

Supplementary Table 1

Term	Count	%		Term	Count	%	
GO:0005622~intracellular	571	74.44		GO:0006631~fatty acid metabolic process	18	2.346	
GO:0044424~intracellular part	555	72.35		GO:0006633~fatty acid biosynthetic process	8	1.043	
GO:0043226~organelle	525	68.44		GO:0006636~unsaturated fatty acid biosynthetic process	4	0.521	
GO:0043227~membrane-bounded organelle	486	63.36		GO:0072330~monocarboxylic acid biosynthetic process	9	1.173	
GO:0043231~intracellular membrane-bounded organelle	440	57.36		GO:0033559~unsaturated fatty acid metabolic process	6	0.782	
GO:0043229~intracellular organelle	479	62.45		GO:0008610~lipid biosynthetic process	21	2.737	
GO:0005737~cytoplasm	427	55.67		GO:0046394~carboxylic acid biosynthetic process	10	1.303	
GO:0005623~cell	622	81.09		GO:0016053~organic acid biosynthetic process	10	1.303	
GO:0044464~cell part	620	80.83		GO:0044283~small molecule biosynthetic process	17	2.216	
Term	Count	%		Term	Count	%	
GO:0043167~ion binding	191	24.90		GO:0038061~NIK/NF-kappaB signaling	4	0.521	
GO:0043169~cation binding	182	23.72		GO:1901224~positive regulation of NIK/NF-kappaB signaling	3	0.391	
GO:0046872~metal ion binding	179	23.33		GO:1901222~regulation of NIK/NF-kappaB signaling	3	0.391	
GO:0046914~transition metal ion binding	79	10.29					
Term	Count	%		Term	Count	%	
GO:0005634~nucleus	274	35.72		GO:0016835~carbon-oxygen lyase activity	5	0.651	
GO:0044446~intracellular organelle part	299	38.98		GO:0016836~hydro-lyase activity	4	0.521	
GO:0044422~organelle part	304	39.63		GO:0016829~lyase activity	6	0.782	
GO:0044428~nuclear part	157	20.46					
GO:0043233~organelle lumen	151	19.68		Term	Count	%	
GO:0031974~membrane-enclosed lumen	153	19.94		GO:0006376~mRNA splice site selection	3	0.391	
GO:0070013~intracellular organelle lumen	150	19.55		GO:0016071~mRNA metabolic process	22	2.868	
GO:0031981~nuclear lumen	136	17.73		GO:0000245~spliceosomal complex assembly	4	0.521	
GO:0005654~nucleoplasm	96	12.51		GO:1903311~regulation of mRNA metabolic process	8	1.043	
				GO:0043484~regulation of RNA splicing	7	0.912	
Term	Count	%		GO:0050684~regulation of mRNA processing	6	0.782	
GO:0044237~cellular metabolic process	422	55.01		GO:0008380~RNA splicing	13	1.694	
GO:0044238~primary metabolic process	421	54.88		GO:0048024~regulation of mRNA splicing, via spliceosome	4	0.521	
GO:0071704~organic substance metabolic process	437	56.97		GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	9	1.173	
GO:0008152~metabolic process	453	59.06		GO:0000398~mRNA splicing, via spliceosome	9	1.173	
GO:0043170~macromolecule metabolic process	377	49.15		GO:0000375~RNA splicing, via transesterification reactions	9	1.173	
GO:0044260~cellular macromolecule metabolic process	347	45.24		GO:0006397~mRNA processing	13	1.694	
GO:0006807~nitrogen compound metabolic process	281	36.63					
GO:0010467~gene expression	224	29.20		Term	Count	%	
GO:0034641~cellular nitrogen compound metabolic process	264	34.41		GO:0015748~organophosphate ester transport	6	0.782	
GO:0090304~nucleic acid metabolic process	206	26.85		GO:0015914~phospholipid transport	4	0.521	
GO:0006725~cellular aromatic compound metabolic process	235	30.63		GO:0005548~phospholipid transporter activity	3	0.391	
GO:0019222~regulation of metabolic process	253	32.98		GO:0005319~lipid transporter activity	4	0.521	
GO:0080090~regulation of primary metabolic process	238	31.02					
GO:0031323~regulation of cellular metabolic process	240	31.29		Term	Count	%	
GO:0046483~heterocycle metabolic process	231	30.11		GO:0097186~amelogenesis	3	0.391	
GO:0006139~nucleobase-containing compound metabolic process	226	29.46		GO:0042475~odontogenesis of dentin-containing tooth	5	0.651	
GO:0060255~regulation of macromolecule metabolic process	235	30.63		GO:0042476~odontogenesis	5	0.651	
GO:0010468~regulation of gene expression	173	22.55					
GO:1901360~organic cyclic compound metabolic process	235	30.63		Term	Count	%	
GO:0034645~cellular macromolecule biosynthetic process	200	26.07		GO:0097186~amelogenesis	3	0.391	
GO:0009059~macromolecule biosynthetic process	204	26.59		GO:0042475~odontogenesis of dentin-containing tooth	5	0.651	
GO:0016070~RNA metabolic process	178	23.20		GO:0042476~odontogenesis	5	0.651	
GO:0051171~regulation of nitrogen compound metabolic process	172	22.42					
GO:0019219~regulation of nucleobase-containing compound metabolic process	161	20.99		Term	Count	%	
GO:0051252~regulation of RNA metabolic process	145	18.90		GO:0005912~adherens junction	28	3.650	
GO:0044249~cellular biosynthetic process	232	30.24		GO:0070161~anchoring junction	28	3.650	
GO:0009889~regulation of biosynthetic process	166	21.64		GO:0005911~cell-cell junction	25	3.259	
GO:0009058~biosynthetic process	237	30.89		GO:0005924~cell-substrate adherens junction	17	2.216	
GO:0010556~regulation of macromolecule biosynthetic process	156	20.33		GO:0030055~cell-substrate junction	17	2.216	
GO:0006351~transcription, DNA-templated	124	16.16		GO:0005925~focal adhesion	16	2.086	
GO:2000112~regulation of cellular macromolecule biosynthetic process	151	19.68		GO:0030054~cell junction	48	6.258	
GO:1901576~organic substance biosynthetic process	232	30.24					
GO:2001141~regulation of RNA biosynthetic process	136	17.73		Term	Count	%	
GO:0031326~regulation of cellular biosynthetic process	162	21.12		GO:0048660~regulation of smooth muscle cell proliferation	8	1.043	
GO:1903506~regulation of nucleic acid-templated transcription	135	17.60		GO:0048659~smooth muscle cell proliferation	7	0.912	
GO:0006355~regulation of transcription, DNA-templated	134	17.47		GO:0033002~muscle cell proliferation	9	1.173	
GO:0034654~nucleobase-containing compound biosynthetic process	156	20.33		GO:0048661~positive regulation of smooth muscle cell proliferation	5	0.651	
GO:0018130~heterocycle biosynthetic process	158	20.59					
GO:0019438~aromatic compound biosynthetic process	158	20.59		Term	Count	%	
GO:0032774~RNA biosynthetic process	139	18.12		GO:0042274~ribosomal small subunit biogenesis	6	0.782	
GO:0010604~positive regulation of macromolecule metabolic process	124	16.16		GO:0030490~maturation of SSU-rRNA	4	0.521	
GO:0009893~positive regulation of metabolic process	132	17.20		GO:0000462~maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3	0.391	
GO:0044271~cellular nitrogen compound biosynthetic process	188	24.51					
GO:0097659~nucleic acid-templated transcription	137	17.86		Term	Count	%	
GO:0031325~positive regulation of cellular metabolic process	122	15.90		GO:0034614~cellular response to reactive oxygen species	9	1.173	
GO:1901362~organic cyclic compound biosynthetic process	159	20.73		GO:0034599~cellular response to oxidative stress	13	1.694	
GO:0010628~positive regulation of gene expression	73	9.517		GO:0070301~cellular response to hydrogen peroxide	6	0.782	
GO:0045935~positive regulation of nucleobase-containing compound metabolic process	71	9.256		GO:0000302~response to reactive oxygen species	12	1.564	
GO:0006366~transcription from RNA polymerase II promoter	72	9.387		GO:0042542~response to hydrogen peroxide	8	1.043	
GO:0051173~positive regulation of nitrogen compound metabolic process	74	9.647		GO:0006979~response to oxidative stress	18	2.346	
GO:0051254~positive regulation of RNA metabolic process	59	7.692					
GO:0006357~regulation of transcription from RNA polymerase II promoter	74	9.647		Term	Count	%	
GO:1902680~positive regulation of RNA biosynthetic process	56	7.301		GO:0031984~organelle subcompartment	13	1.694	
GO:0045893~positive regulation of transcription, DNA-templated	56	7.301		GO:0098791~Golgi subcompartment	12	1.564	
GO:1903508~positive regulation of nucleic acid-templated transcription	56	7.301		GO:0005802~trans-Golgi network	8	1.043	
GO:0009891~positive regulation of biosynthetic process	71	9.256		GO:0005795~Golgi stack	5	0.651	
GO:0010557~positive regulation of macromolecule biosynthetic process	64	8.344					
GO:0031328~positive regulation of cellular biosynthetic process	68	8.865		Term	Count	%	
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	42	5.475		GO:0048857~neural nucleus development	5	0.651	
				GO:0030901~midbrain development	5	0.651	
Term	Count	%		GO:0021762~substantia nigra development	3	0.391	
GO:0019222~regulation of metabolic process	253	32.98					
GO:0080090~regulation of primary metabolic process	238	31.02		Term	Count	%	
GO:0031323~regulation of cellular metabolic process	240	31.29		GO:0035091~phosphatidylinositol binding	11	1.434	
GO:0048519~negative regulation of biological process	197	25.68		GO:1901981~phosphatidylinositol phosphate binding	7	0.912	
GO:0048523~negative regulation of cellular process	184	23.98		GO:0005543~phospholipid binding	13	1.694	
GO:0009892~negative regulation of metabolic process	111	14.47		GO:0008289~lipid binding	22	2.868	
GO:0031324~negative regulation of cellular metabolic process	104	13.55					
GO:0010605~negative regulation of macromolecule metabolic process	101	13.16		Term	Count	%	
				GO:0044427~chromosomal part	37	4.823	
Term	Count	%		GO:0005694~chromosome	40	5.215	
GO:1901265~nucleoside phosphate binding	111	14.47		GO:0044454~nuclear chromosome part	22	2.868	
GO:0000166~nucleotide binding	111	14.47		GO:0000228~nuclear chromosome	22	2.868	
GO:0036094~small molecule binding	118	15.38		GO:0000785~chromatin	14	1.825	
GO:0032555~purine ribonucleotide binding	88	11.47		GO:0000790~nuclear chromatin	8	1.043	
GO:0035639~purine ribonucleoside triphosphate binding	86	11.21					
GO:0017076~purine nucleotide binding	88	11.47		Term	Count	%	
GO:0032550~purine ribonucleoside binding	86	11.21		GO:0007167~enzyme linked receptor protein signaling pathway	40	5.215	
GO:0001883~purine nucleoside binding	86	11.21		GO:0007179~transforming growth factor beta receptor signaling pathway	8	1.043	
GO:0032549~ribonucleoside binding	86	11.21		GO:0071560~cellular response to transforming growth factor beta stimulus	11	1.434	
GO:0032553~ribonucleotide binding	88	11.47		GO:0071559~response to transforming growth factor beta	11	1.434	
GO:0001882~nucleoside binding	86	11.21		GO:0071363~cellular response to growth factor stimulus	27	3.520	
GO:1901363~heterocyclic compound binding	233	30.37		GO:0070848~response to growth factor	28	3.650	
GO:0032559~adenyl ribonucleotide binding	70	9.126		GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	14	1.825	
GO:0030554~adenyl nucleotide binding	70	9.126		GO:0030512~negative regulation of transforming growth factor beta receptor signaling pathway	3	0.391	
GO:0005524~ATP binding	68	8.865		GO:1903845~negative regulation of cellular response to transforming growth factor beta stimulus	3	0.391	
GO:0097367~carbohydrate derivative binding	98	12.77		GO:0090092~regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	8	1.043	
GO:0097159~organic cyclic compound binding	233	30.37		GO:0017015~regulation of transforming growth factor beta receptor signaling pathway	4	0.521	
GO:0016772~transferase activity, transferring phosphorus-containing groups	47	6.127		GO:0090288~negative regulation of cellular response to growth factor stimulus	5	0.651	
GO:0016301~kinase activity	37	4.823		GO:1903844~regulation of cellular response to transforming growth factor beta stimulus	4	0.521	
GO:0046777~protein autophosphorylation	12	1.564		GO:0090101~negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	4	0.521	
GO:0016773~phosphotransferase activity, alcohol group as acceptor	30	3.911		GO:0090287~regulation of cellular response to growth factor stimulus	8	1.043	
GO:0004674~protein serine/threonine kinase activity	18	2.346					
GO:0004672~protein kinase activity	25	3.259					

Term	Count	%		Term	Count	%	
GO:0071840~cellular component organization or biogenesis	263	34.28		GO:0006692~prostanoid metabolic process	3	0.391	
GO:0044085~cellular component biogenesis	131	17.07		GO:0006693~prostaglandin metabolic process	3	0.391	
GO:0071822~protein complex subunit organization	74	9.647		GO:0033559~unsaturated fatty acid metabolic process	6	0.782	
GO:0016043~cellular component organization	248	32.33		GO:0006690~icosanoid metabolic process	4	0.521	
GO:0022607~cellular component assembly	115	14.99					
GO:0043933~macromolecular complex subunit organization	105	13.68					
GO:0051259~protein oligomerization	32	4.172		Term	Count	%	
GO:0006461~protein complex assembly	65	8.474		GO:0030520~intracellular estrogen receptor signaling pathway	4	0.521	
GO:0070271~protein complex biogenesis	65	8.474		GO:0033146~regulation of intracellular estrogen receptor signaling pathway	3	0.391	
GO:0065003~macromolecular complex assembly	75	9.778		GO:0030518~intracellular steroid hormone receptor signaling pathway	6	0.782	
GO:0043623~cellular protein complex assembly	24	3.129		GO:0030522~intracellular receptor signaling pathway	10	1.303	
GO:0034622~cellular macromolecular complex assembly	39	5.084		GO:0009755~hormone-mediated signaling pathway	9	1.173	
				GO:0071383~cellular response to steroid hormone stimulus	11	1.434	
Term	Count	%		GO:0043401~steroid hormone mediated signaling pathway	6	0.782	
GO:1902589~single-organism organelle organization	86	11.21		GO:0033143~regulation of intracellular steroid hormone receptor signaling pathway	3	0.391	
GO:0007010~cytoskeleton organization	62	8.083					
GO:0030036~actin cytoskeleton organization	31	4.041		Term	Count	%	
GO:0006996~organelle organization	148	19.29		GO:0032612~interleukin-1 production	6	0.782	
				GO:0032611~interleukin-1 beta production	5	0.651	
Term	Count	%		GO:0032755~positive regulation of interleukin-6 production	4	0.521	
GO:0048365~Rac GTPase binding	7	0.912		GO:0032675~regulation of interleukin-6 production	4	0.521	
GO:0017048~Rho GTPase binding	10	1.303		GO:0032635~interleukin-6 production	4	0.521	
GO:0017016~Ras GTPase binding	16	2.086		GO:0002831~regulation of response to biotic stimulus	6	0.782	
GO:0031267~small GTPase binding	16	2.086					
GO:0051020~GTPase binding	17	2.216					
				Term	Count	%	
Term	Count	%		GO:0014070~response to organic cyclic compound	59	7.692	
GO:0006396~RNA processing	40	5.215		GO:0010033~response to organic substance	129	16.81	
GO:0034470~ncRNA processing	21	2.737		GO:0009605~response to external stimulus	97	12.64	
GO:0006364~rRNA processing	14	1.825		GO:0071310~cellular response to organic substance	90	11.73	
GO:0016072~rRNA metabolic process	14	1.825		GO:1901698~response to nitrogen compound	50	6.518	
GO:0022613~ribonucleoprotein complex biogenesis	26	3.389		GO:1901700~response to oxygen-containing compound	77	10.03	
GO:0042254~ribosome biogenesis	18	2.346		GO:0010243~response to organonitrogen compound	45	5.867	
GO:0034660~ncRNA metabolic process	23	2.998		GO:0071495~cellular response to endogenous stimulus	53	6.910	
				GO:0070887~cellular response to chemical stimulus	104	13.55	
Term	Count	%		GO:0032870~cellular response to hormone stimulus	28	3.650	
GO:0032446~protein modification by small protein conjugation	42	5.475		GO:0009719~response to endogenous stimulus	72	9.387	
GO:0016567~protein ubiquitination	38	4.954		GO:1901699~cellular response to nitrogen compound	26	3.389	
GO:0019787~ubiquitin-like protein transferase activity	25	3.259		GO:0008286~insulin receptor signaling pathway	5	0.651	
GO:0070647~protein modification by small protein conjugation or removal	45	5.867		GO:1901653~cellular response to peptide	14	1.825	
GO:0004842~ubiquitin-protein transferase activity	24	3.129		GO:1901701~cellular response to oxygen-containing compound	42	5.475	
GO:0061630~ubiquitin protein ligase activity	11	1.434		GO:0071417~cellular response to organonitrogen compound	22	2.868	
GO:0061659~ubiquitin-like protein ligase activity	11	1.434		GO:0033993~response to lipid	45	5.867	
GO:0000209~protein polyubiquitination	10	1.303		GO:0009725~response to hormone	39	5.084	
				GO:0071375~cellular response to peptide hormone stimulus	11	1.434	
Term	Count	%		GO:0048545~response to steroid hormone	18	2.346	
GO:0044260~cellular macromolecule metabolic process	347	45.24		GO:1900076~regulation of cellular response to insulin stimulus	3	0.391	
GO:0019222~regulation of metabolic process	253	32.98		GO:0032869~cellular response to insulin stimulus	7	0.912	
GO:0080090~regulation of primary metabolic process	238	31.02		GO:1901652~response to peptide	18	2.346	
GO:0031323~regulation of cellular metabolic process	240	31.29		GO:0032868~response to insulin	8	1.043	
GO:0043412~macromolecule modification	173	22.55		GO:0043434~response to peptide hormone	14	1.825	
GO:0007166~cell surface receptor signaling pathway	111	14.47		GO:0042221~response to chemical	159	20.73	
GO:0060255~regulation of macromolecule metabolic process	235	30.63					
GO:0048583~regulation of response to stimulus	155	20.20		Term	Count	%	
GO:0042325~regulation of phosphorylation	76	9.908		GO:0045746~negative regulation of Notch signaling pathway	3	0.391	
GO:0001932~regulation of protein phosphorylation	70	9.126		GO:0008593~regulation of Notch signaling pathway	4	0.521	
GO:0048518~positive regulation of biological process	230	29.98		GO:0007219~Notch signaling pathway	7	0.912	
GO:0019220~regulation of phosphate metabolic process	84	10.95					
GO:0051174~regulation of phosphorus metabolic process	84	10.95		Term	Count	%	
GO:0035556~intracellular signal transduction	115	14.99		GO:0001667~ameboidal-type cell migration	17	2.216	
GO:0019538~protein metabolic process	233	30.37		GO:1901343~negative regulation of vasculature development	6	0.782	
GO:0036211~protein modification process	159	20.73		GO:0030334~regulation of cell migration	32	4.172	
GO:0006464~cellular protein modification process	159	20.73		GO:0043535~regulation of blood vessel endothelial cell migration	4	0.521	
GO:0006796~phosphate-containing compound metabolic process	135	17.60		GO:1901342~regulation of vasculature development	12	1.564	
GO:0006793~phosphorus metabolic process	135	17.60		GO:0030336~negative regulation of cell migration	11	1.434	
GO:0031399~regulation of protein modification process	81	10.56		GO:0045766~positive regulation of angiogenesis	7	0.912	
GO:0016310~phosphorylation	101	13.16		GO:2000181~negative regulation of blood vessel morphogenesis	5	0.651	
GO:0051246~regulation of protein metabolic process	117	15.25		GO:0010633~negative regulation of epithelial cell migration	4	0.521	
GO:0044267~cellular protein metabolic process	205	26.72		GO:2000146~negative regulation of cell motility	11	1.434	
GO:0006468~protein phosphorylation	84	10.95		GO:0051271~negative regulation of cellular component movement	12	1.564	
GO:0006351~transcription, DNA-templated	124	16.16		GO:0010596~negative regulation of endothelial cell migration	3	0.391	
GO:0032268~regulation of cellular protein metabolic process	108	14.08		GO:0040013~negative regulation of locomotion	12	1.564	
GO:0043408~regulation of MAPK cascade	38	4.954		GO:0045765~regulation of angiogenesis	10	1.303	
GO:0009966~regulation of signal transduction	112	14.60		GO:1904018~positive regulation of vasculature development	7	0.912	
GO:0048522~positive regulation of cellular process	203	26.46		GO:0043542~endothelial cell migration	7	0.912	
GO:0010604~positive regulation of macromolecule metabolic process	124	16.16		GO:0010631~epithelial cell migration	10	1.303	
GO:1902531~regulation of intracellular signal transduction	73	9.517		GO:0090132~epithelium migration	10	1.303	
GO:0009893~positive regulation of metabolic process	132	17.20		GO:0043534~blood vessel endothelial cell migration	4	0.521	
GO:0051247~positive regulation of protein metabolic process	70	9.126		GO:0090130~tissue migration	10	1.303	
GO:0065009~regulation of molecular function	116	15.12		GO:0016525~negative regulation of angiogenesis	4	0.521	
GO:0042327~positive regulation of phosphorylation	47	6.127		GO:0010594~regulation of endothelial cell migration	5	0.651	
GO:0043085~positive regulation of catalytic activity	61	7.953		GO:0010632~regulation of epithelial cell migration	7	0.912	
GO:0051345~positive regulation of hydrolase activity	38	4.954		GO:0001525~angiogenesis	15	1.955	
GO:0031325~positive regulation of cellular metabolic process	122	15.90		GO:0048514~blood vessel morphogenesis	18	2.346	
GO:0010562~positive regulation of phosphorus metabolic process	51	6.649					
GO:0045937~positive regulation of phosphate metabolic process	51	6.649		Term	Count	%	
GO:0001934~positive regulation of protein phosphorylation	44	5.736		GO:0022411~cellular component disassembly	18	2.346	
GO:0031401~positive regulation of protein modification process	52	6.779		GO:0032984~macromolecular complex disassembly	8	1.043	
GO:0032270~positive regulation of cellular protein metabolic process	64	8.344		GO:0043244~regulation of protein complex disassembly	5	0.651	
GO:0044093~positive regulation of molecular function	72	9.387		GO:0043241~protein complex disassembly	7	0.912	
GO:0048584~positive regulation of response to stimulus	82	10.69		GO:0043624~cellular protein complex disassembly	6	0.782	
GO:0023014~signal transduction by protein phosphorylation	37	4.823		GO:0051261~protein depolymerization	5	0.651	
GO:0050790~regulation of catalytic activity	91	11.86		GO:1901879~regulation of protein depolymerization	4	0.521	
GO:0000165~MAPK cascade	35	4.563		GO:0030042~actin filament depolymerization	3	0.391	
GO:0045859~regulation of protein kinase activity	33	4.302					
GO:0010646~regulation of cell communication	118	15.38		Term	Count	%	
GO:0051338~regulation of transferase activity	39	5.084		GO:0000315~organellar large ribosomal subunit	3	0.391	
GO:0043549~regulation of kinase activity	35	4.563		GO:0005762~mitochondrial large ribosomal subunit	3	0.391	
GO:0051336~regulation of hydrolase activity	54	7.040		GO:0005759~mitochondrial matrix	12	1.564	
GO:0023051~regulation of signaling	118	15.38		GO:0000313~organellar ribosome	4	0.521	
GO:0032147~activation of protein kinase activity	14	1.825		GO:0005761~mitochondrial ribosome	4	0.521	
GO:0010628~positive regulation of gene expression	73	9.517					
GO:0043410~positive regulation of MAPK cascade	24	3.129		Term	Count	%	
GO:0045860~positive regulation of protein kinase activity	21	2.737		GO:0006612~protein targeting to membrane	6	0.782	
GO:0033674~positive regulation of kinase activity	21	2.737		GO:0006497~protein lipidation	5	0.651	
GO:0070371~ERK1 and ERK2 cascade	13	1.694		GO:0042158~lipoprotein biosynthetic process	5	0.651	
GO:1902533~positive regulation of intracellular signal transduction	39	5.084		GO:0042157~lipoprotein metabolic process	5	0.651	
GO:0009967~positive regulation of signal transduction	56	7.301					
GO:0070372~regulation of ERK1 and ERK2 cascade	13	1.694		Term	Count	%	
GO:0051347~positive regulation of transferase activity	23	2.998		GO:0033036~macromolecule localization	110	14.34	
GO:0010647~positive regulation of cell communication	60	7.822		GO:0008104~protein localization	93	12.12	
GO:0023056~positive regulation of signaling	60	7.822		GO:0051234~establishment of localization	173	22.55	
GO:0043405~regulation of MAP kinase activity	13	1.694		GO:0051641~cellular localization	92	11.99	
GO:0071902~positive regulation of protein serine/threonine kinase activity	11	1.434		GO:0070727~cellular macromolecule localization	59	7.692	
GO:0070374~positive regulation of ERK1 and ERK2 cascade	8	1.043		GO:0072594~establishment of protein localization to organelle	22	2.868	
GO:0071900~regulation of protein serine/threonine kinase activity	17	2.216		GO:0034613~cellular protein localization	58	7.561	
GO:0043406~positive regulation of MAP kinase activity	7	0.912		GO:0006605~protein targeting	24	3.129	
GO:0051716~cellular response to stimulus	267	34.81		GO:0015031~protein transport	61	7.953	
GO:0007165~signal transduction	215	28.03		GO:1902580~single-organism cellular localization	37	4.823	
GO:0050789~regulation of biological process	406	52.93		GO:0033365~protein localization to organelle	30	3.911	
GO:0050794~regulation of cellular process	389	50.71		GO:0051649~establishment of localization in cell	64	8.344	
GO:0050896~response to stimulus	321	41.85		GO:0071702~organic substance transport	87	11.34	
GO:0007154~cell communication	226	29.46		GO:0045184~establishment of protein localization	65	8.474	
GO:0065007~biological regulation	425	55.41		GO:0006886~intracellular protein transport	32	4.172	
GO:0044700~single organism signaling	221	28.81		GO:0046907~intracellular transport	44	5.736	
GO:0023052~signaling	222	28.94					

