growth	GO:GO:0030308	Dnajc2	Grem1
positive regulation of transcription from RNA polymerase II promoter	GO:GO:0045944	Neurog3	Top2a
ribonucleoside-diphosphate reductase activity	GO:GO:0004748	Rrm1	Rrm2
hyaluronic acid binding	GO:GO:0005540	Cd44	Hmmr
barrier septum	GO:GO:0000935	Pck2	Scd1
synaptic vesicle	GO:GO:0008021	Sypl	Syt9
methenyltetrahydrofolate cyclohydrolase activity	GO:GO:0004477	Mthfd2	
regulation of circadian rhythm	GO:GO:0042752	Timeless	
imidazolonepropionase activity	GO:GO:0050480	Amdhd1	
cytoplasmic sequestering of transcription factor	GO:GO:0042994	Tacc3	
specific transcriptional repressor activity	GO:GO:0016566	Recc1	
SAGA complex	GO:GO:0000124	Taf9	
malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity	GO:GO:0004473	Mod1	
regulation of neuronal synaptic plasticity	GO:GO:0048168	Ephb2	
calcium-dependent protein serine/threonine phosphatase activity	GO:GO:0004723	Ppp3cb	
complement component C1q binding	GO:GO:0001849	C1qbp	
phosphoenolpyruvate carboxykinase activity	GO:GO:0004611	Pck2	
sterol metabolism	GO:GO:0016125	Ins1	
gap-junction forming channel activity	GO:GO:0005243	Gjb2	

centromeric DNA binding	GO:GO:0019237	Kif2c
morphogenesis of an epithelium	GO:GO:0002009	Timeless
voltage-gated potassium channel complex	GO:GO:0008076	Kcnn4
barrier septum formation	GO:GO:0000917	Scd1
UTP biosynthesis	GO:GO:0006228	Nme1
guard mother cell cytokinesis	GO:GO:0010235	Scd1
induction of an organ	GO:GO:0001759	Hoxa11
transcription cofactor activity	GO:GO:0003712	Trip13
nuclear export	GO:GO:0051168	Xpo1
copper, zinc superoxide dismutase activity	GO:GO:0004785	Scd1
phosphorylation	GO:GO:0016310	Galk1
neuronal Cdc2-like kinase binding	GO:GO:0042808	Cdk5rap2
p53 binding	GO:GO:0002039	Tfam
physiological process	GO:GO:0007582	Ins1
cyclin-dependent protein kinase inhibitor activity	GO:GO:0004861	Cdkn2c
chromatin silencing at silent mating-type cassette	GO:GO:0030466	Mcm10
blood vessel remodeling	GO:GO:0001974	Tgm2
tracheal system development (sensu Insecta)	GO:GO:0007424	Cdk4
spindle organization and biogenesis	GO:GO:0007051	Scd1
thyroid hormone receptor binding	GO:GO:0046966	Nup62
prostaglandin transport	GO:GO:0015732	Slco3a1
vasculogenesis	GO:GO:0001570	Amot
cell migration during gastrulation	GO:GO:0042074	Amot
isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine	GO:GO:0018153	Tgm2
neuromuscular junction development	GO:GO:0007528	Utrn
caspase inhibitor activity	GO:GO:0043027	Birc5
site-specific DNA-methyltransferase (cytosine-specific) activity	GO:GO:0008326	Dnmt1
folic acid and derivative biosynthesis	GO:GO:0009396	Mthfd2
dopamine metabolism	GO:GO:0042417	Park2
protein N-terminus binding	GO:GO:0047485	Rpa2
tryptophan-tRNA ligase activity	GO:GO:0004830	Wars
CD27 receptor binding	GO:GO:0005175	Siva

chemoattractant activity	GO:GO:0042056	Ccl9
CXCR3 chemokine receptor binding	GO:GO:0048248	Cxcl9
regulation of cell volume	GO:GO:0006884	Clns1a
mRNA cleavage and polyadenylation specificity factor complex	GO:GO:0005847	Cpsf2
regulation of cell cycle	GO:GO:0051726	Ccnb1
methylated-DNA-[protein]-cysteine S-methyltransferase activity	GO:GO:0003908	Ada
RNA ligase (ATP) activity	GO:GO:0003972	Lig1
transcription initiation from RNA polymerase II promoter	GO:GO:0006367	Taf9
signal transduction during conjugation with cellular fusion	GO:GO:0032005	Scd1
deoxyribonucleotide metabolism	GO:GO:0009262	Rrm2
maintenance of DNA methylation	GO:GO:0010216	Dnmt1
peptidyl-proline hydroxylation to 4-hydroxy-L-proline	GO:GO:0018401	P4hb
monovalent inorganic cation transport	GO:GO:0015672	Atp4a
startle response	GO:GO:0001964	Park2
positive regulation of protein secretion	GO:GO:0050714	Kcnn4
filopodium formation	GO:GO:0046847	Itga6
negative regulation of astrocyte differentiation	GO:GO:0048712	Id4
regulation of neuron differentiation	GO:GO:0045664	Cdk5rap2
integral to endoplasmic reticulum membrane	GO:GO:0030176	Scd1
peptide cross-linking	GO:GO:0018149	Tgm2
cytosolic small ribosomal subunit (sensu Eukaryota)	GO:GO:0005843	Rps6
purinergic nucleotide receptor activity, G-protein coupled	GO:GO:0045028	Ffar2
calcium- and calmodulin-dependent protein kinase activity	GO:GO:0004685	Itpka
regulation of Ras protein signal transduction	GO:GO:0046578	Nup62
transcription-coupled nucleotide-excision repair	GO:GO:0006283	Hmgn1

connexon complex	GO:GO:0005922	Gjb2
'de novo' IMP biosynthesis	GO:GO:0006189	Gart
methylenetetrahydrofolate dehydrogenase (NADP+) activity	GO:GO:0004488	Mthfd2
glutamate biosynthesis	GO:GO:0006537	Idh1
rRNA export from nucleus	GO:GO:0006407	Nup107
flap endonuclease activity	GO:GO:0048256	Fen1
nucleoside metabolism	GO:GO:0009116	Prps2
enzyme activator activity	GO:GO:0008047	Recc1
regulation of lipid metabolism	GO:GO:0019216	Ppap2a
aster	GO:GO:0005818	Tpx2
re-entry into mitotic cell cycle	GO:GO:0000320	Ccnd1
metal ion transporter activity	GO:GO:0046873	Slc39a8
apical plasma membrane	GO:GO:0016324	Slc12a2
ribonuclease P activity	GO:GO:0004526	Rpp14
androgen receptor signaling pathway	GO:GO:0030521	Ppap2a
Ran GTPase activator activity	GO:GO:0005098	Rangap1
positive regulation of transcription	GO:GO:0045941	Nup62
prolyl aminopeptidase activity	GO:GO:0016804	Lap3
dynein binding	GO:GO:0045502	Cenpf
gene silencing	GO:GO:0016458	Rpa2
negative regulation of DNA replication	GO:GO:0008156	Gmnn
vesicle fusion	GO:GO:0006906	Vav3
lipid biosynthesis	GO:GO:0008610	Scd1
embryonic limb morphogenesis	GO:GO:0030326	Grem1
tryptophan metabolism	GO:GO:0006568	Indo
positive regulation of inflammatory response	GO:GO:0050729	Tgm2
stearoyl-CoA 9-desaturase activity	GO:GO:0004768	Scd1
tropomyosin binding	GO:GO:0005523	Cnn3
eukaryotic initiation factor 4E binding	GO:GO:0008190	Eif4ebp2
FAD binding	GO:GO:0050660	Steap1
AMP deaminase activity	GO:GO:0003876	Amd1
DNA polymerase processivity factor activity	GO:GO:0030337	Pcna
protein polymerization	GO:GO:0051258	Tubb5

deoxyribonucleoside diphosphate metabolism	GO:GO:0009186	Rrm2
positive transcription elongation factor activity	GO:GO:0008159	Hmgn1
PCNA complex	GO:GO:0043626	Pcna
positive regulation of cell adhesion	GO:GO:0045785	Vav3
viral capsid assembly	GO:GO:0019069	Abce1
cation:chloride symporter activity	GO:GO:0015377	Slc12a2
snoRNA binding	GO:GO:0030515	Nola1
spermine biosynthesis	GO:GO:0006597	Amd1
strand invasion	GO:GO:0042148	Rad51
UV protection	GO:GO:0009650	Fen1
lateral plasma membrane	GO:GO:0016328	Gjb2
nuclear envelope lumen	GO:GO:0005641	Hrasls
polyribonucleotide nucleotidyltransferase activity	GO:GO:0004654	Pnpt1
response to toxin	GO:GO:0009636	Blmh
receptor signaling complex scaffold activity	GO:GO:0030159	Nup62
pyrimidine ribonucleoside triphosphate biosynthesis	GO:GO:0009209	Nme1
protein phosphatase inhibitor activity	GO:GO:0004864	Ppp1r14b
caspase activation	GO:GO:0006919	Stat1
protein amino acid O-linked glycosylation	GO:GO:0006493	Pomt1
rhythmic process	GO:GO:0048511	Timeless
telomere maintenance via recombination	GO:GO:0000722	Rad51
odontogenesis (sensu Vertebrata	GO:GO:0042475	Itga6
dopamine uptake	GO:GO:0051583	Park2
ESC/E(Z) complex	GO:GO:0035098	Suz12
protein amino acid N-linked glycosylation via asparagine	GO:GO:0018279	Mgat2
citrate metabolism	GO:GO:0006101	Polr3h
defense response to pathogenic bacteria, incompatible interaction	GO:GO:0009816	Rrs1
DNA ligase (NAD+) activity	GO:GO:0003911	Recc1
carrier activity	GO:GO:0005386	Slc12a2
RNA localization	GO:GO:0006403	Ran
chorion gene amplification	GO:GO:0007307	Mcm6

ubiquitin binding	GO:GO:0043130	Nup62
exocytosis	GO:GO:0006887	Zwint
adenosine deaminase activity	GO:GO:0004000	Ada
translation elongation factor activity	GO:GO:0003746	Eftud2
regulation of body size	GO:GO:0040014	Atrn
skeletal development	GO:GO:0001501	Hoxa11
protein import into nucleus, translocation	GO:GO:0000060	Kpnb1
negative regulation of neuron apoptosis	GO:GO:0043524	Birc5
epidermal growth factor receptor binding	GO:GO:0005154	Vav3
tumor necrosis factor receptor activity	GO:GO:0005031	Tnfrsf1b
cytosolic ribosome (sensu Eukaryota)	GO:GO:0005830	Rps6
positive regulation of nitric-oxide synthase activity	GO:GO:0051000	Ins1
protein amino acid N-linked glycosylation	GO:GO:0006487	Mgat2
cell septum	GO:GO:0030428	Pck2
oligosaccharide biosynthesis	GO:GO:0009312	Mgat2
sarcomere	GO:GO:0030017	Lman1
vacuole (sensu Fungi)	GO:GO:0000324	Prc1
pronucleus	GO:GO:0045120	Cenpf
myo-inositol metabolism	GO:GO:0006020	Itpka
prefoldin complex	GO:GO:0016272	C80913
lipoate-protein ligase B activity	GO:GO:0016978	Prps2
heteroduplex formation	GO:GO:0030491	Rad51
protein targeting to lysosome	GO:GO:0006622	Ap3m1
protein homooligomerization	GO:GO:0051260	Tgm2
gastric acid secretion	GO:GO:0001696	Atp4a
ureteric bud branching	GO:GO:0001658	Cd44
regulation of axonogenesis	GO:GO:0050770	Ephb2
regulation of bone mineralization	GO:GO:0030500	Omd
ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	GO:GO:0015662	Atp4a
positive regulation of mitosis	GO:GO:0045840	Nusap1
cytokinesis after mitosis	GO:GO:0000281	Nusap1
response to virus	GO:GO:0009615	Xpo1
DNA topoisomerase activity	GO:GO:0003916	Top2a
mannose binding	GO:GO:0005537	Lman1

neuron projection	GO:GO:0043005	Park2
regulation of synaptic transmission	GO:GO:0050804	Park2
ceramide metabolism	GO:GO:0006672	Ppap2a
SLIK (SAGA-like) complex	GO:GO:0046695	Taf9
transmembrane receptor protein tyrosine phosphatase activity	GO:GO:0005001	Ptpro
synaptic transmission	GO:GO:0007268	Kcnk3
primary spermatocyte growth	GO:GO:0007285	Boc
tubulin binding	GO:GO:0015631	Stmn1
protein kinase C activity	GO:GO:0004697	Pck2
Barr body	GO:GO:0001740	H2afz
amino acid transport	GO:GO:0006865	Slc12a2
sulfur amino acid biosynthesis	GO:GO:0000097	Cdo1
induction of positive chemotaxis	GO:GO:0050930	Cxcl9
recombinase activity	GO:GO:0000150	Rad51
protein-hormone receptor activity	GO:GO:0016500	Lgr5
galactose metabolism	GO:GO:0006012	Galk1
protein kinase cascade	GO:GO:0007243	Socs3
blastoderm segmentation	GO:GO:0007350	Cdk4
M phase specific microtubule process	GO:GO:0000072	Rangap1
cysteine dioxygenase activity	GO:GO:0017172	Cdo1
vacuolar lumen (sensu Fungi)	GO:GO:0000328	Prc1
nuclear matrix	GO:GO:0016363	Cenpf
STAT protein nuclear translocation	GO:GO:0007262	Stat1
neutral amino acid transporter activity	GO:GO:0015175	Slc1a4
axonemal dynein complex	GO:GO:0005858	Dynlt1
insulin-like growth factor receptor signaling pathway	GO:GO:0048009	Perq1
DNA replication checkpoint	GO:GO:0000076	Rfc2
heterochromatin	GO:GO:0000792	Dnmt1
olfactory receptor activity	GO:GO:0004984	Olfr157
G1 phase of mitotic cell cycle	GO:GO:0000080	Cdc2a
clathrin vesicle coat	GO:GO:0030125	Ap3m1
nucleotide kinase activity	GO:GO:0019201	Taf9
hydrolase activity, hydrolyzing O-glycosyl compounds	GO:GO:0004553	Pnpt1
Rho protein signal transduction	GO:GO:0007266	Ctnnal1

indoleamine-pyrrole 2,3-dioxygenase activity	GO:GO:0004426	Indo
embryonic eye morphogenesis	GO:GO:0048048	Cct3
exosome (RNase complex)	GO:GO:0000178	Ran
B cell differentiation	GO:GO:0030183	Bcl11a
alpha-beta T cell activation	GO:GO:0046631	Ins1
cadherin binding	GO:GO:0045296	Ctnnal1
cell redox homeostasis	GO:GO:0045454	Apex1
angiogenesis	GO:GO:0001525	Narg1
negative regulation of protein biosynthesis	GO:GO:0017148	Eif4ebp2
nuclear inner membrane	GO:GO:0005637	Tmpo
TATA-binding protein binding	GO:GO:0017025	Taf9
cobalt ion binding	GO:GO:0050897	Pa2g4
bleomycin hydrolase activity	GO:GO:0008423	Blmh
mitotic spindle organization and biogenesis	GO:GO:0007052	Stmn1
hydroxymethyl-, formyl- and related transferase activity	GO:GO:0016742	Gart
fin regeneration	GO:GO:0031101	Hspd1
gamma-aminobutyric acid signaling pathway	GO:GO:0007214	Slc12a2
adenylate kinase activity	GO:GO:0004017	Taf9
female pronucleus	GO:GO:0001939	Rif1
linoleoyl-CoA desaturase activity	GO:GO:0016213	Fads1
multidimensional cell growth	GO:GO:0009825	Scd1
synaptic transmission, glutamatergic	GO:GO:0035249	Park2
snoRNP binding	GO:GO:0030519	Nol5
biosynthesis	GO:GO:0009058	Gart
phosphoribosylamine-glycine ligase activity	GO:GO:0004637	Gart
chaperone binding	GO:GO:0051087	Hspd1
ATPase activity, coupled	GO:GO:0042623	Hspe1
negative regulation of neuron differentiation	GO:GO:0045665	Id4
cell migration	GO:GO:0016477	Vav3
cell projection biogenesis	GO:GO:0030031	Vav3
nucleoside triphosphate biosynthesis	GO:GO:0009142	Nme1
meiotic chromosome segregation	GO:GO:0045132	Sgol1

negative regulation of translational initiation	GO:GO:0045947	Eif4ebp2
cell wall (sensu Fungi)	GO:GO:0009277	Gas5
Golgi medial cisterna	GO:GO:0005797	Nucb2
paraxial mesoderm development	GO:GO:0048339	Epb4.1l5
L-serine catabolism	GO:GO:0006565	Shmt1
actin filament polymerization	GO:GO:0030041	Diap2

main pathways of carbohydrate metabolism	GO:GO:0006092	Idh1
male genitalia development	GO:GO:0030539	Gjb2
sex chromatin	GO:GO:0001739	Suz12
protein disulfide isomerase activity	GO:GO:0003756	P4hb
nuclear heterochromatin	GO:GO:0005720	Cbx5
oxidoreductase activity, acting on iron-sulfur proteins as donors	GO:GO:0016730	Lats2
Nup107-160 complex	GO:GO:0031080	Nup107
peptidyl-threonine phosphorylation	GO:GO:0018107	Pbk
polynucleotide adenylyltransferase activity	GO:GO:0004652	Pap
L-cysteine catabolism to taurine	GO:GO:0019452	Cdo1
regulation of JAK-STAT cascade	GO:GO:0046425	Statip1
positive regulation of smooth muscle cell proliferation	GO:GO:0048661	Tgm2
chromatin silencing	GO:GO:0006342	Hells
dynein complex	GO:GO:0030286	Dynlt1
delta DNA polymerase activity	GO:GO:0003891	Pold3
nucleosome	GO:GO:0000786	H2afz
ribonucleoside-diphosphate reductase complex	GO:GO:0005971	Rrm1
auxin polar transport	GO:GO:0009926	Rcn1
female meiosis chromosome segregation	GO:GO:0016321	Mcm10
insoluble fraction	GO:GO:0005626	Ppp3cb
pyrimidine nucleotide biosynthesis	GO:GO:0006221	Ctps
cortical actin cytoskeleton	GO:GO:0030864	Utrn
vasodilation	GO:GO:0042311	Vip
glucose metabolism	GO:GO:0006006	Ins1
gap junction	GO:GO:0005921	Gjb2
urogenital system development	GO:GO:0001655	Hells
carboxypeptidase activity	GO:GO:0004180	Blmh

neuroblast proliferation (sensu Vertebrata)	GO:GO:0043350	Id4
extracellular matrix structural constituent	GO:GO:0005201	Omd
entry of virus into host cell	GO:GO:0046718	Wwp1
telomere cap complex	GO:GO:0000782	Rif1
regulation of cell migration	GO:GO:0030334	Amot
septation initiation signaling	GO:GO:0031028	Cdc7
chloroplast	GO:GO:0009507	Wwp1
cytoplasmic dynein complex	GO:GO:0005868	Dynlt1
response to pathogenic fungi	GO:GO:0009621	Rpp14
regulation of smooth muscle contraction	GO:GO:0006940	Cnn1
hyperosmotic response	GO:GO:0006972	Slc12a2
regulation of mitosis	GO:GO:0007088	Nek2
protein oligomerization	GO:GO:0051259	Tgm2
dicarboxylic acid transport	GO:GO:0006835	Slc1a4
positive regulation of embryonic development	GO:GO:0040019	Amot
deoxyribonuclease activity	GO:GO:0004536	Nme1
negative regulation of transforming growth factor beta receptor signaling pathway	GO:GO:0030512	Strap
nucleoside-diphosphatase activity	GO:GO:0017110	Entpd4
ribosome assembly	GO:GO:0042255	Pa2g4
exodeoxyribonuclease activity	GO:GO:0004529	Fen1
connexon channel activity	GO:GO:0015285	Gjb2
5'-3' exonuclease activity	GO:GO:0008409	Fen1
metallochaperone activity	GO:GO:0016530	Mtm1
protein amino acid acetylation	GO:GO:0006473	Taf9
insulin-like growth factor binding protein complex	GO:GO:0016942	Igfbp5
transcription elongation factor complex	GO:GO:0008023	Statip1
fatty acid metabolism	GO:GO:0006631	Acsl5
nuclear outer membrane	GO:GO:0005640	Nucb2
chaperonin-containing T-complex	GO:GO:0005832	Cct3
adult somatic muscle development	GO:GO:0007527	Utrn
serine-type endopeptidase inhibitor activity	GO:GO:0004867	Serpina10
S-adenosylmethionine metabolism	GO:GO:0046500	Pnmt
purine ribonucleoside monophosphate biosynthesis	GO:GO:0009168	Ada

central element	GO:GO:0000801	Incenp
cell junction	GO:GO:0030054	Utrn
mitotic checkpoint	GO:GO:0007093	Brca2
DNA topological change	GO:GO:0006265	Top2a
pyrimidine nucleotide binding	GO:GO:0019103	Pola1

