

Table S5. Functional enrichment analysis of the genes in the turquoise module.

Category	Term description	Term ID	Adjusted p value
GO:MF	protein binding	GO:0005515	6.43E-48
GO:MF	catalytic activity	GO:0003824	6.84E-33
GO:MF	binding	GO:0005488	1.01E-30
GO:MF	enzyme binding	GO:0019899	3.26E-17
GO:MF	transferase activity	GO:0016740	6.49E-14
GO:MF	nucleoside phosphate binding	GO:1901265	1.74E-12
GO:MF	nucleotide binding	GO:0000166	1.74E-12
GO:MF	identical protein binding	GO:0042802	3.86E-12
GO:MF	ion binding	GO:0043167	1.03E-11
GO:MF	anion binding	GO:0043168	2.78E-11
GO:MF	carbohydrate derivative binding	GO:0097367	3.06E-11
GO:MF	small molecule binding	GO:0036094	8.57E-11
GO:MF	purine nucleotide binding	GO:0017076	8.57E-11
GO:MF	ribonucleotide binding	GO:0032553	1.44E-09
GO:MF	catalytic activity, acting on a protein	GO:0140096	1.63E-09
GO:MF	purine ribonucleoside triphosphate binding	GO:0035639	1.85E-09
GO:MF	adenyl nucleotide binding	GO:0030554	2.40E-09
GO:MF	purine ribonucleotide binding	GO:0032555	4.59E-09
GO:MF	phosphatase activity	GO:0016791	6.25E-08
GO:MF	adenyl ribonucleotide binding	GO:0032559	1.23E-07
GO:MF	ATP binding	GO:0005524	1.23E-07
GO:MF	protein kinase binding	GO:0019901	1.99E-07
GO:MF	oxidoreductase activity	GO:0016491	3.31E-07
GO:MF	protein-containing complex binding	GO:0044877	4.90E-07
GO:MF	kinase binding	GO:0019900	6.09E-07
GO:MF	enzyme regulator activity	GO:0030234	9.94E-07
GO:MF	phosphoprotein phosphatase activity	GO:0004721	1.92E-06
GO:MF	cytoskeletal protein binding	GO:0008092	2.14E-06
GO:MF	phosphoric ester hydrolase activity	GO:0042578	1.77E-05
GO:MF	acyltransferase activity	GO:0016746	2.51E-05
GO:MF	protein domain specific binding	GO:0019904	4.50E-05
GO:MF	phosphotransferase activity, alcohol group as acceptor	GO:0016773	5.77E-05
GO:MF	hydrolase activity, acting on acid anhydrides	GO:0016817	6.37E-05
GO:MF	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	GO:0016818	6.90E-05
GO:MF	protein homodimerization activity	GO:0042803	8.91E-05
GO:MF	pyrophosphatase activity	GO:0016462	9.05E-05
GO:MF	ribonucleoside triphosphate phosphatase activity	GO:0017111	0.0001422
GO:MF	protein serine/threonine kinase activity	GO:0004674	0.0001684
GO:MF	kinase activity	GO:0016301	0.0003395
GO:MF	ATP-dependent activity	GO:0140657	0.0003755
GO:MF	protein kinase activity	GO:0004672	0.0005199
GO:MF	nucleoside-triphosphatase regulator activity	GO:0060589	0.0005346
GO:MF	GTPase regulator activity	GO:0030695	0.0008505
GO:MF	transferase activity, transferring phosphorus-containing groups	GO:0016772	0.0008505
GO:MF	protein tyrosine/serine/threonine phosphatase activity	GO:0008138	0.0015209
GO:MF	protein dimerization activity	GO:0046983	0.0018046
GO:MF	aminoacyltransferase activity	GO:0016755	0.0018181
GO:MF	histone binding	GO:0042393	0.0018889
GO:MF	guanyl-nucleotide exchange factor activity	GO:0005085	0.0024827
GO:MF	ubiquitin-like protein transferase activity	GO:0019787	0.0027675
GO:MF	protein-macromolecule adaptor activity	GO:0030674	0.0037102