Term	Count	%							
GO:0032561~guanyl ribonucleotide binding	22	2.868							
GO:0019001~guanyl nucleotide binding	22	2.868			Term	Count	%		
GO:0005525~GTP binding	21	2.737			GO:0001046~core promoter sequence-specific DNA binding	6	0.782		
					GO:0000979~RNA polymerase II core promoter sequence-specific DNA binding	4	0.521		
					GO:0001047~core promoter binding	7	0.912		
Term	Count	%							
GO:0006351~transcription, DNA-templated	124	16.16			Term	Count	%		
GO:2000112~regulation of cellular macromolecule biosynthetic process	151	19.68			GO:0001706~endoderm formation	4	0.521		
GO:0010629~negative regulation of gene expression	70	9.126			GO:0007492~endoderm development	5	0.651		
GO:2001141~regulation of RNA biosynthetic process	136	17.73			GO:0007369~gastrulation	9	1.173		
GO:1903506~regulation of nucleic acid-templated transcription	135	17.60			GO:0035987~endodermal cell differentiation	3	0.391		
GO:0006355~regulation of transcription, DNA-templated	134	17.47			GO:0001704~formation of primary germ layer	4	0.521		
GO:0009892~negative regulation of metabolic process	111	14.47							
GO:0031324~negative regulation of cellular metabolic process	104	13.55							
GO:0010605~negative regulation of macromolecule metabolic process	101	13.16			Term	Count	%		
GO:0051172~negative regulation of nitrogen compound metabolic process	68	8.865			GO:0051053~negative regulation of DNA metabolic process	7	0.912		
GO:0045934~negative regulation of nucleobase-containing compound metabolic process	62	8.083			GO:0032200~telomere organization	6	0.782		
GO:0051253~negative regulation of RNA metabolic process	56	7.301			GO:0000723~telomere maintenance	6	0.782		
GO:2000113~negative regulation of cellular macromolecule biosynthetic process	60	7.822			GO:0000784~nuclear chromosome, telomeric region	6	0.782		
GO:0000122~negative regulation of transcription from RNA polymerase II promoter	38	4.954			GO:1904356~regulation of telomere maintenance via telomere lengthening	3	0.391		
GO:0045892~negative regulation of transcription, DNA-templated	52	6.779			GO:0000781~chromosome, telomeric region	6	0.782		
GO:1902679~negative regulation of RNA biosynthetic process	53	6.910			GO:0010833~telomere maintenance via telomere lengthening	3	0.391		
GO:1903507~negative regulation of nucleic acid-templated transcription	52	6.779			GO:0032204~regulation of telomere maintenance	3	0.391		
GO:0010558~negative regulation of macromolecule biosynthetic process	61	7.953							
GO:0009890~negative regulation of biosynthetic process	64	8.344							
GO:0031327~negative regulation of cellular biosynthetic process	62	8.083			Term	Count	%		
GO:0006366~transcription from RNA polymerase II promoter	72	9.387			GO:0004527~exonuclease activity	5	0.651		
GO:0006357~regulation of transcription from RNA polymerase II promoter	74	9.647			GO:0004518~nuclease activity	9	1.173		
					GO:0008408~3'-5' exonuclease activity	3	0.391		
Term	Count	%			GO:0004536~deoxyribonuclease activity	4	0.521		
GO:0000776~kinetochore	11	1.434			GO:0090305~nucleic acid phosphodiester bond hydrolysis	9	1.173		
GO:0000777~condensed chromosome kinetochore	6	0.782			GO:0004519~endonuclease activity	5	0.651		
GO:0000775~chromosome, centromeric region	11	1.434							
GO:0098687~chromosomal region	17	2.216			Term	Count	%		
GO:0000779~condensed chromosome, centromeric region	6	0.782			GO:0048589~developmental growth	31	4.041		
GO:0000793~condensed chromosome	10	1.303			GO:0001558~regulation of cell growth	18	2.346		
					GO:0040007~growth	41	5.345		
Term	Count	%			GO:0048638~regulation of developmental growth	15	1.955		
GO:0051090~regulation of sequence-specific DNA binding transcription factor activity	22	2.868			GO:0040008~regulation of growth	26	3.389		
GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity	14	1.825			GO:0016049~cell growth	12	1.564		
GO:0051092~positive regulation of NF-kappaB transcription factor activity	8	1.043							
					Term	Count	%		
Term	Count	%			GO:0010038~response to metal ion	22	2.868		
GO:0009966~regulation of signal transduction	112	14.60			GO:0071248~cellular response to metal ion	8	1.043		
GO:0009968~negative regulation of signal transduction	52	6.779			GO:0071241~cellular response to inorganic substance	9	1.173		
GO:0010648~negative regulation of cell communication	54	7.040			GO:0071277~cellular response to calcium ion	3	0.391		
GO:0023057~negative regulation of signaling	54	7.040			GO:0051592~response to calcium ion	4	0.521		
GO:1902532~negative regulation of intracellular signal transduction	25	3.259							
GO:0048585~negative regulation of response to stimulus	61	7.953			Term	Count	%		
GO:0010646~regulation of cell communication	118	15.38			GO:0052548~regulation of endopeptidase activity	21	2.737		
GO:0023051~regulation of signaling	118	15.38			GO:0052547~regulation of peptidase activity	22	2.868		
					GO:0043154~negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	6	0.782		
Term	Count	%			GO:2000117~negative regulation of cysteine-type endopeptidase activity	6	0.782		
GO:0098813~nuclear chromosome segregation	18	2.346			GO:0004857~enzyme inhibitor activity	16	2.086		
GO:0051303~establishment of chromosome localization	7	0.912			GO:0061135~endopeptidase regulator activity	8	1.043		
GO:0050000~chromosome localization	7	0.912			GO:0061134~peptidase regulator activity	9	1.173		
GO:0051310~metaphase plate congression	5	0.651			GO:0051346~negative regulation of hydrolase activity	16	2.086		
GO:0051640~organelle localization	21	2.737			GO:0010951~negative regulation of endopeptidase activity	10	1.303		
GO:0051656~establishment of organelle localization	17	2.216			GO:0004869~cysteine-type endopeptidase inhibitor activity	3	0.391		
					GO:0004866~endopeptidase inhibitor activity	7	0.912		
Term	Count	%			GO:0010466~negative regulation of peptidase activity	10	1.303		
GO:0000993~RNA polymerase II core binding	4	0.521			GO:0030414~peptidase inhibitor activity	7	0.912		
GO:0043175~RNA polymerase core enzyme binding	4	0.521			GO:0045861~negative regulation of proteolysis	12	1.564		
GO:0070063~RNA polymerase binding	5	0.651			GO:0004867~serine-type endopeptidase inhibitor activity	3	0.391		
GO:0001099~basal RNA polymerase II transcription machinery binding	4	0.521							
GO:0001098~basal transcription machinery binding	4	0.521			Term	Count	%		
					GO:0006612~protein targeting to membrane	6	0.782		
Term	Count	%			GO:0072657~protein localization to membrane	17	2.216		
GO:0043281~regulation of cysteine-type endopeptidase activity involved in apoptotic process	16	2.086			GO:0090150~establishment of protein localization to membrane	9	1.173		
GO:0010952~positive regulation of peptidase activity	12	1.564							
GO:0043280~positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	10	1.303			Term	Count	%		
GO:2000116~regulation of cysteine-type endopeptidase activity	16	2.086			GO:0019207~kinase regulator activity	12	1.564		
GO:0010950~positive regulation of endopeptidase activity	11	1.434			GO:0004860~protein kinase inhibitor activity	5	0.651		
GO:2001056~positive regulation of cysteine-type endopeptidase activity	10	1.303			GO:0019210~kinase inhibitor activity	5	0.651		
GO:0006919~activation of cysteine-type endopeptidase activity involved in apoptotic process	6	0.782			GO:0019887~protein kinase regulator activity	8	1.043		
GO:0052548~regulation of endopeptidase activity	21	2.737			GO:0051348~negative regulation of transferase activity	12	1.564		
GO:0052547~regulation of peptidase activity	22	2.868			GO:1904893~negative regulation of STAT cascade	3	0.391		
GO:0045862~positive regulation of proteolysis	15	1.955			GO:0046426~negative regulation of JAK-STAT cascade	3	0.391		
GO:0030162~regulation of proteolysis	29	3.780			GO:0033673~negative regulation of kinase activity	10	1.303		
					GO:0006469~negative regulation of protein kinase activity	9	1.173		
Term	Count	%			GO:0007259~JAK-STAT cascade	6	0.782		
GO:0051239~regulation of multicellular organismal process	128	16.68			GO:0097696~STAT cascade	6	0.782		
GO:2000026~regulation of multicellular organismal development	87	11.34			GO:0043407~negative regulation of MAP kinase activity	3	0.391		
GO:0009653~anatomical structure morphogenesis	121	15.77			GO:1904892~regulation of STAT cascade	5	0.651		
GO:0050793~regulation of developmental process	102	13.29			GO:0046425~regulation of JAK-STAT cascade	5	0.651		
GO:0048513~animal organ development	152	19.81			GO:0071901~negative regulation of protein serine/threonine kinase activity	4	0.521		
GO:0044767~single-organism developmental process	231	30.11							
GO:0044707~single-multicellular organism process	241	31.42			Term	Count	%		
GO:0045595~regulation of cell differentiation	77	10.03			GO:0005911~cell-cell junction	25	3.259		
GO:0032502~developmental process	234	30.50			GO:0098632~protein binding involved in cell-cell adhesion	10	1.303		
GO:0048869~cellular developmental process	171	22.29			GO:0098631~protein binding involved in cell adhesion	10	1.303		
GO:0048856~anatomical structure development	226	29.46			GO:0098641~cadherin binding involved in cell-cell adhesion	9	1.173		
GO:0007275~multicellular organism development	203	26.46			GO:0005913~cell-cell adherens junction	11	1.434		
GO:0048731~system development	185	24.11			GO:0050839~cell adhesion molecule binding	15	1.955		
GO:0030154~cell differentiation	153	19.94			GO:0045296~cadherin binding	9	1.173		
GO:0032501~multicellular organismal process	257	33.50							
					Term	Count	%		
Term	Count	%			GO:2000484~positive regulation of interleukin-8 secretion	3	0.391		
GO:0019899~enzyme binding	84	10.95			GO:0032637~interleukin-8 production	6	0.782		
GO:0019901~protein kinase binding	30	3.911			GO:2000482~regulation of interleukin-8 secretion	3	0.391		
GO:0019900~kinase binding	30	3.911			GO:0072606~interleukin-8 secretion	3	0.391		
					GO:0032677~regulation of interleukin-8 production	5	0.651		
Term	Count	%			GO:0032757~positive regulation of interleukin-8 production	4	0.521		
GO:0012501~programmed cell death	85	11.08			GO:0050715~positive regulation of cytokine secretion	6	0.782		
GO:0006915~apoptotic process	79	10.29			GO:0046903~secretion	43	5.606		
GO:0043280~positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	10	1.303			GO:0050663~cytokine secretion	8	1.043		
GO:0010950~positive regulation of endopeptidase activity	11	1.434			GO:0032940~secretion by cell	35	4.563		
GO:0043067~regulation of programmed cell death	69	8.996			GO:0032880~regulation of protein localization	37	4.823		
GO:2001056~positive regulation of cysteine-type endopeptidase activity	10	1.303			GO:0050714~positive regulation of protein secretion	9	1.173		
GO:0008219~cell death	86	11.21			GO:0051223~regulation of protein transport	28	3.650		
GO:0010941~regulation of cell death	73	9.517			GO:0050708~regulation of protein secretion	15	1.955		
GO:0042981~regulation of apoptotic process	67	8.735			GO:0050707~regulation of cytokine secretion	6	0.782		
GO:0060548~negative regulation of cell death	47	6.127			GO:0009306~protein secretion	17	2.216		
GO:0043065~positive regulation of apoptotic process	28	3.650			GO:0051222~positive regulation of protein transport	17	2.216		
GO:0043069~negative regulation of programmed cell death	40	5.215			GO:0033157~regulation of intracellular protein transport	13	1.694		
GO:0043068~positive regulation of programmed cell death	28	3.650			GO:0070201~regulation of establishment of protein localization	28	3.650		
GO:0045862~positive regulation of proteolysis	15	1.955			GO:1904951~positive regulation of establishment of protein localization	17	2.216		
GO:0043066~negative regulation of apoptotic process	37	4.823			GO:0051050~positive regulation of transport	33	4.302		
GO:0010942~positive regulation of cell death	28	3.650			GO:0051046~regulation of secretion	24	3.129		
					GO:0032386~regulation of intracellular transport	14	1.825		
					GO:0051047~positive regulation of secretion	12	1.564		
					GO:1903530~regulation of secretion by cell	21	2.737		