protein phosphatase type 1 regulator activity	GO:GO:0008599	Ppp1r14b
cAMP-mediated signaling	GO:GO:0019933	Eif4ebp2
fat cell differentiation	GO:GO:0045444	Ccnd1
nucleoside diphosphate kinase activity	GO:GO:0004550	Nme1
response to oxidative stress	GO:GO:0006979	Idh1
glutamate-5-semialdehyde dehydrogenase activity	GO:GO:0004350	Aldh18a1
Cajal body	GO:GO:0015030	Nolc1
nuclear localization sequence binding	GO:GO:0008139	Kpnb1
insulin receptor binding	GO:GO:0005158	Ins1
protein localization	GO:GO:0008104	Incenp
DNA-directed RNA polymerase II, core complex	GO:GO:0005665	Polr2a
site of polarized growth	GO:GO:0030427	Scd1
response to antibiotic	GO:GO:0046677	Lap3
purine base metabolism	GO:GO:0006144	Ada
dense fibrillar component	GO:GO:0001651	Nola1
transmembrane receptor activity	GO:GO:0004888	Utrn
lamin binding	GO:GO:0005521	Tmpo
amino acid-polyamine transporter activity	GO:GO:0005279	Slc12a2
cysteine metabolism	GO:GO:0006534	Cdo1

protein amino acid terminal N-glycosylation	GO:GO:0006496	Mgat2
malate metabolism	GO:GO:0006108	Mod1
negative regulation of signal transduction	GO:GO:0009968	Socs3
endocytic vesicle	GO:GO:0030139	Amot
autophagy	GO:GO:0006914	Wipi2
positive regulation of transcription, DNA-dependent	GO:GO:0045893	Tfam

hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	GO:GO:0016814	Apobec3
nuclear membrane	GO:GO:0031965	Nup107
regulation of cyclin-dependent protein kinase activity	GO:GO:0000079	Chek1
L-cysteine metabolism	GO:GO:0046439	Cdo1
Hsp70 protein binding	GO:GO:0030544	Cdc2a
cell communication	GO:GO:0007154	Gjb2
zinc ion transporter activity	GO:GO:0005385	Slc39a8
telomeric 3' overhang formation	GO:GO:0031860	Rif1
GMP biosynthesis	GO:GO:0006177	Impdh2
response to methylmercury	GO:GO:0051597	Rad51
transaminase activity	GO:GO:0008483	Psat1
chemokine receptor binding	GO:GO:0042379	Cxcl11
circulation	GO:GO:0008015	Clns1a
tryptophanyl-tRNA aminoacylation	GO:GO:0006436	Wars
malate dehydrogenase (decarboxylating) activity	GO:GO:0004471	Mod1
lamellipodium	GO:GO:0030027	Amot
lipid metabolism	GO:GO:0006629	Acsl5
catecholamine biosynthesis	GO:GO:0042423	Pnmt
spermidine biosynthesis	GO:GO:0008295	Amd1
proximal/distal pattern formation	GO:GO:0009954	Grem1
epsilon DNA polymerase complex	GO:GO:0008622	Pole2
NuRD complex	GO:GO:0016581	Rbbp4
regulation of protein amino acid phosphorylation	GO:GO:0001932	Socs3
mannosyltransferase activity	GO:GO:0000030	Pomt1
protein kinase activator activity	GO:GO:0030295	1190002H23Rik
sodium:potassium:chloride symporter activity	GO:GO:0008511	Slc12a2
rRNA binding	GO:GO:0019843	Nola1
chromatin assembly complex	GO:GO:0005678	Nap1l1
ribulose-phosphate 3-epimerase activity	GO:GO:0004750	Rpe
transmembrane receptor protein tyrosine phosphatase signaling pathway	GO:GO:0007185	Ptpro

negative regulation of vasodilation	GO:GO:0045908	Ins1
positive regulation of cell volume	GO:GO:0045795	Slc12a2
vesicular fraction	GO:GO:0042598	Wnk1
phosphoric monoester hydrolase activity	GO:GO:0016791	Cdc25b
phosphoenolpyruvate carboxykinase (GTP) activity	GO:GO:0004613	Pck2
axonogenesis	GO:GO:0007409	Stmn1
metal ion transport	GO:GO:0030001	Slc39a8
double-strand break repair via single-strand annealing	GO:GO:0045002	Rad51
neuron migration	GO:GO:0001764	Pomt1
transcription initiation	GO:GO:0006352	Taf9
response to cadmium ion	GO:GO:0046686	Rad51
N-methyltransferase activity	GO:GO:0008170	Aurkb
release of cytoplasmic sequestered NF-kappaB	GO:GO:0008588	Tgm2
regulation of DNA replication initiation	GO:GO:0030174	Cdt1
large ribosomal subunit	GO:GO:0015934	Rpl7l1
calcium-activated potassium channel activity	GO:GO:0015269	Kcnn4
procollagen-proline 4-dioxygenase activity	GO:GO:0004656	P4hb
cation transport	GO:GO:0006812	Atp4a
S-methyl-5-thioadenosine phosphorylase activity	GO:GO:0017061	Mtap
mitotic nuclear envelope reassembly	GO:GO:0007084	Tmpo
histone methyltransferase activity	GO:GO:0042054	Suz12
negative regulation of retinal programmed cell death	GO:GO:0046671	Cct3
galactokinase activity	GO:GO:0004335	Galk1
regulation of stomatal movement	GO:GO:0010119	Rcn1
phosphatidate phosphatase activity	GO:GO:0008195	Ppap2a
regulation of muscle contraction	GO:GO:0006937	Tpm3
lactation	GO:GO:0007595	Nme1
SWI/SNF complex	GO:GO:0016514	Smarcc1
sodium:dicarboxylate symporter activity	GO:GO:0017153	Slc1a4
nuclear lamina	GO:GO:0005652	Pcna
locomotory behavior	GO:GO:0007626	Park2

poly(A) binding	GO:GO:0008143	Syncrip
norepinephrine metabolism	GO:GO:0042415	Park2
nucleotide-excision repair	GO:GO:0006289	Rpa2
peptidyl-prolyl cis-trans isomerase activity	GO:GO:0003755	Fkbp3
positive regulation of cell migration	GO:GO:0030335	Cxcl10
MAP kinase kinase kinase activity	GO:GO:0004709	B230120H23Rik
fatty acid desaturation	GO:GO:0006636	Fads1
fatty acid elongation, unsaturated fatty acid	GO:GO:0019368	Elovl5
mRNA splice site selection	GO:GO:0006376	Sfrs2
protection from non-homologous end joining at telomere	GO:GO:0031848	Rif1
35S primary transcript processing	GO:GO:0006365	Rcl1
positive regulation of epidermal growth factor receptor signaling pathway	GO:GO:0045742	Nup62
auxiliary transport protein activity	GO:GO:0015457	Clns1a
oocyte maturation	GO:GO:0001556	Ccnb1
positive regulation of progression through cell cycle	GO:GO:0045787	Cdk4
RNA helicase activity	GO:GO:0003724	Hnrpab
nucleocytoplasmic shuttling complex	GO:GO:0031074	Nup62
lamellipodium biogenesis	GO:GO:0030032	Vav3
ribonuclease MRP activity	GO:GO:0000171	Nme1
nuclear speck	GO:GO:0016607	Sfrs2
GTP biosynthesis	GO:GO:0006183	Nme1
nuclear telomeric heterochromatin	GO:GO:0005724	Rif1
deaminase activity	GO:GO:0019239	Ada
skeletal muscle growth	GO:GO:0048630	Igfbp5
histone ubiquitination	GO:GO:0016574	Suz12
nuclear envelope-endoplasmic reticulum network	GO:GO:0042175	Tmpo
1,3-beta-glucanosyltransferase activity	GO:GO:0042124	Gas5
DNA-(apurinic or apyrimidinic site) lyase activity	GO:GO:0003906	Apex1
3'-5'-exoribonuclease activity	GO:GO:0000175	Pnpt1
sodium ion binding	GO:GO:0031402	Slc12a2
phosphoglycerate dehydrogenase activity	GO:GO:0004617	Phgdh

diacylglycerol biosynthesis	GO:GO:0006651	Ppap2a
nuclear envelope reassembly	GO:GO:0031468	Tmpo
response to stress	GO:GO:0006950	Tacc3
spindle stabilization	GO:GO:0043146	Ccdc5
protein import into mitochondrial matrix	GO:GO:0030150	Hspd1
oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor	GO:GO:0016652	Idh1
negative regulation of coagulation	GO:GO:0050819	Proc
nitric-oxide synthase regulator activity	GO:GO:0030235	Hmgb1
chaperonin-mediated tubulin folding	GO:GO:0007022	Cct3
synaptic vesicle endocytosis	GO:GO:0048488	Cd24a
origin recognition complex	GO:GO:0000808	Orc2l
Rac guanyl-nucleotide exchange factor activity	GO:GO:0030676	Vav3
G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	GO:GO:0007200	Tgm2
transcription from mitochondrial promoter	GO:GO:0006390	Tfam
L-serine transporter activity	GO:GO:0015194	Slc1a4
double-strand break repair	GO:GO:0006302	Fen1
transcription factor TFIID complex	GO:GO:0005669	Taf9
sensory perception of smell	GO:GO:0007608	Olfr157
actin filament organization	GO:GO:0007015	Ran
potassium channel activity	GO:GO:0005267	Kcnk3
embryonic cleavage	GO:GO:0040016	Top2a
positive regulation of phosphoinositide 3-kinase activity	GO:GO:0043552	Vav3
nuclear telomere cap complex	GO:GO:0000783	Rif1
centrosome cycle	GO:GO:0007098	Nek2
sensory perception	GO:GO:0007600	Cxcl10
enzyme binding	GO:GO:0019899	Tgm2
double-stranded telomeric DNA binding	GO:GO:0003691	Terf1
axial mesoderm development	GO:GO:0048318	Epb4.1l5
hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	GO:GO:0016820	Atp4a
actin nucleation	GO:GO:0045010	Proc
oogenesis (sensu Insecta	GO:GO:0009993	Mcm6

neuromuscular synaptic transmission	GO:GO:0007274	Cd24a
long-chain-fatty-acid-CoA ligase activity	GO:GO:0004467	Acsl5
tRNA aminoacylation for protein translation	GO:GO:0006418	Wars
spliceosome assembly	GO:GO:0000245	Gemin6
muscle thin filament tropomyosin	GO:GO:0005862	Tpm3
DNA topoisomerase (ATP-hydrolyzing) activity	GO:GO:0003918	Top2a
taurine biosynthesis	GO:GO:0042412	Cdo1
enoyl-[acyl-carrier protein] reductase activity	GO:GO:0016631	Mod1
phosphodiesterase I activity	GO:GO:0004528	Apex1
ribonucleoside monophosphate biosynthesis	GO:GO:0009156	Prps2
mitotic centrosome separation	GO:GO:0007100	Kif11
pyrimidine dimer repair via nucleotide-excision repair	GO:GO:0000720	Hmgn1
cyclin catabolism	GO:GO:0008054	Ube2c
general RNA polymerase II transcription factor activity	GO:GO:0016251	Taf9
metanephros development	GO:GO:0001656	Hoxa11
inner cell mass cell proliferation	GO:GO:0001833	Luzp5
lung development	GO:GO:0030324	Timeless
taurine metabolism	GO:GO:0019530	Cdo1
growth cone	GO:GO:0030426	Utrn
inositol or phosphatidylinositol phosphatase activity	GO:GO:0004437	Mtm1
hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity	GO:GO:0005062	Stat1
polyamine metabolism	GO:GO:0006595	Amd1
NLS-bearing substrate import into nucleus	GO:GO:0006607	Kpnb1
asparagine synthase (glutamine-hydrolyzing) activity	GO:GO:0004066	Asns
monovalent inorganic cation transporter activity	GO:GO:0015077	Atp4a
traversing start control point of mitotic cell cycle	GO:GO:0007089	Dbf4

viral envelope	GO:GO:0019031	D17H6S56E-5
glutathione metabolism	GO:GO:0006749	Idh1
negative regulation of blood coagulation	GO:GO:0030195	Proc
galactoside binding	GO:GO:0016936	Lgals2
protein binding, bridging	GO:GO:0030674	Cnn3
histone methylation	GO:GO:0016571	Suz12
Rho GTPase activator activity	GO:GO:0005100	Lrg1
structural constituent of chromatin	GO:GO:0030527	Hmgb1
cyclin-dependent protein kinase activity	GO:GO:0004693	Cdk4
negative regulation of non-apoptotic programmed cell death	GO:GO:0043072	Nup62
response to UV-C	GO:GO:0010225	Hmgn1
condensin complex	GO:GO:0000796	Smc4l1
mitochondrial DNA replication	GO:GO:0006264	Tfam
secretory pathway	GO:GO:0045045	Rpe
protein C (activated) activity	GO:GO:0003808	Proc
ruffle	GO:GO:0001726	Amot
RNA-3'-phosphate cyclase activity	GO:GO:0003963	Rcl1
RNA metabolism	GO:GO:0016070	Hnrpa1
acyltransferase activity	GO:GO:0008415	Tgm2
bud neck	GO:GO:0005935	Lrg1
cytokinesis by cell plate formation	GO:GO:0000911	Scd1
regulation of progression through mitotic cell cycle	GO:GO:0007346	Nek2
sphingosine metabolism	GO:GO:0006670	Ppap2a
calcium-mediated signaling	GO:GO:0019722	Rcn1
negative regulation of phosphorylation	GO:GO:0042326	Prkrip1
kinetochore assembly	GO:GO:0051382	Cenpf
manganese ion transport	GO:GO:0006828	Mtm1
isocitrate dehydrogenase (NAD+) activity	GO:GO:0004449	Idh1
leucyl aminopeptidase activity	GO:GO:0004178	Lap3
phosphotransferase activity, alcohol group as acceptor	GO:GO:0016773	Galk1
morphogenesis	GO:GO:0009653	Lig1

oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	GO:GO:0016717	Scd1
regulation of circadian sleep/wake cycle, sleep	GO:GO:0045187	Ada
glutamate 5-kinase activity	GO:GO:0004349	Aldh18a1
thymidine kinase activity	GO:GO:0004797	Tk1
5'-flap endonuclease activity	GO:GO:0017108	Fen1
malic enzyme activity	GO:GO:0004470	Mod1
positive regulation of nitric oxide biosynthesis	GO:GO:0045429	Ins1
rRNA modification	GO:GO:0000154	Nol5
transferase activity, transferring pentosyl groups	GO:GO:0016763	Mtap
alpha DNA polymerase activity	GO:GO:0003889	Pola1
regulation of protein secretion	GO:GO:0050708	Ins1
regulation of osteoblast differentiation	GO:GO:0045667	Fzd1
mitochondrial nucleoid	GO:GO:0042645	Idh1
cell cycle arrest	GO:GO:0007050	Pa2g4
synaptonemal complex	GO:GO:0000795	Incenp
mating projection tip	GO:GO:0043332	Scd1
WW domain binding	GO:GO:0050699	Wbp5
inositol trisphosphate 3-kinase activity	GO:GO:0008440	Itpka
embryonic development	GO:GO:0009790	Birc5
response to ethylene stimulus	GO:GO:0009723	Rcn1
L-serine transport	GO:GO:0015825	Slc1a4
inositol or phosphatidylinositol kinase activity	GO:GO:0004428	Itpka
tight junction	GO:GO:0005923	Cldn2
mRNA binding	GO:GO:0003729	Hnrpab
adenosylmethionine decarboxylase activity	GO:GO:0004014	Amd1
water channel activity	GO:GO:0015250	Aqp1
cell plate	GO:GO:0009504	Rangap1
voltage-gated ion channel activity	GO:GO:0005244	Kcnk3
microtubule depolymerization	GO:GO:0007019	Stmn1
DNA ligase activity	GO:GO:0003909	Lig1

response to amphetamine	GO:GO:0001975	Ppp3cb
neuromuscular junction	GO:GO:0031594	Utrn
digestion	GO:GO:0007586	Gkn1
tyrosine phosphorylation of STAT protein	GO:GO:0007260	Stat1
phenylethanolamine N-methyltransferase activity	GO:GO:0004603	Pnmt
peroxisome	GO:GO:0005777	Acsl5
aminoacyl-tRNA ligase activity	GO:GO:0004812	Wars
regulation of neurotransmitter secretion	GO:GO:0046928	Park2
positive regulation of vasodilation	GO:GO:0045909	Ins1
response to heat	GO:GO:0009408	Hspd1
voltage-gated potassium channel activity	GO:GO:0005249	Kcnn4
hormone-mediated signaling	GO:GO:0009755	Nup62
elevation of cytosolic calcium ion concentration during G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	GO:GO:0051482	Tgm2
insulin receptor signaling pathway	GO:GO:0008286	Eif4ebp2
vacuolar protein catabolism	GO:GO:0007039	Prc1
intracellular transport	GO:GO:0046907	Ap3m1
male pronucleus	GO:GO:0001940	Rif1
nitric oxide biosynthesis	GO:GO:0006809	Hmgb1
fatty acid synthase complex	GO:GO:0005835	Mod1
negative regulation of insulin receptor signaling pathway	GO:GO:0046627	Socs3
troponin C binding	GO:GO:0030172	Cnn3
CTP synthase activity	GO:GO:0003883	Ctps
lymphocyte differentiation	GO:GO:0030098	Hells
hydrogen:potassium-exchanging ATPase activity	GO:GO:0008900	Atp4a
protein secretion	GO:GO:0009306	Cxcl10
microvillus	GO:GO:0005902	Aqp1
oligodendrocyte differentiation	GO:GO:0048709	Cdkn2c
double-stranded RNA binding	GO:GO:0003725	Prkrip1
glyoxylate cycle	GO:GO:0006097	Idh1
tubulin	GO:GO:0045298	Tubb5
guard cell differentiation	GO:GO:0010052	Scd1

IMP dehydrogenase activity	GO:GO:0003938	Impdh2
S-adenosylhomocysteine metabolism	GO:GO:0046498	Pnmt
synaptic transmission, dopaminergic	GO:GO:0001963	Park2
tubulin folding	GO:GO:0007021	Cct3
ribonuclease MRP complex	GO:GO:0000172	Nme1
growth factor binding	GO:GO:0019838	Igfbp5
ubiquitin protein ligase binding	GO:GO:0031625	Aurka
COPII vesicle coat	GO:GO:0030127	Sec23b
CTP biosynthesis	GO:GO:0006241	Nme1
gluconeogenesis	GO:GO:0006094	Pck2
very-long-chain fatty acid biosynthesis	GO:GO:0042761	Elovl5
DNA (cytosine-5-)-methyltransferase activity	GO:GO:0003886	Dnmt1
epinephrine biosynthesis	GO:GO:0042418	Pnmt
tryptophan catabolism to kynurenine	GO:GO:0019441	Indo
G1/S-specific transcription in mitotic cell cycle	GO:GO:0000083	Bzw1
ribosomal protein import into nucleus	GO:GO:0006610	Kpnb1
SRP-dependent cotranslational protein targeting to membrane	GO:GO:0006614	Dek
positive regulation of cytokine secretion	GO:GO:0050715	Ins1
cell organization and biogenesis	GO:GO:0016043	Diap2
negative regulation of protein catabolism	GO:GO:0042177	Ins1
G1-specific transcription in mitotic cell cycle	GO:GO:0000114	Taf9
anti-inflammatory response	GO:GO:0030236	Proc
methylenetetrahydrofolate dehydrogenase (NAD+) activity	GO:GO:0004487	Mthfd2
phosphoserine transaminase activity	GO:GO:0004648	Psat1
isocitrate metabolism	GO:GO:0006102	Idh1
calcineurin complex	GO:GO:0005955	Rcn1
regulation of signal transduction	GO:GO:0009966	Nup62
two-component signal transduction system (phosphorelay)	GO:GO:0000160	Rem2
carbohydrate phosphorylation	GO:GO:0046835	Galk1
complement activation	GO:GO:0006956	C1qbp
protein kinase C activation	GO:GO:0007205	Ppap2a

eye morphogenesis (sensu Vertebrata)	GO:GO:0048593	Ccnd1
base-excision repair, gap-filling	GO:GO:0006287	Pcna
fertilization (sensu Metazoa)	GO:GO:0007338	Nhp2l1
zinc ion transport	GO:GO:0006829	Slc39a8
response to UV-B	GO:GO:0010224	Hmgn1
N-acetyltransferase activity	GO:GO:0008080	Narg1
RNA destabilization	GO:GO:0050779	Tnfrsf1b
asparagine biosynthesis	GO:GO:0006529	Asns
positive regulation of cell motility	GO:GO:0051272	Stmn1
carboxypeptidase C activity	GO:GO:0004186	Prc1
epsilon DNA polymerase activity	GO:GO:0003893	Pole2
protein complex assembly	GO:GO:0006461	Sf3b3
meiotic joint molecule formation	GO:GO:0000709	Rad51
acetylglucosaminyltransferase activity	GO:GO:0008375	Mgat2
sensory perception of sound	GO:GO:0007605	Gjb2
cell-substrate junction assembly	GO:GO:0007044	Itga6
protein catabolism	GO:GO:0030163	Psmc6
protein-glutamine gamma-glutamyltransferase activity	GO:GO:0003810	Tgm2
phosphoribosylformylglycinamidine cyclo-ligase activity	GO:GO:0004641	Gart
visual perception	GO:GO:0007601	Clns1a
water transport	GO:GO:0006833	Aqp1
peptidyl-serine phosphorylation	GO:GO:0018105	Pbk
regulation of protein import into nucleus	GO:GO:0042306	Nolc1
DNA topoisomerase complex (ATP-hydrolyzing)	GO:GO:0009330	Top2a
hemostasis	GO:GO:0007599	Gp1ba
chromatin remodeling complex	GO:GO:0016585	Actl6a
regulation of cell redox homeostasis	GO:GO:0030503	Apex1
rRNA methyltransferase activity	GO:GO:0008649	Nol5
positive regulation of abscisic acid mediated signaling	GO:GO:0009789	Rcn1
double-stranded DNA specific exodeoxyribonuclease activity	GO:GO:0008309	Fen1
isocitrate dehydrogenase (NADP+) activity	GO:GO:0004450	Idh1

establishment of mitotic spindle localization	GO:GO:0040001	Nusap1
inner kinetochore of condensed chromosome	GO:GO:0000939	Orc2l
endocytosis	GO:GO:0006897	Scd1
vacuole	GO:GO:0005773	Entpd4
positive regulation of long-term neuronal synaptic plasticity	GO:GO:0048170	Ephb2
purine base biosynthesis	GO:GO:0009113	Gart
GDP binding	GO:GO:0019003	Iigp1
lymphocyte proliferation	GO:GO:0046651	Impdh2
integrin complex	GO:GO:0008305	Itga6
tRNA splicing	GO:GO:0006388	Lig1
transcription initiation from mitochondrial promoter	GO:GO:0006391	Tfam
superoxide metabolism	GO:GO:0006801	Scd1
phosphoribosylglycinamide formyltransferase activity	GO:GO:0004644	Gart
double-strand break repair via synthesis-dependent strand annealing	GO:GO:0045003	Rad51
negative regulation of protein kinase activity	GO:GO:0006469	Prkrip1
activation of NF-kappaB transcription factor	GO:GO:0051092	Tgm2
alpha-glucan biosynthesis	GO:GO:0030979	Pck2
alpha-1,6-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity	GO:GO:0008455	Mgat2
Rho GTPase binding	GO:GO:0017048	Diap2
sphingolipid biosynthesis	GO:GO:0030148	Fen1
negative regulation of microtubule polymerization	GO:GO:0031115	Stmn1
DNA ligase (ATP) activity	GO:GO:0003910	Lig1
mRNA editing	GO:GO:0006381	Hnrpab
smoothened signaling pathway	GO:GO:0007224	Boc
adenosine metabolism	GO:GO:0046085	Ada
histone binding	GO:GO:0042393	Asf1b
mitotic metaphase/anaphase transition	GO:GO:0007091	Ccdc5
pentose-phosphate shunt	GO:GO:0006098	Rpe