GO:MF	cell adhesion molecule binding	GO:0050839	0.0037102
GO:MF	phosphatase binding	GO:0019902	0.0037837
GO:MF	translation regulator activity, nucleic acid binding	GO:0090079	0.0038054
GO:MF	modification-dependent protein binding	GO:0140030	0.0038054
GO:MF	oxidoreductase activity, acting on CH-OH group of donors	GO:0016614	0.0039328
GO:MF	enzyme activator activity	GO:0008047	0.0040782
GO:MF	transcription coregulator activity	GO:0003712	0.0045546
GO:MF	magnesium ion binding	GO:0000287	0.0048959
GO:MF	ATP hydrolysis activity	GO:0016887	0.0048959
GO:MF	protein tyrosine phosphatase activity	GO:0004725	0.0051425
GO:MF	transcription factor binding	GO:0008134	0.0064557
GO:MF	histone modifying activity	GO:0140993	0.0088561
GO:MF	ubiquitin-protein transferase activity	GO:0004842	0.0089203
GO:MF	actin binding	GO:0003779	0.0098505
GO:MF	flavin adenine dinucleotide binding	GO:0050660	0.0105634
GO:MF	molecular adaptor activity	GO:0060090	0.0105634
GO:MF	DNA-binding transcription factor binding	GO:0140297	0.0119819
GO:MF	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0016616	0.0140014
GO:MF	hydrolase activity	GO:0016787	0.0229192
GO:MF	translation regulator activity	GO:0045182	0.0236966
GO:MF	cation binding	GO:0043169	0.0236966
GO:MF	ubiquitin-like protein ligase activity	GO:0061659	0.0236966
GO:MF	ubiquitin protein ligase activity	GO:0061630	0.0236966
GO:MF	metal ion binding	GO:0046872	0.0236966
GO:MF	translation factor activity, RNA binding	GO:0008135	0.0246867
GO:MF	protease binding	GO:0002020	0.0308363
GO:MF	primary active transmembrane transporter activity	GO:0015399	0.0332428
GO:MF	protein heterodimerization activity	GO:0046982	0.0348961
GO:MF	translation initiation factor activity	GO:0003743	0.0348961
GO:MF	active transmembrane transporter activity	GO:0022804	0.0350347
GO:MF	telomeric DNA binding	GO:0042162	0.0410808
GO:MF	ribonucleoprotein complex binding	GO:0043021	0.0422236
GO:MF	ubiquitin-like protein binding	GO:0032182	0.0468246
GO:MF	protein serine/threonine phosphatase activity	GO:0004722	0.0468246
GO:MF	iron-sulfur cluster binding	GO:0051536	0.0468246
GO:MF	metal cluster binding	GO:0051540	0.0468246
GO:MF	carbohydrate derivative transmembrane transporter activity	GO:1901505	0.0491267
GO:BP	organonitrogen compound metabolic process	GO:1901564	4.50E-46
GO:BP	protein metabolic process	GO:0019538	4.89E-39
GO:BP	macromolecule modification	GO:0043412	6.09E-36
GO:BP	protein modification process	GO:0036211	6.29E-32
GO:BP	positive regulation of biological process	GO:0048518	1.11E-26
GO:BP	response to stress	GO:0006950	4.82E-24
GO:BP	catabolic process	GO:0009056	1.09E-21
GO:BP	positive regulation of cellular process	GO:0048522	5.09E-21
GO:BP	cellular localization	GO:0051641	2.63E-20
GO:BP	regulation of protein metabolic process	GO:0051246	1.31E-19
GO:BP	localization	GO:0051179	1.62E-19
GO:BP	intracellular signal transduction	GO:0035556	2.14E-19
GO:BP	regulation of response to stimulus	GO:0048583	2.92E-19
GO:BP	phosphorus metabolic process	GO:0006793	1.08E-17
GO:BP	phosphate-containing compound metabolic process	GO:0006796	1.74E-17
GO:BP	organic substance catabolic process	GO:1901575	7.86E-17
GO:BP	cellular response to stress	GO:0033554	1.22E-16
GO:BP	macromolecule localization	GO:0033036	1.27E-16

GO:BP	primary metabolic process	GO:0044238	1.98E-16
GO:BP	regulation of cellular component organization	GO:0051128	4.41E-16
GO:BP	cellular macromolecule localization	GO:0070727	5.26E-16
GO:BP	cellular component organization or biogenesis	GO:0071840	6.61E-16
GO:BP	protein localization	GO:0008104	8.61E-16
GO:BP	amide metabolic process	GO:0043603	2.68E-15
GO:BP	intracellular transport	GO:0046907	4.00E-15
GO:BP	positive regulation of molecular function	GO:0044093	5.43E-15
GO:BP	positive regulation of metabolic process	GO:0009893	6.35E-15
GO:BP	establishment of localization	GO:0051234	1.57E-14
GO:BP	regulation of molecular function	GO:0065009	2.26E-14
GO:BP	transport	GO:0006810	2.65E-14
GO:BP	macromolecule catabolic process	GO:0009057	6.16E-14
GO:BP	nitrogen compound metabolic process	GO:0006807	7.16E-14
GO:BP	organonitrogen compound catabolic process	GO:1901565	1.34E-13
GO:BP	cellular component organization	GO:0016043	2.17E-13
GO:BP	cellular response to chemical stimulus	GO:0070887	2.19E-13
GO:BP	small molecule metabolic process	GO:0044281	3.42E-13
GO:BP	establishment of localization in cell	GO:0051649	3.42E-13
GO:BP	response to chemical	GO:0042221	4.74E-13
GO:BP	regulation of primary metabolic process	GO:0080090	8.45E-13
GO:BP	regulation of intracellular signal transduction	GO:1902531	9.34E-13
GO:BP	organonitrogen compound biosynthetic process	GO:1901566	1.27E-12
GO:BP	peptide metabolic process	GO:0006518	1.38E-12
GO:BP	response to external stimulus	GO:0009605	1.79E-12
GO:BP	amide biosynthetic process	GO:0043604	2.19E-12
GO:BP	positive regulation of macromolecule metabolic process	GO:0010604	2.54E-12
GO:BP	immune system process	GO:0002376	3.96E-12
GO:BP	regulation of nitrogen compound metabolic process	GO:0051171	6.19E-12
GO:BP	regulation of catalytic activity	GO:0050790	6.84E-12
GO:BP	regulation of response to stress	GO:0080134	1.03E-11
GO:BP	establishment of protein localization	GO:0045184	2.36E-11
GO:BP	negative regulation of response to stimulus	GO:0048585	2.36E-11
GO:BP	positive regulation of cellular metabolic process	GO:0031325	2.79E-11
GO:BP	locomotion	GO:0040011	2.97E-11
GO:BP	positive regulation of nitrogen compound metabolic process	GO:0051173	3.60E-11
GO:BP	protein transport	GO:0015031	4.09E-11
GO:BP	regulation of cell motility	GO:2000145	4.80E-11
GO:BP	cellular catabolic process	GO:0044248	4.98E-11
GO:BP	cell death	GO:0008219	5.23E-11
GO:BP	protein catabolic process	GO:0030163	5.44E-11
GO:BP	positive regulation of protein metabolic process	GO:0051247	5.46E-11
GO:BP	programmed cell death	GO:0012501	5.57E-11
GO:BP	regulation of signal transduction	GO:0009966	6.37E-11
GO:BP	negative regulation of intracellular signal transduction	GO:1902532	6.73E-11
GO:BP	regulation of immune system process	GO:0002682	6.73E-11
GO:BP	positive regulation of response to stimulus	GO:0048584	6.73E-11
GO:BP	positive regulation of catalytic activity	GO:0043085	6.73E-11
GO:BP	response to organic substance	GO:0010033	7.35E-11
GO:BP	phosphorylation	GO:0016310	7.36E-11
GO:BP	regulation of cell migration	GO:0030334	1.00E-10
GO:BP	peptide biosynthetic process	GO:0043043	1.20E-10
GO:BP	regulation of protein modification process	GO:0031399	1.22E-10
GO:BP	apoptotic process	GO:0006915	2.44E-10
GO:BP	response to other organism	GO:0051707	2.44E-10
GO:BP	response to biotic stimulus	GO:0009607	2.44E-10