Term	Count	%		GO:1903532~positive regulation of secretion by cell	10	1.303	
GO:0032649~regulation of interferon-gamma production	9	1.173					
GO:0032609~interferon-gamma production	9	1.173					
GO:0032729~positive regulation of interferon-gamma production	5	0.651		Term	Count	%	
				GO:0030323~respiratory tube development	11	1.434	
				GO:0030324~lung development	10	1.303	
				GO:0060541~respiratory system development	11	1.434	
Term	Count	%					
GO:0048146~positive regulation of fibroblast proliferation	7	0.912					
GO:0048145~regulation of fibroblast proliferation	8	1.043		Term	Count	%	
GO:0048144~fibroblast proliferation	8	1.043		GO:0071385~cellular response to glucocorticoid stimulus	6	0.782	
				GO:0071549~cellular response to dexamethasone stimulus	4	0.521	
				GO:0071384~cellular response to corticosteroid stimulus	6	0.782	
Term	Count	%		GO:1901655~cellular response to ketone	6	0.782	
GO:0002684~positive regulation of immune system process	43	5.606		GO:0071383~cellular response to steroid hormone stimulus	11	1.434	
GO:0001819~positive regulation of cytokine production	24	3.129		GO:0031960~response to corticosteroid	12	1.564	
GO:0001817~regulation of cytokine production	31	4.041		GO:0071548~response to dexamethasone	4	0.521	
GO:0001816~cytokine production	33	4.302		GO:1901654~response to ketone	12	1.564	
GO:0050852~T cell receptor signaling pathway	7	0.912		GO:0051384~response to glucocorticoid	10	1.303	
GO:0031349~positive regulation of defense response	18	2.346					
GO:0002253~activation of immune response	18	2.346					
GO:0050778~positive regulation of immune response	25	3.259		Term	Count	%	
GO:0002764~immune response-regulating signaling pathway	16	2.086		GO:0021544~subpallium development	4	0.521	
GO:0002768~immune response-regulating cell surface receptor signaling pathway	11	1.434		GO:0021756~striatum development	3	0.391	
GO:0050851~antigen receptor-mediated signaling pathway	9	1.173		GO:0021680~cerebellar Purkinje cell layer development	3	0.391	
GO:0002757~immune response-activating signal transduction	15	1.955		GO:0022037~metencephalon development	6	0.782	
GO:0002429~immune response-activating cell surface receptor signaling pathway	10	1.303		GO:0021695~cerebellar cortex development	3	0.391	
GO:0050776~regulation of immune response	30	3.911		GO:0021549~cerebellum development	5	0.651	
GO:0045088~regulation of innate immune response	12	1.564		GO:0030902~hindbrain development	7	0.912	
GO:0045087~innate immune response	25	3.259		GO:0021537~telencephalon development	9	1.173	
GO:0006955~immune response	46	5.997		GO:0030900~forebrain development	12	1.564	
GO:0002252~immune effector process	26	3.389		GO:0021987~cerebral cortex development	3	0.391	
GO:0006952~defense response	48	6.258		GO:0021543~pallium development	4	0.521	
Term	Count	%		Term	Count	%	
GO:0042578~phosphoric ester hydrolase activity	23	2.998		GO:1901981~phosphatidylinositol phosphate binding	7	0.912	
GO:0016791~phosphatase activity	18	2.346		GO:0005546~phosphatidylinositol-4,5-bisphosphate binding	3	0.391	
GO:0016788~hydrolase activity, acting on ester bonds	38	4.954		GO:1902936~phosphatidylinositol bisphosphate binding	3	0.391	
GO:0004721~phosphoprotein phosphatase activity	11	1.434					
GO:0016311~dephosphorylation	22	2.868					
GO:0004725~protein tyrosine phosphatase activity	7	0.912		Term	Count	%	
GO:0035335~peptidyl-tyrosine dephosphorylation	7	0.912		GO:0002761~regulation of myeloid leukocyte differentiation	7	0.912	
GO:0006470~protein dephosphorylation	13	1.694		GO:0045638~negative regulation of myeloid cell differentiation	5	0.651	
GO:0008138~protein tyrosine/serine/threonine phosphatase activity	3	0.391		GO:0002762~negative regulation of myeloid leukocyte differentiation	3	0.391	
				GO:1903707~negative regulation of hemopoiesis	6	0.782	
				GO:1902106~negative regulation of leukocyte differentiation	4	0.521	
				GO:0002683~negative regulation of immune system process	12	1.564	
Term	Count	%					
GO:0042802~identical protein binding	63	8.213		Term	Count	%	
GO:0042803~protein homodimerization activity	37	4.823		GO:0014003~oligodendrocyte development	3	0.391	
GO:0046983~protein dimerization activity	49	6.388		GO:0021782~glial cell development	5	0.651	
				GO:0010001~glial cell differentiation	10	1.303	
Term	Count	%		GO:0048709~oligodendrocyte differentiation	5	0.651	
GO:0009790~embryo development	57	7.431		GO:0042063~gliogenesis	11	1.434	
GO:0048568~embryonic organ development	27	3.520					
GO:0009792~embryo development ending in birth or egg hatching	34	4.432		Term	Count	%	
GO:0043009~chordate embryonic development	33	4.302		GO:0034695~response to prostaglandin E	3	0.391	
GO:0001701~in utero embryonic development	19	2.477		GO:0034694~response to prostaglandin	3	0.391	
				GO:0016324~apical plasma membrane	8	1.043	
Term	Count	%					
GO:1901575~organic substance catabolic process	77	10.03		Term	Count	%	
GO:0044712~single-organism catabolic process	37	4.823		GO:0033209~tumor necrosis factor-mediated signaling pathway	4	0.521	
GO:0009056~catabolic process	78	10.16		GO:0034612~response to tumor necrosis factor	9	1.173	
GO:0044248~cellular catabolic process	59	7.692		GO:0071356~cellular response to tumor necrosis factor	7	0.912	
GO:0009057~macromolecule catabolic process	36	4.693					
Term	Count	%		Term	Count	%	
GO:0042127~regulation of cell proliferation	72	9.387		GO:0010830~regulation of myotube differentiation	5	0.651	
GO:0008283~cell proliferation	81	10.56		GO:0045663~positive regulation of myoblast differentiation	3	0.391	
GO:0008284~positive regulation of cell proliferation	42	5.475		GO:0051154~negative regulation of striated muscle cell differentiation	3	0.391	
				GO:0051147~regulation of muscle cell differentiation	9	1.173	
Term	Count	%		GO:0051153~regulation of striated muscle cell differentiation	6	0.782	
GO:0019221~cytokine-mediated signaling pathway	20	2.607		GO:0051148~negative regulation of muscle cell differentiation	4	0.521	
GO:0034097~response to cytokine	36	4.693		GO:0014902~myotube differentiation	5	0.651	
GO:0071345~cellular response to cytokine stimulus	29	3.780		GO:0045445~myoblast differentiation	4	0.521	
				GO:0045661~regulation of myoblast differentiation	3	0.391	
Term	Count	%		GO:0051149~positive regulation of muscle cell differentiation	4	0.521	
GO:0007051~spindle organization	10	1.303		GO:0051146~striated muscle cell differentiation	9	1.173	
GO:1902850~microtubule cytoskeleton organization involved in mitosis	5	0.651		GO:0042692~muscle cell differentiation	12	1.564	
GO:0090307~mitotic spindle assembly	5	0.651		GO:0055002~striated muscle cell development	4	0.521	
GO:0051225~spindle assembly	7	0.912		GO:0055001~muscle cell development	4	0.521	
GO:0007067~mitotic nuclear division	14	1.825					
				Term	Count	%	
Term	Count	%		GO:0016853~isomerase activity	8	1.043	
GO:0006259~DNA metabolic process	40	5.215		GO:0003755~peptidyl-prolyl cis-trans isomerase activity	3	0.391	
GO:0006281~DNA repair	21	2.737		GO:0000413~protein peptidyl-prolyl isomerization	3	0.391	
GO:0006974~cellular response to DNA damage stimulus	32	4.172		GO:0016859~cis-trans isomerase activity	3	0.391	
				GO:0018208~peptidyl-proline modification	3	0.391	
				GO:0006457~protein folding	5	0.651	
Term	Count	%					
GO:0003170~heart valve development	7	0.912		Term	Count	%	
GO:0003199~endocardial cushion to mesenchymal transition involved in heart valve formation	3	0.391		GO:0032153~cell division site	4	0.521	
GO:0003188~heart valve formation	4	0.521		GO:0032155~cell division site part	4	0.521	
GO:0090500~endocardial cushion to mesenchymal transition	3	0.391		GO:0097610~cell surface furrow	3	0.391	
GO:0003283~atrial septum development	4	0.521		GO:0032154~cleavage furrow	3	0.391	
GO:0003179~heart valve morphogenesis	5	0.651		GO:0043297~apical junction assembly	3	0.391	
GO:0003181~atrioventricular valve morphogenesis	4	0.521		GO:0034329~cell junction assembly	6	0.782	
GO:0003171~atrioventricular valve development	4	0.521		GO:0007044~cell-substrate junction assembly	3	0.391	
GO:0060317~cardiac epithelial to mesenchymal transition	4	0.521		GO:0007043~cell-cell junction assembly	3	0.391	
GO:0003281~ventricular septum development	6	0.782		GO:0034330~cell junction organization	7	0.912	
GO:0003230~cardiac atrium development	4	0.521		GO:0045216~cell-cell junction organization	6	0.782	
GO:0003197~endocardial cushion development	4	0.521					
GO:0003231~cardiac ventricle development	8	1.043		Term	Count	%	
GO:0072132~mesenchyme morphogenesis	4	0.521		GO:0051593~response to folic acid	3	0.391	
GO:0003203~endocardial cushion morphogenesis	3	0.391		GO:0033273~response to vitamin	5	0.651	
GO:0014031~mesenchymal cell development	8	1.043		GO:0007584~response to nutrient	7	0.912	
GO:0048762~mesenchymal cell differentiation	8	1.043					
GO:0001837~epithelial to mesenchymal transition	5	0.651					
GO:0060485~mesenchyme development	10	1.303					
				Term	Count	%	
Term	Count	%		GO:0072657~protein localization to membrane	17	2.216	
GO:0010842~retina layer formation	5	0.651		GO:0061024~membrane organization	33	4.302	
GO:0043010~camera-type eye development	21	2.737		GO:1902580~single-organism cellular localization	37	4.823	
GO:0060042~retina morphogenesis in camera-type eye	6	0.782		GO:0044802~single-organism membrane organization	28	3.650	
GO:0001654~eye development	21	2.737					
GO:0048592~eye morphogenesis	10	1.303		Term	Count	%	
GO:0048593~camera-type eye morphogenesis	8	1.043		GO:0014066~regulation of phosphatidylinositol 3-kinase signaling	5	0.651	
GO:0007423~sensory organ development	28	3.650		GO:0014068~positive regulation of phosphatidylinositol 3-kinase signaling	4	0.521	
GO:0090596~sensory organ morphogenesis	15	1.955		GO:0048015~phosphatidylinositol-mediated signaling	6	0.782	
GO:0003407~neural retina development	5	0.651		GO:0048017~inositol lipid-mediated signaling	6	0.782	
GO:0060041~retina development in camera-type eye	9	1.173		GO:0014065~phosphatidylinositol 3-kinase signaling	4	0.521	
Term	Count	%		Term	Count	%	
GO:0007059~chromosome segregation	26	3.389		GO:0016706~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	3	0.391	
GO:0098813~nuclear chromosome segregation	18	2.346					

GO:0005819~spindle	19	2.477	GO:0051213~dioxygenase activity	4	0.521
GO:0045143~homologous chromosome segregation	7	0.912	GO:0016705~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	8	1.043
GO:0022402~cell cycle process	52	6.779			
GO:0045132~meiotic chromosome segregation	8	1.043			
GO:0007049~cell cycle	62	8.083	Term	Count	%
GO:0000278~mitotic cell cycle	36	4.693	GO:0060041~retina development in camera-type eye	9	1.173
GO:0045787~positive regulation of cell cycle	18	2.346	GO:0001754~eye photoreceptor cell differentiation	3	0.391
GO:0000819~sister chromatid segregation	10	1.303	GO:0046530~photoreceptor cell differentiation	3	0.391
GO:1903047~mitotic cell cycle process	30	3.911			
GO:0051301~cell division	20	2.607			
GO:0007127~meiosis I	7	0.912	Term	Count	%
GO:0007126~meiotic nuclear division	10	1.303	GO:0071453~cellular response to oxygen levels	8	1.043
GO:0045931~positive regulation of mitotic cell cycle	8	1.043	GO:0055093~response to hyperoxia	3	0.391
GO:0000070~mitotic sister chromatid segregation	8	1.043	GO:0036296~response to increased oxygen levels	3	0.391
GO:0010564~regulation of cell cycle process	23	2.998			
GO:0051726~regulation of cell cycle	36	4.693			
GO:1903046~meiotic cell cycle process	10	1.303	Term	Count	%
GO:0051321~meiotic cell cycle	11	1.434	GO:0032760~positive regulation of tumor necrosis factor production	4	0.521
GO:0090068~positive regulation of cell cycle process	10	1.303	GO:1903555~regulation of tumor necrosis factor superfamily cytokine production	6	0.782
GO:0000280~nuclear division	21	2.737	GO:1903557~positive regulation of tumor necrosis factor superfamily cytokine production	4	0.521
GO:0070192~chromosome organization involved in meiotic cell cycle	4	0.521	GO:0071706~tumor necrosis factor superfamily cytokine production	6	0.782
GO:0007067~mitotic nuclear division	14	1.825	GO:0032640~tumor necrosis factor production	5	0.651
GO:0007129~synapsis	3	0.391	GO:0032680~regulation of tumor necrosis factor production	5	0.651
GO:0048285~organelle fission	21	2.737			
GO:0007346~regulation of mitotic cell cycle	16	2.086			
			Term	Count	%
Term	Count	%	GO:0044295~axonal growth cone	3	0.391
GO:0000453~enzyme-directed rRNA 2'-O-methylation	3	0.391	GO:0030427~site of polarized growth	8	1.043
GO:0000451~rRNA 2'-O-methylation	3	0.391	GO:0030426~growth cone	7	0.912
GO:0009451~RNA modification	12	1.564	GO:0048675~axon extension	4	0.521
GO:0016435~rRNA (guanine) methyltransferase activity	3	0.391			
GO:0008168~methyltransferase activity	15	1.955	Term	Count	%
GO:0008757~S-adenosylmethionine-dependent methyltransferase activity	12	1.564	GO:0003081~regulation of systemic arterial blood pressure by renin-angiotensin	3	0.391
GO:0016741~transferase activity, transferring one-carbon groups	15	1.955	GO:0001990~regulation of systemic arterial blood pressure by hormone	3	0.391
GO:0008649~rRNA methyltransferase activity	4	0.521	GO:0050886~endocrine process	5	0.651
GO:0000154~rRNA modification	5	0.651	GO:0003044~regulation of systemic arterial blood pressure mediated by a chemical signal	3	0.391
GO:0061087~positive regulation of histone H3-K27 methylation	3	0.391	GO:0003073~regulation of systemic arterial blood pressure	4	0.521
GO:0008171~O-methyltransferase activity	4	0.521	GO:0008217~regulation of blood pressure	6	0.782
GO:0008173~RNA methyltransferase activity	6	0.782			
GO:0031167~rRNA methylation	4	0.521			
GO:0061085~regulation of histone H3-K27 methylation	3	0.391	Term	Count	%
GO:0032259~methylation	19	2.477	GO:1901564~organonitrogen compound metabolic process	87	11.34
GO:0001510~RNA methylation	6	0.782	GO:0043603~cellular amide metabolic process	46	5.997
GO:0031062~positive regulation of histone methylation	4	0.521	GO:0015934~large ribosomal subunit	10	1.303
GO:0070734~histone H3-K27 methylation	3	0.391	GO:0030529~intracellular ribonucleoprotein complex	38	4.954
GO:0051276~chromosome organization	46	5.997	GO:1990904~ribonucleoprotein complex	38	4.954
GO:0043414~macromolecule methylation	14	1.825	GO:0043604~amide biosynthetic process	35	4.563
GO:0031060~regulation of histone methylation	5	0.651	GO:0006518~peptide metabolic process	37	4.823
GO:0016279~protein-lysine N-methyltransferase activity	4	0.521	GO:0044445~cytosolic part	16	2.086
GO:0016278~lysine N-methyltransferase activity	4	0.521	GO:0003735~structural constituent of ribosome	16	2.086
GO:0008170~N-methyltransferase activity	5	0.651	GO:0022625~cytosolic large ribosomal subunit	7	0.912
GO:0016571~histone methylation	7	0.912	GO:0006412~translation	30	3.911
GO:0018022~peptidyl-lysine methylation	6	0.782	GO:0043043~peptide biosynthetic process	30	3.911
GO:0031058~positive regulation of histone modification	5	0.651	GO:0005198~structural molecule activity	29	3.780
GO:0008213~protein alkylation	8	1.043	GO:0005840~ribosome	16	2.086
GO:0006479~protein methylation	8	1.043	GO:0044391~ribosomal subunit	12	1.564
GO:0018205~peptidyl-lysine modification	14	1.825	GO:1901566~organonitrogen compound biosynthetic process	50	6.518
GO:1905269~positive regulation of chromatin organization	5	0.651	GO:0022626~cytosolic ribosome	8	1.043
GO:2001252~positive regulation of chromosome organization	7	0.912			
GO:0034968~histone lysine methylation	5	0.651			
GO:0033044~regulation of chromosome organization	12	1.564	Term	Count	%
GO:0008276~protein methyltransferase activity	4	0.521	GO:0045580~regulation of T cell differentiation	7	0.912
GO:0016570~histone modification	17	2.216	GO:0046632~alpha-beta T cell differentiation	5	0.651
GO:0031056~regulation of histone modification	6	0.782	GO:0046631~alpha-beta T cell activation	6	0.782
GO:0016569~covalent chromatin modification	17	2.216	GO:0046634~regulation of alpha-beta T cell activation	4	0.521
GO:0006325~chromatin organization	24	3.129	GO:0046637~regulation of alpha-beta T cell differentiation	3	0.391
GO:1902275~regulation of chromatin organization	6	0.782	GO:0035710~CD4-positive, alpha-beta T cell activation	3	0.391
Term	Count	%	Term	Count	%
GO:0001078~transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding	11	1.434	GO:0050807~regulation of synapse organization	7	0.912
GO:0003690~double-stranded DNA binding	39	5.084	GO:0051965~positive regulation of synapse assembly	4	0.521
GO:1990837~sequence-specific double-stranded DNA binding	34	4.432	GO:0050808~synapse organization	10	1.303
GO:0044212~transcription regulatory region DNA binding	39	5.084	GO:0051963~regulation of synapse assembly	4	0.521
GO:0000975~regulatory region DNA binding	39	5.084	GO:0007416~synapse assembly	5	0.651
GO:0001227~transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding	12	1.564	GO:0050803~regulation of synapse structure or activity	9	1.173
GO:0001067~regulatory region nucleic acid binding	39	5.084			
GO:0000982~transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	20	2.607			
GO:0003677~DNA binding	80	10.43	Term	Count	%
GO:0000977~RNA polymerase II regulatory region sequence-specific DNA binding	28	3.650	GO:0042379~chemokine receptor binding	4	0.521
GO:0000976~transcription regulatory region sequence-specific DNA binding	31	4.041	GO:0048246~macrophage chemotaxis	3	0.391
GO:0001012~RNA polymerase II regulatory region DNA binding	28	3.650	GO:0097529~myeloid leukocyte migration	8	1.043
GO:0043565~sequence-specific DNA binding	44	5.736	GO:0008009~chemokine activity	3	0.391
GO:0000987~core promoter proximal region sequence-specific DNA binding	18	2.346	GO:0070555~response to interleukin-1	7	0.912
GO:0001159~core promoter proximal region DNA binding	18	2.346	GO:0072676~lymphocyte migration	4	0.521
GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	17	2.216	GO:0048247~lymphocyte chemotaxis	3	0.391
GO:0000981~RNA polymerase II transcription factor activity, sequence-specific DNA binding	28	3.650	GO:0030593~neutrophil chemotaxis	4	0.521
GO:0001071~nucleic acid binding transcription factor activity	41	5.345	GO:0030595~leukocyte chemotaxis	8	1.043
GO:0003700~transcription factor activity, sequence-specific DNA binding	41	5.345	GO:0002548~monocyte chemotaxis	3	0.391
GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	9	1.173	GO:0050900~leukocyte migration	11	1.434
GO:0001228~transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	10	1.303	GO:1990266~neutrophil migration	4	0.521
Term	Count	%	GO:0005125~cytokine activity	7	0.912
GO:0032091~negative regulation of protein binding	7	0.912	GO:0071621~granulocyte chemotaxis	4	0.521
GO:0043393~regulation of protein binding	12	1.564	GO:0002688~regulation of leukocyte chemotaxis	4	0.521
GO:0051098~regulation of binding	17	2.216	GO:0071346~cellular response to interferon-gamma	3	0.391
GO:0051100~negative regulation of binding	9	1.173	GO:0097530~granulocyte migration	4	0.521
			GO:0071347~cellular response to interleukin-1	4	0.521
			GO:0060326~cell chemotaxis	8	1.043
			GO:0034341~response to interferon-gamma	3	0.391
Term	Count	%	Term	Count	%
GO:0071214~cellular response to abiotic stimulus	21	2.737	GO:0031965~nuclear membrane	13	1.694
GO:0071478~cellular response to radiation	12	1.564	GO:0005635~nuclear envelope	19	2.477
GO:0071493~cellular response to UV-B	3	0.391	GO:0019866~organelle inner membrane	18	2.346
GO:0034644~cellular response to UV	7	0.912	GO:0031967~organelle envelope	36	4.693
GO:0071479~cellular response to ionizing radiation	6	0.782	GO:0044429~mitochondrial part	29	3.780
GO:0071482~cellular response to light stimulus	7	0.912	GO:0031975~envelope	36	4.693
GO:0009411~response to UV	9	1.173	GO:0005743~mitochondrial inner membrane	13	1.694
GO:0010224~response to UV-B	3	0.391	GO:0031966~mitochondrial membrane	17	2.216
GO:0010212~response to ionizing radiation	10	1.303	GO:0005740~mitochondrial envelope	17	2.216
GO:0009628~response to abiotic stimulus	53	6.910			
GO:0009314~response to radiation	20	2.607			
GO:0009416~response to light stimulus	13	1.694			
			Term	Count	%
Term	Count	%	GO:0035257~nuclear hormone receptor binding	7	0.912
GO:0009451~RNA modification	12	1.564	GO:0030518~intracellular steroid hormone receptor signaling pathway	6	0.782
GO:0006400~tRNA modification	5	0.651	GO:0001104~RNA polymerase II transcription cofactor activity	4	0.521
GO:0008033~tRNA processing	6	0.782	GO:0043401~steroid hormone mediated signaling pathway	6	0.782
GO:0006399~tRNA metabolic process	7	0.912	GO:0003713~transcription coactivator activity	8	1.043
			GO:0001076~transcription factor activity, RNA polymerase II transcription factor binding	4	0.521
Term	Count	%	Term	Count	%
GO:0051495~positive regulation of cytoskeleton organization	18	2.346	GO:0002761~regulation of myeloid leukocyte differentiation	7	0.912
GO:0051125~regulation of actin nucleation	5	0.651	GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	14	1.825
GO:0034315~regulation of Arp2/3 complex-mediated actin nucleation	4	0.521	GO:0030510~regulation of BMP signaling pathway	4	0.521
GO:0030036~actin cytoskeleton organization	31	4.041	GO:0030509~BMP signaling pathway	5	0.651
GO:0045010~actin nucleation	6	0.782	GO:0071772~response to BMP	5	0.651