DNA primase activity	GO:GO:0003896	Prim1
uracil DNA N-glycosylase activity	GO:GO:0004844	Tdg
negative regulation of angiogenesis	GO:GO:0016525	Amot
branching morphogenesis of a tube	GO:GO:0048754	Timeless
regulation of Cdc42 GTPase activity	GO:GO:0043088	Scd1
negative regulation of mitotic metaphase/anaphase transition	GO:GO:0045841	Mad2l1
mitotic G2 checkpoint	GO:GO:0007095	Cdc2a
actin filament binding	GO:GO:0051015	Utrn
glucose transport	GO:GO:0015758	Ins1
negative regulation of actin filament polymerization	GO:GO:0030837	Proc
dolichyl-phosphate-mannose-protein mannosyltransferase activity	GO:GO:0004169	Pomt1
mammary gland development	GO:GO:0030879	Nme1
calcium-dependent protein serine/threonine phosphatase regulator activity	GO:GO:0008597	Rcn1
cysteine protease inhibitor activity	GO:GO:0004869	Birc5
sex determination	GO:GO:0007530	2010012C16Rik
snRNP protein import into nucleus	GO:GO:0006608	Nol5

Anp32e	Apex1	Api5	Apobec3	Aspm	Aurkb	B230120H	BC027344	Bcl11a	Bclaf1	Birc5	Blmh	Brca2
Bclaf1	Birc5	Boc	Brca2	Bysl	C1qbp	Car8	Cbx5	Ccna2	Ccnb1	Ccnb2	Ccnd1	Cct3
Cct3	Cdc2a	Cdc6	Cdc7	Cdk4	Chek1	Chek2	Cstf2	Ddx39	Diap2	Eftud2	Ephb2	Ephb3
Dnajc2	Dnmt1	E2f8	Fancm	Fen1	H1f0	H2afz	Hells	Hmga2	Hmgb1	Hmgn1	Hnrpab	Hnrpdl
Bcl11a	Birc5	Blmh	Brca2	Car8	Ccna2	Cct3	Cdc6	Cenpf	Ect2	Eif4e2	Eif4g1	Eif5a
Atrn	Boc	Car12	Cd24a	Cd44	Cldn2	Dek	Eif1a	Entpd4	Ephb2	Ephb3	Ffar2	Fignl1
Bub1b	Cct3	Cdc2a	Cdc6	Cdc7	Cdk4	Chek1	Chek2	Ddx39	Ephb2	Ephb3	Fancm	Fignl1
Boc	Car12	Cd44	Cldn2	Elovl5	Entpd4	Ephb2	Ephb3	Ffar2	Fzd1	Fzd7	Gjb2	Gp1ba
B230120H	BC027344	Bcl11a	Birc5	Car12	Car8	Chek2	Cnot6	Dbf4	Dnmt1	Fads1	Fancl	Impdh2
Brrn1	Bub1b	Ccdc5	Ccna2	Ccnb1	Ccnb1-rs1	Ccnb2	Ccnd1	Ccne2	Cdc25b	Cdc2a	Cdc6	Cdc7
Cdc2a	Cdc7	Cdk4	Chek1	Chek2	Diap2	Dnmt1	Ephb2	Ephb3	Galk1	Gart	Itpka	Lats2
Eif1a	Eif5a	Fancm	Fen1	Gpatc4	Gtf2h2	Hells	Hnrpa1	Hnrpab	Hnrpdl	Lap3	Mcm2	Mcm3
Asns	Aspm	Blmh	Bxdc1	Bysl	Ccdc5	Cdc7	Cdk5rap2	Cpsf2	Cstf2	Eif4ebp2	Gbp2	Iigp1
Cnot6	Dnmt1	E2f8	Hmga2	Hmgb1	Hnrpab	Hod	Hoxa11	Hoxa9	Mcm2	Mcm3	Mcm5	Mcm6
Hmga2	Hnrpab	Hod	Hoxa11	Hoxa9	Mcm2	Mcm3	Mcm5	Mcm6	Mcm7	Narg1	Neurog3	Nono
Cxcl10	Cxcl11	Cxcl9	Ephb3	Ffar2	Fzd7	Gkn1	Grem1	Hdgf	Hmgb1	Igfbp5	Ins1	Kap
Ccdc5	Cdk5rap2	Ckap4	Cpsf2	Gas5	Gnl3	Iigp2	Kpnb1	Lin9	Mki67ip	Nola1	Nudcd2	Nusap1
Car8	Cdc6	Dbf4	Dnmt1	Fancl	Gtf2h2	Kpnb1	Lap3	Lyar	Mcm2	Park2	Pck2	Pola1
Clns1a	Eif1a	Gjb2	Hmgb1	Hnrpa1	Kcnk3	Kcnn4	Kpnb1	Lman1	Mtm1	Nup107	Nup155	Nup37
Eif4e2	Eif4g1	Gbp2	Hnrpa1	Hnrpab	Hnrpdl	Idh1	Mki67ip	Ncl	Nhp2l1	Nol5a	Nola1	Nola2
Cdk5rap2	Cenpf	Cnn1	Cpsf2	Ctnnal1	Gmnn	Gnl3	Hrasls	Kpnb1	Lin9	Mad2l1	Nudcd2	Rad51ap1
Ccnd1	Cdc2a	Cdc7	Cdk4	Cdkn2c	Chek1	Chek2	Cks1b	Dbf4	Diap2	Ephb2	Ephb3	Galk1
Ccna2	Ccnb1	Ccnb2	Ccnd1	Ccne2	Cdc25b	Cdc2a	Cdc6	Cdc7	Cdca5	Cdk4	Cenpf	Cep55
Mcm2	Mcm3	Mcm5	Mcm6	Mcm7	Nap1l1	Orc2l	Pcna	Pola1	Pold3	Pole	Pole2	Prim1
Cnot6	Ddx39	Entpd4	Fancm	Fen1	Iigp1	Isg20l1	Lap3	Mthfd2	Mtm1	Pa2g4	Pole	Ppap2a
Lap3	Nedd4	Nras	Park2	Pitpnm2	Racgap1	Rad51	Ran	Recc1	Rexo2	Rpl7l1	Rps6	Smarcc1
Ccna2	Ccnb1	Ccnb1-rs1	Ccnb2	Cdc25b	Cdc2a	Cdc6	Cdca5	Cdk4	Cep55	Incenp	Kif22	Kif2c
Gtf2h2	Lig1	Nono	Pcna	Pole	Pole2	Rad51	Rad51ap1	Rad54l	Recc1	Rfc5	Rpa1	Rpa2
Igtp	Indo	Mcm2	Mcm3	Mcm5	Mcm6	Nedd4	Nucb2	Nup107	Psmc6	Rfc2	Rfc4	Rfc5
Ccne2	Cdk4	Ect2	Gkn1	Gmnn	Gnl3	Mcm5	Nek2	Nhp2l1	Nras	Pcna	Ran	Skp2
Fzd1	Fzd7	Hmmr	Itga6	Lgr5	Lin9	Narg1	Neto1	Olfr157	Pprc1	Ptpro	Strap	Tnfrsf1b
Hspe1	Kif11	Lap3	Lrg1	Mthfd2	Mtm1	Pck2	Polr3h	Rexo2	Rpa2	Shmt1	Shmt2	Tfam
Cdc7	Cdk4	Chek1	Chek2	Dbf4	Ephb2	Ephb3	Lats2	Melk	Nek2	Pbk	Pck2	Plk4
Chek1	Chek2	Dbf4	Ephb2	Ephb3	Lats2	Melk	Nek2	Nup62	Pbk	Plk4	Tgm2	Wnk1
Lman1	Nucb2	P4hb	Park2	Pomt1	Prc1	Rcn1	Scd1	Sec23b	Set	Tmed5	Txndc5	
Igfbp5	Itpka	Lgr5	Ppap2a	Ppp2r2b	Racgap1	Rangap1	Socs3	Stat1	Utrn	Wwp1		
Mcm10	Mcm2	Mcm3	Mcm5	Mcm6	Mcm7	Nup62	Rpa1	Smarcc1	Suz12	Tmpo		

Cdk4	Chek1	Chek2	Ephb2	Ephb3	Lats2	Melk	Nek2	Pbk	Plk4	Wnk1
Indo	Mod1	Mthfd2	Phgdh	Pitpnm2	Pycr1	Rrm1	Rrm2	Scd1	Steap1	
Nhp2l1	Nono	Sfpq	Sfrs2	Snrpd3	Snrpg	Syncrip	Thoc3	Usp39	Xpo1	
Nono	Pole	Rad51	Rad51ap1	Rad54l	Rif1	Sfpq	Ssrp1	Tdg	Topbp1	
H2afz	Hod	Hoxa11	Hoxa9	Narg1	Neurog3	Pomt1	Timeless	Zipro1		
Pa2g4	Rbmx	Rbmxrt	Rpl7l1	Rps6	Snrpa1	Snrpd3	Snrpg	Syncrip		
Entpd4	Fen1	Lap3	Lats2	Mthfd2	Nek2	Nme1	Pomt1	Prps2		
Nolc1	Nusap1	Polr2a	Prkrip1	Rcl1	Rif1	Rpa2	Top2a			
Nolc1	Nras	Pck2	Ran	Rem2	Tgm2	Tgtp	Tubb5			
Gp1ba	Gpiap1	Kcnk3	Kcnn4	Olfr157	Ppap2a	Ptpro	Slc12a2			
Mcm5	Mcm6	Mcm7	Orc2l	Pola1	Rfc2	Rfc5				
Mcm2	Mcm7	Mia1	Mki67	Pa2g4	Pcna	Tnfrsf1b				
Nucb2	Ppap2a	Ptpro	Tgm2	Utrn	Vav3					
Ran	Sec23b	Snx10	Snx6	Xpo1	Xpo4					
Park2	Ube2c	Uble1a	Uble1b	Wars	Wwp1					
Ephb3	Melk	Nek2	Pbk	Plk4						
Gbp4	Ifitm2	Indo	Rps6	Tnfrsf1b						
Spdef	Stat1	Tcf19	Tfam	Zipro1						
Snrpd3	Snrpg	Syncrip	Thoc3	Usp39						
Neurog3	Smarcc1	Terf1	Tfam	Tmpo						
Mia1	P4hb	Proc	Retnlb	Vip						
Snx6	Socs3	Stat1	Stmn1	Vav3						
Recc1	Rfc2	Rfc4	Rfc5	Trip13						
Orc2l	Smarcc1	Ssrp1	Taf9							
Ppp3cb	Rangap1	Wars	Wnk1							
Uble1b	Uchl5	Ufm1	Wwp1							
Hspd1	Hspe1	Lman1	P4hb							
Stat1	Syt9	Tgm2	Utrn							
Steap1	Trip6	Txndc5	Uble1b							
Ssrp1	Terf1	Tmpo	Top2a							
Mthfd2	Rrm1	Uble1a	Uble1b							
Polr3h	Prim1	Rpo1-4								
Lman1	Nol5	P4hb								
Ran	Rem2	Tubb5								
Rfc2	Rfc4	Rfc5								
Prc1	Stmn1	Tubb5								
Rrm2	Scd1	Steap1								

Rps6
Sypl
Txndc5
Rpl7l1
Xpo1
Phgdh
Utrn
Tdg
Rrs1
Tnfrsf1b
Ran
Mcm7
Wars
Syt9
Uble1b
Ssrp1
Xpo4
Psat1

		Colon TA	TA Avg	SC Avg	DC Avg
nucleus	GO:GO:0005634	0.466019	0.457368	0.348404	0.219441
protein binding	GO:GO:0005515	0.300971	0.313872	0.311195	0.302361
nucleotide binding	GO:GO:0000166	0.194175	0.201331	0.151085	0.124064
DNA binding	GO:GO:0003677	0.177184	0.198481	0.144077	0.094037
cytoplasm	GO:GO:0005737	0.157767	0.163231	0.158419	0.14562
membrane	GO:GO:0016020	0.145631	0.148839	0.226493	0.317531
ATP binding	GO:GO:0005524	0.143204	0.144868	0.111496	0.100783
integral to membrane	GO:GO:0016021	0.135922	0.1184	0.192388	0.271179
metal ion binding	GO:GO:0046872	0.128641	0.111287	0.137616	0.136152
cell cycle	GO:GO:0007049	0.118932	0.092444	0.045123	0.031116
transferase activity	GO:GO:0016740	0.116505	0.11	0.100952	0.105465
nucleic acid binding	GO:GO:0003676	0.114078	0.134093	0.098443	0.041588
cellular component unknown	GO:GO:0008372	0.114078	0.112379	0.1398	0.107205
regulation of transcription, DNA-dependent	GO:GO:0006355	0.106796	0.121536	0.136303	0.088038
transcription	GO:GO:0006350	0.104369	0.104542	0.112522	0.07041
extracellular space	GO:GO:0005615	0.099515	0.084797	0.110147	0.173148
biological process unknown	GO:GO:0000004	0.092233	0.091496	0.102027	0.084367
zinc ion binding	GO:GO:0008270	0.092233	0.086943	0.107604	0.09178
transport	GO:GO:0006810	0.089806	0.103749	0.10595	0.118486
RNA binding	GO:GO:0003723	0.087379	0.116647	0.079098	0.024458
molecular function unknown	GO:GO:0005554	0.084951	0.105675	0.098758	0.077548
kinase activity	GO:GO:0016301	0.082524	0.074829	0.058592	0.070805
cell division	GO:GO:0051301	0.07767	0.068847	0.022291	0.015506
DNA replication	GO:GO:0006260	0.07767	0.069401	0.017939	0.008719
hydrolase activity	GO:GO:0016787	0.075243	0.082868	0.091108	0.107355
intracellular	GO:GO:0005622	0.065534	0.079157	0.097598	0.067172
mitosis	GO:GO:0007067	0.063107	0.051115	0.018903	0.012506
DNA repair	GO:GO:0006281	0.058252	0.04165	0.02013	0.009944
cytosol	GO:GO:0005829	0.058252	0.060522	0.06775	0.054648
regulation of progression through cell cycle	GO:GO:0000074	0.053398	0.047919	0.036325	0.028422
receptor activity	GO:GO:0004872	0.050971	0.048779	0.06661	0.08866
mitochondrion	GO:GO:0005739	0.050971	0.078872	0.092153	0.073037
protein amino acid phosphorylation	GO:GO:0006468	0.050971	0.050179	0.041236	0.049824
protein serine/threonine kinase activity	GO:GO:0004674	0.048544	0.047556	0.034339	0.044149
endoplasmic reticulum	GO:GO:0005783	0.046117	0.032289	0.052649	0.057424
signal transduction	GO:GO:0007165	0.043689	0.037929	0.065944	0.087629
chromatin binding	GO:GO:0003682	0.043689	0.039491	0.018223	0.009385
protein kinase activity	GO:GO:0004672	0.043689	0.047032	0.036175	0.045803
oxidoreductase activity	GO:GO:0016491	0.041262	0.040638	0.04932	0.056252
mRNA processing	GO:GO:0006397	0.041262	0.066981	0.02755	0.005828
response to DNA damage stimulus	GO:GO:0006974	0.041262	0.027096	0.015049	0.010346
development	GO:GO:0007275	0.038835	0.039529	0.05272	0.048514
ribonucleoprotein complex	GO:GO:0030529	0.038835	0.056916	0.040612	0.012348
magnesium ion binding	GO:GO:0000287	0.038835	0.025365	0.021921	0.027666
nucleolus	GO:GO:0005730	0.036408	0.043946	0.023695	0.008851
GTP binding	GO:GO:0005525	0.036408	0.018856	0.03035	0.030533
integral to plasma membrane	GO:GO:0005887	0.036408	0.040163	0.045645	0.073951
DNA replication initiation	GO:GO:0006270	0.033981	0.019153	0.004542	0.002233
cell proliferation	GO:GO:0008283	0.033981	0.036606	0.026471	0.024702
plasma membrane	GO:GO:0005886	0.031553	0.024109	0.053374	0.088638

protein transport	GO:GO:0015031	0.031553	0.026614	0.040245	0.035907
ligase activity	GO:GO:0016874	0.031553	0.027034	0.023376	0.012945
protein-tyrosine kinase activity	GO:GO:0004713	0.029126	0.03482	0.026241	0.032423
immune response	GO:GO:0006955	0.029126	0.008019	0.018963	0.037667
transcription factor activity	GO:GO:0003700	0.029126	0.051718	0.068735	0.057125
nuclear mRNA splicing, via spliceosome	GO:GO:0000398	0.029126	0.047055	0.019689	0.003957
regulation of transcription	GO:GO:0045449	0.029126	0.031442	0.030295	0.024194
extracellular region	GO:GO:0005576	0.029126	0.011868	0.023539	0.046488
intracellular signaling cascade	GO:GO:0007242	0.029126	0.024153	0.026258	0.037685
nucleoside-triphosphatase activity	GO:GO:0017111	0.029126	0.029744	0.012156	0.010313
chromatin	GO:GO:0000785	0.026699	0.022968	0.01135	0.005677
soluble fraction	GO:GO:0005625	0.026699	0.013667	0.018935	0.020625
ubiquitin cycle	GO:GO:0006512	0.026699	0.025554	0.030847	0.017896
protein folding	GO:GO:0006457	0.026699	0.03014	0.025433	0.015824
calcium ion binding	GO:GO:0005509	0.026699	0.033863	0.04372	0.065329
electron transport	GO:GO:0006118	0.026699	0.018012	0.029154	0.031308
chromosome	GO:GO:0005694	0.026699	0.030247	0.012323	0.006327
catalytic activity	GO:GO:0003824	0.026699	0.029631	0.031557	0.035198
nucleotidyltransferase activity	GO:GO:0016779	0.024272	0.015574	0.010206	0.007585
unfolded protein binding	GO:GO:0051082	0.024272	0.026532	0.019002	0.011294
GTPase activity	GO:GO:0003924	0.024272	0.009841	0.017669	0.020451
S phase of mitotic cell cycle	GO:GO:0000084	0.024272	0.022078	0.005386	0.002194
microtubule	GO:GO:0005874	0.024272	0.021054	0.014634	0.014663
iron ion binding	GO:GO:0005506	0.024272	0.01513	0.018524	0.023989
protein biosynthesis	GO:GO:0006412	0.021845	0.055458	0.045138	0.014561
transporter activity	GO:GO:0005215	0.021845	0.022106	0.019984	0.02713
electron carrier activity	GO:GO:0009055	0.021845	0.01178	0.012659	0.011639
transcription regulator activity	GO:GO:0030528	0.021845	0.018973	0.018689	0.012604
binding	GO:GO:0005488	0.021845	0.032622	0.038137	0.031429
metabolism	GO:GO:0008152	0.021845	0.019098	0.03087	0.035249
cytoskeleton	GO:GO:0005856	0.019417	0.024433	0.032518	0.048527
carbohydrate metabolism	GO:GO:0005975	0.019417	0.010636	0.015228	0.01998
rRNA processing	GO:GO:0006364	0.019417	0.027157	0.012408	0.005954
inflammatory response	GO:GO:0006954	0.019417	0.006195	0.009305	0.018928
cell adhesion	GO:GO:0007155	0.019417	0.018506	0.033729	0.048822
pre-replicative complex	GO:GO:0005656	0.019417	0.011886	0.00278	0.001124
DNA-directed RNA polymerase activity	GO:GO:0003899	0.01699	0.011276	0.004862	0.002147
apoptosis	GO:GO:0006915	0.01699	0.018216	0.030008	0.029604
DNA replication origin binding	GO:GO:0003688	0.01699	0.008899	0.002582	0.000914
DNA-dependent ATPase activity	GO:GO:0008094	0.01699	0.012532	0.002493	0.001255
cyclin-dependent protein kinase regulator activity	GO:GO:0016538	0.01699	0.011036	0.00428	0.004099
condensed chromosome	GO:GO:0000793	0.01699	0.013782	0.00395	0.002328
chromosome, pericentric region	GO:GO:0000775	0.01699	0.013728	0.003172	0.0016
negative regulation of transcription from RNA polymerase II promoter	GO:GO:0000122	0.01699	0.026017	0.015306	0.011971
spliceosome complex	GO:GO:0005681	0.01699	0.025984	0.012528	0.003431
nuclear pore	GO:GO:0005643	0.01699	0.016718	0.008809	0.002974
peptidase activity	GO:GO:0008233	0.01699	0.020011	0.030161	0.039733
membrane fraction	GO:GO:0005624	0.01699	0.021208	0.028433	0.042672