GO:BP	proteolysis involved in protein catabolic process	GO:0051603	2.46E-10
GO:BP	biological process involved in interspecies interaction between organisms	GO:0044419	2.62E-10
GO:BP	nitrogen compound transport	GO:0071705	2.79E-10
GO:BP	protein phosphorylation	GO:0006468	3.24E-10
GO:BP	organic substance transport	GO:0071702	3.38E-10
GO:BP	response to external biotic stimulus	GO:0043207	3.94E-10
GO:BP	post-translational protein modification	GO:0043687	4.05E-10
GO:BP	translation	GO:0006412	4.14E-10
GO:BP	cellular component biogenesis	GO:0044085	4.80E-10
GO:BP	regulation of locomotion	GO:0040012	5.25E-10
GO:BP	positive regulation of immune system process	GO:0002684	6.14E-10
GO:BP	regulation of catabolic process	GO:0009894	6.22E-10
GO:BP	metabolic process	GO:0008152	7.36E-10
GO:BP	developmental process	GO:0032502	7.49E-10
GO:BP	regulation of multicellular organismal process	GO:0051239	1.04E-09
GO:BP	modification-dependent macromolecule catabolic process	GO:0043632	1.52E-09
GO:BP	regulation of developmental process	GO:0050793	1.54E-09
GO:BP	immune response	GO:0006955	1.78E-09
GO:BP	modification-dependent protein catabolic process	GO:0019941	2.30E-09
GO:BP	anatomical structure development	GO:0048856	2.82E-09
GO:BP	regulation of response to external stimulus	GO:0032101	3.03E-09
GO:BP	ubiquitin-dependent protein catabolic process	GO:0006511	3.03E-09
GO:BP	organic acid metabolic process	GO:0006082	4.48E-09
GO:BP	mitochondrion organization	GO:0007005	4.70E-09
GO:BP	regulation of immune response	GO:0050776	4.79E-09
GO:BP	regulation of cellular localization	GO:0060341	5.63E-09
GO:BP	dephosphorylation	GO:0016311	5.68E-09
GO:BP	oxoacid metabolic process	GO:0043436	6.35E-09
GO:BP	cellular response to organic substance	GO:0071310	7.62E-09
GO:BP	negative regulation of nitrogen compound metabolic process	GO:0051172	9.03E-09
GO:BP	defense response to other organism	GO:0098542	9.29E-09
GO:BP	negative regulation of signal transduction	GO:0009968	1.13E-08
GO:BP	positive regulation of locomotion	GO:0040017	1.13E-08
GO:BP	regulation of protein serine/threonine kinase activity	GO:0071900	1.26E-08
GO:BP	regulation of signaling	GO:0023051	1.37E-08
GO:BP	vesicle-mediated transport	GO:0016192	1.38E-08
GO:BP	protein dephosphorylation	GO:0006470	1.45E-08
GO:BP	carboxylic acid metabolic process	GO:0019752	1.45E-08
GO:BP	positive regulation of cell migration	GO:0030335	2.04E-08
GO:BP	positive regulation of cellular component organization	GO:0051130	2.06E-08
GO:BP	cell motility	GO:0048870	2.22E-08
GO:BP	regulation of cell communication	GO:0010646	2.47E-08
GO:BP	cell migration	GO:0016477	2.72E-08
GO:BP	positive regulation of cell motility	GO:2000147	3.07E-08
GO:BP	negative regulation of protein metabolic process	GO:0051248	3.63E-08
GO:BP	hemopoiesis	GO:0030097	4.01E-08
GO:BP	negative regulation of biological process	GO:0048519	4.20E-08
GO:BP	regulation of phosphorus metabolic process	GO:0051174	4.44E-08
GO:BP	regulation of phosphate metabolic process	GO:0019220	4.93E-08
GO:BP	regulation of localization	GO:0032879	5.83E-08
GO:BP	protein modification by small protein conjugation or removal	GO:0070647	5.98E-08
GO:BP	intracellular protein transport	GO:0006886	6.28E-08
GO:BP	cell surface receptor signaling pathway	GO:0007166	7.70E-08
GO:BP	protein localization to organelle	GO:0033365	1.11E-07
GO:BP	regulation of organelle organization	GO:0033043	1.21E-07