GO:0007015~actin filament organization	20	2.607	GO:0071773~cellular response to BMP stimulus	5	0.651
GO:0032273~positive regulation of protein polymerization	9	1.173			
GO:0044089~positive regulation of cellular component biogenesis	24	3.129			
GO:0034314~Arp2/3 complex-mediated actin nucleation	4	0.521	Term	Count	%
GO:0030029~actin filament-based process	32	4.172	GO:0035023~regulation of Rho protein signal transduction	7	0.912
GO:0051493~regulation of cytoskeleton organization	23	2.998	GO:0005085~guanyl-nucleotide exchange factor activity	7	0.912
GO:0051127~positive regulation of actin nucleation	3	0.391	GO:0005088~Ras guanyl-nucleotide exchange factor activity	5	0.651
GO:0030838~positive regulation of actin filament polymerization	7	0.912	GO:0005089~Rho guanyl-nucleotide exchange factor activity	3	0.391
GO:0032956~regulation of actin cytoskeleton organization	16	2.086			
GO:0031334~positive regulation of protein complex assembly	12	1.564			
GO:0032970~regulation of actin filament-based process	17	2.216	Term	Count	%
GO:0032271~regulation of protein polymerization	10	1.303	GO:0042345~regulation of NF-kappaB import into nucleus	4	0.521
GO:0032535~regulation of cellular component size	18	2.346	GO:1900180~regulation of protein localization to nucleus	11	1.434
GO:0008154~actin polymerization or depolymerization	10	1.303	GO:0042306~regulation of protein import into nucleus	9	1.173
GO:0030832~regulation of actin filament length	9	1.173	GO:1900182~positive regulation of protein localization to nucleus	7	0.912
GO:0008064~regulation of actin polymerization or depolymerization	9	1.173	GO:1904589~regulation of protein import	9	1.173
GO:0010638~positive regulation of organelle organization	27	3.520	GO:0042990~regulation of transcription factor import into nucleus	5	0.651
GO:0044087~regulation of cellular component biogenesis	35	4.563	GO:0042348~NF-kappaB import into nucleus	3	0.391
GO:0043254~regulation of protein complex assembly	17	2.216	GO:0042991~transcription factor import into nucleus	5	0.651
GO:0090066~regulation of anatomical structure size	24	3.129	GO:0072594~establishment of protein localization to organelle	22	2.868
GO:0030833~regulation of actin filament polymerization	8	1.043	GO:0006606~protein import into nucleus	12	1.564
GO:0030041~actin filament polymerization	8	1.043	GO:1902593~single-organism nuclear import	12	1.564
GO:0051130~positive regulation of cellular component organization	52	6.779	GO:0044744~protein targeting to nucleus	12	1.564
GO:0051258~protein polymerization	11	1.434	GO:0051170~nuclear import	12	1.564
GO:0051128~regulation of cellular component organization	90	11.73	GO:0006605~protein targeting	24	3.129
GO:0033043~regulation of organelle organization	41	5.345	GO:0034504~protein localization to nucleus	15	1.955
			GO:0042307~positive regulation of protein import into nucleus	5	0.651
Term	Count	%	GO:0042993~positive regulation of transcription factor import into nucleus	3	0.391
GO:0010390~histone monoubiquitination	4	0.521	GO:1904591~positive regulation of protein import	5	0.651
GO:0006513~protein monoubiquitination	5	0.651	GO:0033365~protein localization to organelle	30	3.911
GO:0016574~histone ubiquitination	4	0.521	GO:0046822~regulation of nucleocytoplasmic transport	9	1.173
			GO:1902582~single-organism intracellular transport	22	2.868
			GO:0017038~protein import	13	1.694
Term	Count	%	GO:0032880~regulation of protein localization	37	4.823
GO:0002684~positive regulation of immune system process	43	5.606	GO:0046824~positive regulation of nucleocytoplasmic transport	5	0.651
GO:0002521~leukocyte differentiation	28	3.650	GO:0006913~nucleocytoplasmic transport	15	1.955
GO:0002682~regulation of immune system process	58	7.561	GO:0051169~nuclear transport	15	1.955
GO:1902105~regulation of leukocyte differentiation	16	2.086	GO:0051223~regulation of protein transport	28	3.650
GO:0002573~myeloid leukocyte differentiation	13	1.694	GO:1903533~regulation of protein targeting	11	1.434
GO:1903708~positive regulation of hemopoiesis	12	1.564	GO:0006886~intracellular protein transport	32	4.172
GO:1903706~regulation of hemopoiesis	20	2.607	GO:1903827~regulation of cellular protein localization	20	2.607
GO:1902107~positive regulation of leukocyte differentiation	10	1.303	GO:0051222~positive regulation of protein transport	17	2.216
GO:0030097~hemopoiesis	39	5.084	GO:0033157~regulation of intracellular protein transport	13	1.694
GO:0045639~positive regulation of myeloid cell differentiation	7	0.912	GO:0070201~regulation of establishment of protein localization	28	3.650
GO:0045637~regulation of myeloid cell differentiation	12	1.564	GO:1904951~positive regulation of establishment of protein localization	17	2.216
GO:0002520~immune system development	42	5.475	GO:0090316~positive regulation of intracellular protein transport	8	1.043
GO:0048534~hematopoietic or lymphoid organ development	40	5.215	GO:1903829~positive regulation of cellular protein localization	11	1.434
GO:0030099~myeloid cell differentiation	19	2.477	GO:0032386~regulation of intracellular transport	14	1.825
GO:0030316~osteoclast differentiation	6	0.782	GO:0032388~positive regulation of intracellular transport	8	1.043
GO:0046649~lymphocyte activation	29	3.780	GO:0060341~regulation of cellular localization	26	3.389
GO:0045619~regulation of lymphocyte differentiation	9	1.173			
GO:0045621~positive regulation of lymphocyte differentiation	6	0.782	Term	Count	%
GO:0030098~lymphocyte differentiation	16	2.086	GO:0031214~biomineral tissue development	7	0.912
GO:0002761~regulation of myeloid leukocyte differentiation	7	0.912	GO:0030501~positive regulation of bone mineralization	3	0.391
GO:0002376~immune system process	89	11.60	GO:0070169~positive regulation of biomineral tissue development	3	0.391
GO:0045321~leukocyte activation	32	4.172	GO:0045778~positive regulation of ossification	5	0.651
GO:0002763~positive regulation of myeloid leukocyte differentiation	4	0.521	GO:0030500~regulation of bone mineralization	4	0.521
GO:0045670~regulation of osteoclast differentiation	4	0.521	GO:0070167~regulation of biomineral tissue development	4	0.521
			GO:0001503~ossification	15	1.955
Term	Count	%	GO:0030278~regulation of ossification	8	1.043
GO:2000242~negative regulation of reproductive process	6	0.782	GO:0030282~bone mineralization	4	0.521
GO:2000241~regulation of reproductive process	10	1.303	GO:0001649~osteoblast differentiation	7	0.912
GO:0051447~negative regulation of meiotic cell cycle	3	0.391	GO:0045667~regulation of osteoblast differentiation	4	0.521
GO:0051445~regulation of meiotic cell cycle	4	0.521			
			Term	Count	%
Term	Count	%	GO:1901616~organic hydroxy compound catabolic process	4	0.521
GO:0000226~microtubule cytoskeleton organization	26	3.389	GO:0046164~alcohol catabolic process	3	0.391
GO:0015630~microtubule cytoskeleton	49	6.388	GO:0019751~polyol metabolic process	5	0.651
GO:0005813~centrosome	24	3.129	GO:0046173~polyol biosynthetic process	3	0.391
GO:0005815~microtubule organizing center	28	3.650	GO:0046165~alcohol biosynthetic process	4	0.521
GO:0007017~microtubule-based process	29	3.780	GO:0006066~alcohol metabolic process	8	1.043
GO:0044430~cytoskeletal part	59	7.692	GO:1901615~organic hydroxy compound metabolic process	12	1.564
GO:0005856~cytoskeleton	71	9.256	GO:1901617~organic hydroxy compound biosynthetic process	4	0.521
Term	Count	%	Term	Count	%
GO:0071044~histone mRNA catabolic process	4	0.521	GO:0001655~urogenital system development	16	2.086
GO:0008334~histone mRNA metabolic process	4	0.521	GO:0001822~kidney development	13	1.694
GO:1901361~organic cyclic compound catabolic process	19	2.477	GO:0072001~renal system development	13	1.694
GO:0019439~aromatic compound catabolic process	17	2.216	GO:0072006~nephron development	6	0.782
GO:1901565~organonitrogen compound catabolic process	16	2.086			
GO:0046700~heterocycle catabolic process	16	2.086	Term	Count	%
GO:0044270~cellular nitrogen compound catabolic process	16	2.086	GO:0035326~enhancer binding	7	0.912
GO:0034661~ncRNA catabolic process	3	0.391	GO:0001158~enhancer sequence-specific DNA binding	6	0.782
GO:0034655~nucleobase-containing compound catabolic process	12	1.564	GO:0072006~nephron development	6	0.782
GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	3	0.391	GO:0072009~nephron epithelium development	4	0.521
GO:0000956~nuclear-transcribed mRNA catabolic process	6	0.782	GO:0072080~nephron tubule development	3	0.391
GO:0006402~mRNA catabolic process	6	0.782	GO:0061326~renal tubule development	3	0.391
GO:0031123~RNA 3'-end processing	4	0.521	GO:0072073~kidney epithelium development	4	0.521
GO:0006401~RNA catabolic process	6	0.782			
Term	Count	%	Term	Count	%
GO:0051216~cartilage development	12	1.564	GO:0016444~somatic cell DNA recombination	4	0.521
GO:0032330~regulation of chondrocyte differentiation	5	0.651	GO:0002562~somatic diversification of immune receptors via germline recombination within a single locus	4	0.521
GO:0061448~connective tissue development	15	1.955	GO:0002200~somatic diversification of immune receptors	4	0.521
GO:0001501~skeletal system development	25	3.259	GO:0016064~immunoglobulin mediated immune response	6	0.782
GO:0002062~chondrocyte differentiation	7	0.912	GO:0045190~isotype switching	3	0.391
GO:0061035~regulation of cartilage development	5	0.651	GO:0002208~somatic diversification of immunoglobulins involved in immune response	3	0.391
GO:0048705~skeletal system morphogenesis	11	1.434	GO:0002204~somatic recombination of immunoglobulin genes involved in immune response	3	0.391
			GO:0019724~B cell mediated immunity	6	0.782
Term	Count	%	GO:0016447~somatic recombination of immunoglobulin gene segments	3	0.391
GO:0005975~carbohydrate metabolic process	37	4.823	GO:0002381~immunoglobulin production involved in immunoglobulin mediated immune response	3	0.391
GO:0044723~single-organism carbohydrate metabolic process	32	4.172	GO:0016445~somatic diversification of immunoglobulins	3	0.391
GO:0006487~protein N-linked glycosylation	7	0.912	GO:0002440~production of molecular mediator of immune response	7	0.912
GO:0009101~glycoprotein biosynthetic process	17	2.216	GO:0051054~positive regulation of DNA metabolic process	8	1.043
GO:0009100~glycoprotein metabolic process	18	2.346	GO:0002312~B cell activation involved in immune response	3	0.391
GO:0043413~macromolecule glycosylation	13	1.694	GO:0002377~immunoglobulin production	3	0.391
GO:0006486~protein glycosylation	13	1.694	GO:0002285~lymphocyte activation involved in immune response	4	0.521
GO:0070085~glycosylation	13	1.694	GO:0002366~leukocyte activation involved in immune response	5	0.651
GO:0016758~transferase activity, transferring hexosyl groups	10	1.303	GO:0002263~cell activation involved in immune response	5	0.651
GO:0016757~transferase activity, transferring glycosyl groups	12	1.564			
GO:1901137~carbohydrate derivative biosynthetic process	27	3.520	Term	Count	%
GO:1901135~carbohydrate derivative metabolic process	42	5.475	GO:0048704~embryonic skeletal system morphogenesis	5	0.651
GO:0008194~UDP-glycosyltransferase activity	5	0.651	GO:0048701~embryonic cranial skeleton morphogenesis	3	0.391
			GO:0048706~embryonic skeletal system development	6	0.782
			GO:1904888~cranial skeletal system development	3	0.391
Term	Count	%	Term	Count	%
GO:0030674~protein binding, bridging	8	1.043	GO:0061515~myeloid cell development	4	0.521
GO:0060090~binding, bridging	8	1.043	GO:0045646~regulation of erythrocyte differentiation	3	0.391
GO:0035591~signaling adaptor activity	4	0.521	GO:0030218~erythrocyte differentiation	5	0.651
GO:0005070~SH3/SH2 adaptor activity	3	0.391	GO:0048872~homeostasis of number of cells	11	1.434
			GO:0034101~erythrocyte homeostasis	5	0.651
Term	Count	%	GO:0002262~myeloid cell homeostasis	5	0.651
GO:0036159~inner dynein arm assembly	4	0.521			
GO:0070286~axonemal dynein complex assembly	4	0.521			
GO:0060271~cilium morphogenesis	15	1.955	Term	Count	%
GO:0070925~organelle assembly	33	4.302	GO:0040029~regulation of gene expression, epigenetic	10	1.303

GO:0030031~cell projection assembly	22	2.868	GO:0035195~gene silencing by miRNA	3	0.391
GO:0042384~cilium assembly	12	1.564	GO:0017148~negative regulation of translation	6	0.782
GO:0044782~cilium organization	12	1.564	GO:0035194~posttranscriptional gene silencing by RNA	3	0.391
GO:0035082~axoneme assembly	4	0.521	GO:0016441~posttranscriptional gene silencing	3	0.391
GO:0010927~cellular component assembly involved in morphogenesis	14	1.825	GO:0034249~negative regulation of cellular amide metabolic process	6	0.782
GO:0001578~microtubule bundle formation	5	0.651	GO:0031047~gene silencing by RNA	3	0.391
GO:0005929~cilium	18	2.346	GO:0016458~gene silencing	5	0.651
GO:0044441~ciliary part	9	1.173			
Term	Count	%	Term	Count	%
GO:0031999~negative regulation of fatty acid beta-oxidation	3	0.391	GO:0042593~glucose homeostasis	14	1.825
GO:0046322~negative regulation of fatty acid oxidation	3	0.391	GO:0033500~carbohydrate homeostasis	14	1.825
GO:0050995~negative regulation of lipid catabolic process	4	0.521	GO:0001678~cellular glucose homeostasis	8	1.043
GO:0072329~monocarboxylic acid catabolic process	8	1.043	GO:0071453~cellular response to oxygen levels	8	1.043
GO:0044282~small molecule catabolic process	16	2.086	GO:0009749~response to glucose	9	1.173
GO:0009062~fatty acid catabolic process	7	0.912	GO:0070482~response to oxygen levels	16	2.086
GO:0046395~carboxylic acid catabolic process	11	1.434	GO:0009746~response to hexose	9	1.173
GO:0009895~negative regulation of catabolic process	10	1.303	GO:0036294~cellular response to decreased oxygen levels	6	0.782
GO:0016054~organic acid catabolic process	12	1.564	GO:0036293~response to decreased oxygen levels	14	1.825
GO:0006635~fatty acid beta-oxidation	6	0.782	GO:0034284~response to monosaccharide	9	1.173
GO:0031998~regulation of fatty acid beta-oxidation	3	0.391	GO:0071333~cellular response to glucose stimulus	5	0.651
GO:0016042~lipid catabolic process	15	1.955	GO:0071326~cellular response to monosaccharide stimulus	5	0.651
GO:0019395~fatty acid oxidation	7	0.912	GO:0071331~cellular response to hexose stimulus	5	0.651
GO:0034440~lipid oxidation	7	0.912	GO:0071456~cellular response to hypoxia	5	0.651
GO:0033539~fatty acid beta-oxidation using acyl-CoA dehydrogenase	3	0.391	GO:0071322~cellular response to carbohydrate stimulus	5	0.651
GO:0031330~negative regulation of cellular catabolic process	6	0.782	GO:0009743~response to carbohydrate	9	1.173
GO:0019217~regulation of fatty acid metabolic process	6	0.782	GO:0001666~response to hypoxia	11	1.434
GO:0045833~negative regulation of lipid metabolic process	6	0.782			
GO:0030258~lipid modification	11	1.434	Term	Count	%
GO:0045922~negative regulation of fatty acid metabolic process	3	0.391	GO:0030968~endoplasmic reticulum unfolded protein response	4	0.521
GO:0044242~cellular lipid catabolic process	10	1.303	GO:0034620~cellular response to unfolded protein	4	0.521
GO:0019216~regulation of lipid metabolic process	15	1.955	GO:0035967~cellular response to topologically incorrect protein	4	0.521
GO:0046320~regulation of fatty acid oxidation	3	0.391	GO:0006986~response to unfolded protein	4	0.521
GO:0050994~regulation of lipid catabolic process	4	0.521	GO:0035966~response to topologically incorrect protein	4	0.521
GO:0010565~regulation of cellular ketone metabolic process	6	0.782	GO:0034976~response to endoplasmic reticulum stress	6	0.782
GO:0042180~cellular ketone metabolic process	8	1.043			
GO:0031329~regulation of cellular catabolic process	12	1.564	Term	Count	%
GO:0031331~positive regulation of cellular catabolic process	6	0.782	GO:0030141~secretory granule	14	1.825
			GO:0099503~secretory vesicle	18	2.346
Term	Count	%	GO:0016023~cytoplasmic, membrane-bounded vesicle	34	4.432
GO:0001906~cell killing	11	1.434	GO:0097708~intracellular vesicle	38	4.954
GO:0001909~leukocyte mediated cytotoxicity	9	1.173	GO:0031410~cytoplasmic vesicle	37	4.823
GO:0031341~regulation of cell killing	8	1.043			
GO:0001910~regulation of leukocyte mediated cytotoxicity	7	0.912	Term	Count	%
GO:0002706~regulation of lymphocyte mediated immunity	10	1.303	GO:0014031~mesenchymal cell development	8	1.043
GO:0002703~regulation of leukocyte mediated immunity	12	1.564	GO:0048762~mesenchymal cell differentiation	8	1.043
GO:0001912~positive regulation of leukocyte mediated cytotoxicity	5	0.651	GO:0001755~neural crest cell migration	3	0.391
GO:0031343~positive regulation of cell killing	5	0.651	GO:0014032~neural crest cell development	3	0.391
GO:0002443~leukocyte mediated immunity	15	1.955	GO:0014033~neural crest cell differentiation	3	0.391
GO:0042267~natural killer cell mediated cytotoxicity	4	0.521			
GO:0002228~natural killer cell mediated immunity	4	0.521	Term	Count	%
GO:0042269~regulation of natural killer cell mediated cytotoxicity	3	0.391	GO:0042089~cytokine biosynthetic process	5	0.651
GO:0002715~regulation of natural killer cell mediated immunity	3	0.391	GO:0042107~cytokine metabolic process	5	0.651
GO:0045582~positive regulation of T cell differentiation	4	0.521	GO:0042108~positive regulation of cytokine biosynthetic process	3	0.391
GO:0002697~regulation of immune effector process	15	1.955	GO:0042035~regulation of cytokine biosynthetic process	4	0.521
GO:0002274~myeloid leukocyte activation	6	0.782			
Term	Count	%	Term	Count	%
GO:0002521~leukocyte differentiation	28	3.650	GO:0010508~positive regulation of autophagy	5	0.651
GO:0002682~regulation of immune system process	58	7.561	GO:0010506~regulation of autophagy	7	0.912
GO:0050863~regulation of T cell activation	17	2.216	GO:0016241~regulation of macroautophagy	3	0.391
GO:0051249~regulation of lymphocyte activation	22	2.868			
GO:0002694~regulation of leukocyte activation	25	3.259	Term	Count	%
GO:1903037~regulation of leukocyte cell-cell adhesion	17	2.216	GO:0000077~DNA damage checkpoint	5	0.651
GO:0050867~positive regulation of cell activation	17	2.216	GO:0031570~DNA integrity checkpoint	5	0.651
GO:0050865~regulation of cell activation	26	3.389	GO:0000075~cell cycle checkpoint	7	0.912
GO:0007159~leukocyte cell-cell adhesion	25	3.259			
GO:0002696~positive regulation of leukocyte activation	16	2.086	Term	Count	%
GO:0050670~regulation of lymphocyte proliferation	13	1.694	GO:0046890~regulation of lipid biosynthetic process	7	0.912
GO:0045579~positive regulation of B cell differentiation	3	0.391	GO:0046889~positive regulation of lipid biosynthetic process	4	0.521
GO:0032944~regulation of mononuclear cell proliferation	13	1.694	GO:0045834~positive regulation of lipid metabolic process	4	0.521
GO:0022610~biological adhesion	65	8.474			
GO:0070663~regulation of leukocyte proliferation	13	1.694	Term	Count	%
GO:0098602~single organism cell adhesion	36	4.693	GO:0072331~signal transduction by p53 class mediator	6	0.782
GO:0051251~positive regulation of lymphocyte activation	14	1.825	GO:0030330~DNA damage response, signal transduction by p53 class mediator	3	0.391
GO:0042129~regulation of T cell proliferation	10	1.303	GO:0042770~signal transduction in response to DNA damage	3	0.391
GO:0002520~immune system development	42	5.475			
GO:0050671~positive regulation of lymphocyte proliferation	9	1.173	Term	Count	%
GO:0070489~T cell aggregation	22	2.868	GO:0046486~glycerolipid metabolic process	13	1.694
GO:0042110~T cell activation	22	2.868	GO:0046488~phosphatidylinositol metabolic process	5	0.651
GO:0071593~lymphocyte aggregation	22	2.868	GO:0006644~phospholipid metabolic process	11	1.434
GO:0007155~cell adhesion	64	8.344	GO:0006650~glycerophospholipid metabolic process	6	0.782
GO:0032946~positive regulation of mononuclear cell proliferation	9	1.173			
GO:0022407~regulation of cell-cell adhesion	19	2.477	Term	Count	%
GO:0070486~leukocyte aggregation	22	2.868	GO:0006417~regulation of translation	13	1.694
GO:0070665~positive regulation of leukocyte proliferation	9	1.173	GO:0017148~negative regulation of translation	6	0.782
GO:0042098~T cell proliferation	11	1.434	GO:0010608~posttranscriptional regulation of gene expression	15	1.955
GO:0016337~single organismal cell-cell adhesion	32	4.172	GO:0034249~negative regulation of cellular amide metabolic process	6	0.782
GO:0030155~regulation of cell adhesion	29	3.780	GO:0034248~regulation of cellular amide metabolic process	13	1.694
GO:0046649~lymphocyte activation	29	3.780			
GO:0070661~leukocyte proliferation	15	1.955	Term	Count	%
GO:0045621~positive regulation of lymphocyte differentiation	6	0.782	GO:0005506~iron ion binding	11	1.434
GO:0050871~positive regulation of B cell activation	6	0.782	GO:0020037~heme binding	4	0.521
GO:0030098~lymphocyte differentiation	16	2.086	GO:0046906~tetrapyrrole binding	4	0.521
GO:0046651~lymphocyte proliferation	14	1.825			
GO:0030217~T cell differentiation	12	1.564	Term	Count	%
GO:0032943~mononuclear cell proliferation	14	1.825	GO:0048878~chemical homeostasis	48	6.258
GO:0050870~positive regulation of T cell activation	9	1.173	GO:0032844~regulation of homeostatic process	23	2.998
GO:0045577~regulation of B cell differentiation	3	0.391	GO:0042592~homeostatic process	71	9.256
GO:0001775~cell activation	37	4.823	GO:2000021~regulation of ion homeostasis	10	1.303
GO:0042102~positive regulation of T cell proliferation	6	0.782	GO:0032845~negative regulation of homeostatic process	9	1.173
GO:0045321~leukocyte activation	32	4.172	GO:0050801~ion homeostasis	29	3.780
GO:0098609~cell-cell adhesion	44	5.736	GO:0060401~cytosolic calcium ion transport	7	0.912
GO:1903039~positive regulation of leukocyte cell-cell adhesion	9	1.173	GO:0051928~positive regulation of calcium ion transport	6	0.782
GO:0030183~B cell differentiation	6	0.782	GO:0070509~calcium ion import	8	1.043
GO:0050864~regulation of B cell activation	7	0.912	GO:0098771~inorganic ion homeostasis	27	3.520
GO:0022409~positive regulation of cell-cell adhesion	10	1.303	GO:0055080~cation homeostasis	26	3.389
GO:0042113~B cell activation	10	1.303	GO:0007204~positive regulation of cytosolic calcium ion concentration	12	1.564
GO:0045785~positive regulation of cell adhesion	13	1.694	GO:0051238~sequestering of metal ion	6	0.782
			GO:0060402~calcium ion transport into cytosol	6	0.782
Term	Count	%	GO:0090279~regulation of calcium ion import	5	0.651
GO:0030198~extracellular matrix organization	12	1.564	GO:0043270~positive regulation of ion transport	10	1.303
GO:0043062~extracellular structure organization	12	1.564	GO:0055065~metal ion homeostasis	22	2.868
GO:0030199~collagen fibril organization	4	0.521	GO:0019722~calcium-mediated signaling	6	0.782
			GO:0051282~regulation of sequestering of calcium ion	5	0.651
Term	Count	%	GO:0051208~sequestering of calcium ion	5	0.651
GO:0004620~phospholipase activity	7	0.912	GO:0055082~cellular chemical homeostasis	28	3.650
GO:0016298~lipase activity	8	1.043	GO:0090280~positive regulation of calcium ion import	3	0.391
GO:0004435~phosphatidylinositol phospholipase C activity	3	0.391	GO:0051924~regulation of calcium ion transport	9	1.173
GO:0004629~phospholipase C activity	3	0.391	GO:0051480~regulation of cytosolic calcium ion concentration	12	1.564
GO:0004623~phospholipase A2 activity	3	0.391	GO:0010522~regulation of calcium ion transport into cytosol	4	0.521
GO:0008081~phosphoric diester hydrolase activity	5	0.651	GO:0051209~release of sequestered calcium ion into cytosol	4	0.521
GO:0052689~carboxylic ester hydrolase activity	5	0.651	GO:0051283~negative regulation of sequestering of calcium ion	4	0.521