pre-replicative complex formation and maintenance	GO:GO:0006267	0.01699	0.009829	0.002489	0.000949
proteolysis	GO:GO:0006508	0.014563	0.02415	0.031696	0.04158
negative regulation of cell proliferation	GO:GO:0008285	0.014563	0.017772	0.015868	0.015581
chemotaxis	GO:GO:0006935	0.014563	0.005733	0.006965	0.009633
protein heterodimerization activity	GO:GO:0046982	0.014563	0.019162	0.015213	0.014709
protein modification	GO:GO:0006464	0.014563	0.010001	0.0167	0.009585
organ morphogenesis	GO:GO:0009887	0.014563	0.013665	0.013337	0.014322
positive regulation of cell proliferation	GO:GO:0008284	0.014563	0.016096	0.013781	0.011403
ion transport	GO:GO:0006811	0.014563	0.020019	0.020774	0.035616
ribosome biogenesis	GO:GO:0007046	0.014563	0.024197	0.015802	0.007897
helicase activity	GO:GO:0004386	0.014563	0.014996	0.014466	0.004112
mRNA export from nucleus	GO:GO:0006406	0.014563	0.021335	0.005754	0.001456
ubiquitin-dependent protein catabolism	GO:GO:0006511	0.014563	0.014329	0.020202	0.010354
calmodulin binding	GO:GO:0005516	0.014563	0.014304	0.007258	0.012352
methyltransferase activity	GO:GO:0008168	0.014563	0.011061	0.007105	0.003107
cytokine activity	GO:GO:0005125	0.014563	0.005494	0.009143	0.013756
translation initiation factor activity	GO:GO:0003743	0.014563	0.009698	0.01144	0.003914
small GTPase mediated signal transduction	GO:GO:0007264	0.014563	0.007722	0.017317	0.021412
actin binding	GO:GO:0003779	0.014563	0.023362	0.021952	0.03071
DNA recombination	GO:GO:0006310	0.014563	0.010113	0.00455	0.002341
single-stranded DNA binding	GO:GO:0003697	0.014563	0.018577	0.005994	0.003516
kinetochore	GO:GO:0000776	0.014563	0.009695	0.004042	0.002502
cell-cell signaling	GO:GO:0007267	0.014563	0.009102	0.010898	0.017409
amino acid biosynthesis	GO:GO:0008652	0.012136	0.004182	0.002472	0.001589
regulation of cell growth	GO:GO:0001558	0.012136	0.009281	0.010474	0.006151
ribosome	GO:GO:0005840	0.012136	0.034452	0.025405	0.007028
nucleosome assembly	GO:GO:0006334	0.012136	0.015044	0.007032	0.005044
transcription factor complex	GO:GO:0005667	0.012136	0.019594	0.025675	0.020085
cell surface receptor linked signal transduction	GO:GO:0007166	0.012136	0.005185	0.009857	0.015905
isomerase activity	GO:GO:0016853	0.012136	0.015708	0.015906	0.0096
G-protein coupled receptor protein signaling pathway	GO:GO:0007186	0.012136	0.009821	0.020213	0.028267
ATP-dependent helicase activity	GO:GO:0008026	0.012136	0.013277	0.012714	0.003729
nucleocytoplasmic transport	GO:GO:0006913	0.012136	0.007882	0.003366	0.001289
cytokinesis	GO:GO:0000910	0.012136	0.008474	0.005286	0.005501
nuclease activity	GO:GO:0004518	0.012136	0.014651	0.004393	0.002808
porin activity	GO:GO:0015288	0.012136	0.007482	0.002148	0.001565
cysteine-type endopeptidase activity	GO:GO:0004197	0.012136	0.007162	0.010523	0.010849
small nucleolar ribonucleoprotein complex	GO:GO:0005732	0.012136	0.010001	0.003939	0.000359
sugar binding	GO:GO:0005529	0.012136	0.002827	0.006367	0.010593
ubiquitin-protein ligase activity	GO:GO:0004842	0.012136	0.011675	0.013568	0.006796
chromatin modification	GO:GO:0016568	0.012136	0.012316	0.012964	0.004923
outer membrane	GO:GO:0019867	0.012136	0.008085	0.00487	0.003251
DNA-directed DNA polymerase activity	GO:GO:0003887	0.012136	0.011203	0.003988	0.002269
MCM complex	GO:GO:0042555	0.012136	0.010592	0.002186	0.000949
DNA helicase activity	GO:GO:0003678	0.012136	0.012125	0.003922	0.001643
protein amino acid dephosphorylation	GO:GO:0006470	0.012136	0.01223	0.011829	0.01192
3'-5' exonuclease activity	GO:GO:0008408	0.012136	0.009342	0.002535	0.001009
DNA unwinding during replication	GO:GO:0006268	0.012136	0.013375	0.003865	0.00186

structural molecule activity	GO:GO:0005198	0.012136	0.022408	0.021164	0.033072
GTPase activator activity	GO:GO:0005096	0.012136	0.007765	0.009011	0.011412
meiosis	GO:GO:0007126	0.012136	0.009004	0.003928	0.00264
protein complex	GO:GO:0043234	0.012136	0.018479	0.013733	0.00853
regulation of translation	GO:GO:0006445	0.012136	0.014403	0.006848	0.004994
Golgi stack	GO:GO:0005795	0.012136	0.005265	0.011831	0.014315
nuclear envelope	GO:GO:0005635	0.012136	0.008696	0.005115	0.006552
exonuclease activity	GO:GO:0004527	0.012136	0.012169	0.002637	0.001181
signal transducer activity	GO:GO:0004871	0.012136	0.014095	0.027294	0.036522
RNA splicing	GO:GO:0008380	0.012136	0.008369	0.006501	0.002436
spindle	GO:GO:0005819	0.012136	0.010538	0.006439	0.005221
DNA replication factor C complex	GO:GO:0005663	0.012136	0.007791	0.001905	0.000333
chromosome segregation	GO:GO:0007059	0.009709	0.012489	0.004992	0.002846
replication fork	GO:GO:0005657	0.009709	0.012835	0.004203	0.001113
negative regulation of transcription	GO:GO:0016481	0.009709	0.010777	0.008473	0.007191
chromatin remodeling	GO:GO:0006338	0.009709	0.00726	0.004457	0.00301
microtubule binding	GO:GO:0008017	0.009709	0.013251	0.005961	0.005722
cellular physiological process	GO:GO:0050875	0.009709	0.010753	0.012606	0.01275
microtubule-based process	GO:GO:0007017	0.009709	0.007039	0.00583	0.006831
nervous system development	GO:GO:0007399	0.009709	0.020992	0.022294	0.025039
transcription factor binding	GO:GO:0008134	0.009709	0.006559	0.008712	0.00694
DNA-dependent DNA replication	GO:GO:0006261	0.009709	0.0042	0.001122	0.001043
protein targeting	GO:GO:0006605	0.009709	0.009009	0.011687	0.008288
defense response	GO:GO:0006952	0.009709	0.01175	0.0104	0.018256
chemokine activity	GO:GO:0008009	0.009709	0.00202	0.001858	0.003743
condensed nuclear chromosome	GO:GO:0000794	0.009709	0.005716	0.000991	0.000852
midbody	GO:GO:0030496	0.009709	0.007488	0.000903	0.000801
cell differentiation	GO:GO:0030154	0.009709	0.030501	0.03031	0.030262
cytoskeleton organization and biogenesis	GO:GO:0007010	0.009709	0.009103	0.012018	0.016721
RNA processing	GO:GO:0006396	0.009709	0.014625	0.009449	0.002132
ER-Golgi intermediate compartment	GO:GO:0005793	0.009709	0.003855	0.002499	0.003301
chromosome organization and biogenesis (sensu Eukaryota)	GO:GO:0007001	0.009709	0.011251	0.006046	0.004612
centrosome	GO:GO:0005813	0.009709	0.008474	0.008348	0.005161
potassium ion binding	GO:GO:0030955	0.009709	0.012593	0.004978	0.006563
nucleoplasm	GO:GO:0005654	0.009709	0.013695	0.007478	0.003555
axon guidance	GO:GO:0007411	0.009709	0.009342	0.006272	0.007798
lyase activity	GO:GO:0016829	0.009709	0.011459	0.010982	0.010148
one-carbon compound metabolism	GO:GO:0006730	0.009709	0.004299	0.003983	0.00304
chromosome condensation	GO:GO:0030261	0.009709	0.006337	0.002286	0.00247
DNA metabolism	GO:GO:0006259	0.009709	0.011923	0.004425	0.002964
DNA clamp loader activity	GO:GO:0003689	0.009709	0.008216	0.001443	0.0006
transcriptional repressor activity	GO:GO:0016564	0.009709	0.015814	0.012245	0.009855
intracellular protein transport	GO:GO:0006886	0.009709	0.015549	0.028462	0.028435
sequence-specific DNA binding	GO:GO:0043565	0.009709	0.016361	0.023654	0.024247
protein domain specific binding	GO:GO:0019904	0.009709	0.006454	0.007155	0.006857
ATPase activity	GO:GO:0016887	0.009709	0.025359	0.012783	0.009341
plastid	GO:GO:0009536	0.009709	0.018481	0.010257	0.00393
G-protein coupled receptor activity	GO:GO:0004930	0.009709	0.00718	0.010201	0.015147
motor activity	GO:GO:0003774	0.009709	0.007348	0.008445	0.012699
manganese ion binding	GO:GO:0030145	0.009709	0.00779	0.008638	0.00974

nuclear chromatin	GO:GO:0000790	0.009709	0.008844	0.002221	0.001326
transcription from RNA polymerase II promoter	GO:GO:0006366	0.009709	0.009114	0.011616	0.009784
potassium ion transport	GO:GO:0006813	0.009709	0.014674	0.004766	0.009587
regulation of protein biosynthesis	GO:GO:0006417	0.009709	0.006231	0.003126	0.002568
mitochondrial inner membrane	GO:GO:0005743	0.009709	0.014777	0.026525	0.024631
protein kinase binding	GO:GO:0019901	0.009709	0.003855	0.003649	0.003396
leading strand elongation	GO:GO:0006272	0.009709	0.008216	0.001554	0.000333
anti-apoptosis	GO:GO:0006916	0.009709	0.008812	0.011235	0.013502
hormone activity	GO:GO:0005179	0.009709	0.005105	0.003294	0.006913
mismatch repair	GO:GO:0006298	0.009709	0.010396	0.001883	0.000821
sister chromatid cohesion	GO:GO:0007062	0.007282	0.007286	0.001714	0.001076
cysteine-type peptidase activity	GO:GO:0008234	0.007282	0.003972	0.008893	0.008673
G2/M transition of mitotic cell cycle	GO:GO:0000086	0.007282	0.006319	0.002129	0.00251
microsome	GO:GO:0005792	0.007282	0.005814	0.014339	0.016343
Rho guanyl-nucleotide exchange factor activity	GO:GO:0005089	0.007282	0.003067	0.002994	0.002946
embryonic development (sensu Mammalia)	GO:GO:0001701	0.007282	0.003972	0.004489	0.003188
spindle microtubule	GO:GO:0005876	0.007282	0.004281	0.001121	0.000969
G1/S transition of mitotic cell cycle	GO:GO:0000082	0.007282	0.008314	0.005439	0.004253
Elg1 RFC-like complex	GO:GO:0031391	0.007282	0.005229	0.000897	0.000333
cell death	GO:GO:0008219	0.007282	0.003997	0.001653	0.003644
receptor binding	GO:GO:0005102	0.007282	0.009767	0.008377	0.011254
negative regulation of apoptosis	GO:GO:0043066	0.007282	0.005807	0.006539	0.006937
purine nucleotide binding	GO:GO:0017076	0.007282	0.003997	0.000486	0.000894
mitotic chromosome condensation	GO:GO:0007076	0.007282	0.006152	0.00152	0.000796
perinuclear region	GO:GO:0048471	0.007282	0.005222	0.005786	0.006061
regulation of Rho protein signal transduction	GO:GO:0035023	0.007282	0.003067	0.002657	0.002847
protein C-terminus binding	GO:GO:0008022	0.007282	0.004095	0.003706	0.004867
regulation of S phase of mitotic cell cycle	GO:GO:0007090	0.007282	0.00367	0.000746	0.000754
rhodopsin-like receptor activity	GO:GO:0001584	0.007282	0.00577	0.006169	0.011928
response to unfolded protein	GO:GO:0006986	0.007282	0.004557	0.008733	0.004949
protein kinase inhibitor activity	GO:GO:0004860	0.007282	0.001817	0.002943	0.003666
regulation of apoptosis	GO:GO:0042981	0.007282	0.01037	0.012976	0.011025
Rad17 RFC-like complex	GO:GO:0031389	0.007282	0.005229	0.000957	0.000333
structural constituent of ribosome	GO:GO:0003735	0.007282	0.034656	0.028015	0.008558
tissue regeneration	GO:GO:0042246	0.007282	0.00335	0.002877	0.002976
Ctf18 RFC-like complex	GO:GO:0031390	0.007282	0.005229	0.000961	0.000333
mitotic cell cycle	GO:GO:0000278	0.007282	0.001613	0.002269	0.001112
external side of plasma membrane	GO:GO:0009897	0.007282	0.00577	0.005851	0.012948
structural constituent of cytoskeleton	GO:GO:0005200	0.007282	0.007075	0.009922	0.015497
ATP-dependent DNA helicase activity	GO:GO:0004003	0.007282	0.006257	0.002665	0.001057
JAK-STAT cascade	GO:GO:0007259	0.007282	0.002747	0.002939	0.002444
diacylglycerol binding	GO:GO:0019992	0.007282	0.001817	0.00243	0.004963
cell growth	GO:GO:0016049	0.007282	0.003979	0.004298	0.004041
microtubule motor activity	GO:GO:0003777	0.007282	0.006417	0.004636	0.004362
transferase activity, transferring glycosyl groups	GO:GO:0016757	0.007282	0.008233	0.010075	0.012585
microtubule-based movement	GO:GO:0007018	0.007282	0.007642	0.006469	0.005862
kinesin complex	GO:GO:0005871	0.007282	0.004582	0.002738	0.002893
meiotic recombination	GO:GO:0007131	0.007282	0.005538	0.001531	0.000671

muscle development	GO:GO:0007517	0.007282	0.00824	0.005682	0.007735
DNA packaging	GO:GO:0006323	0.007282	0.012161	0.003097	0.001051
phosphoinositide-mediated signaling	GO:GO:0048015	0.007282	0.007728	0.001682	0.002893
phosphoprotein phosphatase activity	GO:GO:0004721	0.007282	0.007888	0.012076	0.012313
protein import into nucleus	GO:GO:0006606	0.007282	0.00282	0.004336	0.002432
cytoplasmic membrane-bound vesicle	GO:GO:0016023	0.007282	0.003972	0.005136	0.007133
mitochondrial matrix	GO:GO:0005759	0.007282	0.005424	0.006181	0.004012
ubiquitin ligase complex	GO:GO:0000151	0.007282	0.005123	0.004518	0.002223
protein tyrosine phosphatase activity	GO:GO:0004725	0.007282	0.009145	0.008428	0.009438
transcription corepressor activity	GO:GO:0003714	0.007282	0.004575	0.011304	0.007759
regulation of translational initiation	GO:GO:0006446	0.007282	0.005123	0.005171	0.001648
DNA-directed RNA polymerase I complex	GO:GO:0005736	0.007282	0.003067	0.000854	0.000582
telomere maintenance via telomerase	GO:GO:0007004	0.007282	0.00194	0.000578	0
cellular morphogenesis	GO:GO:0000902	0.007282	0.00638	0.002778	0.003547
microtubule cytoskeleton organization and biogenesis	GO:GO:0000226	0.007282	0.001915	0.003241	0.003716
actin filament	GO:GO:0005884	0.007282	0.005549	0.002444	0.005856
Golgi apparatus	GO:GO:0005794	0.007282	0.009237	0.017782	0.021142
DNA methylation	GO:GO:0006306	0.007282	0.006479	0.002463	0.00172
proline biosynthesis	GO:GO:0006561	0.007282	0.002445	0.000437	0.000372
growth factor activity	GO:GO:0008083	0.007282	0.00335	0.00752	0.011909
secretory granule	GO:GO:0030141	0.007282	0.001515	0.003057	0.003677
acute-phase response	GO:GO:0006953	0.007282	0.002445	0.001153	0.005187
protein homodimerization activity	GO:GO:0042803	0.007282	0.011212	0.010557	0.019143
extracellular matrix (sensu Metazoa)	GO:GO:0005578	0.007282	0.01876	0.013743	0.020697
ribosome biogenesis and assembly	GO:GO:0042254	0.007282	0.009686	0.002884	0.000469
cyclin-dependent protein kinase holoenzyme complex	GO:GO:0000307	0.007282	0.005832	0.003103	0.001383
nucleobase, nucleoside, nucleotide and nucleic acid metabolism	GO:GO:0006139	0.007282	0.009848	0.00536	0.004742
base-excision repair	GO:GO:0006284	0.007282	0.007507	0.002199	0.001125
Golgi membrane	GO:GO:0000139	0.007282	0.001817	0.004606	0.00428
negative regulation of transcription, DNA-dependent	GO:GO:0045892	0.007282	0.005825	0.00678	0.005303
transcriptional activator activity	GO:GO:0016563	0.007282	0.00681	0.015638	0.014044
endoplasmic reticulum membrane	GO:GO:0005789	0.007282	0.004909	0.007557	0.00866
chromatin assembly or disassembly	GO:GO:0006333	0.007282	0.010345	0.006746	0.002809
ubiquitin thiolesterase activity	GO:GO:0004221	0.007282	0.00492	0.005477	0.003838
protein transporter activity	GO:GO:0008565	0.007282	0.011871	0.01667	0.0125
mitotic sister chromatid segregation	GO:GO:0000070	0.007282	0.012391	0.00305	0.002438
regulation of cell proliferation	GO:GO:0042127	0.007282	0.014933	0.009611	0.006284
protein ubiquitination	GO:GO:0016567	0.007282	0.006126	0.006826	0.003774
basolateral plasma membrane	GO:GO:0016323	0.007282	0.008455	0.003319	0.004065
phosphatase inhibitor activity	GO:GO:0019212	0.007282	0.005123	0.001151	0.000536
mRNA metabolism	GO:GO:0016071	0.007282	0.006207	0.003738	0.001112
nucleotide metabolism	GO:GO:0009117	0.007282	0.003997	0.002877	0.00263
establishment and/or maintenance of chromatin architecture	GO:GO:0006325	0.007282	0.008829	0.00406	0.002412
telomere maintenance	GO:GO:0000723	0.007282	0.005327	0.005803	0.003474
nucleocytoplasmic transporter activity	GO:GO:0005487	0.007282	0.00492	0.001374	0.00044
ER to Golgi vesicle-mediated transport	GO:GO:0006888	0.007282	0.003954	0.00829	0.008115