GO:BP	DNA damage response	GO:0006974	1.33E-07
GO:BP	regulation of amide metabolic process	GO:0034248	1.34E-07
GO:BP	regulation of protein localization	GO:0032880	1.34E-07
GO:BP	negative regulation of signaling	GO:0023057	1.45E-07
GO:BP	regulation of cellular component biogenesis	GO:0044087	1.53E-07
GO:BP	cellular component assembly	GO:0022607	1.66E-07
GO:BP	cell differentiation	GO:0030154	1.80E-07
GO:BP	cellular developmental process	GO:0048869	1.80E-07
GO:BP	organelle organization	GO:0006996	2.08E-07
GO:BP	cell adhesion	GO:0007155	2.25E-07
GO:BP	protein modification by small protein conjugation	GO:0032446	2.25E-07
GO:BP	proteasomal protein catabolic process	GO:0010498	2.57E-07
GO:BP	regulation of programmed cell death	GO:0043067	2.88E-07
GO:BP	negative regulation of cell communication	GO:0010648	3.62E-07
GO:BP	regulation of phosphorylation	GO:0042325	4.27E-07
GO:BP	negative regulation of cellular process	GO:0048523	4.46E-07
GO:BP	cellular lipid metabolic process	GO:0044255	4.46E-07
GO:BP	cell activation	GO:0001775	5.14E-07
GO:BP	actin filament-based process	GO:0030029	6.49E-07
GO:BP	regulation of transferase activity	GO:0051338	7.00E-07
GO:BP	positive regulation of hydrolase activity	GO:0051345	7.51E-07
GO:BP	positive regulation of catabolic process	GO:0009896	7.89E-07
GO:BP	positive regulation of response to external stimulus	GO:0032103	1.00E-06
GO:BP	regulation of proteolysis	GO:0030162	1.04E-06
GO:BP	positive regulation of immune response	GO:0050778	1.12E-06
GO:BP	ameboidal-type cell migration	GO:0001667	1.14E-06
GO:BP	immune response-regulating cell surface receptor signaling	GO:0002768	1.16E-06
GO:BP	regulation of kinase activity	GO:0043549	1.22E-06
GO:BP	response to oxygen-containing compound	GO:1901700	1.23E-06
GO:BP	regulation of apoptotic process	GO:0042981	1.25E-06
GO:BP	defense response	GO:0006952	1.34E-06
GO:BP	carbohydrate metabolic process	GO:0005975	1.49E-06
GO:BP	regulation of protein phosphorylation	GO:0001932	1.51E-06
GO:BP	actin cytoskeleton organization	GO:0030036	1.63E-06
GO:BP	activation of immune response	GO:0002253	1.69E-06
GO:BP	proteasome-mediated ubiquitin-dependent protein catabolic process	GO:0043161	1.87E-06
GO:BP	regulation of cell adhesion	GO:0030155	1.90E-06
GO:BP	negative regulation of molecular function	GO:0044092	1.90E-06
GO:BP	carbohydrate derivative metabolic process	GO:1901135	2.05E-06
GO:BP	lipid metabolic process	GO:0006629	2.14E-06
GO:BP	protein maturation	GO:0051604	2.37E-06
GO:BP	epithelial cell migration	GO:0010631	2.40E-06
GO:BP	immune response-activating cell surface receptor signaling pathway	GO:0002429	2.40E-06
GO:BP	regulation of protein kinase activity	GO:0045859	2.74E-06
GO:BP	regulation of hydrolase activity	GO:0051336	2.92E-06
GO:BP	organic substance metabolic process	GO:0071704	2.93E-06
GO:BP	regulation of cellular catabolic process	GO:0031329	3.07E-06
GO:BP	regulation of MAPK cascade	GO:0043408	3.13E-06
GO:BP	MAPK cascade	GO:0000165	3.55E-06
GO:BP	leukocyte activation	GO:0045321	3.57E-06
GO:BP	regulation of cellular response to stress	GO:0080135	3.74E-06
GO:BP	generation of precursor metabolites and energy	GO:0006091	3.74E-06
GO:BP	tissue migration	GO:0090130	3.86E-06
GO:BP	cellular metabolic process	GO:0044237	4.01E-06
GO:BP	regulation of biological quality	GO:0065008	4.49E-06
GO:BP	protein ubiquitination	GO:0016567	4.49E-06

GO:BP	myeloid cell differentiation	GO:0030099	4.62E-06
GO:BP	regulation of intracellular transport	GO:0032386	4.62E-06
GO:BP	regulation of defense response	GO:0031347	5.03E-06
GO:BP	epithelium migration	GO:0090132	5.16E-06
GO:BP	regulation of protein-containing complex assembly	GO:0043254	7.12E-06
GO:BP	immune response-regulating signaling pathway	GO:0002764	7.15E-06
GO:BP	positive regulation of protein serine/threonine kinase activity	GO:0071902	7.21E-06
GO:BP	protein-DNA complex organization	GO:0071824	7.22E-06
GO:BP	immune effector process	GO:0002252	7.67E-06
GO:BP	response to cytokine	GO:0034097	8.50E-06
GO:BP	cellular nitrogen compound biosynthetic process	GO:0044271	9.28E-06
GO:BP	regulation of translation	GO:0006417	9.39E-06
GO:BP	cellular response to oxygen-containing compound	GO:1901701	9.68E-06
GO:BP	apoptotic signaling pathway	GO:0097190	9.72E-06
GO:BP	regulation of cell differentiation	GO:0045595	1.07E-05
GO:BP	chromatin organization	GO:0006325	1.08E-05
GO:BP	positive regulation of biosynthetic process	GO:0009891	1.26E-05
GO:BP	protein-containing complex organization	GO:0043933	1.52E-05
GO:BP	cytokine production	GO:0001816	1.53E-05
GO:BP	immune response-activating signaling pathway	GO:0002757	1.71E-05
GO:BP	positive regulation of proteolysis	GO:0045862	1.73E-05
GO:BP	multicellular organismal process	GO:0032501	2.04E-05
GO:BP	positive regulation of cellular biosynthetic process	GO:0031328	2.11E-05
GO:BP	endocytosis	GO:0006897	2.15E-05
GO:BP	circulatory system development	GO:0072359	2.15E-05
GO:BP	regulation of cell population proliferation	GO:0042127	2.25E-05
GO:BP	actin filament organization	GO:0007015	2.38E-05
GO:BP	response to lipid	GO:0033993	2.60E-05
GO:BP	regulation of cytokine production	GO:0001817	2.72E-05
GO:BP	positive regulation of cell adhesion	GO:0045785	2.74E-05
GO:BP	positive regulation of protein modification process	GO:0031401	2.76E-05
GO:BP	process utilizing autophagic mechanism	GO:0061919	2.76E-05
GO:BP	autophagy	GO:0006914	2.76E-05
GO:BP	cell cycle	GO:0007049	2.76E-05
GO:BP	muscle structure development	GO:0061061	2.99E-05
GO:BP	regulation of actin cytoskeleton organization	GO:0032956	3.05E-05
GO:BP	muscle cell differentiation	GO:0042692	3.33E-05
GO:BP	chromatin remodeling	GO:0006338	3.38E-05
GO:BP	supramolecular fiber organization	GO:0097435	3.40E-05
GO:BP	negative regulation of protein modification process	GO:0031400	3.45E-05
GO:BP	small molecule catabolic process	GO:0044282	3.50E-05
GO:BP	homeostatic process	GO:0042592	3.59E-05
GO:BP	membrane organization	GO:0061024	3.80E-05
GO:BP	enzyme-linked receptor protein signaling pathway	GO:0007167	3.93E-05
GO:BP	alcohol metabolic process	GO:0006066	4.64E-05
GO:BP	regulation of transport	GO:0051049	4.75E-05
GO:BP	regulation of epithelial cell migration	GO:0010632	5.04E-05
GO:BP	peptidyl-amino acid modification	GO:0018193	5.25E-05
GO:BP	tissue development	GO:0009888	5.25E-05
GO:BP	positive regulation of macromolecule biosynthetic process	GO:0010557	5.25E-05
GO:BP	regulation of MAP kinase activity	GO:0043405	5.28E-05
GO:BP	innate immune response	GO:0045087	5.30E-05
GO:BP	regulation of actin filament-based process	GO:0032970	5.69E-05
GO:BP	regulation of actin filament organization	GO:0110053	5.76E-05
GO:BP	lipid biosynthetic process	GO:0008610	5.76E-05
GO:BP	regulation of cell cycle	GO:0051726	5.76E-05