				GO:0097553~calcium ion transmembrane import into cytosol	4	0.521
				GO:1902656~calcium ion import into cytosol	4	0.521
Term	Count	%		GO:0019725~cellular homeostasis	30	3.911
GO:0003158~endothelium development	9	1.173		GO:0072507~divalent inorganic cation homeostasis	16	2.086
GO:0045446~endothelial cell differentiation	8	1.043		GO:0051279~regulation of release of sequestered calcium ion into cytosol	3	0.391
GO:0061028~establishment of endothelial barrier	4	0.521		GO:0010959~regulation of metal ion transport	12	1.564
GO:0001885~endothelial cell development	5	0.651		GO:0055074~calcium ion homeostasis	14	1.825
GO:0002064~epithelial cell development	12	1.564		GO:0006873~cellular ion homeostasis	19	2.477
GO:0045601~regulation of endothelial cell differentiation	3	0.391		GO:0006874~cellular calcium ion homeostasis	13	1.694
				GO:0030003~cellular cation homeostasis	18	2.346
				GO:0070838~divalent metal ion transport	13	1.694
Term	Count	%		GO:0072511~divalent inorganic cation transport	13	1.694
GO:0010799~regulation of peptidyl–threonine phosphorylation	4	0.521		GO:0072503~cellular divalent inorganic cation homeostasis	13	1.694
GO:0018107~peptidyl–threonine phosphorylation	6	0.782		GO:0006816~calcium ion transport	11	1.434
GO:0018210~peptidyl–threonine modification	6	0.782		GO:0006875~cellular metal ion homeostasis	15	1.955
				GO:0070588~calcium ion transmembrane transport	7	0.912
				GO:1903169~regulation of calcium ion transmembrane transport	3	0.391
Term	Count	%				
GO:0051536~iron–sulfur cluster binding	5	0.651				
GO:0051540~metal cluster binding	5	0.651		Term	Count	%
GO:0051539~4 iron, 4 sulfur cluster binding	3	0.391		GO:0055067~monovalent inorganic cation homeostasis	7	0.912
				GO:0006885~regulation of pH	4	0.521
				GO:0051453~regulation of intracellular pH	3	0.391
Term	Count	%		GO:0030641~regulation of cellular pH	3	0.391
GO:0046330~positive regulation of JNK cascade	9	1.173		GO:0030004~cellular monovalent inorganic cation homeostasis	3	0.391
GO:0032874~positive regulation of stress–activated MAPK cascade	10	1.303				
GO:0070304~positive regulation of stress–activated protein kinase signaling cascade	10	1.303				
GO:0043410~positive regulation of MAPK cascade	24	3.129		Term	Count	%
GO:0032872~regulation of stress–activated MAPK cascade	12	1.564		GO:0009798~axis specification	5	0.651
GO:0070302~regulation of stress–activated protein kinase signaling cascade	12	1.564		GO:0009948~anterior/posterior axis specification	3	0.391
GO:0051403~stress–activated MAPK cascade	12	1.564		GO:0003002~regionalization	13	1.694
GO:0031098~stress–activated protein kinase signaling cascade	12	1.564		GO:0009952~anterior/posterior pattern specification	6	0.782
GO:0046328~regulation of JNK cascade	9	1.173				
GO:0007254~JNK cascade	9	1.173				
GO:0080135~regulation of cellular response to stress	21	2.737		Term	Count	%
				GO:0051241~negative regulation of multicellular organismal process	43	5.606
				GO:0051093~negative regulation of developmental process	31	4.041
				GO:0045596~negative regulation of cell differentiation	23	2.998
Term	Count	%				
GO:0051496~positive regulation of stress fiber assembly	5	0.651				
GO:0031032~actomyosin structure organization	10	1.303				
GO:0051492~regulation of stress fiber assembly	6	0.782		Term	Count	%
GO:0032956~regulation of actin cytoskeleton organization	16	2.086		GO:0006906~vesicle fusion	6	0.782
GO:0043149~stress fiber assembly	6	0.782		GO:0090174~organelle membrane fusion	6	0.782
GO:0030038~contractile actin filament bundle assembly	6	0.782		GO:0044801~single–organism membrane fusion	7	0.912
GO:0032233~positive regulation of actin filament bundle assembly	5	0.651		GO:0016050~vesicle organization	10	1.303
GO:0032970~regulation of actin filament–based process	17	2.216		GO:0061025~membrane fusion	7	0.912
GO:0032231~regulation of actin filament bundle assembly	6	0.782		GO:0048284~organelle fusion	6	0.782
GO:0051017~actin filament bundle assembly	6	0.782		GO:0045055~regulated exocytosis	6	0.782
GO:0061572~actin filament bundle organization	6	0.782		GO:0006887~exocytosis	9	1.173
				GO:1903305~regulation of regulated secretory pathway	3	0.391
				GO:0017157~regulation of exocytosis	3	0.391
Term	Count	%				
GO:0048736~appendage development	12	1.564				
GO:0060173~limb development	12	1.564		Term	Count	%
GO:0035107~appendage morphogenesis	11	1.434		GO:1901031~regulation of response to reactive oxygen species	3	0.391
GO:0035108~limb morphogenesis	11	1.434		GO:1900407~regulation of cellular response to oxidative stress	4	0.521
GO:0035136~forelimb morphogenesis	4	0.521		GO:1902882~regulation of response to oxidative stress	4	0.521
GO:0030326~embryonic limb morphogenesis	8	1.043		GO:1903201~regulation of oxidative stress–induced cell death	3	0.391
GO:0035113~embryonic appendage morphogenesis	8	1.043		GO:0036473~cell death in response to oxidative stress	3	0.391
GO:0042733~embryonic digit morphogenesis	4	0.521				
Term	Count	%		Term	Count	%
GO:0007264~small GTPase mediated signal transduction	29	3.780		GO:0072376~protein activation cascade	4	0.521
GO:0051056~regulation of small GTPase mediated signal transduction	12	1.564		GO:0006956~complement activation	3	0.391
GO:0046578~regulation of Ras protein signal transduction	11	1.434		GO:0006959~humoral immune response	5	0.651
GO:0007265~Ras protein signal transduction	15	1.955				
GO:0035023~regulation of Rho protein signal transduction	7	0.912		Term	Count	%
				GO:0035265~organ growth	10	1.303
				GO:0060419~heart growth	5	0.651
Term	Count	%		GO:0060420~regulation of heart growth	4	0.521
GO:0016502~nucleotide receptor activity	3	0.391		GO:0046620~regulation of organ growth	5	0.651
GO:0001614~purinergic nucleotide receptor activity	3	0.391		GO:0016202~regulation of striated muscle tissue development	6	0.782
GO:0035590~purinergic nucleotide receptor signaling pathway	3	0.391		GO:0048634~regulation of muscle organ development	6	0.782
GO:0035586~purinergic receptor activity	3	0.391		GO:1901861~regulation of muscle tissue development	6	0.782
GO:0035587~purinergic receptor signaling pathway	3	0.391		GO:0055021~regulation of cardiac muscle tissue growth	3	0.391
				GO:0007517~muscle organ development	13	1.694
				GO:0060538~skeletal muscle organ development	7	0.912
Term	Count	%		GO:0055024~regulation of cardiac muscle tissue development	3	0.391
GO:0060396~growth hormone receptor signaling pathway	3	0.391		GO:0007519~skeletal muscle tissue development	6	0.782
GO:0071378~cellular response to growth hormone stimulus	3	0.391		GO:0055017~cardiac muscle tissue growth	3	0.391
GO:0060416~response to growth hormone	3	0.391		GO:0060537~muscle tissue development	13	1.694
				GO:0014706~striated muscle tissue development	11	1.434
				GO:0048738~cardiac muscle tissue development	5	0.651
Term	Count	%				
GO:0050431~transforming growth factor beta binding	3	0.391				
GO:0019838~growth factor binding	8	1.043		Term	Count	%
GO:0019955~cytokine binding	6	0.782		GO:0009987~cellular process	607	79.13
				GO:0044763~single–organism cellular process	466	60.75
				GO:0044699~single–organism process	514	67.01
Term	Count	%				
GO:0072686~mitotic spindle	7	0.912				
GO:0051988~regulation of attachment of spindle microtubules to kinetochore	3	0.391		Term	Count	%
GO:0000819~sister chromatid segregation	10	1.303		GO:0048638~regulation of developmental growth	15	1.955
GO:0051983~regulation of chromosome segregation	6	0.782		GO:0045927~positive regulation of growth	10	1.303
GO:0000070~mitotic sister chromatid segregation	8	1.043		GO:0048639~positive regulation of developmental growth	6	0.782
GO:0033045~regulation of sister chromatid segregation	3	0.391				
GO:0051304~chromosome separation	3	0.391				
GO:0051783~regulation of nuclear division	5	0.651		Term	Count	%
				GO:0051651~maintenance of location in cell	5	0.651
				GO:0045185~maintenance of protein location	4	0.521
Term	Count	%		GO:0032507~maintenance of protein location in cell	3	0.391
GO:0048565~digestive tract development	10	1.303				
GO:0055123~digestive system development	10	1.303				
GO:0035050~embryonic heart tube development	5	0.651		Term	Count	%
				GO:1901605~alpha–amino acid metabolic process	9	1.173
				GO:0009066~aspartate family amino acid metabolic process	3	0.391
Term	Count	%		GO:0009064~glutamine family amino acid metabolic process	3	0.391
GO:0032006~regulation of TOR signaling	7	0.912		GO:0006520~cellular amino acid metabolic process	7	0.912
GO:0031929~TOR signaling	5	0.651		GO:0043648~dicarboxylic acid metabolic process	3	0.391
GO:0032007~negative regulation of TOR signaling	3	0.391				
Term	Count	%		Term	Count	%
GO:0043596~nuclear replication fork	5	0.651		GO:0005783~endoplasmic reticulum	56	7.301
GO:0005657~replication fork	5	0.651		GO:0005789~endoplasmic reticulum membrane	25	3.259
GO:0071103~DNA conformation change	8	1.043		GO:0042175~nuclear outer membrane–endoplasmic reticulum membrane network	25	3.259
				GO:0044432~endoplasmic reticulum part	27	3.520
Term	Count	%		Term	Count	%
GO:1901136~carbohydrate derivative catabolic process	9	1.173		GO:0046849~bone remodeling	4	0.521
GO:0072523~purine–containing compound catabolic process	5	0.651		GO:0045453~bone resorption	3	0.391
GO:0006195~purine nucleotide catabolic process	4	0.521		GO:0048771~tissue remodeling	7	0.912
GO:0046434~organophosphate catabolic process	7	0.912		GO:0001894~tissue homeostasis	8	1.043
GO:0009166~nucleotide catabolic process	4	0.521				
GO:0009154~purine ribonucleotide catabolic process	3	0.391				
GO:0009261~ribonucleotide catabolic process	3	0.391		Term	Count	%
GO:1901292~nucleoside phosphate catabolic process	4	0.521		GO:0008144~drug binding	6	0.782
				GO:0005231~excitatory extracellular ligand–gated ion channel activity	3	0.391
				GO:0022834~ligand–gated channel activity	5	0.651
Term	Count	%		GO:0015276~ligand–gated ion channel activity	5	0.651
GO:1902911~protein kinase complex	7	0.912		GO:0042391~regulation of membrane potential	14	1.825
GO:0061695~transferase complex, transferring phosphorus–containing groups	12	1.564		GO:0005230~extracellular ligand–gated ion channel activity	3	0.391
GO:1902554~serine/threonine protein kinase complex	5	0.651		GO:0001508~action potential	4	0.521