translational initiation	GO:GO:0006413	0.007282	0.00242	0.005872	0.001968
regulation of DNA replication	GO:GO:0006275	0.007282	0.004299	0.001728	0.001697
amino acid metabolism	GO:GO:0006520	0.004854	0.001312	0.005363	0.004084
symporter activity	GO:GO:0015293	0.004854	0.006195	0.004413	0.006607
fatty acid elongation	GO:GO:0030497	0.004854	0.002242	0.001129	0.000828
cell cycle checkpoint	GO:GO:0000075	0.004854	0.003474	0.001128	0.000618
aminopeptidase activity	GO:GO:0004177	0.004854	0.001613	0.003373	0.003717
antimicrobial humoral response (sensu Vertebrata)	GO:GO:0019735	0.004854	0.00101	0.00229	0.003926
lipid binding	GO:GO:0008289	0.004854	0.006453	0.007881	0.011607
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:GO:0016616	0.004854	0.000302	0.001755	0.001562
glutamine metabolism	GO:GO:0006541	0.004854	0.00226	0.001738	0.000862
nuclear chromosome	GO:GO:0000228	0.004854	0.00585	0.002646	0.001781
heat shock protein binding	GO:GO:0031072	0.004854	0.002562	0.003775	0.003732
histone phosphorylation	GO:GO:0016572	0.004854	0.003713	0.001034	0.000337
hemopoiesis	GO:GO:0030097	0.004854	0.002217	0.004169	0.004704
identical protein binding	GO:GO:0042802	0.004854	0.008953	0.008429	0.010659
response to biotic stimulus	GO:GO:0009607	0.004854	0.00101	0.001046	0.000298
non-G-protein coupled 7TM receptor activity	GO:GO:0004926	0.004854	0.001613	0.001324	0.000229
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	GO:GO:0016702	0.004854	0.001312	0.003106	0.003984
brain development	GO:GO:0007420	0.004854	0.001712	0.005908	0.006594
smooth muscle contraction	GO:GO:0006939	0.004854	0.006584	0.000913	0.001939
sodium ion transport	GO:GO:0006814	0.004854	0.0067	0.004474	0.007481
protein export from nucleus	GO:GO:0006611	0.004854	0.004212	0.002255	0.001276
generation of precursor metabolites and energy	GO:GO:0006091	0.004854	0.001312	0.004102	0.00683
mRNA polyadenylylation	GO:GO:0006378	0.004854	0.002242	0.002879	0.001215
heart development	GO:GO:0007507	0.004854	0.009211	0.00946	0.010261
purine nucleotide biosynthesis	GO:GO:0006164	0.004854	0.010537	0.002378	0.001316
ribose phosphate diphosphokinase activity	GO:GO:0004749	0.004854	0.002562	0.000942	0.000261
guanyl-nucleotide exchange factor activity	GO:GO:0005085	0.004854	0.003165	0.006273	0.006647
carbonate dehydratase activity	GO:GO:0004089	0.004854	0.000505	0.001111	0.001736
small nuclear ribonucleoprotein complex	GO:GO:0030532	0.004854	0.002544	0.001588	0.001401
metaphase plate congression	GO:GO:0051310	0.004854	0.004643	0.000314	0
positive regulation of apoptosis	GO:GO:0043065	0.004854	0.004175	0.004528	0.004377
L-serine metabolism	GO:GO:0006563	0.004854	0.00226	0.000465	0.000242
glycine hydroxymethyltransferase activity	GO:GO:0004372	0.004854	0.00226	0.000465	9.15E-05
RNA splicing factor activity, transesterification mechanism	GO:GO:0031202	0.004854	0.011206	0.00559	0.001462
GPI anchor binding	GO:GO:0048503	0.004854	0.006805	0.005573	0.012457
nuclear origin of replication recognition complex	GO:GO:0005664	0.004854	0.002863	0.000788	0.000267
cellular protein metabolism	GO:GO:0044267	0.004854	0.004372	0.004293	0.0007
circadian rhythm	GO:GO:0007623	0.004854	0.001312	0.002446	0.002436
chloride transport	GO:GO:0006821	0.004854	0.007746	0.003572	0.004421
pyridoxal phosphate binding	GO:GO:0030170	0.004854	0.002562	0.001	0.001023

protein serine/threonine phosphatase activity	GO:GO:0004722	0.004854	0.005548	0.003647	0.003484
cell tip	GO:GO:0051286	0.004854	0.00101	0.001469	0.000957
phospholipid binding	GO:GO:0005543	0.004854	0.00101	0.004102	0.003676
DNA strand elongation	GO:GO:0006271	0.004854	0.004724	0.001895	0.000516
pattern specification	GO:GO:0007389	0.004854	0.002544	0.002841	0.002211
tricarboxylic acid cycle	GO:GO:0006099	0.004854	0.002845	0.003704	0.002629
alpha DNA polymerase:primase complex	GO:GO:0005658	0.004854	0.003812	0.000895	0.00084
mitotic spindle assembly	GO:GO:0051227	0.004854	0.004095	0.001381	0.000832
insulin-like growth factor binding	GO:GO:0005520	0.004854	0.001613	0.001503	0.00177
ubiquitin activating enzyme activity	GO:GO:0004839	0.004854	0	0.001083	0.000446
protein phosphatase type 2A regulator activity	GO:GO:0008601	0.004854	0.002544	0.001219	0.000693
ribonuclease activity	GO:GO:0004540	0.004854	0.00351	0.000869	0.000529
mitochondrion organization and biogenesis	GO:GO:0007005	0.004854	0.003794	0.001519	0.001575
histone acetylation	GO:GO:0016573	0.004854	0.004095	0.002452	0.001664
G2 phase of mitotic cell cycle	GO:GO:0000085	0.004854	0.003492	0.000593	0.000989
blood coagulation	GO:GO:0007596	0.004854	0.001915	0.004317	0.007249
cell motility	GO:GO:0006928	0.004854	0.008225	0.01123	0.014334
heme binding	GO:GO:0020037	0.004854	0.005604	0.00792	0.012153
pyrroline-5-carboxylate reductase activity	GO:GO:0004735	0.004854	0.00194	0.000377	0.000315
nucleotide biosynthesis	GO:GO:0009165	0.004854	0.006294	0.00165	0.000675
transmembrane receptor protein tyrosine kinase signaling pathway	GO:GO:0007169	0.004854	0.009294	0.005817	0.009499
microtubule associated complex	GO:GO:0005875	0.004854	0.006516	0.004811	0.00613
transmembrane-ephrin receptor activity	GO:GO:0005005	0.004854	0.005573	0.000234	9.87E-05
actin cytoskeleton organization and biogenesis	GO:GO:0030036	0.004854	0.006541	0.00929	0.013115
negative regulation of inflammatory response	GO:GO:0050728	0.004854	0.00101	0.000638	0.001424
chromosome, telomeric region	GO:GO:0000781	0.004854	0.000807	0.001464	0.000148
vesicle-mediated transport	GO:GO:0016192	0.004854	0.006151	0.010428	0.014224
DNA replication, synthesis of RNA primer	GO:GO:0006269	0.004854	0.00351	0.000795	0.000524
receptor signaling protein serine/threonine kinase activity	GO:GO:0004702	0.004854	0.007408	0.002784	0.002597
response to drug	GO:GO:0042493	0.004854	0.002544	0.001942	0.002689
nucleolus organization and biogenesis	GO:GO:0007000	0.004854	0.00226	0.001188	0.000302
serine-type endopeptidase activity	GO:GO:0004252	0.004854	0.00351	0.004983	0.011708
regulation of transcription from RNA polymerase II promoter	GO:GO:0006357	0.004854	0.012704	0.023576	0.016431
Ras protein signal transduction	GO:GO:0007265	0.004854	0.001312	0.002949	0.002884
structural constituent of nuclear pore	GO:GO:0017056	0.004854	0.003794	0.000592	9.87E-05
DNA synthesis during DNA repair	GO:GO:0000731	0.004854	0.004742	0.000527	0.000457
ion channel activity	GO:GO:0005216	0.004854	0.010129	0.008119	0.017069
spindle pole	GO:GO:0000922	0.004854	0.003677	0.001224	0.0008
S-adenosylmethionine-dependent methyltransferase activity	GO:GO:0008757	0.004854	0.005327	0.002729	0.00214
phosphoinositide binding	GO:GO:0035091	0.004854	0.001613	0.003253	0.003002
calcium ion homeostasis	GO:GO:0006874	0.004854	0.00101	0.003971	0.006476
endonuclease activity	GO:GO:0004519	0.004854	0.007526	0.003471	0.003615
axon guidance receptor activity	GO:GO:0008046	0.004854	0.006823	0.000506	0.000199
oogenesis	GO:GO:0048477	0.004854	0.000505	0.000381	0
regulation of cell shape	GO:GO:0008360	0.004854	0.002944	0.006653	0.008137

protein phosphatase type 2A complex	GO:GO:0000159	0.004854	0.002544	0.001084	0.001203
NAD binding	GO:GO:0051287	0.004854	0.001552	0.003274	0.003522
synapse	GO:GO:0045202	0.004854	0.002845	0.006103	0.009316
DNA damage checkpoint	GO:GO:0000077	0.004854	0.005334	0.002409	0.000955
Wnt receptor signaling pathway	GO:GO:0016055	0.004854	0.005284	0.00932	0.005542
heparin binding	GO:GO:0008201	0.004854	0.007107	0.006742	0.008104
learning	GO:GO:0007612	0.004854	0.005875	0.000829	0.000555
spindle pole body	GO:GO:0005816	0.004854	0.003474	0.00189	0.00196
glycine metabolism	GO:GO:0006544	0.004854	0.002562	0.000815	9.15E-05
double-stranded DNA binding	GO:GO:0003690	0.004854	0.011915	0.008206	0.007147
delta DNA polymerase complex	GO:GO:0043625	0.004854	0.005672	0.000527	0.000457
long-chain fatty acid biosynthesis	GO:GO:0042759	0.004854	0.004014	0.001171	0.00063
outer kinetochore of condensed chromosome	GO:GO:0000940	0.004854	0.00194	0.00049	0.000451
tRNA processing	GO:GO:0008033	0.004854	0.00101	0.00313	0.000813
cell surface	GO:GO:0009986	0.004854	0.00771	0.009842	0.012201
L-serine biosynthesis	GO:GO:0006564	0.004854	0.000807	0.00171	0.000523
epithelial cell differentiation	GO:GO:0030855	0.004854	0.001613	0.002647	0.003277
fatty acid elongase activity	GO:GO:0009922	0.004854	0.002242	0.001129	0.000828
hydrolase activity, acting on glycosyl bonds	GO:GO:0016798	0.004854	0.001108	0.004086	0.006926
positive regulation of I-kappaB kinase/NF-kappaB cascade	GO:GO:0043123	0.004854	0.004372	0.005316	0.004432
purine nucleotide metabolism	GO:GO:0006163	0.004854	0.00101	0.001303	0.000461
transcription from RNA polymerase I promoter	GO:GO:0006360	0.004854	0.002562	0.001	0.000451
double-strand break repair via homologous recombination	GO:GO:0000724	0.004854	0.002544	0.000876	0.0009
protein disulfide oxidoreductase activity	GO:GO:0015035	0.004854	0.003768	0.003483	0.00172
integrin-mediated signaling pathway	GO:GO:0007229	0.004854	0.002845	0.004366	0.008535
RNA polymerase II transcription factor activity	GO:GO:0003702	0.004854	0.004052	0.012049	0.011377
lagging strand elongation	GO:GO:0006273	0.004854	0.003492	0.000758	0.000149
mitotic spindle checkpoint	GO:GO:0007094	0.004854	0.003776	0.001816	0.000625
induction of apoptosis	GO:GO:0006917	0.004854	0.008135	0.011235	0.011884
establishment and/or maintenance of cell polarity (sensu Fungi)	GO:GO:0030467	0.004854	0.001312	0.001519	0.000791
cytokine and chemokine mediated signaling pathway	GO:GO:0019221	0.004854	0.00101	0.00339	0.00431
endopeptidase inhibitor activity	GO:GO:0004866	0.004854	0.002242	0.003808	0.009187
protein import into nucleus, docking	GO:GO:0000059	0.004854	0.0071	0.003935	0.001968
I-kappaB kinase/NF-kappaB cascade	GO:GO:0007249	0.004854	0.00101	0.001276	0.002568
SH2 domain binding	GO:GO:0042169	0.004854	0.004113	0.001428	0.001409
protein metabolism	GO:GO:0019538	0.004854	0.00194	0.003368	0.003988
DNA replication factor A complex	GO:GO:0005662	0.004854	0.00226	0.000379	0.000267
actin cytoskeleton	GO:GO:0015629	0.004854	0.016095	0.008748	0.015901
ephrin receptor activity	GO:GO:0005003	0.004854	0.006504	0.000904	0.001318
transcription coactivator activity	GO:GO:0003713	0.004854	0.009328	0.013105	0.007212
spermatogenesis	GO:GO:0007283	0.004854	0.015784	0.01191	0.011391
poly(A)+ mRNA export from nucleus	GO:GO:0016973	0.004854	0.001613	0.001408	0.000248
M phase of mitotic cell cycle	GO:GO:0000087	0.004854	0.003801	0.001003	0.000886
chromatin silencing at telomere	GO:GO:0006348	0.004854	0.000807	0.001353	0.000789

mRNA cleavage	GO:GO:0006379	0.004854	0.002242	0.001672	0.000597
fatty acid biosynthesis	GO:GO:0006633	0.004854	0.004759	0.004274	0.003312
central nervous system development	GO:GO:0007417	0.004854	0.003776	0.005795	0.008643
lysosome	GO:GO:0005764	0.004854	0.001613	0.011589	0.020817
negative regulation of progression through cell cycle	GO:GO:0045786	0.004854	0.005345	0.006298	0.006647
telomeric DNA binding	GO:GO:0042162	0.004854	0.000505	0.000373	0
cell wall biosynthesis (sensu Fungi)	GO:GO:0009272	0.004854	0.00101	0.000457	0.000205
extracellular matrix organization and biogenesis	GO:GO:0030198	0.004854	0.00194	0.002668	0.005099
gametogenesis	GO:GO:0007276	0.004854	0.002544	0.001671	0.000414
gastrulation (sensu Mammalia)	GO:GO:0010003	0.004854	0.001312	0.002355	0.000894
proton transport	GO:GO:0015992	0.004854	0.002562	0.006775	0.009182
damaged DNA binding	GO:GO:0003684	0.004854	0.005931	0.004008	0.002508
muscle contraction	GO:GO:0006936	0.004854	0.001613	0.003648	0.009533
regulation of striated muscle development	GO:GO:0016202	0.004854	0.00194	0.000132	0.000537
phospholipid dephosphorylation	GO:GO:0046839	0.004854	0.003713	0.000356	0.001049
cell-matrix adhesion	GO:GO:0007160	0.004854	0.002845	0.003517	0.007297
carboxy-lyase activity	GO:GO:0016831	0.004854	0.006195	0.002268	0.001152
T cell differentiation	GO:GO:0030217	0.004854	0.001312	0.001449	0.001771
cyclin binding	GO:GO:0030332	0.004854	0.005548	0.002052	0.001463
muscle maintenance	GO:GO:0046716	0.004854	0.003713	0.000325	0.000563
ribonuclease H activity	GO:GO:0004523	0.004854	0.005044	0.001367	0.000484
spermatid development	GO:GO:0007286	0.004854	0.00141	0.002052	0.001903
hydrogen ion transporter activity	GO:GO:0015078	0.004854	0.00101	0.004785	0.007604
regulation of GTPase activity	GO:GO:0043087	0.004854	0.00101	0.001986	0.002793
actomyosin structure organization and biogenesis	GO:GO:0031032	0.004854	0.003492	0.000373	0.001179
negative regulation of cell growth	GO:GO:0030308	0.004854	0.004121	0.002481	0.004128
positive regulation of transcription from RNA polymerase II promoter	GO:GO:0045944	0.004854	0.014088	0.019622	0.01476
ribonucleoside-diphosphate reductase activity	GO:GO:0004748	0.004854	0.006496	0.000731	0.000385
hyaluronic acid binding	GO:GO:0005540	0.004854	0.003713	0.000936	0.000922
barrier septum	GO:GO:0000935	0.004854	0.00101	0.001743	0.002132
synaptic vesicle	GO:GO:0008021	0.004854	0.00226	0.003423	0.0043
methenyltetrahydrofolate cyclohydrolase activity	GO:GO:0004477	0.002427	0.001737	0.000404	0.000367
regulation of circadian rhythm	GO:GO:0042752	0.002427	0.000505	0.000738	0
imidazolonepropionase activity	GO:GO:0050480	0.002427	0.000505	0	0
specific transcriptional repressor activity	GO:GO:0016566	0.002427	0.000807	0.001233	0.000619
cytoplasmic sequestering of transcription factor	GO:GO:0042994	0.002427	0.000505	0.000221	0.000952
SAGA complex	GO:GO:0000124	0.002427	0.002057	0.001135	0.000514
malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity	GO:GO:0004473	0.002427	0	0.000158	0.000155
regulation of neuronal synaptic plasticity	GO:GO:0048168	0.002427	0.005068	0.001618	0.001309
calcium-dependent protein serine/threonine phosphatase activity	GO:GO:0004723	0.002427	0.000505	0.000373	0.000272
complement component C1q binding	GO:GO:0001849	0.002427	0.000505	0.000189	5.66E-05
phosphoenolpyruvate carboxykinase activity	GO:GO:0004611	0.002427	0.000505	0.00019	0.000157

sterol metabolism	GO:GO:0016125	0.002427	0.001737	0.000795	0.00113
gap-junction forming channel activity	GO:GO:0005243	0.002427	0.000807	0.000716	0.000387
centromeric DNA binding	GO:GO:0019237	0.002427	0.00141	0.00102	0.000573
voltage-gated potassium channel complex	GO:GO:0008076	0.002427	0.006841	0.002532	0.003875
morphogenesis of an epithelium	GO:GO:0002009	0.002427	0.001435	0.000487	0.000869
barrier septum formation	GO:GO:0000917	0.002427	0.001108	0.001529	0.001191
UTP biosynthesis	GO:GO:0006228	0.002427	0.001737	0.001167	0.000832
guard mother cell cytokinesis	GO:GO:0010235	0.002427	0.000505	0.000362	0.000521
induction of an organ	GO:GO:0001759	0.002427	0.001435	0.000837	0.000256
transcription cofactor activity	GO:GO:0003712	0.002427	0.000807	0.003612	0.004287
nuclear export	GO:GO:0051168	0.002427	0.002057	0.000448	5.66E-05
copper, zinc superoxide dismutase activity	GO:GO:0004785	0.002427	0.000505	0.001416	0.000728
phosphorylation	GO:GO:0016310	0.002427	0.000807	0.003521	0.002464
neuronal Cdc2-like kinase binding	GO:GO:0042808	0.002427	0.000505	0.000145	0
p53 binding	GO:GO:0002039	0.002427	0.001755	0.000184	5.66E-05
physiological process	GO:GO:0007582	0.002427	0.000807	0.000787	0.002221
cyclin-dependent protein kinase inhibitor activity	GO:GO:0004861	0.002427	0.001108	0.001583	0.001714
chromatin silencing at silent mating-type cassette	GO:GO:0030466	0.002427	0.000505	0.000655	0.000239
blood vessel remodeling	GO:GO:0001974	0.002427	0.000505	0.000827	0.001002
tracheal system development (sensu Insecta)	GO:GO:0007424	0.002427	0.001737	0.001052	0.002767
thyroid hormone receptor binding	GO:GO:0046966	0.002427	0.002057	0.001216	0.000662
spindle organization and biogenesis	GO:GO:0007051	0.002427	0.002358	0.001314	0.000577
prostaglandin transport	GO:GO:0015732	0.002427	0.000505	0.000178	0.000397
vasculogenesis	GO:GO:0001570	0.002427	0.004741	0.003076	0.002548
cell migration during gastrulation	GO:GO:0042074	0.002427	0.001737	0.003508	0.002307
isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine	GO:GO:0018153	0.002427	0.000505	0.000477	0.000123
neuromuscular junction development	GO:GO:0007528	0.002427	0.000807	0.000953	0.000739
caspase inhibitor activity	GO:GO:0043027	0.002427	0.001108	0.000704	0.000638
site-specific DNA-methyltransferase (cytosine-specific) activity	GO:GO:0008326	0.002427	0.002987	0.000248	0.000175
folic acid and derivative biosynthesis	GO:GO:0009396	0.002427	0.002667	0.000565	0.000367
dopamine metabolism	GO:GO:0042417	0.002427	0.000505	0.000441	0.000806
protein N-terminus binding	GO:GO:0047485	0.002427	0.001435	0.001106	0.002317
tryptophan-tRNA ligase activity	GO:GO:0004830	0.002427	0.000505	0.000426	9.15E-05
CD27 receptor binding	GO:GO:0005175	0.002427	0	0.000106	0
chemoattractant activity	GO:GO:0042056	0.002427	0.000505	0.000398	0.000895
CXCR3 chemokine receptor binding	GO:GO:0048248	0.002427	0.000505	0	5.66E-05
regulation of cell volume	GO:GO:0006884	0.002427	0.000505	0.000658	0.000586
mRNA cleavage and polyadenylation specificity factor complex	GO:GO:0005847	0.002427	0.001435	0.001027	0.000451
methylated-DNA-[protein]-cysteine S-methyltransferase activity	GO:GO:0003908	0.002427	0.000505	0.00033	5.66E-05
regulation of cell cycle	GO:GO:0051726	0.002427	0.001737	0.000598	0.000627
RNA ligase (ATP) activity	GO:GO:0003972	0.002427	0.000807	0.000242	0.000118
transcription initiation from RNA polymerase II promoter	GO:GO:0006367	0.002427	0.002962	0.004398	0.002107
deoxyribonucleotide metabolism	GO:GO:0009262	0.002427	0.002987	0.00029	0.000267