GO:BP	regulation of cell activation	GO:0050865	5.78E-05
GO:BP	response to oxidative stress	GO:0006979	5.78E-05
GO:BP	ncRNA processing	GO:0034470	6.06E-05
GO:BP	proteolysis	GO:0006508	6.58E-05
GO:BP	nuclear transport	GO:0051169	6.86E-05
GO:BP	monocarboxylic acid metabolic process	GO:0032787	7.27E-05
GO:BP	positive regulation of gene expression	GO:0010628	7.38E-05
GO:BP	nucleocytoplasmic transport	GO:0006913	7.90E-05
GO:BP	regulation of metabolic process	GO:0019222	8.07E-05
GO:BP	cell population proliferation	GO:0008283	8.20E-05
GO:BP	oxidative phosphorylation	GO:0006119	8.52E-05
GO:BP	regulation of multicellular organismal development	GO:2000026	8.87E-05
GO:BP	response to abiotic stimulus	GO:0009628	9.24E-05
GO:BP	vasculature development	GO:0001944	9.27E-05
GO:BP	cellular response to cytokine stimulus	GO:0071345	9.47E-05
GO:BP	lymphocyte activation	GO:0046649	9.65E-05
GO:BP	aerobic respiration	GO:0009060	0.0001117
GO:BP	multicellular organism development	GO:0007275	0.0001132
GO:BP	cell development	GO:0048468	0.0001163
GO:BP	ncRNA metabolic process	GO:0034660	0.0001202
GO:BP	actomyosin structure organization	GO:0031032	0.0001279
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GO:BP	positive regulation of phosphorus metabolic process	GO:0010562	0.0001453
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GO:BP	response to molecule of bacterial origin	GO:0002237	0.0001509
GO:BP	cellular respiration	GO:0045333	0.0001522
GO:BP	electron transport chain	GO:0022900	0.0001698
GO:BP	regulation of supramolecular fiber organization	GO:1902903	0.0001805
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GO:BP	regulation of leukocyte activation	GO:0002694	0.0002033
GO:BP	glycoprotein metabolic process	GO:0009100	0.0002072
GO:BP	positive regulation of protein localization	GO:1903829	0.0002073
GO:BP	regulation of lipid metabolic process	GO:0019216	0.0002073
GO:BP	sulfur compound metabolic process	GO:0006790	0.0002148
GO:BP	negative regulation of response to external stimulus	GO:0032102	0.000218
GO:BP	production of molecular mediator of immune response	GO:0002440	0.000218
GO:BP	signal transduction in response to DNA damage	GO:0042770	0.000218
GO:BP	anatomical structure formation involved in morphogenesis	GO:0048646	0.0002342
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GO:BP	myeloid leukocyte differentiation	GO:0002573	0.0002536
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GO:BP	establishment of protein localization to organelle	GO:0072594	0.0002721
GO:BP	small molecule biosynthetic process	GO:0044283	0.0002839
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GO:BP	response to lipopolysaccharide	GO:0032496	0.0003955
GO:BP	growth	GO:0040007	0.0004033

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GO:BP	regulation of intracellular protein transport	GO:0033157	0.0014346

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GO:BP	regulation of actin filament length	GO:0030832	0.0055061
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GO:BP	leukocyte cell-cell adhesion	GO:0007159	0.0232859
GO:BP	mesenchymal cell differentiation	GO:0048762	0.0232859
GO:BP	Golgi vesicle transport	GO:0048193	0.0233483
GO:BP	innate immune response-activating signaling pathway	GO:0002758	0.0237622
GO:BP	activation of cysteine-type endopeptidase activity involved in apoptotic process	GO:0006919	0.0239033
GO:BP	regulation of Rho protein signal transduction	GO:0035023	0.0239033
GO:BP	response to type II interferon	GO:0034341	0.0241835