Term	Count	%		GO:0050818~regulation of coagulation	3	0.391	
GO:0016477~cell migration	54	7.040		GO:0030168~platelet activation	3	0.391	
GO:0040011~locomotion	67	8.735					
GO:0048870~cell motility	59	7.692					
GO:0051674~localization of cell	59	7.692		Term	Count	%	
GO:0006928~movement of cell or subcellular component	72	9.387		GO:0005615~extracellular space	53	6.910	
GO:0040012~regulation of locomotion	37	4.823		GO:0031988~membrane-bounded vesicle	120	15.64	
GO:0051270~regulation of cellular component movement	38	4.954		GO:1903561~extracellular vesicle	95	12.38	
GO:2000145~regulation of cell motility	34	4.432		GO:0031982~vesicle	125	16.29	
GO:0030334~regulation of cell migration	32	4.172		GO:0043230~extracellular organelle	95	12.38	
GO:0051272~positive regulation of cellular component movement	19	2.477		GO:0070062~extracellular exosome	94	12.25	
GO:0030335~positive regulation of cell migration	17	2.216		GO:0044421~extracellular region part	129	16.81	
GO:0040017~positive regulation of locomotion	18	2.346		GO:0005576~extracellular region	136	17.73	
GO:2000147~positive regulation of cell motility	17	2.216					
Term	Count	%		Term	Count	%	
GO:0010866~regulation of triglyceride biosynthetic process	3	0.391		GO:0051784~negative regulation of nuclear division	3	0.391	
GO:0006639~acylglycerol metabolic process	7	0.912		GO:0000075~cell cycle checkpoint	7	0.912	
GO:0090207~regulation of triglyceride metabolic process	4	0.521		GO:0051783~regulation of nuclear division	5	0.651	
GO:0006638~neutral lipid metabolic process	7	0.912					
GO:0006641~triglyceride metabolic process	6	0.782		Term	Count	%	
GO:0046486~glycerolipid metabolic process	13	1.694		GO:0005215~transporter activity	50	6.518	
				GO:0022832~voltage-gated channel activity	9	1.173	
				GO:0005244~voltage-gated ion channel activity	9	1.173	
Term	Count	%		GO:0022892~substrate-specific transporter activity	42	5.475	
GO:0005874~microtubule	18	2.346		GO:0022843~voltage-gated cation channel activity	6	0.782	
GO:0044430~cytoskeletal part	59	7.692		GO:0022836~gated channel activity	12	1.564	
GO:0099512~supramolecular fiber	24	3.129		GO:0005249~voltage-gated potassium channel activity	4	0.521	
GO:0099513~polymeric cytoskeletal fiber	24	3.129		GO:0005261~cation channel activity	11	1.434	
				GO:0022834~ligand-gated channel activity	5	0.651	
				GO:0015276~ligand-gated ion channel activity	5	0.651	
Term	Count	%		GO:0005216~ion channel activity	14	1.825	
GO:0002705~positive regulation of leukocyte mediated immunity	9	1.173		GO:0022891~substrate-specific transmembrane transporter activity	31	4.041	
GO:0002708~positive regulation of lymphocyte mediated immunity	8	1.043		GO:0098655~cation transmembrane transport	25	3.259	
GO:0050870~positive regulation of T cell activation	9	1.173		GO:0022857~transmembrane transporter activity	34	4.432	
GO:1903039~positive regulation of leukocyte cell-cell adhesion	9	1.173		GO:0055085~transmembrane transport	46	5.997	
GO:0032743~positive regulation of interleukin-2 production	3	0.391		GO:0022838~substrate-specific channel activity	14	1.825	
GO:0032663~regulation of interleukin-2 production	3	0.391		GO:0008324~cation transmembrane transporter activity	19	2.477	
GO:0032623~interleukin-2 production	3	0.391		GO:0005267~potassium channel activity	4	0.521	
				GO:0022803~passive transmembrane transporter activity	14	1.825	
				GO:0015267~channel activity	14	1.825	
Term	Count	%		GO:0043269~regulation of ion transport	20	2.607	
GO:0060761~negative regulation of response to cytokine stimulus	4	0.521		GO:0030001~metal ion transport	27	3.520	
GO:0060759~regulation of response to cytokine stimulus	6	0.782		GO:0006812~cation transport	33	4.302	
GO:0010803~regulation of tumor necrosis factor-mediated signaling pathway	3	0.391		GO:0046873~metal ion transmembrane transporter activity	12	1.564	
GO:0001959~regulation of cytokine-mediated signaling pathway	5	0.651		GO:0098662~inorganic cation transmembrane transport	20	2.607	
GO:0001960~negative regulation of cytokine-mediated signaling pathway	3	0.391		GO:0015075~ion transmembrane transporter activity	23	2.998	
				GO:0015079~potassium ion transmembrane transporter activity	4	0.521	
				GO:0098660~inorganic ion transmembrane transport	22	2.868	
Term	Count	%		GO:0034220~ion transmembrane transport	29	3.780	
GO:0021517~ventral spinal cord development	7	0.912		GO:0006811~ion transport	45	5.867	
GO:0021515~cell differentiation in spinal cord	6	0.782		GO:0015077~monovalent inorganic cation transmembrane transporter activity	9	1.173	
GO:0021522~spinal cord motor neuron differentiation	4	0.521		GO:0015672~monovalent inorganic cation transport	13	1.694	
GO:0021511~spinal cord patterning	3	0.391		GO:0022890~inorganic cation transmembrane transporter activity	13	1.694	
GO:0021510~spinal cord development	7	0.912					
GO:0048663~neuron fate commitment	5	0.651		Term	Count	%	
GO:0048665~neuron fate specification	3	0.391		GO:0000988~transcription factor activity, protein binding	17	2.216	
GO:0009953~dorsal/ventral pattern formation	6	0.782		GO:0003714~transcription corepressor activity	6	0.782	
GO:0021953~central nervous system neuron differentiation	9	1.173		GO:0000989~transcription factor activity, transcription factor binding	16	2.086	
GO:0003002~regionalization	13	1.694		GO:0003713~transcription coactivator activity	8	1.043	
GO:0001708~cell fate specification	3	0.391		GO:0003712~transcription cofactor activity	13	1.694	
GO:0001764~neuron migration	4	0.521					
Term	Count	%		Term	Count	%	
GO:0044437~vacuolar part	23	2.998		GO:0045104~intermediate filament cytoskeleton organization	3	0.391	
GO:0005774~vacuolar membrane	21	2.737		GO:0045103~intermediate filament-based process	3	0.391	
GO:0031901~early endosome membrane	5	0.651		GO:0005882~intermediate filament	3	0.391	
GO:0005769~early endosome	13	1.694		GO:0045111~intermediate filament cytoskeleton	4	0.521	
GO:0044440~endosomal part	12	1.564					
GO:0010008~endosome membrane	11	1.434					
GO:0005768~endosome	27	3.520		Term	Count	%	
				GO:0008080~N-acetyltransferase activity	5	0.651	
				GO:0016407~acetyltransferase activity	5	0.651	
Term	Count	%		GO:0016747~transferase activity, transferring acyl groups other than amino-acyl groups	9	1.173	
GO:0006508~proteolysis	70	9.126		GO:0016410~N-acyltransferase activity	5	0.651	
GO:0070011~peptidase activity, acting on L-amino acid peptides	28	3.650		GO:0004402~histone acetyltransferase activity	3	0.391	
GO:0008233~peptidase activity	28	3.650		GO:0061733~peptide-lysine-N-acetyltransferase activity	3	0.391	
				GO:0034212~peptide N-acetyltransferase activity	3	0.391	
Term	Count	%		GO:0016746~transferase activity, transferring acyl groups	9	1.173	
GO:0031349~positive regulation of defense response	18	2.346		GO:0043543~protein acylation	8	1.043	
GO:0050729~positive regulation of inflammatory response	8	1.043		GO:0006473~protein acetylation	6	0.782	
GO:0050727~regulation of inflammatory response	16	2.086		GO:0018394~peptidyl-lysine acetylation	5	0.651	
GO:0031347~regulation of defense response	28	3.650		GO:0016573~histone acetylation	4	0.521	
GO:0080134~regulation of response to stress	50	6.518		GO:0018393~internal peptidyl-lysine acetylation	4	0.521	
GO:0032101~regulation of response to external stimulus	32	4.172		GO:0006475~internal protein amino acid acetylation	4	0.521	
GO:0032103~positive regulation of response to external stimulus	11	1.434					
GO:0006952~defense response	48	6.258		Term	Count	%	
GO:0006954~inflammatory response	20	2.607		GO:0015297~antiporter activity	5	0.651	
				GO:0015698~inorganic anion transport	6	0.782	
				GO:0015103~inorganic anion transmembrane transporter activity	5	0.651	
Term	Count	%		GO:0015291~secondary active transmembrane transporter activity	8	1.043	
GO:0033198~response to ATP	4	0.521		GO:0006821~chloride transport	4	0.521	
GO:0046683~response to organophosphorus	11	1.434		GO:0098656~anion transmembrane transport	6	0.782	
GO:0014074~response to purine-containing compound	12	1.564		GO:0098661~inorganic anion transmembrane transport	4	0.521	
GO:0051591~response to cAMP	7	0.912		GO:0015108~chloride transmembrane transporter activity	3	0.391	
GO:0071320~cellular response to cAMP	4	0.521		GO:1902476~chloride transmembrane transport	3	0.391	
				GO:0022804~active transmembrane transporter activity	11	1.434	
				GO:0006820~anion transport	13	1.694	
Term	Count	%		GO:0008509~anion transmembrane transporter activity	5	0.651	
GO:0006096~glycolytic process	7	0.912					
GO:0009135~purine nucleoside diphosphate metabolic process	8	1.043		Term	Count	%	
GO:0009179~purine ribonucleoside diphosphate metabolic process	8	1.043		GO:0010948~negative regulation of cell cycle process	9	1.173	
GO:0006165~nucleoside diphosphate phosphorylation	8	1.043		GO:2000134~negative regulation of G1/S transition of mitotic cell cycle	3	0.391	
GO:0006757~ATP generation from ADP	7	0.912		GO:0044843~cell cycle G1/S phase transition	7	0.912	
GO:0016052~carbohydrate catabolic process	10	1.303		GO:1902807~negative regulation of cell cycle G1/S phase transition	3	0.391	
GO:0044724~single-organism carbohydrate catabolic process	9	1.173		GO:0000082~G1/S transition of mitotic cell cycle	6	0.782	
GO:0009185~ribonucleoside diphosphate metabolic process	8	1.043		GO:0000075~cell cycle checkpoint	7	0.912	
GO:0009132~nucleoside diphosphate metabolic process	9	1.173		GO:1901988~negative regulation of cell cycle phase transition	5	0.651	
GO:0046939~nucleotide phosphorylation	8	1.043		GO:0044770~cell cycle phase transition	12	1.564	
GO:0046031~ADP metabolic process	7	0.912		GO:0045786~negative regulation of cell cycle	13	1.694	
GO:0019362~pyridine nucleotide metabolic process	9	1.173		GO:0044839~cell cycle G2/M phase transition	4	0.521	
GO:0046496~nicotinamide nucleotide metabolic process	9	1.173		GO:1902806~regulation of cell cycle G1/S phase transition	4	0.521	
GO:0006732~coenzyme metabolic process	17	2.216		GO:1901991~negative regulation of mitotic cell cycle phase transition	4	0.521	
GO:0072524~pyridine-containing compound metabolic process	9	1.173		GO:0007093~mitotic cell cycle checkpoint	4	0.521	
GO:0006110~regulation of glycolytic process	4	0.521		GO:0044772~mitotic cell cycle phase transition	10	1.303	
GO:0006090~pyruvate metabolic process	7	0.912		GO:0045930~negative regulation of mitotic cell cycle	6	0.782	
GO:0006733~oxidoreduction coenzyme metabolic process	9	1.173		GO:2000045~regulation of G1/S transition of mitotic cell cycle	3	0.391	
GO:0051186~cofactor metabolic process	18	2.346		GO:1901987~regulation of cell cycle phase transition	7	0.912	
GO:0051196~regulation of coenzyme metabolic process	4	0.521		GO:1901990~regulation of mitotic cell cycle phase transition	5	0.651	
GO:0043470~regulation of carbohydrate catabolic process	4	0.521					
GO:0051193~regulation of cofactor metabolic process	4	0.521					
GO:0009118~regulation of nucleoside metabolic process	4	0.521		Term	Count	%	
GO:1903578~regulation of ATP metabolic process	4	0.521		GO:0032309~icosanoid secretion	3	0.391	
GO:0046128~purine ribonucleoside metabolic process	14	1.825		GO:0071715~icosanoid transport	3	0.391	
GO:0042278~purine nucleoside metabolic process	14	1.825		GO:0015908~fatty acid transport	4	0.521	
GO:0009116~nucleoside metabolic process	15	1.955		GO:0015718~monocarboxylic acid transport	4	0.521	
GO:1901135~carbohydrate derivative metabolic process	42	5.475		GO:0046942~carboxylic acid transport	7	0.912	
GO:0043467~regulation of generation of precursor metabolites and energy	5	0.651		GO:0015711~organic anion transport	7	0.912	
GO:0009119~ribonucleoside metabolic process	14	1.825					
GO:0009123~nucleoside monophosphate metabolic process	12	1.564					
GO:0009126~purine nucleoside monophosphate metabolic process	11	1.434					

GO:0009167~purine ribonucleoside monophosphate metabolic process	11	1.434	Term	Count	%	
GO:0072521~purine-containing compound metabolic process	21	2.737	GO:0050770~regulation of axonogenesis	9	1.173	
GO:0009161~ribonucleoside monophosphate metabolic process	11	1.434	GO:0008361~regulation of cell size	9	1.173	
GO:1901657~glycosyl compound metabolic process	15	1.955	GO:0048640~negative regulation of developmental growth	5	0.651	
GO:0009144~purine nucleoside triphosphate metabolic process	10	1.303	GO:0060560~developmental growth involved in morphogenesis	9	1.173	
GO:0006163~purine nucleotide metabolic process	19	2.477	GO:0061387~regulation of extent of cell growth	5	0.651	
GO:0019637~organophosphate metabolic process	35	4.563	GO:0030516~regulation of axon extension	4	0.521	
GO:0009205~purine ribonucleoside triphosphate metabolic process	9	1.173	GO:0050772~positive regulation of axonogenesis	3	0.391	
GO:0009141~nucleoside triphosphate metabolic process	10	1.303	GO:0048675~axon extension	4	0.521	
GO:0009117~nucleotide metabolic process	22	2.868	GO:0048588~developmental cell growth	7	0.912	
GO:0055086~nucleobase-containing small molecule metabolic process	24	3.129	GO:1990138~neuron projection extension	5	0.651	
GO:0009150~purine ribonucleotide metabolic process	17	2.216	GO:0030308~negative regulation of cell growth	5	0.651	
GO:0009199~ribonucleoside triphosphate metabolic process	9	1.173	GO:0045926~negative regulation of growth	7	0.912	
GO:0006753~nucleoside phosphate metabolic process	22	2.868	GO:0016049~cell growth	12	1.564	
GO:0046034~ATP metabolic process	8	1.043				
GO:0009259~ribonucleotide metabolic process	17	2.216	Term	Count	%	
GO:0019693~ribose phosphate metabolic process	17	2.216	GO:0044459~plasma membrane part	83	10.82	
GO:0006091~generation of precursor metabolites and energy	10	1.303	GO:0031226~intrinsic component of plasma membrane	43	5.606	
			GO:0005887~integral component of plasma membrane	38	4.954	
Term	Count	%				
GO:0014888~striated muscle adaptation	5	0.651				
GO:0043500~muscle adaptation	8	1.043	Term	Count	%	
GO:0014897~striated muscle hypertrophy	5	0.651	GO:0006826~iron ion transport	3	0.391	
GO:0014896~muscle hypertrophy	5	0.651	GO:0055076~transition metal ion homeostasis	5	0.651	
GO:0003300~cardiac muscle hypertrophy	4	0.521	GO:0055072~iron ion homeostasis	3	0.391	
			GO:0000041~transition metal ion transport	3	0.391	
Term	Count	%				
GO:0033598~mammary gland epithelial cell proliferation	3	0.391	Term	Count	%	
GO:0061180~mammary gland epithelium development	5	0.651	GO:0030595~leukocyte chemotaxis	8	1.043	
GO:0030879~mammary gland development	9	1.173	GO:0050920~regulation of chemotaxis	8	1.043	
			GO:0050900~leukocyte migration	11	1.434	
Term	Count	%	GO:0002688~regulation of leukocyte chemotaxis	4	0.521	
GO:0000910~cytokinesis	8	1.043	GO:0002685~regulation of leukocyte migration	6	0.782	
GO:0000281~mitotic cytokinesis	3	0.391	GO:0060326~cell chemotaxis	8	1.043	
GO:0061640~cytoskeleton-dependent cytokinesis	3	0.391	GO:0002690~positive regulation of leukocyte chemotaxis	3	0.391	
			GO:0002687~positive regulation of leukocyte migration	4	0.521	
Term	Count	%	GO:0050921~positive regulation of chemotaxis	4	0.521	
GO:0006261~DNA-dependent DNA replication	8	1.043	GO:0045807~positive regulation of endocytosis	4	0.521	
GO:0031297~replication fork processing	3	0.391				
GO:0051053~negative regulation of DNA metabolic process	7	0.912	Term	Count	%	
GO:0045005~DNA-dependent DNA replication maintenance of fidelity	3	0.391	GO:2000179~positive regulation of neural precursor cell proliferation	3	0.391	
			GO:2000177~regulation of neural precursor cell proliferation	4	0.521	
Term	Count	%	GO:0061351~neural precursor cell proliferation	5	0.651	
GO:0050660~flavin adenine dinucleotide binding	6	0.782				
GO:0048037~cofactor binding	14	1.825	Term	Count	%	
GO:0050662~coenzyme binding	10	1.303	GO:0032102~negative regulation of response to external stimulus	11	1.434	
			GO:0050728~negative regulation of inflammatory response	4	0.521	
Term	Count	%	GO:0031348~negative regulation of defense response	5	0.651	
GO:0051000~positive regulation of nitric-oxide synthase activity	3	0.391				
GO:0051353~positive regulation of oxidoreductase activity	4	0.521	Term	Count	%	
GO:0032770~positive regulation of monooxygenase activity	3	0.391	GO:0007595~lactation	3	0.391	
GO:0051341~regulation of oxidoreductase activity	5	0.651	GO:0032941~secretion by tissue	4	0.521	
GO:0050999~regulation of nitric-oxide synthase activity	3	0.391	GO:0007589~body fluid secretion	4	0.521	
GO:0032768~regulation of monooxygenase activity	3	0.391				
			Term	Count	%	
Term	Count	%	GO:0016817~hydrolase activity, acting on acid anhydrides	27	3.520	
GO:0009267~cellular response to starvation	9	1.173	GO:0016462~pyrophosphatase activity	25	3.259	
GO:0071496~cellular response to external stimulus	17	2.216	GO:0016818~hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	25	3.259	
GO:0042594~response to starvation	11	1.434	GO:0016887~ATPase activity	14	1.825	
GO:0031668~cellular response to extracellular stimulus	12	1.564	GO:0017111~nucleoside-triphosphatase activity	21	2.737	
GO:0031669~cellular response to nutrient levels	10	1.303				
GO:0009991~response to extracellular stimulus	24	3.129	Term	Count	%	
GO:0031667~response to nutrient levels	22	2.868	GO:0043525~positive regulation of neuron apoptotic process	4	0.521	
			GO:0043523~regulation of neuron apoptotic process	9	1.173	
Term	Count	%	GO:1901216~positive regulation of neuron death	4	0.521	
GO:0044255~cellular lipid metabolic process	44	5.736	GO:0051402~neuron apoptotic process	9	1.173	
GO:0006631~fatty acid metabolic process	18	2.346	GO:0070997~neuron death	12	1.564	
GO:0032787~monocarboxylic acid metabolic process	25	3.259	GO:1901215~negative regulation of neuron death	7	0.912	
GO:0006629~lipid metabolic process	48	6.258	GO:0043524~negative regulation of neuron apoptotic process	5	0.651	
GO:0043436~oxoacid metabolic process	33	4.302	GO:1901214~regulation of neuron death	10	1.303	
GO:0006082~organic acid metabolic process	36	4.693				
GO:0019752~carboxylic acid metabolic process	32	4.172	Term	Count	%	
GO:0044281~small molecule metabolic process	68	8.865	GO:0044853~plasma membrane raft	5	0.651	
GO:0008610~lipid biosynthetic process	21	2.737	GO:0005901~caveola	4	0.521	
			GO:0098857~membrane microdomain	10	1.303	
Term	Count	%	GO:0045121~membrane raft	10	1.303	
GO:0090090~negative regulation of canonical Wnt signaling pathway	8	1.043	GO:0098589~membrane region	11	1.434	
GO:0060070~canonical Wnt signaling pathway	13	1.694				
GO:0030178~negative regulation of Wnt signaling pathway	8	1.043	Term	Count	%	
GO:1905114~cell surface receptor signaling pathway involved in cell-cell signaling	20	2.607	GO:0044433~cytoplasmic vesicle part	11	1.434	
GO:0016055~Wnt signaling pathway	17	2.216	GO:0012506~vesicle membrane	11	1.434	
GO:0198738~cell-cell signaling by wnt	17	2.216	GO:0030659~cytoplasmic vesicle membrane	9	1.173	
GO:0060828~regulation of canonical Wnt signaling pathway	9	1.173				
GO:0030111~regulation of Wnt signaling pathway	11	1.434	Term	Count	%	
GO:0007267~cell-cell signaling	39	5.084	GO:0009607~response to biotic stimulus	37	4.823	
			GO:0002237~response to molecule of bacterial origin	15	1.955	
Term	Count	%	GO:0051704~multi-organism process	75	9.778	
GO:0061098~positive regulation of protein tyrosine kinase activity	4	0.521	GO:0009617~response to bacterium	22	2.868	
GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	10	1.303	GO:0032496~response to lipopolysaccharide	14	1.825	
GO:0018108~peptidyl-tyrosine phosphorylation	16	2.086	GO:0051707~response to other organism	32	4.172	
GO:0018212~peptidyl-tyrosine modification	16	2.086	GO:0043207~response to external biotic stimulus	32	4.172	
GO:0050730~regulation of peptidyl-tyrosine phosphorylation	11	1.434				
GO:0061097~regulation of protein tyrosine kinase activity	4	0.521	Term	Count	%	
			GO:0072657~protein localization to membrane	17	2.216	
Term	Count	%	GO:0048770~pigment granule	5	0.651	
GO:0031463~Cul3-RING ubiquitin ligase complex	5	0.651	GO:0042470~melanosome	5	0.651	
GO:0000151~ubiquitin ligase complex	14	1.825	GO:0010256~endomembrane system organization	18	2.346	
GO:0031461~cullin-RING ubiquitin ligase complex	8	1.043	GO:0072659~protein localization to plasma membrane	7	0.912	
			GO:0051650~establishment of vesicle localization	6	0.782	
Term	Count	%	GO:0007009~plasma membrane organization	9	1.173	
GO:0032612~interleukin-1 production	6	0.782	GO:0051648~vesicle localization	6	0.782	
GO:0032611~interleukin-1 beta production	5	0.651	GO:1990778~protein localization to cell periphery	7	0.912	
GO:0050702~interleukin-1 beta secretion	3	0.391	GO:0099003~vesicle mediated transport in synapse	3	0.391	
GO:0050701~interleukin-1 secretion	3	0.391	GO:0099504~synaptic vesicle cycle	3	0.391	
GO:0042742~defense response to bacterium	8	1.043	GO:0097480~establishment of synaptic vesicle localization	3	0.391	
			GO:0048489~synaptic vesicle transport	3	0.391	
Term	Count	%	GO:0097479~synaptic vesicle localization	3	0.391	
GO:1905155~positive regulation of membrane invagination	3	0.391	GO:0090002~establishment of protein localization to plasma membrane	3	0.391	
GO:0060100~positive regulation of phagocytosis, engulfment	3	0.391				
GO:0060099~regulation of phagocytosis, engulfment	3	0.391	Term	Count	%	
GO:1905153~regulation of membrane invagination	3	0.391	GO:0043296~apical junction complex	5	0.651	
GO:0006909~phagocytosis	9	1.173	GO:0005923~bicellular tight junction	4	0.521	
GO:0006911~phagocytosis, engulfment	4	0.521	GO:0070160~occluding junction	4	0.521	
GO:0050764~regulation of phagocytosis	5	0.651				
GO:0010324~membrane invagination	4	0.521	Term	Count	%	
GO:0050766~positive regulation of phagocytosis	3	0.391	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	12	1.564	
GO:0030100~regulation of endocytosis	7	0.912	GO:0043632~modification-dependent macromolecule catabolic process	19	2.477	
GO:0045807~positive regulation of endocytosis	4	0.521	GO:0009057~macromolecule catabolic process	36	4.693	
GO:0060627~regulation of vesicle-mediated transport	12	1.564	GO:0019941~modification-dependent protein catabolic process	18	2.346	
			GO:0010498~proteasomal protein catabolic process	12	1.564	
			GO:0030163~protein catabolic process	26	3.389	