signal transduction during conjugation with cellular fusion	GO:GO:0032005	0.002427	0.000505	0.000463	0.000577
maintenance of DNA methylation	GO:GO:0010216	0.002427	0.002057	0.000157	0.000118
peptidyl-proline hydroxylation to 4-hydroxy-L-proline	GO:GO:0018401	0.002427	0.000505	0.000532	0.001054
monovalent inorganic cation transport	GO:GO:0015672	0.002427	0.000505	0.000683	0.001144
startle response	GO:GO:0001964	0.002427	0.000505	6.5E-05	0
positive regulation of protein secretion	GO:GO:0050714	0.002427	0.004138	0.00018	0.000823
filopodium formation	GO:GO:0046847	0.002427	0.000807	0.00109	0.000916
negative regulation of astrocyte differentiation	GO:GO:0048712	0.002427	0.000505	6.42E-05	0
regulation of neuron differentiation	GO:GO:0045664	0.002427	0.000505	0.000733	0.002055
integral to endoplasmic reticulum membrane	GO:GO:0030176	0.002427	0.001108	0.004244	0.005401
peptide cross-linking	GO:GO:0018149	0.002427	0.000505	0.000646	0.000808
cytosolic small ribosomal subunit (sensu Eukaryota)	GO:GO:0005843	0.002427	0.012195	0.005726	0.001866
purinergic nucleotide receptor activity, G-protein coupled	GO:GO:0045028	0.002427	0.003509	0.001875	0.002748
calcium- and calmodulin-dependent protein kinase activity	GO:GO:0004685	0.002427	0.000505	0.000142	0.000762
regulation of Ras protein signal transduction	GO:GO:0046578	0.002427	0.002057	0.000101	0
transcription-coupled nucleotide-excision repair	GO:GO:0006283	0.002427	0.000505	0.000372	0.000184
connexon complex	GO:GO:0005922	0.002427	0.000807	0.000716	0.000387
'de novo' IMP biosynthesis	GO:GO:0006189	0.002427	0.00662	0.000492	0
methylenetetrahydrofolate dehydrogenase (NADP+) activity	GO:GO:0004488	0.002427	0.001737	0.000404	0.000367
glutamate biosynthesis	GO:GO:0006537	0.002427	0.001108	0.001118	0.000118
rRNA export from nucleus	GO:GO:0006407	0.002427	0.002057	0.000389	0
flap endonuclease activity	GO:GO:0048256	0.002427	0.002667	0.000259	0.000149
nucleoside metabolism	GO:GO:0009116	0.002427	0.001755	0.001872	0.000994
enzyme activator activity	GO:GO:0008047	0.002427	0.002667	0.004294	0.005401
regulation of lipid metabolism	GO:GO:0019216	0.002427	0.001435	0.000481	0.000758
aster	GO:GO:0005818	0.002427	0.001435	0	0
re-entry into mitotic cell cycle	GO:GO:0000320	0.002427	0.001108	0.000866	0.000362
metal ion transporter activity	GO:GO:0046873	0.002427	0.001435	0.001381	0.000638
apical plasma membrane	GO:GO:0016324	0.002427	0.006318	0.004221	0.007968
ribonuclease P activity	GO:GO:0004526	0.002427	0.000505	0.000853	0.00019
androgen receptor signaling pathway	GO:GO:0030521	0.002427	0.001108	0.002108	0.001421
Ran GTPase activator activity	GO:GO:0005098	0.002427	0.000807	0.000361	0.000247
positive regulation of transcription	GO:GO:0045941	0.002427	0.007606	0.005912	0.007696
prolyl aminopeptidase activity	GO:GO:0016804	0.002427	0.001755	0.000107	0
dynein binding	GO:GO:0045502	0.002427	0.001435	0.000704	0.000541
gene silencing	GO:GO:0016458	0.002427	0.003208	0.000242	0.000395
negative regulation of DNA replication	GO:GO:0008156	0.002427	0.002667	0.000558	0.000619
vesicle fusion	GO:GO:0006906	0.002427	0.000807	0.00151	0.00082
lipid biosynthesis	GO:GO:0008610	0.002427	0.007419	0.009152	0.005383
embryonic limb morphogenesis	GO:GO:0030326	0.002427	0.00234	0.002845	0.002708
tryptophan metabolism	GO:GO:0006568	0.002427	0.000505	0.00016	0.000449
positive regulation of inflammatory response	GO:GO:0050729	0.002427	0.000505	0.001273	0.001044
stearoyl-CoA 9-desaturase activity	GO:GO:0004768	0.002427	0.000505	0.001409	0.000851

tropomyosin binding	GO:GO:0005523	0.002427	0.002358	0.000879	0.001039
eukaryotic initiation factor 4E binding	GO:GO:0008190	0.002427	0.000807	0.000617	0.0001
FAD binding	GO:GO:0050660	0.002427	0.000807	0.00247	0.003554
AMP deaminase activity	GO:GO:0003876	0.002427	0.000505	0.000426	0.000446
DNA polymerase processivity factor activity	GO:GO:0030337	0.002427	0.002057	0.000716	0
protein polymerization	GO:GO:0051258	0.002427	0.00266	0.001554	0.00224
deoxyribonucleoside diphosphate metabolism	GO:GO:0009186	0.002427	0.002987	0.00029	0.000267
positive transcription elongation factor activity	GO:GO:0008159	0.002427	0.000505	0.001114	0.00058
PCNA complex	GO:GO:0043626	0.002427	0.002057	0.000656	0
positive regulation of cell adhesion	GO:GO:0045785	0.002427	0.000505	6.42E-05	0.000846
viral capsid assembly	GO:GO:0019069	0.002427	0.003208	0.000302	0
cation:chloride symporter activity	GO:GO:0015377	0.002427	0.005388	0.00087	0.00055
snoRNA binding	GO:GO:0030515	0.002427	0.00141	0.001007	0.000398
spermine biosynthesis	GO:GO:0006597	0.002427	0.000505	0.000385	9.15E-05
strand invasion	GO:GO:0042148	0.002427	0.001435	9.19E-05	0.000249
nuclear envelope lumen	GO:GO:0005641	0.002427	0.000505	0.000587	0.000715
lateral plasma membrane	GO:GO:0016328	0.002427	0.000807	0.00058	0.000634
UV protection	GO:GO:0009650	0.002427	0.001737	0.000481	0.000149
polyribonucleotide nucleotidyltransferase activity	GO:GO:0004654	0.002427	0.000505	8.85E-05	0
response to toxin	GO:GO:0009636	0.002427	0.000505	0.001543	0.002586
receptor signaling complex scaffold activity	GO:GO:0030159	0.002427	0.002057	0.00044	0.000916
pyrimidine ribonucleoside triphosphate biosynthesis	GO:GO:0009209	0.002427	0.001737	0.000656	0.000596
protein phosphatase inhibitor activity	GO:GO:0004864	0.002427	0.002057	0.000729	0.000701
protein amino acid O-linked glycosylation	GO:GO:0006493	0.002427	0.003208	0.00179	0.001606
caspase activation	GO:GO:0006919	0.002427	0.00234	0.002998	0.001197
telomere maintenance via recombination	GO:GO:0000722	0.002427	0.001435	0.000216	0.00033
rhythmic process	GO:GO:0048511	0.002427	0.000505	0.001018	0.001873
odontogenesis (sensu Vertebrata)	GO:GO:0042475	0.002427	0.001108	0.002761	0.001774
dopamine uptake	GO:GO:0051583	0.002427	0.000505	0.000225	0
ESC/E(Z) complex	GO:GO:0035098	0.002427	0.003307	0.000509	0.000385
protein amino acid N-linked glycosylation via asparagine	GO:GO:0018279	0.002427	0.000505	0.001244	0.000658
citrate metabolism	GO:GO:0006101	0.002427	0.000505	0.00058	0.000665
DNA ligase (NAD+) activity	GO:GO:0003911	0.002427	0.000505	0.000227	0
defense response to pathogenic bacteria, incompatible interaction	GO:GO:0009816	0.002427	0.003208	0.000217	0.000184
carrier activity	GO:GO:0005386	0.002427	0.006318	0.005494	0.006211
chorion gene amplification	GO:GO:0007307	0.002427	0.004237	0.000627	0.000293
RNA localization	GO:GO:0006403	0.002427	0.000905	0.001374	0.00059
ubiquitin binding	GO:GO:0043130	0.002427	0.002358	0.000962	0.001883
exocytosis	GO:GO:0006887	0.002427	0.003289	0.004045	0.005014
adenosine deaminase activity	GO:GO:0004000	0.002427	0.000505	0.000696	0.000362
translation elongation factor activity	GO:GO:0003746	0.002427	0.006275	0.004644	0.002666
regulation of body size	GO:GO:0040014	0.002427	0.000505	0.002119	0.00246
skeletal development	GO:GO:0001501	0.002427	0.005106	0.00764	0.009935
protein import into nucleus, translocation	GO:GO:0000060	0.002427	0.002642	0.001513	0.000497
negative regulation of neuron apoptosis	GO:GO:0043524	0.002427	0.001712	0.001413	0.001551

epidermal growth factor receptor binding	GO:GO:0005154	0.002427	0.000807	0.000854	0.001012
cytosolic ribosome (sensu Eukaryota)	GO:GO:0005830	0.002427	0.014401	0.009978	0.002584
tumor necrosis factor receptor activity	GO:GO:0005031	0.002427	0.000505	0.000273	0.000276
positive regulation of nitric-oxide synthase activity	GO:GO:0051000	0.002427	0.000505	0	0.000289
protein amino acid N-linked glycosylation	GO:GO:0006487	0.002427	0.001435	0.001945	0.002674
cell septum	GO:GO:0030428	0.002427	0.000807	0.000436	5.66E-05
oligosaccharide biosynthesis	GO:GO:0009312	0.002427	0.000505	0.000642	0.000914
sarcomere	GO:GO:0030017	0.002427	0.000807	0.00122	0.001303
vacuole (sensu Fungi)	GO:GO:0000324	0.002427	0.002039	0.000641	0.000849
myo-inositol metabolism	GO:GO:0006020	0.002427	0.000505	0.000199	0.000389
pronucleus	GO:GO:0045120	0.002427	0.004539	0.00118	0.000542
prefoldin complex	GO:GO:0016272	0.002427	0.003208	0.000767	0.000425
lipoate-protein ligase B activity	GO:GO:0016978	0.002427	0.001755	0.000222	0.000148
heteroduplex formation	GO:GO:0030491	0.002427	0.001435	9.19E-05	0.000249
protein targeting to lysosome	GO:GO:0006622	0.002427	0.000505	0.000585	0.000402
gastric acid secretion	GO:GO:0001696	0.002427	0.000505	0.000135	0.0001
protein homooligomerization	GO:GO:0051260	0.002427	0.000505	0.001681	0.00189
regulation of axonogenesis	GO:GO:0050770	0.002427	0.00444	0.000786	0.001161
ureteric bud branching	GO:GO:0001658	0.002427	0.00591	0.001567	0.00135
ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	GO:GO:0015662	0.002427	0.001435	0.002208	0.002769
regulation of bone mineralization	GO:GO:0030500	0.002427	0.000505	0.000241	0.000369
cytokinesis after mitosis	GO:GO:0000281	0.002427	0.001737	0.000211	0.000267
positive regulation of mitosis	GO:GO:0045840	0.002427	0.002667	0.000749	0.000684
response to virus	GO:GO:0009615	0.002427	0.002358	0.002719	0.004995
DNA topoisomerase activity	GO:GO:0003916	0.002427	0.005345	0.001536	0.000521
mannose binding	GO:GO:0005537	0.002427	0.000807	0.000481	0.000603
neuron projection	GO:GO:0043005	0.002427	0.001435	0.001988	0.003284
regulation of synaptic transmission	GO:GO:0050804	0.002427	0.000505	0.000129	0.000356
ceramide metabolism	GO:GO:0006672	0.002427	0.000505	0.000776	0.00125
SLIK (SAGA-like) complex	GO:GO:0046695	0.002427	0.002057	0.001245	0.000341
transmembrane receptor protein tyrosine phosphatase activity	GO:GO:0005001	0.002427	0.001737	0.000879	0.001972
synaptic transmission	GO:GO:0007268	0.002427	0.00234	0.005297	0.014005
primary spermatocyte growth	GO:GO:0007285	0.002427	0.000505	3.47E-05	0
tubulin binding	GO:GO:0015631	0.002427	0.002987	0.000919	0.000684
protein kinase C activity	GO:GO:0004697	0.002427	0.000505	0.000787	0.001743
Barr body	GO:GO:0001740	0.002427	0.000905	0.001192	0.000502
amino acid transport	GO:GO:0006865	0.002427	0.005388	0.002764	0.003406
sulfur amino acid biosynthesis	GO:GO:0000097	0.002427	0.000505	6.42E-05	0
induction of positive chemotaxis	GO:GO:0050930	0.002427	0.000505	0.000538	0.00096
recombinase activity	GO:GO:0000150	0.002427	0.001435	0.000181	0.00033
protein-hormone receptor activity	GO:GO:0016500	0.002427	0.001755	0.0002	0.00033
galactose metabolism	GO:GO:0006012	0.002427	0.000505	0.000644	0.001152
protein kinase cascade	GO:GO:0007243	0.002427	0.001435	0.005276	0.007724
blastoderm segmentation	GO:GO:0007350	0.002427	0.001737	0.000855	0.00053
M phase specific microtubule process	GO:GO:0000072	0.002427	0.00141	0.000651	0.000671
cysteine dioxygenase activity	GO:GO:0017172	0.002427	0.000505	6.42E-05	0
vacuolar lumen (sensu Fungi)	GO:GO:0000328	0.002427	0.001108	0.000535	0.000451

nuclear matrix	GO:GO:0016363	0.002427	0.00537	0.001796	0.000704
STAT protein nuclear translocation	GO:GO:0007262	0.002427	0.000807	0.000943	0.00075
neutral amino acid transporter activity	GO:GO:0015175	0.002427	0.001435	0.00111	0.001496
axonemal dynein complex	GO:GO:0005858	0.002427	0	0.000381	0.000339
insulin-like growth factor receptor signaling pathway	GO:GO:0048009	0.002427	0.000807	0.000729	0.000543
DNA replication checkpoint	GO:GO:0000076	0.002427	0.001737	0.0011	0.000704
heterochromatin	GO:GO:0000792	0.002427	0.003892	0.002091	0.001778
olfactory receptor activity	GO:GO:0004984	0.002427	0.000505	0.000202	0.000634
clathrin vesicle coat	GO:GO:0030125	0.002427	0.000505	0.002543	0.002865
G1 phase of mitotic cell cycle	GO:GO:0000080	0.002427	0.005991	0.002005	0.001088
nucleotide kinase activity	GO:GO:0019201	0.002427	0.002057	0.000944	0.001228
Rho protein signal transduction	GO:GO:0007266	0.002427	0.001712	0.003215	0.005862
hydrolase activity, hydrolyzing O-glycosyl compounds	GO:GO:0004553	0.002427	0.000505	0.002204	0.002076
indoleamine-pyrrole 2,3-dioxygenase activity	GO:GO:0004426	0.002427	0.000505	6.42E-05	0.000392
embryonic eye morphogenesis	GO:GO:0048048	0.002427	0.00234	0.001345	0.000628
exosome (RNase complex)	GO:GO:0000178	0.002427	0.004335	0.004733	0.003425
B cell differentiation	GO:GO:0030183	0.002427	0.000807	0.000764	0.001006
alpha-beta T cell activation	GO:GO:0046631	0.002427	0.000505	8.67E-05	0.000353
cadherin binding	GO:GO:0045296	0.002427	0.001108	0.000177	0.000664
cell redox homeostasis	GO:GO:0045454	0.002427	0.00391	0.002281	0.000517
angiogenesis	GO:GO:0001525	0.002427	0.002039	0.00892	0.010058
negative regulation of protein biosynthesis	GO:GO:0017148	0.002427	0.000807	0.000619	0.000369
nuclear inner membrane	GO:GO:0005637	0.002427	0.004539	0.002159	0.00112
TATA-binding protein binding	GO:GO:0017025	0.002427	0.002358	0.001379	0.000151
bleomycin hydrolase activity	GO:GO:0008423	0.002427	0.000505	0.000359	0
cobalt ion binding	GO:GO:0050897	0.002427	0.001435	0.001255	0.001285
mitotic spindle organization and biogenesis	GO:GO:0007052	0.002427	0.002057	0.00082	0.000456
hydroxymethyl-, formyl- and related transferase activity	GO:GO:0016742	0.002427	0.000807	0.000239	0.000246
fin regeneration	GO:GO:0031101	0.002427	0.000807	0.000376	0.0001
gamma-aminobutyric acid signaling pathway	GO:GO:0007214	0.002427	0.005388	0.001009	0.001329
adenylate kinase activity	GO:GO:0004017	0.002427	0.002057	0.000885	0.000533
female pronucleus	GO:GO:0001939	0.002427	0	0.00028	0.000118
linoleoyl-CoA desaturase activity	GO:GO:0016213	0.002427	0.000505	0.000336	0
multidimensional cell growth	GO:GO:0009825	0.002427	0.000505	0.000404	0.000619
synaptic transmission, glutamatergic	GO:GO:0035249	0.002427	0.000505	6.5E-05	5.66E-05
snoRNP binding	GO:GO:0030519	0.002427	0.001737	0.000577	0.000184
biosynthesis	GO:GO:0009058	0.002427	0.003811	0.00445	0.003322
phosphoribosylamine-glycine ligase activity	GO:GO:0004637	0.002427	0.000807	0.000357	0
chaperone binding	GO:GO:0051087	0.002427	0.001108	0.001073	0.000163
ATPase activity, coupled	GO:GO:0042623	0.002427	0.00141	0.001709	0.000483
negative regulation of neuron differentiation	GO:GO:0045665	0.002427	0.002642	0.002785	0.001122
cell migration	GO:GO:0016477	0.002427	0.001737	0.00378	0.006862
cell projection biogenesis	GO:GO:0030031	0.002427	0.000807	0.001013	0.001901
nucleoside triphosphate biosynthesis	GO:GO:0009142	0.002427	0.001435	0.000296	0
meiotic chromosome segregation	GO:GO:0045132	0.002427	0.000505	0.000375	0.000341
negative regulation of translational initiation	GO:GO:0045947	0.002427	0.000807	0.00058	0.000319
cell wall (sensu Fungi)	GO:GO:0009277	0.002427	0.003208	0.002139	0.000659
Golgi medial cisterna	GO:GO:0005797	0.002427	0.000505	0.00052	0.00093

paraxial mesoderm development	GO:GO:0048339	0.002427	0.000505	0.000126	0
L-serine catabolism	GO:GO:0006565	0.002427	0.001755	0.000423	0
actin filament polymerization	GO:GO:0030041	0.002427	0.000807	0.001744	0.003513
main pathways of carbohydrate metabolism	GO:GO:0006092	0.002427	0.001108	0.001138	0.000743
male genitalia development	GO:GO:0030539	0.002427	0.000807	0.000651	0.000566
sex chromatin	GO:GO:0001739	0.002427	0.001755	0.000955	0.000118
protein disulfide isomerase activity	GO:GO:0003756	0.002427	0.000807	0.000677	0.000972
nuclear heterochromatin	GO:GO:0005720	0.002427	0.000807	0.001454	0.000959
oxidoreductase activity, acting on iron-sulfur proteins as donors	GO:GO:0016730	0.002427	0	3.29E-05	0.000308
Nup107-160 complex	GO:GO:0031080	0.002427	0.000807	0.000266	0
peptidyl-threonine phosphorylation	GO:GO:0018107	0.002427	0.001755	0.000892	6.41E-05
polynucleotide adenylyltransferase activity	GO:GO:0004652	0.002427	0.001755	0.00053	0.000683
L-cysteine catabolism to taurine	GO:GO:0019452	0.002427	0.000505	0.000277	0
regulation of JAK-STAT cascade	GO:GO:0046425	0.002427	0.000505	0.000582	5.66E-05
positive regulation of smooth muscle cell proliferation	GO:GO:0048661	0.002427	0.000505	0.000833	0.00043
chromatin silencing	GO:GO:0006342	0.002427	0.001755	0.001041	0.000667
dynein complex	GO:GO:0030286	0.002427	0.000302	0.001298	0.001332
delta DNA polymerase activity	GO:GO:0003891	0.002427	0.004237	0.000532	0.000477
nucleosome	GO:GO:0000786	0.002427	0.006632	0.004317	0.003977
ribonucleoside-diphosphate reductase complex	GO:GO:0005971	0.002427	0.003509	0.000442	0.000118
auxin polar transport	GO:GO:0009926	0.002427	0.001737	0.000562	9.87E-05
female meiosis chromosome segregation	GO:GO:0016321	0.002427	0.000505	0.000174	0.000118
insoluble fraction	GO:GO:0005626	0.002427	0.003296	0.002908	0.003999
pyrimidine nucleotide biosynthesis	GO:GO:0006221	0.002427	0.001755	0.001741	0.000544
cortical actin cytoskeleton	GO:GO:0030864	0.002427	0.001737	0.001385	0.001551
vasodilation	GO:GO:0042311	0.002427	0.000505	0.000696	0.0001
glucose metabolism	GO:GO:0006006	0.002427	0.004759	0.00221	0.003733
gap junction	GO:GO:0005921	0.002427	0.000807	0.000867	0.000478
urogenital system development	GO:GO:0001655	0.002427	0.004458	0.000553	0.000157
carboxypeptidase activity	GO:GO:0004180	0.002427	0.000505	0.002086	0.004052
neuroblast proliferation (sensu Vertebrata)	GO:GO:0043350	0.002427	0.000807	0.000383	0.000151
extracellular matrix structural constituent	GO:GO:0005201	0.002427	0.004528	0.00497	0.007423
entry of virus into host cell	GO:GO:0046718	0.002427	0.000505	0.000688	0.000683
telomere cap complex	GO:GO:0000782	0.002427	0	6.42E-05	0
regulation of cell migration	GO:GO:0030334	0.002427	0.001737	0.004167	0.004015
septation initiation signaling	GO:GO:0031028	0.002427	0.001435	0.000347	0.000267
chloroplast	GO:GO:0009507	0.002427	0.00537	0.001812	0.001246
cytoplasmic dynein complex	GO:GO:0005868	0.002427	0.000302	0.000467	0.001234
response to pathogenic fungi	GO:GO:0009621	0.002427	0.000505	0.000225	0
regulation of smooth muscle contraction	GO:GO:0006940	0.002427	0.001435	0.000512	0.000398
hyperosmotic response	GO:GO:0006972	0.002427	0.005388	0.000629	0.00063
regulation of mitosis	GO:GO:0007088	0.002427	0.00359	0.00124	0.000958
protein oligomerization	GO:GO:0051259	0.002427	0.000505	0.000685	0.00056
dicarboxylic acid transport	GO:GO:0006835	0.002427	0.000505	0.000569	0.000742
positive regulation of embryonic development	GO:GO:0040019	0.002427	0.000505	0.000476	5.66E-05
deoxyribonuclease activity	GO:GO:0004536	0.002427	0.001435	0.000329	0.000297
negative regulation of transforming growth factor beta receptor signaling pathway	GO:GO:0030512	0.002427	0.002057	0.000396	0.000192