GO:BP	blood vessel endothelial cell migration	GO:0043534	0.0245346
GO:BP	positive regulation of phagocytosis	GO:0050766	0.0247357
GO:BP	multicellular organismal movement	GO:0050879	0.0247357
GO:BP	regulation of nucleobase-containing compound metabolic process	GO:0019219	0.0249094
GO:BP	positive regulation of small GTPase mediated signal transduction	GO:0051057	0.0250739
GO:BP	maintenance of location in cell	GO:0051651	0.0267406
GO:BP	pattern recognition receptor signaling pathway	GO:0002221	0.0267406
GO:BP	regulation of post-translational protein modification	GO:1901873	0.0274809
GO:BP	positive regulation of cell cycle	GO:0045787	0.0278928
GO:BP	cytosolic transport	GO:0016482	0.028
GO:BP	sphingolipid biosynthetic process	GO:0030148	0.0282668
GO:BP	regulation of macroautophagy	GO:0016241	0.0282779
GO:BP	regulation of lipid biosynthetic process	GO:0046890	0.0282779
GO:BP	regulation of leukocyte migration	GO:0002685	0.0282779
GO:BP	DNA integrity checkpoint signaling	GO:0031570	0.0285345
GO:BP	organic acid biosynthetic process	GO:0016053	0.0287324
GO:BP	regulation of T cell activation	GO:0050863	0.0287557
GO:BP	negative regulation of cell differentiation	GO:0045596	0.0289146
GO:BP	glycerophospholipid biosynthetic process	GO:0046474	0.0289151
GO:BP	organophosphate biosynthetic process	GO:0090407	0.0295922
GO:BP	protein localization to cell periphery	GO:1990778	0.0297011
GO:BP	regulation of myoblast differentiation	GO:0045661	0.0303423
GO:BP	musculoskeletal movement	GO:0050881	0.0304273
GO:BP	water-soluble vitamin metabolic process	GO:0006767	0.0304273
GO:BP	positive regulation of reactive oxygen species metabolic process	GO:2000379	0.0304273
GO:BP	nucleobase-containing small molecule metabolic process	GO:0055086	0.0306077
GO:BP	system development	GO:0048731	0.030875
GO:BP	negative regulation of gene expression, epigenetic	GO:0045814	0.030875
GO:BP	regulation of viral life cycle	GO:1903900	0.030875
GO:BP	regulation of protein localization to cell periphery	GO:1904375	0.030875
GO:BP	alpha-beta T cell activation	GO:0046631	0.030875
GO:BP	lipid homeostasis	GO:0055088	0.030875
GO:BP	negative regulation of cytokine production	GO:0001818	0.030875
GO:BP	cell activation involved in immune response	GO:0002263	0.030875
GO:BP	negative regulation of translation	GO:0017148	0.0309518
GO:BP	stress-activated protein kinase signaling cascade	GO:0031098	0.0310866
GO:BP	T cell proliferation	GO:0042098	0.0315788
GO:BP	negative regulation of inflammatory response	GO:0050728	0.0318931
GO:BP	secondary alcohol metabolic process	GO:1902652	0.0319577
GO:BP	negative regulation of protein kinase activity	GO:0006469	0.0319577
GO:BP	negative regulation of post-translational protein modification	GO:1901874	0.0319577
GO:BP	regulation of actin filament bundle assembly	GO:0032231	0.0319577
GO:BP	mitochondrial respiratory chain complex assembly	GO:0033108	0.0319577
GO:BP	regulation of cell shape	GO:0008360	0.0321971
GO:BP	lymphocyte differentiation	GO:0030098	0.0326479
GO:BP	heterochromatin organization	GO:0070828	0.0329025
GO:BP	sphingolipid metabolic process	GO:0006665	0.0331025
GO:BP	DNA damage response, signal transduction by p53 class mediator	GO:0030330	0.0331025
GO:BP	protein N-linked glycosylation	GO:0006487	0.0331025
GO:BP	cellular response to nitrogen compound	GO:1901699	0.033165
GO:BP	extrinsic apoptotic signaling pathway	GO:0097191	0.0333282
GO:BP	tRNA metabolic process	GO:0006399	0.0333282
GO:BP	negative regulation of kinase activity	GO:0033673	0.0333282
GO:BP	regulation of mitotic cell cycle	GO:0007346	0.0333317
GO:BP	chromosome segregation	GO:0007059	0.033675
GO:BP	heterocycle catabolic process	GO:0046700	0.0338867