Term	Count	%		GO:0006511~ubiquitin-dependent protein catabolic process	17	2.216
GO:0002705~positive regulation of leukocyte mediated immunity	9	1.173		GO:0051603~proteolysis involved in cellular protein catabolic process	20	2.607
GO:0002708~positive regulation of lymphocyte mediated immunity	8	1.043		GO:0044265~cellular macromolecule catabolic process	27	3.520
GO:0002706~regulation of lymphocyte mediated immunity	10	1.303		GO:0044257~cellular protein catabolic process	20	2.607
GO:0002703~regulation of leukocyte mediated immunity	12	1.564				
GO:0002824~positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	7	0.912				
GO:0002821~positive regulation of adaptive immune response	7	0.912	Term	Count	%	
GO:0002720~positive regulation of cytokine production involved in immune response	4	0.521	GO:0045604~regulation of epidermal cell differentiation	3	0.391	
GO:0002714~positive regulation of B cell mediated immunity	4	0.521	GO:0045682~regulation of epidermis development	3	0.391	
GO:0002891~positive regulation of immunoglobulin mediated immune response	4	0.521	GO:0060113~inner ear receptor cell differentiation	3	0.391	
GO:0002702~positive regulation of production of molecular mediator of immune response	6	0.782	GO:0042490~mechanoreceptor differentiation	3	0.391	
GO:0002699~positive regulation of immune effector process	11	1.434	GO:0048839~inner ear development	7	0.912	
GO:0002449~lymphocyte mediated immunity	13	1.694	GO:0009913~epidermal cell differentiation	5	0.651	
GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	8	1.043	GO:0043583~ear development	7	0.912	
GO:0002443~leukocyte mediated immunity	15	1.955	GO:0008544~epidermis development	7	0.912	
GO:0002819~regulation of adaptive immune response	8	1.043				
GO:0002712~regulation of B cell mediated immunity	4	0.521	Term	Count	%	
GO:0002889~regulation of immunoglobulin mediated immune response	4	0.521	GO:0098802~plasma membrane receptor complex	7	0.912	
GO:0002709~regulation of T cell mediated immunity	4	0.521	GO:0043235~receptor complex	10	1.303	
GO:0002250~adaptive immune response	14	1.825	GO:0098797~plasma membrane protein complex	12	1.564	
GO:0002718~regulation of cytokine production involved in immune response	4	0.521				
GO:0002711~positive regulation of T cell mediated immunity	3	0.391				
GO:0002700~regulation of production of molecular mediator of immune response	6	0.782				
GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	11	1.434	Term	Count	%	
GO:0016064~immunoglobulin mediated immune response	6	0.782	GO:0007601~visual perception	5	0.651	
GO:0019724~B cell mediated immunity	6	0.782	GO:0050953~sensory perception of light stimulus	5	0.651	
GO:0002367~cytokine production involved in immune response	4	0.521	GO:0007600~sensory perception	12	1.564	
GO:0002252~immune effector process	26	3.389				
GO:0002440~production of molecular mediator of immune response	7	0.912				
GO:0002456~T cell mediated immunity	4	0.521	Term	Count	%	
GO:0002697~regulation of immune effector process	15	1.955	GO:0015179~L-amino acid transmembrane transporter activity	3	0.391	
GO:0002285~lymphocyte activation involved in immune response	4	0.521	GO:0003333~amino acid transmembrane transport	3	0.391	
GO:0002366~leukocyte activation involved in immune response	5	0.651	GO:1905039~carboxylic acid transmembrane transport	3	0.391	
GO:0002263~cell activation involved in immune response	5	0.651	GO:1903825~organic acid transmembrane transport	3	0.391	
			GO:0015171~amino acid transmembrane transporter activity	3	0.391	
			GO:0006865~amino acid transport	3	0.391	
Term	Count	%	GO:0046943~carboxylic acid transmembrane transporter activity	3	0.391	
GO:0051336~regulation of hydrolase activity	54	7.040	GO:0005342~organic acid transmembrane transporter activity	3	0.391	
GO:0030234~enzyme regulator activity	36	4.693	GO:0046942~carboxylic acid transport	7	0.912	
GO:0004857~enzyme inhibitor activity	16	2.086	GO:0015849~organic acid transport	3	0.391	
GO:0098772~molecular function regulator	42	5.475	GO:0015711~organic anion transport	7	0.912	
Term	Count	%	Term	Count	%	
GO:0003007~heart morphogenesis	16	2.086	GO:0071222~cellular response to lipopolysaccharide	7	0.912	
GO:0048646~anatomical structure formation involved in morphogenesis	55	7.170	GO:0002237~response to molecule of bacterial origin	15	1.955	
GO:0007507~heart development	28	3.650	GO:0071219~cellular response to molecule of bacterial origin	7	0.912	
GO:0072359~circulatory system development	44	5.736	GO:0032496~response to lipopolysaccharide	14	1.825	
GO:0072358~cardiovascular system development	44	5.736	GO:0071216~cellular response to biotic stimulus	7	0.912	
GO:1901342~regulation of vasculature development	12	1.564	GO:0071396~cellular response to lipid	19	2.477	
GO:0045766~positive regulation of angiogenesis	7	0.912				
GO:0045765~regulation of angiogenesis	10	1.303	Term	Count	%	
GO:1904018~positive regulation of vasculature development	7	0.912	GO:0098815~modulation of excitatory postsynaptic potential	3	0.391	
GO:0001944~vasculature development	25	3.259	GO:0060079~excitatory postsynaptic potential	4	0.521	
GO:0001568~blood vessel development	23	2.998	GO:0099565~chemical synaptic transmission, postsynaptic	4	0.521	
GO:0001525~angiogenesis	15	1.955	GO:0050806~positive regulation of synaptic transmission	6	0.782	
GO:0048514~blood vessel morphogenesis	18	2.346	GO:0060291~long-term synaptic potentiation	3	0.391	
			GO:0060078~regulation of postsynaptic membrane potential	4	0.521	
Term	Count	%	GO:0007269~neurotransmitter secretion	5	0.651	
GO:0051239~regulation of multicellular organismal process	128	16.68	GO:0099643~signal release from synapse	5	0.651	
GO:0051240~positive regulation of multicellular organismal process	78	10.16	GO:0099531~presynaptic process involved in chemical synaptic transmission	5	0.651	
GO:2000026~regulation of multicellular organismal development	87	11.34	GO:0001505~regulation of neurotransmitter levels	7	0.912	
GO:0050793~regulation of developmental process	102	13.29	GO:0070382~exocytic vesicle	5	0.651	
GO:0045595~regulation of cell differentiation	77	10.03	GO:0008021~synaptic vesicle	4	0.521	
GO:0000902~cell morphogenesis	58	7.561	GO:0098793~presynapse	9	1.173	
GO:0048858~cell projection morphogenesis	39	5.084	GO:0006836~neurotransmitter transport	5	0.651	
GO:0045597~positive regulation of cell differentiation	44	5.736	GO:0050804~modulation of synaptic transmission	8	1.043	
GO:0051094~positive regulation of developmental process	55	7.170	GO:0030133~transport vesicle	6	0.782	
GO:0032990~cell part morphogenesis	39	5.084	GO:0048167~regulation of synaptic plasticity	3	0.391	
GO:0032989~cellular component morphogenesis	60	7.822	GO:0099536~synaptic signaling	12	1.564	
GO:0007409~axonogenesis	21	2.737	GO:0099537~trans-synaptic signaling	12	1.564	
GO:0030030~cell projection organization	60	7.822	GO:0098916~anterograde trans-synaptic signaling	12	1.564	
GO:0061564~axon development	21	2.737	GO:0007268~chemical synaptic transmission	12	1.564	
GO:0051962~positive regulation of nervous system development	24	3.129				
GO:0007411~axon guidance	10	1.303	Term	Count	%	
GO:0097485~neuron projection guidance	10	1.303	GO:0042130~negative regulation of T cell proliferation	3	0.391	
GO:0050770~regulation of axonogenesis	9	1.173	GO:0007162~negative regulation of cell adhesion	9	1.173	
GO:0051960~regulation of nervous system development	37	4.823	GO:0050868~negative regulation of T cell activation	4	0.521	
GO:0030182~neuron differentiation	54	7.040	GO:1903038~negative regulation of leukocyte cell-cell adhesion	4	0.521	
GO:0031346~positive regulation of cell projection organization	16	2.086	GO:0032945~negative regulation of mononuclear cell proliferation	3	0.391	
GO:0045664~regulation of neuron differentiation	27	3.520	GO:0050672~negative regulation of lymphocyte proliferation	3	0.391	
GO:0060284~regulation of cell development	39	5.084	GO:0070664~negative regulation of leukocyte proliferation	3	0.391	
GO:0048812~neuron projection morphogenesis	23	2.998	GO:0022408~negative regulation of cell-cell adhesion	5	0.651	
GO:0048468~cell development	84	10.95	GO:0051250~negative regulation of lymphocyte activation	4	0.521	
GO:0045666~positive regulation of neuron differentiation	16	2.086	GO:0002683~negative regulation of immune system process	12	1.564	
GO:0050767~regulation of neurogenesis	32	4.172	GO:0002695~negative regulation of leukocyte activation	4	0.521	
GO:0048667~cell morphogenesis involved in neuron differentiation	21	2.737	GO:0050866~negative regulation of cell activation	4	0.521	
GO:0000904~cell morphogenesis involved in differentiation	31	4.041				
GO:0048699~generation of neurons	58	7.561	Term	Count	%	
GO:0050769~positive regulation of neurogenesis	19	2.477	GO:0070509~calcium ion import	8	1.043	
GO:0031175~neuron projection development	35	4.563	GO:0072509~divalent inorganic cation transmembrane transporter activity	5	0.651	
GO:0022008~neurogenesis	61	7.953	GO:0005262~calcium channel activity	3	0.391	
GO:0010720~positive regulation of cell development	22	2.868	GO:0015085~calcium ion transmembrane transporter activity	3	0.391	
GO:0048666~neuron development	40	5.215	GO:0070588~calcium ion transmembrane transport	7	0.912	
GO:0007399~nervous system development	85	11.08				
GO:0010976~positive regulation of neuron projection development	11	1.434	Term	Count	%	
GO:0031344~regulation of cell projection organization	24	3.129	GO:0048814~regulation of dendrite morphogenesis	4	0.521	
GO:0010975~regulation of neuron projection development	18	2.346	GO:0016358~dendrite development	8	1.043	
GO:0010769~regulation of cell morphogenesis involved in differentiation	13	1.694	GO:0050773~regulation of dendrite development	5	0.651	
GO:0022604~regulation of cell morphogenesis	20	2.607				
Term	Count	%	Term	Count	%	
GO:1902041~regulation of extrinsic apoptotic signaling pathway via death domain receptors	5	0.651	GO:0035270~endocrine system development	8	1.043	
GO:0008625~extrinsic apoptotic signaling pathway via death domain receptors	6	0.782				
GO:1902043~positive regulation of extrinsic apoptotic signaling pathway via death domain receptors	3	0.391	GO:0031016~pancreas development	5	0.651	
GO:2001236~regulation of extrinsic apoptotic signaling pathway	9	1.173	GO:0031018~endocrine pancreas development	3	0.391	
GO:0097190~apoptotic signaling pathway	26	3.389	GO:0050796~regulation of insulin secretion	6	0.782	
GO:0097191~extrinsic apoptotic signaling pathway	11	1.434	GO:0010817~regulation of hormone levels	17	2.216	
GO:2001235~positive regulation of apoptotic signaling pathway	9	1.173	GO:0032024~positive regulation of insulin secretion	3	0.391	
GO:2001238~positive regulation of extrinsic apoptotic signaling pathway	4	0.521	GO:0015833~peptide transport	9	1.173	
GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	4	0.521	GO:0023061~signal release	14	1.825	
GO:2001233~regulation of apoptotic signaling pathway	14	1.825	GO:0042886~amide transport	9	1.173	
GO:2001234~negative regulation of apoptotic signaling pathway	5	0.651	GO:0046883~regulation of hormone secretion	8	1.043	
			GO:0030073~insulin secretion	5	0.651	
Term	Count	%	GO:0090276~regulation of peptide hormone secretion	6	0.782	
GO:0003283~atrial septum development	4	0.521	GO:0090277~positive regulation of peptide hormone secretion	3	0.391	
GO:0003279~cardiac septum development	9	1.173	GO:0002791~regulation of peptide secretion	6	0.782	
GO:0060976~coronary vasculature development	5	0.651	GO:0090087~regulation of peptide transport	6	0.782	
GO:0060413~atrial septum morphogenesis	3	0.391	GO:0002793~positive regulation of peptide secretion	3	0.391	
GO:0003281~ventricular septum development	6	0.782	GO:0046879~hormone secretion	9	1.173	
GO:0051100~negative regulation of binding	9	1.173	GO:0071705~nitrogen compound transport	20	2.607	
GO:0033613~activating transcription factor binding	5	0.651	GO:0009914~hormone transport	9	1.173	
GO:0003230~cardiac atrium development	4	0.521	GO:0030072~peptide hormone secretion	6	0.782	
GO:0003205~cardiac chamber development	10	1.303	GO:0046887~positive regulation of hormone secretion	3	0.391	
GO:0003231~cardiac ventricle development	8	1.043	GO:0002790~peptide secretion	6	0.782	
GO:0060411~cardiac septum morphogenesis	5	0.651				
GO:0003209~cardiac atrium morphogenesis	3	0.391				

GO:0001102~RNA polymerase II activating transcription factor binding	3	0.391	Term	Count	%	
GO:0035904~aorta development	4	0.521	GO:0004386~helicase activity	5	0.651	
GO:0060412~ventricular septum morphogenesis	3	0.391	GO:0070035~purine NTP-dependent helicase activity	3	0.391	
GO:0055008~cardiac muscle tissue morphogenesis	4	0.521	GO:0008026~ATP-dependent helicase activity	3	0.391	
GO:0014031~mesenchymal cell development	8	1.043	GO:0042623~ATPase activity, coupled	8	1.043	
GO:0060840~artery development	5	0.651				
GO:0003151~outflow tract morphogenesis	4	0.521				
GO:0048762~mesenchymal cell differentiation	8	1.043	Term	Count	%	
GO:0003206~cardiac chamber morphogenesis	6	0.782	GO:0051054~positive regulation of DNA metabolic process	8	1.043	
GO:0003208~cardiac ventricle morphogenesis	4	0.521	GO:0006282~regulation of DNA repair	3	0.391	
GO:0060415~muscle tissue morphogenesis	4	0.521	GO:2001020~regulation of response to DNA damage stimulus	3	0.391	
GO:0055010~ventricular cardiac muscle tissue morphogenesis	3	0.391				
GO:0048644~muscle organ morphogenesis	4	0.521				
GO:0003229~ventricular cardiac muscle tissue development	3	0.391	Term	Count	%	
GO:0001085~RNA polymerase II transcription factor binding	3	0.391	GO:0043200~response to amino acid	6	0.782	
GO:0048738~cardiac muscle tissue development	5	0.651	GO:0001101~response to acid chemical	15	1.955	
			GO:0071230~cellular response to amino acid stimulus	3	0.391	
			GO:0071229~cellular response to acid chemical	5	0.651	
Term	Count	%				
GO:2000377~regulation of reactive oxygen species metabolic process	12	1.564				
GO:2000379~positive regulation of reactive oxygen species metabolic process	7	0.912	Term	Count	%	
GO:0072593~reactive oxygen species metabolic process	12	1.564	GO:1904063~negative regulation of cation transmembrane transport	3	0.391	
GO:1903426~regulation of reactive oxygen species biosynthetic process	5	0.651	GO:0034766~negative regulation of ion transmembrane transport	3	0.391	
GO:1903409~reactive oxygen species biosynthetic process	5	0.651	GO:0034763~negative regulation of transmembrane transport	3	0.391	
GO:1903428~positive regulation of reactive oxygen species biosynthetic process	3	0.391	GO:1904062~regulation of cation transmembrane transport	7	0.912	
GO:0045428~regulation of nitric oxide biosynthetic process	3	0.391	GO:0043271~negative regulation of ion transport	3	0.391	
Term	Count	%	Term	Count	%	
GO:0050680~negative regulation of epithelial cell proliferation	9	1.173	GO:0048477~oogenesis	3	0.391	
GO:0050673~epithelial cell proliferation	17	2.216	GO:0007292~female gamete generation	4	0.521	
GO:0050678~regulation of epithelial cell proliferation	14	1.825	GO:0007281~germ cell development	8	1.043	
Term	Count	%	Term	Count	%	
GO:0051179~localization	228	29.72	GO:0051896~regulation of protein kinase B signaling	5	0.651	
GO:0033036~macromolecule localization	110	14.34	GO:0051897~positive regulation of protein kinase B signaling	3	0.391	
GO:1902578~single-organism localization	137	17.86	GO:0043491~protein kinase B signaling	4	0.521	
GO:0044765~single-organism transport	129	16.81				
GO:0051234~establishment of localization	173	22.55				
GO:0032879~regulation of localization	100	13.03	Term	Count	%	
GO:0006810~transport	163	21.25	GO:0030823~regulation of cGMP metabolic process	3	0.391	
GO:0015031~protein transport	61	7.953	GO:1900542~regulation of purine nucleotide metabolic process	9	1.173	
GO:0071702~organic substance transport	87	11.34	GO:0006140~regulation of nucleotide metabolic process	9	1.173	
GO:0045184~establishment of protein localization	65	8.474	GO:1900543~negative regulation of purine nucleotide metabolic process	3	0.391	
GO:0051049~regulation of transport	64	8.344	GO:0045980~negative regulation of nucleotide metabolic process	3	0.391	
			GO:0045981~positive regulation of nucleotide metabolic process	5	0.651	
			GO:1900544~positive regulation of purine nucleotide metabolic process	5	0.651	
Term	Count	%	GO:0030799~regulation of cyclic nucleotide metabolic process	5	0.651	
GO:0006487~protein N-linked glycosylation	7	0.912	GO:0030814~regulation of cAMP metabolic process	4	0.521	
GO:0030148~sphingolipid biosynthetic process	6	0.782	GO:0030804~positive regulation of cyclic nucleotide biosynthetic process	3	0.391	
GO:0046513~ceramide biosynthetic process	5	0.651	GO:0030802~regulation of cyclic nucleotide biosynthetic process	4	0.521	
GO:0006672~ceramide metabolic process	6	0.782	GO:0042451~purine nucleoside biosynthetic process	3	0.391	
GO:0046467~membrane lipid biosynthetic process	7	0.912	GO:0046129~purine ribonucleoside biosynthetic process	3	0.391	
GO:0001573~ganglioside metabolic process	3	0.391	GO:0030810~positive regulation of nucleotide biosynthetic process	3	0.391	
GO:0006665~sphingolipid metabolic process	7	0.912	GO:1900373~positive regulation of purine nucleotide biosynthetic process	3	0.391	
GO:0006643~membrane lipid metabolic process	8	1.043	GO:0030808~regulation of nucleotide biosynthetic process	4	0.521	
GO:0031300~intrinsic component of organelle membrane	7	0.912	GO:1900371~regulation of purine nucleotide biosynthetic process	4	0.521	
GO:0006687~glycosphingolipid metabolic process	3	0.391	GO:0030801~positive regulation of cyclic nucleotide metabolic process	3	0.391	
GO:0031301~integral component of organelle membrane	6	0.782	GO:0009165~nucleotide biosynthetic process	9	1.173	
GO:0006664~glycolipid metabolic process	4	0.521	GO:0030817~regulation of cAMP biosynthetic process	3	0.391	
GO:0009247~glycolipid biosynthetic process	3	0.391	GO:1901293~nucleoside phosphate biosynthetic process	9	1.173	
GO:1903509~liposaccharide metabolic process	4	0.521	GO:0052652~cyclic purine nucleotide metabolic process	4	0.521	
			GO:0006164~purine nucleotide biosynthetic process	7	0.912	
			GO:0072522~purine-containing compound biosynthetic process	7	0.912	
Term	Count	%	GO:0009190~cyclic nucleotide biosynthetic process	4	0.521	
GO:0007368~determination of left/right symmetry	8	1.043	GO:0042455~ribonucleoside biosynthetic process	3	0.391	
GO:0009855~determination of bilateral symmetry	8	1.043	GO:0009163~nucleoside biosynthetic process	3	0.391	
GO:0009799~specification of symmetry	8	1.043	GO:1901659~glycosyl compound biosynthetic process	3	0.391	
GO:0007224~smoothened signaling pathway	7	0.912	GO:0009187~cyclic nucleotide metabolic process	5	0.651	
GO:0035050~embryonic heart tube development	5	0.651	GO:0006171~cAMP biosynthetic process	3	0.391	
GO:0001947~heart looping	4	0.521	GO:0009152~purine ribonucleotide biosynthetic process	6	0.782	
GO:0009953~dorsal/ventral pattern formation	6	0.782	GO:0090407~organophosphate biosynthetic process	13	1.694	
GO:0061371~determination of heart left/right asymmetry	4	0.521	GO:0009260~ribonucleotide biosynthetic process	6	0.782	
GO:0003143~embryonic heart tube morphogenesis	4	0.521	GO:0046390~ribose phosphate biosynthetic process	6	0.782	
GO:0005930~axoneme	5	0.651	GO:0046058~cAMP metabolic process	3	0.391	
GO:0097014~ciliary plasm	5	0.651				
			Term	Count	%	
	Count	%	GO:0019867~outer membrane	6	0.782	
Term	10	1.303	GO:0031968~organelle outer membrane	5	0.651	
GO:0007051~spindle organization	7	0.912	GO:0005741~mitochondrial outer membrane	4	0.521	
GO:0051225~spindle assembly	4	0.521				
GO:0003777~microtubule motor activity	6	0.782				
GO:0005875~microtubule associated complex	3	0.391	Term	Count	%	
GO:0005871~kinesin complex	5	0.651	GO:0014910~regulation of smooth muscle cell migration	3	0.391	
GO:0003774~motor activity	7	0.912	GO:0014909~smooth muscle cell migration	3	0.391	
GO:0007018~microtubule-based movement			GO:0014812~muscle cell migration	3	0.391	
Term	Count	%	Term	Count	%	
GO:0044272~sulfur compound biosynthetic process	8	1.043	GO:0065004~protein-DNA complex assembly	7	0.912	
GO:0009108~coenzyme biosynthetic process	7	0.912	GO:0071103~DNA conformation change	8	1.043	
GO:0071616~acyl-CoA biosynthetic process	3	0.391	GO:0071824~protein-DNA complex subunit organization	7	0.912	
GO:0035384~thioester biosynthetic process	3	0.391	GO:0006334~nucleosome assembly	3	0.391	
GO:0051188~cofactor biosynthetic process	8	1.043	GO:0006323~DNA packaging	4	0.521	
GO:0006637~acyl-CoA metabolic process	3	0.391	GO:0031497~chromatin assembly	3	0.391	
GO:0035383~thioester metabolic process	3	0.391	GO:0034728~nucleosome organization	3	0.391	
			GO:0006333~chromatin assembly or disassembly	3	0.391	
Term	Count	%				
GO:0046599~regulation of centriole replication	3	0.391	Term	Count	%	
GO:0051298~centrosome duplication	5	0.651	GO:0035725~sodium ion transmembrane transport	5	0.651	
GO:0051297~centrosome organization	7	0.912	GO:0015081~sodium ion transmembrane transporter activity	4	0.521	
GO:0032886~regulation of microtubule-based process	9	1.173	GO:0006814~sodium ion transport	5	0.651	
GO:0007098~centrosome cycle	5	0.651	GO:0015077~monovalent inorganic cation transmembrane transporter activity	9	1.173	
GO:0031023~microtubule organizing center organization	7	0.912	GO:0015672~monovalent inorganic cation transport	13	1.694	
GO:0010824~regulation of centrosome duplication	3	0.391				
GO:0070507~regulation of microtubule cytoskeleton organization	7	0.912				
GO:0046605~regulation of centrosome cycle	3	0.391				
GO:0031109~microtubule polymerization or depolymerization	4	0.521	Term	Count	%	
GO:0031110~regulation of microtubule polymerization or depolymerization	3	0.391	GO:0031329~regulation of cellular catabolic process	12	1.564	
GO:1902115~regulation of organelle assembly	5	0.651	GO:0042176~regulation of protein catabolic process	11	1.434	
			GO:0061136~regulation of proteasomal protein catabolic process	4	0.521	
			GO:0032434~regulation of proteasomal ubiquitin-dependent protein catabolic process	3	0.391	
Term	Count	%	GO:1903050~regulation of proteolysis involved in cellular protein catabolic process	4	0.521	
GO:0009887~organ morphogenesis	51	6.649	GO:1903362~regulation of cellular protein catabolic process	4	0.521	
GO:0048568~embryonic organ development	27	3.520				
GO:0048562~embryonic organ morphogenesis	18	2.346				
GO:0060071~Wnt signaling pathway, planar cell polarity pathway	4	0.521	Term	Count	%	
GO:0005109~frizzled binding	4	0.521	GO:0001756~somitogenesis	3	0.391	
GO:0090175~regulation of establishment of planar polarity	4	0.521	GO:0061053~somite development	3	0.391	
GO:0048598~embryonic morphogenesis	30	3.911	GO:0035282~segmentation	3	0.391	
GO:0035567~non-canonical Wnt signaling pathway	5	0.651	GO:0009952~anterior/posterior pattern specification	6	0.782	
GO:0001736~establishment of planar polarity	4	0.521				
GO:0007164~establishment of tissue polarity	4	0.521				
GO:0090102~cochlea development	4	0.521	Term	Count	%	
GO:0035295~tube development	30	3.911	GO:0034765~regulation of ion transmembrane transport	13	1.694	
GO:2000027~regulation of organ morphogenesis	10	1.303	GO:0034762~regulation of transmembrane transport	13	1.694	
GO:0001841~neural tube formation	7	0.912	GO:0098662~inorganic cation transmembrane transport	20	2.607	
GO:0001843~neural tube closure	6	0.782				
GO:0060606~tube closure	6	0.782				
GO:0050821~protein stabilization	7	0.912	Term	Count	%	
GO:0014020~primary neural tube formation	6	0.782	GO:2001257~regulation of cation channel activity	4	0.521	
GO:0001738~morphogenesis of a polarized epithelium	4	0.521	GO:0032414~positive regulation of ion transmembrane transporter activity	3	0.391	
GO:0001838~embryonic epithelial tube formation	7	0.912	GO:0032411~positive regulation of transporter activity	3	0.391	