nucleoside-diphosphatase activity	GO:GO:0017110	0.002427	0.000505	0.000662	0.002213
ribosome assembly	GO:GO:0042255	0.002427	0.002057	0.000805	0.0001
exodeoxyribonuclease activity	GO:GO:0004529	0.002427	0.001737	0.000321	0.000149
connexon channel activity	GO:GO:0015285	0.002427	0.000807	0.000716	0.000387
5'-3' exonuclease activity	GO:GO:0008409	0.002427	0.002667	0.000323	0.000149
metallochaperone activity	GO:GO:0016530	0.002427	0.003208	0.000233	0.000364
protein amino acid acetylation	GO:GO:0006473	0.002427	0.002057	0.00079	0.000755
insulin-like growth factor binding protein complex	GO:GO:0016942	0.002427	0.000505	0.000228	0.00032
transcription elongation factor complex	GO:GO:0008023	0.002427	0.000505	0.00229	0.001358
fatty acid metabolism	GO:GO:0006631	0.002427	0.000505	0.006838	0.007509
nuclear outer membrane	GO:GO:0005640	0.002427	0.000505	0.000597	0.000798
chaperonin-containing T-complex	GO:GO:0005832	0.002427	0.002962	0.002852	0.000389
adult somatic muscle development	GO:GO:0007527	0.002427	0.000505	0.000442	0.000326
serine-type endopeptidase inhibitor activity	GO:GO:0004867	0.002427	0.001737	0.004779	0.007979
S-adenosylmethionine metabolism	GO:GO:0046500	0.002427	0.002366	0.000559	0.000903
purine ribonucleoside monophosphate biosynthesis	GO:GO:0009168	0.002427	0.000505	0.000435	0.000411
central element	GO:GO:0000801	0.002427	0.003208	0.000347	0
cell junction	GO:GO:0030054	0.002427	0.000807	0.000718	0.000818
mitotic checkpoint	GO:GO:0007093	0.002427	0.001108	0.000764	0.000802
DNA topological change	GO:GO:0006265	0.002427	0.003289	0.001705	0.000521
pyrimidine nucleotide binding	GO:GO:0019103	0.002427	0.000505	0.000101	0.000149
protein phosphatase type 1 regulator activity	GO:GO:0008599	0.002427	0.002057	0.001093	0.000481
cAMP-mediated signaling	GO:GO:0019933	0.002427	0.000807	0.000624	0.001736
fat cell differentiation	GO:GO:0045444	0.002427	0.000807	0.001552	0.001235
nucleoside diphosphate kinase activity	GO:GO:0004550	0.002427	0.001737	0.001167	0.000832
response to oxidative stress	GO:GO:0006979	0.002427	0.004175	0.009496	0.01168
glutamate-5-semialdehyde dehydrogenase activity	GO:GO:0004350	0.002427	0.000505	3.29E-05	0
Cajal body	GO:GO:0015030	0.002427	0.000807	0.001286	0.000213
nuclear localization sequence binding	GO:GO:0008139	0.002427	0.005043	0.001443	0.000667
insulin receptor binding	GO:GO:0005158	0.002427	0.000505	0.000838	0.000804
protein localization	GO:GO:0008104	0.002427	0.006293	0.004082	0.002638
DNA-directed RNA polymerase II, core complex	GO:GO:0005665	0.002427	0.000807	0.001092	0.000963
site of polarized growth	GO:GO:0030427	0.002427	0.000807	0.000607	0.000577
response to antibiotic	GO:GO:0046677	0.002427	0.000505	0.000386	0.000708
purine base metabolism	GO:GO:0006144	0.002427	0.000505	0.000706	0.00103
dense fibrillar component	GO:GO:0001651	0.002427	0.001108	0.000655	0.000113
transmembrane receptor activity	GO:GO:0004888	0.002427	0.003289	0.004343	0.008346
lamin binding	GO:GO:0005521	0.002427	0.003289	0.000783	0.000534
amino acid-polyamine transporter activity	GO:GO:0005279	0.002427	0.005388	0.001883	0.001174
cysteine metabolism	GO:GO:0006534	0.002427	0.000505	0.000437	0.000589
protein amino acid terminal N-glycosylation	GO:GO:0006496	0.002427	0.000505	0.00024	0.000155
malate metabolism	GO:GO:0006108	0.002427	0	0.000577	0.000575
negative regulation of signal transduction	GO:GO:0009968	0.002427	0.000505	0.003425	0.003525
endocytic vesicle	GO:GO:0030139	0.002427	0.000505	0.001529	0.001744
autophagy	GO:GO:0006914	0.002427	0.000807	0.001572	0.002698
positive regulation of transcription, DNA-dependent	GO:GO:0045893	0.002427	0.006349	0.008374	0.007112

hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	GO:GO:0016814	0.002427	0.000505	0.000167	0.000659
nuclear membrane	GO:GO:0031965	0.002427	0.000807	0.000874	0.000313
regulation of cyclin-dependent protein kinase activity	GO:GO:0000079	0.002427	0.00234	0.002824	0.002775
L-cysteine metabolism	GO:GO:0046439	0.002427	0.000505	6.42E-05	0
Hsp70 protein binding	GO:GO:0030544	0.002427	0.001108	0.000747	0.000516
cell communication	GO:GO:0007154	0.002427	0.002039	0.002577	0.000987
zinc ion transporter activity	GO:GO:0005385	0.002427	0.001435	0.001529	0.001757
telomeric 3' overhang formation	GO:GO:0031860	0.002427	0	6.42E-05	0
GMP biosynthesis	GO:GO:0006177	0.002427	0.002987	0.000535	0.00029
response to methylmercury	GO:GO:0051597	0.002427	0.002366	0.001651	0.001428
transaminase activity	GO:GO:0008483	0.002427	0.000807	0.002665	0.001185
chemokine receptor binding	GO:GO:0042379	0.002427	0.000505	0	0
circulation	GO:GO:0008015	0.002427	0.000505	0.002103	0.005877
tryptophanyl-tRNA aminoacylation	GO:GO:0006436	0.002427	0.000505	0.000426	9.15E-05
malate dehydrogenase (decarboxylating) activity	GO:GO:0004471	0.002427	0	0.000235	5.66E-05
lamellipodium	GO:GO:0030027	0.002427	0.005018	0.006951	0.007132
lipid metabolism	GO:GO:0006629	0.002427	0.015092	0.016106	0.023396
catecholamine biosynthesis	GO:GO:0042423	0.002427	0.000505	0.000143	0.000951
spermidine biosynthesis	GO:GO:0008295	0.002427	0.000505	0.000887	0.00029
proximal/distal pattern formation	GO:GO:0009954	0.002427	0.001737	0.000174	0.000199
epsilon DNA polymerase complex	GO:GO:0008622	0.002427	0.002667	0.000457	0.000149
NuRD complex	GO:GO:0016581	0.002427	0.001712	0.001418	0.000389
regulation of protein amino acid phosphorylation	GO:GO:0001932	0.002427	0.000505	0.000786	0.000861
mannosyltransferase activity	GO:GO:0000030	0.002427	0.000505	0.000202	0.000405
protein kinase activator activity	GO:GO:0030295	0.002427	0.000505	0.000584	0.000722
sodium:potassium:chloride symporter activity	GO:GO:0008511	0.002427	0.005388	0.000423	5.66E-05
rRNA binding	GO:GO:0019843	0.002427	0.006374	0.004217	0.000278
chromatin assembly complex	GO:GO:0005678	0.002427	0.002057	0.00112	0.000262
ribulose-phosphate 3-epimerase activity	GO:GO:0004750	0.002427	0.000505	7.18E-05	0
transmembrane receptor protein tyrosine phosphatase signaling pathway	GO:GO:0007185	0.002427	0.001737	0.00264	0.003322
negative regulation of vasodilation	GO:GO:0045908	0.002427	0.000505	4.23E-05	0.000479
positive regulation of cell volume	GO:GO:0045795	0.002427	0.005388	0.000382	0
vesicular fraction	GO:GO:0042598	0.002427	0.000505	0.000492	0.000113
phosphoric monoester hydrolase activity	GO:GO:0016791	0.002427	0.000505	0.001135	0.00085
phosphoenolpyruvate carboxykinase (GTP) activity	GO:GO:0004613	0.002427	0.000505	0.00019	0.000157
axonogenesis	GO:GO:0007409	0.002427	0.00266	0.004528	0.004988
metal ion transport	GO:GO:0030001	0.002427	0.001435	0.001705	0.000638
double-strand break repair via single-strand annealing	GO:GO:0045002	0.002427	0.001435	0.000152	0.00033
neuron migration	GO:GO:0001764	0.002427	0.002944	0.006081	0.005092
transcription initiation	GO:GO:0006352	0.002427	0.003289	0.001365	0.000796
response to cadmium ion	GO:GO:0046686	0.002427	0.001435	0.001871	0.001613
N-methyltransferase activity	GO:GO:0008170	0.002427	0.002667	0.000836	0.000885

release of cytoplasmic sequestered NF-kappaB	GO:GO:0008588	0.002427	0.000505	0.000477	0.000123
regulation of DNA replication initiation	GO:GO:0030174	0.002427	0.002057	0.000222	0
large ribosomal subunit	GO:GO:0015934	0.002427	0.003892	0.004048	0.000849
calcium-activated potassium channel activity	GO:GO:0015269	0.002427	0.005068	0.000196	0.000592
procollagen-proline 4-dioxygenase activity	GO:GO:0004656	0.002427	0.000505	0.000532	0.001054
cation transport	GO:GO:0006812	0.002427	0.002366	0.004087	0.007374
S-methyl-5-thioadenosine phosphorylase activity	GO:GO:0017061	0.002427	0.000505	0.000102	0
mitotic nuclear envelope reassembly	GO:GO:0007084	0.002427	0.002358	0.000746	0.000802
histone methyltransferase activity	GO:GO:0042054	0.002427	0.003608	0.000888	0.000639
negative regulation of retinal programmed cell death	GO:GO:0046671	0.002427	0.000807	0.000647	0.000197
galactokinase activity	GO:GO:0004335	0.002427	0.000505	0.000369	0.0001
regulation of stomatal movement	GO:GO:0010119	0.002427	0.001737	0.000362	9.87E-05
phosphatidate phosphatase activity	GO:GO:0008195	0.002427	0.000505	0.000217	0.000399
regulation of muscle contraction	GO:GO:0006937	0.002427	0.000505	0.002061	0.003677
lactation	GO:GO:0007595	0.002427	0.001435	0.000946	0.001158
SWI/SNF complex	GO:GO:0016514	0.002427	0.001737	0.001447	0.000817
sodium:dicarboxylate symporter activity	GO:GO:0017153	0.002427	0.000505	0.000569	0.000742
nuclear lamina	GO:GO:0005652	0.002427	0.003289	0.001198	0.000367
locomotory behavior	GO:GO:0007626	0.002427	0.000505	0.002003	0.003695
poly(A) binding	GO:GO:0008143	0.002427	0.005043	0.001672	0.000349
norepinephrine metabolism	GO:GO:0042415	0.002427	0.000505	6.5E-05	0
nucleotide-excision repair	GO:GO:0006289	0.002427	0.004201	0.002789	0.000804
peptidyl-prolyl cis-trans isomerase activity	GO:GO:0003755	0.002427	0.007216	0.005948	0.002156
positive regulation of cell migration	GO:GO:0030335	0.002427	0.002685	0.001298	0.000733
MAP kinase kinase kinase activity	GO:GO:0004709	0.002427	0.000505	0.00086	0.00021
fatty acid desaturation	GO:GO:0006636	0.002427	0.000505	0.000484	0.000249
fatty acid elongation, unsaturated fatty acid	GO:GO:0019368	0.002427	0.000505	0.000382	0.000333
mRNA splice site selection	GO:GO:0006376	0.002427	0.006268	0.003658	0.001717
protection from non-homologous end joining at telomere	GO:GO:0031848	0.002427	0	6.42E-05	0
35S primary transcript processing	GO:GO:0006365	0.002427	0.003165	0.001304	0.001013
positive regulation of epidermal growth factor receptor signaling pathway	GO:GO:0045742	0.002427	0.002057	0.000101	0
auxiliary transport protein activity	GO:GO:0015457	0.002427	0.000807	0.000383	0.000184
oocyte maturation	GO:GO:0001556	0.002427	0.001737	0.000405	0.001359
positive regulation of progression through cell cycle	GO:GO:0045787	0.002427	0.001737	0.000643	0.00024
RNA helicase activity	GO:GO:0003724	0.002427	0.006613	0.003042	0.001028
nucleocytoplasmic shuttling complex	GO:GO:0031074	0.002427	0.002057	0.000101	0
lamellipodium biogenesis	GO:GO:0030032	0.002427	0.000505	0.002541	0.002293
ribonuclease MRP activity	GO:GO:0000171	0.002427	0.001435	0.000473	9.87E-05
nuclear speck	GO:GO:0016607	0.002427	0.001108	0.001652	0.000412
GTP biosynthesis	GO:GO:0006183	0.002427	0.001737	0.001328	0.001348
nuclear telomeric heterochromatin	GO:GO:0005724	0.002427	0	6.42E-05	0
deaminase activity	GO:GO:0019239	0.002427	0.000505	0.000435	0.000411
skeletal muscle growth	GO:GO:0048630	0.002427	0.000505	2.67E-05	0.00032
histone ubiquitination	GO:GO:0016574	0.002427	0.000505	0.00066	6.41E-05

nuclear envelope-endoplasmic reticulum network	GO:GO:0042175	0.002427	0.002057	0.001344	0.000934
1,3-beta-glucanosyltransferase activity	GO:GO:0042124	0.002427	0.003208	0.000959	0
DNA-(apurinic or apyrimidinic site) lyase activity	GO:GO:0003906	0.002427	0.002987	0.001014	0.000302
3'-5'-exoribonuclease activity	GO:GO:0000175	0.002427	0.002685	0.00109	0
sodium ion binding	GO:GO:0031402	0.002427	0.006195	0.003458	0.005586
phosphoglycerate dehydrogenase activity	GO:GO:0004617	0.002427	0	0.000367	0.0001
diacylglycerol biosynthesis	GO:GO:0006651	0.002427	0.000505	0.000189	0.000915
nuclear envelope reassembly	GO:GO:0031468	0.002427	0.002057	0.000498	0.000367
response to stress	GO:GO:0006950	0.002427	0.005469	0.00822	0.00943
spindle stabilization	GO:GO:0043146	0.002427	0.000505	6.42E-05	0
protein import into mitochondrial matrix	GO:GO:0030150	0.002427	0.000807	0.000403	0
oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor	GO:GO:0016652	0.002427	0.001108	0.001098	0.00045
negative regulation of coagulation	GO:GO:0050819	0.002427	0.000505	0.000755	0.000978
nitric-oxide synthase regulator activity	GO:GO:0030235	0.002427	0.003811	0.001217	0.000431
chaperonin-mediated tubulin folding	GO:GO:0007022	0.002427	0.00266	0.001221	0
synaptic vesicle endocytosis	GO:GO:0048488	0.002427	0.000807	0.001061	0.000781
origin recognition complex	GO:GO:0000808	0.002427	0.000505	0.000516	9.15E-05
Rac guanyl-nucleotide exchange factor activity	GO:GO:0030676	0.002427	0.000505	6.42E-05	0.000294
G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	GO:GO:0007200	0.002427	0.000505	0.001654	0.001579
transcription from mitochondrial promoter	GO:GO:0006390	0.002427	0.001755	0.000289	0.000303
L-serine transporter activity	GO:GO:0015194	0.002427	0.000505	0.00039	9.87E-05
double-strand break repair	GO:GO:0006302	0.002427	0.003899	0.00157	0.000551
transcription factor TFIID complex	GO:GO:0005669	0.002427	0.002057	0.001013	0.000335
sensory perception of smell	GO:GO:0007608	0.002427	0.001755	0.001193	0.001404
actin filament organization	GO:GO:0007015	0.002427	0.003909	0.003943	0.007371
potassium channel activity	GO:GO:0005267	0.002427	0.004138	0.001923	0.005935
embryonic cleavage	GO:GO:0040016	0.002427	0.003289	0.000691	0.000647
positive regulation of phosphoinositide 3-kinase activity	GO:GO:0043552	0.002427	0.000807	0.000511	0.000556
nuclear telomere cap complex	GO:GO:0000783	0.002427	0	0.000128	0
centrosome cycle	GO:GO:0007098	0.002427	0.005444	0.001635	0.001107
sensory perception	GO:GO:0007600	0.002427	0.000505	0.002682	0.005916
enzyme binding	GO:GO:0019899	0.002427	0.001737	0.002408	0.003179
double-stranded telomeric DNA binding	GO:GO:0003691	0.002427	0.000505	6.42E-05	0
axial mesoderm development	GO:GO:0048318	0.002427	0.000505	6E-05	0
hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	GO:GO:0016820	0.002427	0.000807	0.003121	0.003676
actin nucleation	GO:GO:0045010	0.002427	0.000505	0.000376	0.000971
oogenesis (sensu Insecta)	GO:GO:0009993	0.002427	0.004219	0.002556	0.001001
neuromuscular synaptic transmission	GO:GO:0007274	0.002427	0.000807	0.000932	0.001175
long-chain-fatty-acid-CoA ligase activity	GO:GO:0004467	0.002427	0.000505	0.000592	0.001382
tRNA aminoacylation for protein translation	GO:GO:0006418	0.002427	0.006392	0.007193	0.002543
spliceosome assembly	GO:GO:0000245	0.002427	0.004759	0.002443	0.000437
DNA topoisomerase (ATP-hydrolyzing) activity	GO:GO:0003918	0.002427	0.003289	0.001577	0.000323