GO:BP	regulation of protein modification by small protein conjugation or removal	GO:1903320	0.0342947
GO:BP	T cell differentiation	GO:0030217	0.0342947
GO:BP	protein targeting	GO:0006605	0.0343047
GO:BP	positive regulation of protein binding	GO:0032092	0.0354923
GO:BP	receptor recycling	GO:0001881	0.0354923
GO:BP	intracellular protein transmembrane transport	GO:0065002	0.0354923
GO:BP	positive regulation of proteolysis involved in protein catabolic	GO:1903052	0.0360095
GO:BP	xenobiotic metabolic process	GO:0006805	0.036389
GO:BP	plasma membrane invagination	GO:0099024	0.036389
GO:BP	toll-like receptor 4 signaling pathway	GO:0034142	0.036389
GO:BP	positive regulation of protein dephosphorylation	GO:0035307	0.036389
GO:BP	regulation of lymphocyte mediated immunity	GO:0002706	0.0364895
GO:BP	positive regulation of ubiquitin-dependent protein catabolic process	GO:2000060	0.0364895
GO:BP	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	GO:0043280	0.0365184
GO:BP	nucleobase-containing compound catabolic process	GO:0034655	0.0371623
GO:BP	carbohydrate catabolic process	GO:0016052	0.0372169
GO:BP	vesicle-mediated transport to the plasma membrane	GO:0098876	0.0372169
GO:BP	regulation of leukocyte cell-cell adhesion	GO:1903037	0.0372719
GO:BP	carboxylic acid biosynthetic process	GO:0046394	0.0372719
GO:BP	leukocyte activation involved in immune response	GO:0002366	0.0372719
GO:BP	response to transforming growth factor beta	GO:0071559	0.0375079
GO:BP	response to heat	GO:0009408	0.0379019
GO:BP	positive regulation of binding	GO:0051099	0.0382011
GO:BP	cell-cell adhesion	GO:0098609	0.0384128
GO:BP	regulation of phagocytosis	GO:0050764	0.0385468
GO:BP	negative regulation of autophagy	GO:0010507	0.0385468
GO:BP	cardiocyte differentiation	GO:0035051	0.0390325
GO:BP	epigenetic regulation of gene expression	GO:0040029	0.0393272
GO:BP	cellular ketone metabolic process	GO:0042180	0.0403469
GO:BP	regulation of DNA-binding transcription factor activity	GO:0051090	0.0405447
GO:BP	mitotic nuclear division	GO:0140014	0.0406588
GO:BP	positive regulation of NF-kappaB transcription factor activity	GO:0051092	0.0406699
GO:BP	T cell differentiation in thymus	GO:0033077	0.0407115
GO:BP	stem cell differentiation	GO:0048863	0.0412155
GO:BP	epithelium development	GO:0060429	0.0412155
GO:BP	receptor-mediated endocytosis	GO:0006898	0.0412155
GO:BP	steroid metabolic process	GO:0008202	0.0412155
GO:BP	membrane lipid metabolic process	GO:0006643	0.0414236
GO:BP	regulation of actomyosin structure organization	GO:0110020	0.0416795
GO:BP	transport along microtubule	GO:0010970	0.0417543
GO:BP	endothelial cell development	GO:0001885	0.0418599
GO:BP	mitochondrial transmembrane transport	GO:1990542	0.0418599
GO:BP	cellular response to organic cyclic compound	GO:0071407	0.0426185
GO:BP	regulation of stress-activated protein kinase signaling cascade	GO:0070302	0.0439196
GO:BP	skeletal muscle fiber development	GO:0048741	0.0440378
GO:BP	semaphorin-plexin signaling pathway	GO:0071526	0.0440378
GO:BP	mitochondrial electron transport, NADH to ubiquinone	GO:0006120	0.0440378
GO:BP	lymphocyte migration	GO:0072676	0.044052
GO:BP	nuclear-transcribed mRNA catabolic process	GO:0000956	0.044052
GO:BP	mRNA catabolic process	GO:0006402	0.0454611
GO:BP	RNA catabolic process	GO:0006401	0.0454611
GO:BP	epithelial cell development	GO:0002064	0.0456334
GO:BP	cellular response to nutrient levels	GO:0031669	0.0456334
GO:BP	amino acid metabolic process	GO:0006520	0.0463839

GO:BP	developmental growth	GO:0048589	0.047493
GO:BP	positive regulation of proteasomal protein catabolic process	GO:1901800	0.0475984
GO:BP	regulation of nucleocytoplasmic transport	GO:0046822	0.0475984
GO:BP	B cell activation	GO:0042113	0.0498112
GO:BP	double-strand break repair	GO:0006302	0.0499808
GO:CC	cytoplasm	GO:0005737	1.42E-142
GO:CC	intracellular anatomical structure	GO:0005622	6.42E-67
GO:CC	intracellular membrane-bounded organelle	GO:0043231	2.01E-65
GO:CC	membrane-bounded organelle	GO:0043227	1.42E-64
GO:CC	cytosol	GO:0005829	2.17E-39
GO:CC	intracellular organelle	GO:0043229	5.79E-38
GO:CC	organelle	GO:0043226	9.50E-35
GO:CC	nucleoplasm	GO:0005654	9.02E-33
GO:CC	cellular anatomical entity	GO:0110165	1.02E-31
GO:CC	endomembrane system	GO:0012505	2.28E-31
GO:CC	membrane-enclosed lumen	GO:0031974	3.21E-26
GO:CC	organelle lumen	GO:0043233	3.21E-26
GO:CC	intracellular organelle lumen	GO:0070013	3.21E-26
GO:CC	catalytic complex	GO:1902494	3.97E-25
GO:CC	organelle membrane	GO:0031090	1.33E-22
GO:CC	nuclear lumen	GO:0031981	2.68E-21
GO:CC	mitochondrion	GO:0005739	3.84E-19
GO:CC	Golgi apparatus	GO:0005794	3.78E-18
GO:CC	endoplasmic reticulum	GO:0005783	3.41E-14
GO:CC	intracellular protein-containing complex	GO:0140535	4.13E-13
GO:CC	protein-containing complex	GO:0032991	5.78E-13
GO:CC	organelle envelope	GO:0031967	7.43E-13
GO:CC	envelope	GO:0031975	7.43E-13
GO:CC	nucleus	GO:0005634	1.28E-12
GO:CC	mitochondrial envelope	GO:0005740	2.70E-11
GO:CC	mitochondrial membrane	GO:0031966	2.51E-10
GO:CC	organelle subcompartment	GO:0031984	2.63E-10
GO:CC	actin cytoskeleton	GO:0015629	1.42E-09
GO:CC	mitochondrial protein-containing complex	GO:0098798	6.36E-09
GO:CC	transferase complex	GO:1990234	3.29E-08
GO:CC	mitochondrial inner membrane	GO:0005743	4.45E-08
GO:CC	bounding membrane of organelle	GO:0098588	6.46E-08
GO:CC	endoplasmic reticulum subcompartment	GO:0098827	8.08E-08
GO:CC	nuclear outer membrane-endoplasmic reticulum membrane network	GO:0042175	8.17E-08
GO:CC	endoplasmic reticulum membrane	GO:0005789	8.17E-08
GO:CC	vesicle	GO:0031982	4.41E-07
GO:CC	organelle inner membrane	GO:0019866	9.55E-07
GO:CC	nuclear body	GO:0016604	1.49E-06
GO:CC	endosome	GO:0005768	2.12E-06
GO:CC	Golgi membrane	GO:0000139	2.14E-06
GO:CC	cytoplasmic vesicle	GO:0031410	2.14E-06
GO:CC	plasma membrane	GO:0005886	2.14E-06
GO:CC	cell periphery	GO:0071944	2.48E-06
GO:CC	intracellular vesicle	GO:0097708	3.45E-06
GO:CC	inner mitochondrial membrane protein complex	GO:0098800	5.87E-06
GO:CC	sarcomere	GO:0030017	1.00E-05
GO:CC	ribosomal subunit	GO:0044391	1.37E-05
GO:CC	chromosome	GO:0005694	1.69E-05
GO:CC	perinuclear region of cytoplasm	GO:0048471	2.29E-05
GO:CC	nuclear speck	GO:0016607	2.64E-05
GO:CC	contractile fiber	GO:0043292	5.83E-05