GO:0072175~epithelial tube formation	7	0.912	GO:0032412~regulation of ion transmembrane transporter activity	6	0.782
GO:0021915~neural tube development	8	1.043	GO:0022898~regulation of transmembrane transporter activity	6	0.782
GO:0042472~inner ear morphogenesis	5	0.651	GO:1904062~regulation of cation transmembrane transport	7	0.912
GO:0035148~tube formation	7	0.912	GO:0034767~positive regulation of ion transmembrane transport	4	0.521
GO:0060429~epithelium development	42	5.475	GO:0034764~positive regulation of transmembrane transport	4	0.521
GO:0060562~epithelial tube morphogenesis	14	1.825	GO:0032409~regulation of transporter activity	6	0.782
GO:0016331~morphogenesis of embryonic epithelium	7	0.912	GO:1904064~positive regulation of cation transmembrane transport	3	0.391
GO:0048729~tissue morphogenesis	23	2.998			
GO:0042471~ear morphogenesis	5	0.651			
GO:0035239~tube morphogenesis	14	1.825	Term	Count	%
GO:0048839~inner ear development	7	0.912	GO:0044459~plasma membrane part	83	10.82
GO:0002009~morphogenesis of an epithelium	17	2.216	GO:0071944~cell periphery	146	19.03
GO:0043583~ear development	7	0.912	GO:0005886~plasma membrane	141	18.38
Term	Count	%	Term	Count	%
GO:0005777~peroxisome	9	1.173	GO:0006626~protein targeting to mitochondrion	5	0.651
GO:0042579~microbody	9	1.173	GO:0072655~establishment of protein localization to mitochondrion	5	0.651
GO:0044438~microbody part	3	0.391	GO:0070585~protein localization to mitochondrion	5	0.651
GO:0044439~peroxisomal part	3	0.391	GO:0006839~mitochondrial transport	6	0.782
Term	Count	%	Term	Count	%
GO:0018105~peptidyl-serine phosphorylation	13	1.694	GO:0022836~gated channel activity	12	1.564
GO:0018209~peptidyl-serine modification	13	1.694	GO:1990351~transporter complex	5	0.651
GO:0033135~regulation of peptidyl-serine phosphorylation	6	0.782	GO:0034702~ion channel complex	4	0.521
			GO:1902495~transmembrane transporter complex	4	0.521
Term	Count	%	Term	Count	%
GO:0032648~regulation of interferon-beta production	4	0.521	GO:0007041~lysosomal transport	3	0.391
GO:0032479~regulation of type I interferon production	4	0.521	GO:0016197~endosomal transport	6	0.782
GO:0032606~type I interferon production	4	0.521	GO:0007034~vacuolar transport	6	0.782
GO:0032608~interferon-beta production	3	0.391			
Term	Count	%	Term	Count	%
GO:0045069~regulation of viral genome replication	6	0.782	GO:0008236~serine-type peptidase activity	7	0.912
GO:0019079~viral genome replication	6	0.782	GO:0017171~serine hydrolase activity	7	0.912
GO:1903900~regulation of viral life cycle	9	1.173	GO:0004252~serine-type endopeptidase activity	6	0.782
GO:0045070~positive regulation of viral genome replication	3	0.391			
GO:1903902~positive regulation of viral life cycle	3	0.391			
GO:0043902~positive regulation of multi-organism process	5	0.651	Term	Count	%
GO:0048524~positive regulation of viral process	3	0.391	GO:0043492~ATPase activity, coupled to movement of substances	5	0.651
			GO:0042626~ATPase activity, coupled to transmembrane movement of substances	3	0.391
			GO:0016820~hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	3	0.391
Term	Count	%	GO:0042623~ATPase activity, coupled	8	1.043
GO:0070613~regulation of protein processing	5	0.651	GO:0015399~primary active transmembrane transporter activity	3	0.391
GO:1903317~regulation of protein maturation	5	0.651	GO:0015405~P-P-bond-hydrolysis-driven transmembrane transporter activity	3	0.391
GO:0010955~negative regulation of protein processing	3	0.391			
GO:1903318~negative regulation of protein maturation	3	0.391			
			Term	Count	%
			GO:0008643~carbohydrate transport	5	0.651
Term	Count	%	GO:0008645~hexose transport	4	0.521
GO:0098581~detection of external biotic stimulus	3	0.391	GO:0015749~monosaccharide transport	4	0.521
GO:0009595~detection of biotic stimulus	3	0.391	GO:0015758~glucose transport	3	0.391
GO:0051606~detection of stimulus	5	0.651			
Term	Count	%	Term	Count	%
GO:0060452~positive regulation of cardiac muscle contraction	3	0.391	GO:0033267~axon part	10	1.303
GO:0006937~regulation of muscle contraction	10	1.303	GO:0044306~neuron projection terminus	6	0.782
GO:0045989~positive regulation of striated muscle contraction	3	0.391	GO:0043679~axon terminus	5	0.651
GO:0045823~positive regulation of heart contraction	4	0.521	GO:0043195~terminal bouton	3	0.391
GO:0006940~regulation of smooth muscle contraction	5	0.651			
GO:0055117~regulation of cardiac muscle contraction	5	0.651	Term	Count	%
GO:1903524~positive regulation of blood circulation	7	0.912	GO:0097060~synaptic membrane	10	1.303
GO:0003012~muscle system process	18	2.346	GO:0045211~postsynaptic membrane	6	0.782
GO:0045933~positive regulation of muscle contraction	4	0.521	GO:0060076~excitatory synapse	7	0.912
GO:0090257~regulation of muscle system process	11	1.434	GO:0043197~dendritic spine	4	0.521
GO:0042311~vasodilation	5	0.651	GO:0044309~neuron spine	4	0.521
GO:0006942~regulation of striated muscle contraction	5	0.651	GO:0014069~postsynaptic density	6	0.782
GO:0003018~vascular process in circulatory system	10	1.303	GO:0099572~postsynaptic specialization	6	0.782
GO:0006936~muscle contraction	13	1.694	GO:0045202~synapse	25	3.259
GO:1903522~regulation of blood circulation	12	1.564	GO:0044456~synapse part	18	2.346
GO:0008015~blood circulation	19	2.477	GO:0098794~postsynapse	9	1.173
GO:0050880~regulation of blood vessel size	8	1.043			
GO:0003013~circulatory system process	19	2.477			
GO:0035150~regulation of tube size	8	1.043	Term	Count	%
GO:0044057~regulation of system process	21	2.737	GO:0007417~central nervous system development	35	4.563
GO:0006939~smooth muscle contraction	5	0.651	GO:0007420~brain development	27	3.520
GO:0006941~striated muscle contraction	7	0.912	GO:0060322~head development	27	3.520
GO:0008016~regulation of heart contraction	7	0.912	GO:0030900~forebrain development	12	1.564
GO:0043502~regulation of muscle adaptation	4	0.521			
GO:0060047~heart contraction	7	0.912			
GO:0003015~heart process	7	0.912	Term	Count	%
GO:0060048~cardiac muscle contraction	4	0.521	GO:0090317~negative regulation of intracellular protein transport	3	0.391
GO:0019229~regulation of vasoconstriction	3	0.391	GO:0051224~negative regulation of protein transport	6	0.782
GO:0042310~vasoconstriction	3	0.391	GO:0032387~negative regulation of intracellular transport	3	0.391
			GO:1904950~negative regulation of establishment of protein localization	6	0.782
			GO:1903828~negative regulation of cellular protein localization	3	0.391
Term	Count	%			
GO:0051336~regulation of hydrolase activity	54	7.040			
GO:0008047~enzyme activator activity	17	2.216	Term	Count	%
GO:0043087~regulation of GTPase activity	22	2.868	GO:0030659~cytoplasmic vesicle membrane	9	1.173
GO:0043547~positive regulation of GTPase activity	19	2.477	GO:0030658~transport vesicle membrane	3	0.391
GO:0005096~GTPase activator activity	9	1.173	GO:0030133~transport vesicle	6	0.782
GO:0060589~nucleoside-triphosphatase regulator activity	10	1.303			
GO:0030695~GTPase regulator activity	9	1.173			
			Term	Count	%
			GO:0042552~myelination	3	0.391
Term	Count	%	GO:0007272~ensheathment of neurons	3	0.391
GO:0006111~regulation of gluconeogenesis	4	0.521	GO:0008366~axon ensheathment	3	0.391
GO:0006094~gluconeogenesis	5	0.651			
GO:0019318~hexose metabolic process	11	1.434	Term	Count	%
GO:0019319~hexose biosynthetic process	5	0.651	GO:0042995~cell projection	67	8.735
GO:0046364~monosaccharide biosynthetic process	5	0.651	GO:0036477~somatodendritic compartment	28	3.650
GO:0005996~monosaccharide metabolic process	11	1.434	GO:0044297~cell body	21	2.737
GO:0016051~carbohydrate biosynthetic process	9	1.173	GO:0097458~neuron part	49	6.388
GO:0044262~cellular carbohydrate metabolic process	12	1.564	GO:0043005~neuron projection	37	4.823
GO:0006109~regulation of carbohydrate metabolic process	9	1.173	GO:0043025~neuronal cell body	18	2.346
GO:0010906~regulation of glucose metabolic process	6	0.782	GO:0030425~dendrite	17	2.216
GO:0010675~regulation of cellular carbohydrate metabolic process	7	0.912			
GO:0006006~glucose metabolic process	8	1.043			
GO:0043255~regulation of carbohydrate biosynthetic process	4	0.521			
			Term	Count	%
			GO:0007613~memory	5	0.651
Term	Count	%	GO:0050890~cognition	8	1.043
GO:0007040~lysosome organization	4	0.521	GO:0007612~learning	4	0.521
GO:0080171~lytic vacuole organization	4	0.521	GO:0007611~learning or memory	7	0.912
GO:0007033~vacuole organization	9	1.173	GO:0044708~single-organism behavior	13	1.694
			GO:0007610~behavior	16	2.086
			GO:0050877~neurological system process	22	2.868
Term	Count	%			
GO:0070232~regulation of T cell apoptotic process	4	0.521			
GO:0070228~regulation of lymphocyte apoptotic process	5	0.651	Term	Count	%
GO:0070227~lymphocyte apoptotic process	5	0.651	GO:1903008~organelle disassembly	6	0.782
GO:0070229~negative regulation of lymphocyte apoptotic process	3	0.391	GO:0000422~mitophagy	5	0.651
GO:2000106~regulation of leukocyte apoptotic process	5	0.651	GO:0061726~mitochondrion disassembly	5	0.651
GO:0070231~T cell apoptotic process	3	0.391	GO:0006914~autophagy	12	1.564
GO:0071887~leukocyte apoptotic process	5	0.651	GO:0098779~mitophagy in response to mitochondrial depolarization	3	0.391
GO:2000107~negative regulation of leukocyte apoptotic process	3	0.391	GO:0098780~response to mitochondrial depolarisation	3	0.391
			GO:0000423~macromitophagy	3	0.391
			GO:0016236~macroautophagy	7	0.912
Term	Count	%			

GO:0000910~cytokinesis	8	1.043			
GO:0032467~positive regulation of cytokinesis	3	0.391			
GO:0032465~regulation of cytokinesis	4	0.521	Term	Count	%
GO:0030496~midbody	6	0.782	GO:0051224~negative regulation of protein transport	6	0.782
GO:0051781~positive regulation of cell division	4	0.521	GO:1904950~negative regulation of establishment of protein localization	6	0.782
GO:0051302~regulation of cell division	5	0.651	GO:0051048~negative regulation of secretion	6	0.782
			GO:0051051~negative regulation of transport	14	1.825
			GO:0050709~negative regulation of protein secretion	3	0.391
			GO:1903531~negative regulation of secretion by cell	4	0.521
Term	Count	%			
GO:0033260~nuclear DNA replication	3	0.391			
GO:0006261~DNA-dependent DNA replication	8	1.043	Term	Count	%
GO:0044786~cell cycle DNA replication	3	0.391	GO:0030017~sarcomere	5	0.651
GO:0003678~DNA helicase activity	3	0.391	GO:0044449~contractile fiber part	5	0.651
GO:0032392~DNA geometric change	3	0.391	GO:0030016~myofibril	5	0.651
GO:0004386~helicase activity	5	0.651	GO:0043292~contractile fiber	5	0.651
Term	Count	%	Term	Count	%
GO:0001941~postsynaptic membrane organization	4	0.521	GO:0008344~adult locomotory behavior	3	0.391
GO:0051668~localization within membrane	4	0.521	GO:0030534~adult behavior	4	0.521
GO:0043113~receptor clustering	3	0.391	GO:0007626~locomotory behavior	5	0.651
Term	Count	%	Term	Count	%
GO:1903901~negative regulation of viral life cycle	7	0.912	GO:0044448~cell cortex part	4	0.521
GO:0045069~regulation of viral genome replication	6	0.782	GO:0005938~cell cortex	6	0.782
GO:0019079~viral genome replication	6	0.782	GO:0099568~cytoplasmic region	6	0.782
GO:1903900~regulation of viral life cycle	9	1.173			
GO:0048525~negative regulation of viral process	7	0.912			
GO:0045071~negative regulation of viral genome replication	4	0.521	Term	Count	%
GO:0043901~negative regulation of multi-organism process	9	1.173	GO:0010721~negative regulation of cell development	10	1.303
GO:0019058~viral life cycle	11	1.434	GO:0010771~negative regulation of cell morphogenesis involved in differentiation	3	0.391
GO:0043900~regulation of multi-organism process	19	2.477	GO:0051961~negative regulation of nervous system development	8	1.043
GO:0050792~regulation of viral process	12	1.564	GO:0050768~negative regulation of neurogenesis	7	0.912
GO:0043903~regulation of symbiosis, encompassing mutualism through parasitism	13	1.694	GO:0031345~negative regulation of cell projection organization	4	0.521
GO:0002252~immune effector process	26	3.389	GO:0045665~negative regulation of neuron differentiation	5	0.651
GO:0044764~multi-organism cellular process	19	2.477	GO:0010977~negative regulation of neuron projection development	3	0.391
GO:0051607~defense response to virus	9	1.173			
GO:0044403~symbiosis, encompassing mutualism through parasitism	20	2.607			
GO:0044419~interspecies interaction between organisms	20	2.607	Term	Count	%
GO:0016032~viral process	18	2.346	GO:0016020~membrane	312	40.67
GO:0009615~response to virus	9	1.173	GO:0031224~intrinsic component of membrane	185	24.11
			GO:0016021~integral component of membrane	181	23.59
			GO:0044425~membrane part	220	28.68
Term	Count	%			
GO:0006302~double-strand break repair	10	1.303			
GO:0006310~DNA recombination	11	1.434	Term	Count	%
GO:0000724~double-strand break repair via homologous recombination	4	0.521	GO:0004871~signal transducer activity	50	6.518
GO:0000725~recombinational repair	4	0.521	GO:0004872~receptor activity	38	4.954
			GO:0060089~molecular transducer activity	38	4.954
			GO:0038023~signaling receptor activity	31	4.041
Term	Count	%	GO:0004930~G-protein coupled receptor activity	12	1.564
GO:0009898~cytoplasmic side of plasma membrane	10	1.303	GO:0004888~transmembrane signaling receptor activity	26	3.389
GO:0098562~cytoplasmic side of membrane	10	1.303	GO:0099600~transmembrane receptor activity	27	3.520
GO:0098552~side of membrane	20	2.607			
GO:0019898~extrinsic component of membrane	11	1.434			
GO:0019897~extrinsic component of plasma membrane	6	0.782			
GO:0031234~extrinsic component of cytoplasmic side of plasma membrane	4	0.521			