muscle thin filament tropomyosin	GO:GO:0005862	0.002427	0.000505	0.00055	0.000971
taurine biosynthesis	GO:GO:0042412	0.002427	0.000505	0.000277	0
enoyl-[acyl-carrier protein] reductase activity	GO:GO:0016631	0.002427	0	0.000128	5.66E-05
phosphodiesterase I activity	GO:GO:0004528	0.002427	0.002057	0.000958	0.000629
mitotic centrosome separation	GO:GO:0007100	0.002427	0.000807	0.000309	0.000267
ribonucleoside monophosphate biosynthesis	GO:GO:0009156	0.002427	0.001755	0.000449	0.000148
pyrimidine dimer repair via nucleotide-excision repair	GO:GO:0000720	0.002427	0.000505	0.000119	0
cyclin catabolism	GO:GO:0008054	0.002427	0.00327	0.001483	0.000704
general RNA polymerase II transcription factor activity	GO:GO:0016251	0.002427	0.002358	0.0018	0.001544
metanephros development	GO:GO:0001656	0.002427	0.000505	0.001002	0.001413
inner cell mass cell proliferation	GO:GO:0001833	0.002427	0.000302	0.00063	0.00058
taurine metabolism	GO:GO:0019530	0.002427	0.000505	0.000277	0
lung development	GO:GO:0030324	0.002427	0.00359	0.003925	0.003711
growth cone	GO:GO:0030426	0.002427	0.00141	0.002166	0.003378
inositol or phosphatidylinositol phosphatase activity	GO:GO:0004437	0.002427	0.003208	0.001404	0.002357
polyamine metabolism	GO:GO:0006595	0.002427	0.000807	0.000653	0.000512
hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity	GO:GO:0005062	0.002427	0.000505	0.000121	0.000895
NLS-bearing substrate import into nucleus	GO:GO:0006607	0.002427	0.006293	0.001409	0.000666
monovalent inorganic cation transporter activity	GO:GO:0015077	0.002427	0.000505	0.000683	0.000647
asparagine synthase (glutamine-hydrolyzing) activity	GO:GO:0004066	0.002427	0.000807	0.000102	0.000643
viral envelope	GO:GO:0019031	0.002427	0.000505	0.000267	0.000913
traversing start control point of mitotic cell cycle	GO:GO:0007089	0.002427	0.001435	0.000293	0.000121
glutathione metabolism	GO:GO:0006749	0.002427	0.000807	0.002131	0.003006
negative regulation of blood coagulation	GO:GO:0030195	0.002427	0.000505	9.79E-05	0.000379
galactoside binding	GO:GO:0016936	0.002427	0.000505	4.08E-05	0
protein binding, bridging	GO:GO:0030674	0.002427	0.004822	0.003682	0.004399
histone methylation	GO:GO:0016571	0.002427	0.003608	0.001432	0.001685
Rho GTPase activator activity	GO:GO:0005100	0.002427	0.000505	0.000346	0.000943
structural constituent of chromatin	GO:GO:0030527	0.002427	0.004113	0.001294	0.000267
negative regulation of non-apoptotic programmed cell death	GO:GO:0043072	0.002427	0.002057	0.000101	0
cyclin-dependent protein kinase activity	GO:GO:0004693	0.002427	0.008455	0.002737	0.001771
response to UV-C	GO:GO:0010225	0.002427	0.000505	0.000119	0
condensin complex	GO:GO:0000796	0.002427	0.004113	0.000442	0.000118
secretory pathway	GO:GO:0045045	0.002427	0.00266	0.003623	0.003269
mitochondrial DNA replication	GO:GO:0006264	0.002427	0.001755	0.000346	5.66E-05
protein C (activated) activity	GO:GO:0003808	0.002427	0.000505	6.5E-05	0.000315
ruffle	GO:GO:0001726	0.002427	0.001108	0.003563	0.003875
RNA-3'-phosphate cyclase activity	GO:GO:0003963	0.002427	0.000505	0.000391	9.87E-05
RNA metabolism	GO:GO:0016070	0.002427	0.002057	0.001765	0.000856
acyltransferase activity	GO:GO:0008415	0.002427	0.00694	0.009046	0.009026
bud neck	GO:GO:0005935	0.002427	0.000807	0.000278	0.000205
cytokinesis by cell plate formation	GO:GO:0000911	0.002427	0.000505	0.000362	0.000521

regulation of progression through mitotic cell cycle	GO:GO:0007346	0.002427	0.002969	0.001547	0.001522
sphingosine metabolism	GO:GO:0006670	0.002427	0.000505	0.000348	0.00061
calcium-mediated signaling	GO:GO:0019722	0.002427	0.002039	0.001304	0.002032
negative regulation of phosphorylation	GO:GO:0042326	0.002427	0.000505	9.79E-05	0.00037
kinetochore assembly	GO:GO:0051382	0.002427	0.001435	3.29E-05	0.0001
manganese ion transport	GO:GO:0006828	0.002427	0.003208	0.000297	0.000364
leucyl aminopeptidase activity	GO:GO:0004178	0.002427	0.000505	0.000416	0
isocitrate dehydrogenase (NAD+) activity	GO:GO:0004449	0.002427	0.001108	0.001128	0.00045
phosphotransferase activity, alcohol group as acceptor	GO:GO:0016773	0.002427	0.002057	0.002416	0.002208
morphogenesis	GO:GO:0009653	0.002427	0.002039	0.003461	0.003587
regulation of circadian sleep/wake cycle, sleep	GO:GO:0045187	0.002427	0.000505	0.000526	0.001095
oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	GO:GO:0016717	0.002427	0.000505	0.00117	0.000676
glutamate 5-kinase activity	GO:GO:0004349	0.002427	0.000505	3.29E-05	0
thymidine kinase activity	GO:GO:0004797	0.002427	0.001737	0.000461	0.000339
malic enzyme activity	GO:GO:0004470	0.002427	0	0.000321	0.000326
5'-flap endonuclease activity	GO:GO:0017108	0.002427	0.002667	0.000259	0.000205
positive regulation of nitric oxide biosynthesis	GO:GO:0045429	0.002427	0.000505	8.57E-05	0.000916
rRNA modification	GO:GO:0000154	0.002427	0.002987	0.000736	0.00043
transferase activity, transferring pentosyl groups	GO:GO:0016763	0.002427	0.002358	0.000723	0.000175
alpha DNA polymerase activity	GO:GO:0003889	0.002427	0.000807	0.000101	0.000149
regulation of protein secretion	GO:GO:0050708	0.002427	0.000505	0.000343	0.00063
mitochondrial nucleoid	GO:GO:0042645	0.002427	0.000807	0.000394	0.000118
regulation of osteoblast differentiation	GO:GO:0045667	0.002427	0.002057	0.000346	0.000684
cell cycle arrest	GO:GO:0007050	0.002427	0.008012	0.006012	0.007003
synaptonemal complex	GO:GO:0000795	0.002427	0.003208	0.000734	0
mating projection tip	GO:GO:0043332	0.002427	0.000807	0.00064	0.000779
WW domain binding	GO:GO:0050699	0.002427	0.000807	0.000675	9.87E-05
inositol trisphosphate 3-kinase activity	GO:GO:0008440	0.002427	0.000505	0.000237	0.000484
embryonic development	GO:GO:0009790	0.002427	0.002013	0.004893	0.003076
response to ethylene stimulus	GO:GO:0009723	0.002427	0.001737	0.000233	0.000155
L-serine transport	GO:GO:0015825	0.002427	0.000505	0.00039	9.87E-05
inositol or phosphatidylinositol kinase activity	GO:GO:0004428	0.002427	0.000505	0.000658	0.0009
mRNA binding	GO:GO:0003729	0.002427	0.009735	0.010122	0.003485
tight junction	GO:GO:0005923	0.002427	0.000807	0.004289	0.006816
adenosylmethionine decarboxylase activity	GO:GO:0004014	0.002427	0.000505	0.000385	9.15E-05
water channel activity	GO:GO:0015250	0.002427	0.003005	0.000368	0.000962
cell plate	GO:GO:0009504	0.002427	0.000807	0.000255	0.000247
voltage-gated ion channel activity	GO:GO:0005244	0.002427	0.005061	0.003746	0.007314
microtubule depolymerization	GO:GO:0007019	0.002427	0.002057	0.000315	0.000371
DNA ligase activity	GO:GO:0003909	0.002427	0.000807	0.000283	0.000118
response to amphetamine	GO:GO:0001975	0.002427	0.000505	0.000373	0.000781
digestion	GO:GO:0007586	0.002427	0.000505	0.000922	0.003812

neuromuscular junction	GO:GO:0031594	0.002427	0.000505	0.000412	0.000538
tyrosine phosphorylation of STAT protein	GO:GO:0007260	0.002427	0.000807	0.000943	0.00075
phenylethanolamine N-methyltransferase activity	GO:GO:0004603	0.002427	0.000505	0	0.000348
peroxisome	GO:GO:0005777	0.002427	0.000807	0.007214	0.009609
aminoacyl-tRNA ligase activity	GO:GO:0004812	0.002427	0.007322	0.008588	0.0026
positive regulation of vasodilation	GO:GO:0045909	0.002427	0.000505	6.75E-05	0.000822
regulation of neurotransmitter secretion	GO:GO:0046928	0.002427	0.000505	0.000256	0.001017
response to heat	GO:GO:0009408	0.002427	0.002013	0.005353	0.003849
voltage-gated potassium channel activity	GO:GO:0005249	0.002427	0.006841	0.002012	0.004674
hormone-mediated signaling	GO:GO:0009755	0.002427	0.002057	0.000464	0
insulin receptor signaling pathway	GO:GO:0008286	0.002427	0.001108	0.003185	0.00173
elevation of cytosolic calcium ion concentration during G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	GO:GO:0051482	0.002427	0.000505	0.000477	0.000278
intracellular transport	GO:GO:0046907	0.002427	0.003811	0.003815	0.003987
vacuolar protein catabolism	GO:GO:0007039	0.002427	0.000807	0.000419	0.000323
male pronucleus	GO:GO:0001940	0.002427	0	0.000188	0.000118
fatty acid synthase complex	GO:GO:0005835	0.002427	0	0.000128	5.66E-05
nitric oxide biosynthesis	GO:GO:0006809	0.002427	0.004113	0.00127	0.001891
negative regulation of insulin receptor signaling pathway	GO:GO:0046627	0.002427	0.000505	0.000904	0.001555
troponin C binding	GO:GO:0030172	0.002427	0.002057	0.000202	0.000267
CTP synthase activity	GO:GO:0003883	0.002427	0.001755	0.000531	0.000248
lymphocyte differentiation	GO:GO:0030098	0.002427	0.002057	0.001367	0.000596
hydrogen:potassium-exchanging ATPase activity	GO:GO:0008900	0.002427	0.000505	0.000135	0.0001
microvillus	GO:GO:0005902	0.002427	0.00266	0.001829	0.003408
protein secretion	GO:GO:0009306	0.002427	0.001108	0.001169	0.001517
oligodendrocyte differentiation	GO:GO:0048709	0.002427	0.000807	0.000955	0.000323
double-stranded RNA binding	GO:GO:0003725	0.002427	0.002039	0.002816	0.002465
glyoxylate cycle	GO:GO:0006097	0.002427	0.001108	0.000972	0.000175
tubulin	GO:GO:0045298	0.002427	0.002358	0.000848	0.000983
IMP dehydrogenase activity	GO:GO:0003938	0.002427	0.002987	0.000446	0.00029
guard cell differentiation	GO:GO:0010052	0.002427	0.000505	0.000362	0.000521
S-adenosylhomocysteine metabolism	GO:GO:0046498	0.002427	0.002366	0.000869	0.000903
synaptic transmission, dopaminergic	GO:GO:0001963	0.002427	0.000505	0.000287	0.000592
tubulin folding	GO:GO:0007021	0.002427	0.002962	0.002721	0.000816
ribonuclease MRP complex	GO:GO:0000172	0.002427	0.001435	0.000473	9.87E-05
growth factor binding	GO:GO:0019838	0.002427	0.001108	0.002354	0.002256
ubiquitin protein ligase binding	GO:GO:0031625	0.002427	0.000807	0.000519	0.000361
COPII vesicle coat	GO:GO:0030127	0.002427	0.000505	0.000992	0.000448
CTP biosynthesis	GO:GO:0006241	0.002427	0.001737	0.001167	0.000832
gluconeogenesis	GO:GO:0006094	0.002427	0.001755	0.003011	0.004673
very-long-chain fatty acid biosynthesis	GO:GO:0042761	0.002427	0.000505	0.000446	0.000333
DNA (cytosine-5-)-methyltransferase activity	GO:GO:0003886	0.002427	0.002987	0.000496	0.000275
epinephrine biosynthesis	GO:GO:0042418	0.002427	0.000505	0	0.000348
tryptophan catabolism to kynurenine	GO:GO:0019441	0.002427	0.000505	6.42E-05	0.000392
ribosomal protein import into nucleus	GO:GO:0006610	0.002427	0.002057	0.001382	0

G1/S-specific transcription in mitotic cell cycle	GO:GO:0000083	0.002427	0.000505	0.000487	0.000175
SRP-dependent cotranslational protein targeting to membrane	GO:GO:0006614	0.002427	0.002057	0.000939	0.000982
positive regulation of cytokine secretion	GO:GO:0050715	0.002427	0.000505	0.000124	0.000621
cell organization and biogenesis	GO:GO:0016043	0.002427	0.000505	0.000303	0.000699
negative regulation of protein catabolism	GO:GO:0042177	0.002427	0.000505	0.000341	0.000387
G1-specific transcription in mitotic cell cycle	GO:GO:0000114	0.002427	0.002057	0.000823	0.000897
anti-inflammatory response	GO:GO:0030236	0.002427	0.000505	0.000474	0.000692
methylenetetrahydrofolate dehydrogenase (NAD+) activity	GO:GO:0004487	0.002427	0.000807	0.000292	0.000367
phosphoserine transaminase activity	GO:GO:0004648	0.002427	0.000505	0.000263	5.66E-05
isocitrate metabolism	GO:GO:0006102	0.002427	0.001108	0.000807	0.000118
calcineurin complex	GO:GO:0005955	0.002427	0.001737	0.000656	0.000518
regulation of signal transduction	GO:GO:0009966	0.002427	0.003492	0.001301	0.001137
two-component signal transduction system (phosphorelay)	GO:GO:0000160	0.002427	0.002039	0.00392	0.003162
carbohydrate phosphorylation	GO:GO:0046835	0.002427	0.000505	0.000628	0.000337
complement activation	GO:GO:0006956	0.002427	0.000505	0.000884	0.002261
protein kinase C activation	GO:GO:0007205	0.002427	0.002039	0.001211	0.000937
eye morphogenesis (sensu Vertebrata)	GO:GO:0048593	0.002427	0.000807	0.000696	0.000249
base-excision repair, gap-filling	GO:GO:0006287	0.002427	0.003608	0.001082	0.000149
fertilization (sensu Metazoa)	GO:GO:0007338	0.002427	0.000505	0.001071	0.000458
zinc ion transport	GO:GO:0006829	0.002427	0.001435	0.001529	0.001757
response to UV-B	GO:GO:0010224	0.002427	0.000505	0.000247	0.000175
N-acetyltransferase activity	GO:GO:0008080	0.002427	0.003509	0.002296	0.001823
asparagine biosynthesis	GO:GO:0006529	0.002427	0.000807	0.000102	0.000643
RNA destabilization	GO:GO:0050779	0.002427	0.000505	0.000343	0.000594
positive regulation of cell motility	GO:GO:0051272	0.002427	0.003289	0.001229	0.000697
carboxypeptidase C activity	GO:GO:0004186	0.002427	0.000807	0.000415	0.000759
epsilon DNA polymerase activity	GO:GO:0003893	0.002427	0.002667	0.000457	0.000149
meiotic joint molecule formation	GO:GO:0000709	0.002427	0.001435	9.19E-05	0.000249
protein complex assembly	GO:GO:0006461	0.002427	0.004397	0.006612	0.006694
acetylglucosaminyltransferase activity	GO:GO:0008375	0.002427	0.000505	0.001431	0.001685
sensory perception of sound	GO:GO:0007605	0.002427	0.001108	0.00367	0.003545
cell-substrate junction assembly	GO:GO:0007044	0.002427	0.001435	0.000758	0.001438
protein catabolism	GO:GO:0030163	0.002427	0.002962	0.004158	0.002197
protein-glutamine gamma-glutamyltransferase activity	GO:GO:0003810	0.002427	0.000505	0.000477	0.000359
phosphoribosylformylglycinamidine cyclo-ligase activity	GO:GO:0004641	0.002427	0.000807	0.000239	0
visual perception	GO:GO:0007601	0.002427	0.002642	0.004815	0.006792
water transport	GO:GO:0006833	0.002427	0.003005	0.000402	0.000962
peptidyl-serine phosphorylation	GO:GO:0018105	0.002427	0.001755	0.000826	0.00065
regulation of protein import into nucleus	GO:GO:0042306	0.002427	0.000505	0.000711	0.000451
DNA topoisomerase complex (ATP-hydrolyzing)	GO:GO:0009330	0.002427	0.002987	0.000472	0.000323
hemostasis	GO:GO:0007599	0.002427	0.000505	0.000616	0.001329
chromatin remodeling complex	GO:GO:0016585	0.002427	0.002358	0.000769	9.15E-05
regulation of cell redox homeostasis	GO:GO:0030503	0.002427	0.002057	0.001593	0.001286
rRNA methyltransferase activity	GO:GO:0008649	0.002427	0.001755	0.000474	0.000246

positive regulation of abscisic acid mediated signaling	GO:GO:0009789	0.002427	0.001737	0.000233	9.87E-05
double-stranded DNA specific exodeoxyribonuclease activity	GO:GO:0008309	0.002427	0.001737	0.000193	0.000149
isocitrate dehydrogenase (NADP+) activity	GO:GO:0004450	0.002427	0.001108	0.001055	0.000569
establishment of mitotic spindle localization	GO:GO:0040001	0.002427	0.001737	0.000335	0.000267
inner kinetochore of condensed chromosome	GO:GO:0000939	0.002427	0.001737	0.000364	0.0001
positive regulation of long-term neuronal synaptic plasticity	GO:GO:0048170	0.002427	0.004138	0	9.87E-05
vacuole	GO:GO:0005773	0.002427	0.000505	0.001852	0.002519
endocytosis	GO:GO:0006897	0.002427	0.000505	0.008729	0.012264
GDP binding	GO:GO:0019003	0.002427	0.000505	0.000132	0.000488
purine base biosynthesis	GO:GO:0009113	0.002427	0.000807	0.000329	0
lymphocyte proliferation	GO:GO:0046651	0.002427	0.002987	0.000605	0.000382
integrin complex	GO:GO:0008305	0.002427	0.000807	0.002115	0.00317
tRNA splicing	GO:GO:0006388	0.002427	0.000807	0.000408	0.000118
transcription initiation from mitochondrial promoter	GO:GO:0006391	0.002427	0.001755	0.000151	5.66E-05
phosphoribosylglycinamide formyltransferase activity	GO:GO:0004644	0.002427	0.000807	0.000239	0
superoxide metabolism	GO:GO:0006801	0.002427	0.000505	0.002162	0.001967
double-strand break repair via synthesis-dependent strand annealing	GO:GO:0045003	0.002427	0.001435	0.000152	0.00033
negative regulation of protein kinase activity	GO:GO:0006469	0.002427	0.000807	0.002139	0.003935
activation of NF-kappaB transcription factor	GO:GO:0051092	0.002427	0.002057	0.002033	0.001833
alpha-glucan biosynthesis	GO:GO:0030979	0.002427	0.000505	0.00019	0
alpha-1,6-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity	GO:GO:0008455	0.002427	0.000505	0.00024	0.000155
Rho GTPase binding	GO:GO:0017048	0.002427	0.000807	0.000961	0.001177
sphingolipid biosynthesis	GO:GO:0030148	0.002427	0.001737	0.000351	0.00061
negative regulation of microtubule polymerization	GO:GO:0031115	0.002427	0.002057	0.000225	0
DNA ligase (ATP) activity	GO:GO:0003910	0.002427	0.000807	0.000556	0.000118
mRNA editing	GO:GO:0006381	0.002427	0.003608	0.00107	0.001325
smoothened signaling pathway	GO:GO:0007224	0.002427	0.000505	0.001555	0.001534
histone binding	GO:GO:0042393	0.002427	0.001108	0.001357	0.000599
adenosine metabolism	GO:GO:0046085	0.002427	0.000505	0.00033	5.66E-05
mitotic metaphase/anaphase transition	GO:GO:0007091	0.002427	0.002642	0.001747	0.001954
pentose-phosphate shunt	GO:GO:0006098	0.002427	0.000807	0.002513	0.002341
DNA primase activity	GO:GO:0003896	0.002427	0.003005	0.000942	0.000445
uracil DNA N-glycosylase activity	GO:GO:0004844	0.002427	0.000603	0.000457	0.000442
negative regulation of angiogenesis	GO:GO:0016525	0.002427	0.001435	0.002032	0.001556
regulation of Cdc42 GTPase activity	GO:GO:0043088	0.002427	0.000505	0.000362	0.000521
branching morphogenesis of a tube	GO:GO:0048754	0.002427	0.002358	0.001966	0.001226
negative regulation of mitotic metaphase/anaphase transition	GO:GO:0045841	0.002427	0.001737	0.000358	0.000267
mitotic G2 checkpoint	GO:GO:0007095	0.002427	0.000807	0.00026	0.000358
actin filament binding	GO:GO:0051015	0.002427	0.006903	0.003325	0.007249
glucose transport	GO:GO:0015758	0.002427	0.003811	0.001256	0.003192

negative regulation of actin filament polymerization	GO:GO:0030837	0.002427	0.000505	6.5E-05	0.000315
dolichyl-phosphate-mannose-protein mannosyltransferase activity	GO:GO:0004169	0.002427	0.000505	8.32E-05	0
mammary gland development	GO:GO:0030879	0.002427	0.001435	0.000893	0.000747
calcium-dependent protein serine/threonine phosphatase regulator activity	GO:GO:0008597	0.002427	0.001737	0.000233	9.87E-05
cysteine protease inhibitor activity	GO:GO:0004869	0.002427	0.002039	0.002492	0.003287
sex determination	GO:GO:0007530	0.002427	0.002039	0.00031	0.000118
snRNP protein import into nucleus	GO:GO:0006608	0.002427	0.001755	0.000328	0