GO:CC	membrane protein complex	GO:0098796	5.83E-05
GO:CC	ubiquitin ligase complex	GO:0000151	7.44E-05
GO:CC	cell surface	GO:0009986	8.42E-05
GO:CC	myofibril	GO:0030016	0.0001166
GO:CC	spliceosomal complex	GO:0005681	0.0001295
GO:CC	vacuole	GO:0005773	0.0001419
GO:CC	side of membrane	GO:0098552	0.0002207
GO:CC	lysosome	GO:0005764	0.0003539
GO:CC	microtubule cytoskeleton	GO:0015630	0.0003539
GO:CC	lytic vacuole	GO:0000323	0.0003539
GO:CC	mitochondrial matrix	GO:0005759	0.0004625
GO:CC	chromatin	GO:0000785	0.0005243
GO:CC	I band	GO:0031674	0.0005596
GO:CC	endopeptidase complex	GO:1905369	0.0005621
GO:CC	cytosolic ribosome	GO:0022626	0.0006768
GO:CC	protein-DNA complex	GO:0032993	0.0006773
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GO:CC	cytoplasmic ribonucleoprotein granule	GO:0036464	0.0010449
GO:CC	ribonucleoprotein granule	GO:0035770	0.001124
GO:CC	microtubule organizing center	GO:0005815	0.001174
GO:CC	focal adhesion	GO:0005925	0.0013426
GO:CC	cell-substrate junction	GO:0030055	0.0013696
GO:CC	centrosome	GO:0005813	0.0013738
GO:CC	Z disc	GO:0030018	0.00252
GO:CC	endosome membrane	GO:0010008	0.0025539
GO:CC	nuclear envelope	GO:0005635	0.0030185
GO:CC	membrane raft	GO:0045121	0.0032503
GO:CC	membrane microdomain	GO:0098857	0.0032503
GO:CC	U2-type spliceosomal complex	GO:0005684	0.0039857
GO:CC	respiratory chain complex	GO:0098803	0.0039857
GO:CC	early endosome	GO:0005769	0.0040337
GO:CC	proteasome complex	GO:0000502	0.0040337
GO:CC	oxidoreductase complex	GO:1990204	0.0040934
GO:CC	peroxisome	GO:0005777	0.0056656
GO:CC	microbody	GO:0042579	0.0056656
GO:CC	external side of plasma membrane	GO:0009897	0.006335
GO:CC	respirasome	GO:0070469	0.0078965
GO:CC	Golgi apparatus subcompartment	GO:0098791	0.0086171
GO:CC	lamellipodium	GO:0030027	0.0105525
GO:CC	large ribosomal subunit	GO:0015934	0.0126157
GO:CC	cortical actin cytoskeleton	GO:0030864	0.0133284
GO:CC	organellar ribosome	GO:0000313	0.0133284
GO:CC	mitochondrial ribosome	GO:0005761	0.0133284
GO:CC	spindle	GO:0005819	0.0133284
GO:CC	ATPase complex	GO:1904949	0.0148187
GO:CC	catalytic step 2 spliceosome	GO:0071013	0.0148187
GO:CC	mitochondrial respirasome	GO:0005746	0.0148187
GO:CC	cell leading edge	GO:0031252	0.015122
GO:CC	myosin complex	GO:0016459	0.0223729
GO:CC	cytoplasmic vesicle membrane	GO:0030659	0.0233471
GO:CC	cullin-RING ubiquitin ligase complex	GO:0031461	0.0233603
GO:CC	Cul4-RING E3 ubiquitin ligase complex	GO:0080008	0.0234965
GO:CC	mitotic spindle	GO:0072686	0.0240015
GO:CC	sarcolemma	GO:0042383	0.0240015

GO:CC	respiratory chain complex I	GO:0045271	0.0276796
GO:CC	NADH dehydrogenase complex	GO:0030964	0.0276796
GO:CC	mitochondrial respiratory chain complex I	GO:0005747	0.0276796
GO:CC	vesicle membrane	GO:0012506	0.0334816
GO:CC	mitochondrial outer membrane	GO:0005741	0.0337262
GO:CC	anchoring junction	GO:0070161	0.0339589
GO:CC	endoplasmic reticulum-Golgi intermediate compartment	GO:0005793	0.0348282
GO:CC	cytosolic small ribosomal subunit	GO:0022627	0.0348282
GO:CC	recycling endosome	GO:0055037	0.0348282
GO:CC	chromosomal region	GO:0098687	0.0420025
GO:CC	SWI/SNF superfamily-type complex	GO:0070603	0.0445528
GO:CC	outer membrane	GO:0019867	0.0466654
GO:CC	organelle outer membrane	GO:0031968	0.0466654
GO:CC	heterochromatin	GO:0000792	0.0480823