

Table S4

GO-ID	p-value	n	Total	Description
8151	7.7360E-21	2212	9276	cellular physiological process
5622	1.4058E-20	1716	6910	intracellular
44237	2.8411E-19	1665	6712	cellular metabolism
8152	6.0287E-19	1752	7132	metabolism
44238	4.2413E-16	1586	6442	primary metabolism
43227	2.2560E-15	1264	4993	membrane-bound organelle
43231	2.2560E-15	1264	4993	intracellular membrane-bound organelle
3824	5.3170E-14	1233	4895	catalytic activity
43226	2.9497E-13	1418	5764	organelle
43229	2.9497E-13	1418	5764	intracellular organelle
5737	3.2041E-12	758	2849	cytoplasm
43170	1.9956E-11	850	3272	macromolecule metabolism
44260	2.9870E-11	807	3090	cellular macromolecule metabolism
19538	1.3435E-10	761	2909	protein metabolism
44267	4.5970E-10	752	2886	cellular protein metabolism
5634	4.8937E-9	895	3548	nucleus
6464	8.1933E-8	424	1544	protein modification
7049	1.3856E-6	208	687	cell cycle
166	1.4999E-6	425	1582	nucleotide binding
3723	1.8085E-6	163	514	RNA binding
17076	2.4375E-6	417	1555	purine nucleotide binding
43283	1.1196E-5	431	1634	biopolymer metabolism
74	1.2196E-5	135	420	regulation of cell cycle
6139	1.5698E-5	750	3036	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
5739	1.7091E-5	186	622	mitochondrion
43234	1.8146E-5	426	1621	protein complex
16568	1.8225E-5	48	111	chromatin modification
44249	1.8839E-5	271	969	cellular biosynthesis
9058	2.7932E-5	300	1094	biosynthesis
16772	4.4921E-5	259	929	transferase activity, transferring phosphorus-containing groups
16740	5.7399E-5	410	1570	transferase activity
45308	5.7399E-5	629	2526	protein binding
6259	7.9723E-5	172	581	DNA metabolism
5524	1.0124E-4	321	1199	ATP binding
30554	1.2425E-4	328	1232	adenyl nucleotide binding
6796	1.2425E-4	223	793	phosphate metabolism
6793	1.2425E-4	223	793	phosphorus metabolism
16043	1.7941E-4	251	913	cell organization and biogenesis
16874	2.5111E-4	156	528	ligase activity
6996	2.5820E-4	213	760	organelle organization and biogenesis
46907	3.0320E-4	154	522	intracellular transport
8371	3.7837E-4	63	175	obsolete biological process
16288	4.9354E-4	57	155	cytokinesis
50789	5.4327E-4	769	3199	regulation of biological process
9117	6.0307E-4	67	192	nucleotide metabolism

5488	6.6941E-4	1933	8613	binding
6886	8.2712E-4	101	322	intracellular protein transport
16773	1.1613E-3	186	666	phosphotransferase activity, alcohol group as acceptor
6416	1.5006E-3	158	554	protein biosynthesis
51186	1.5393E-3	57	161	cofactor metabolism
45184	1.5393E-3	144	498	establishment of protein localization
16407	1.5393E-3	24	50	acetyltransferase activity
50794	1.5393E-3	701	2919	regulation of cellular process
50791	1.5393E-3	707	2946	regulation of physiological process
4674	1.7012E-3	125	423	protein serine/threonine kinase activity
9059	1.7080E-3	173	618	macromolecule biosynthesis
15031	1.7630E-3	143	496	protein transport
16301	1.7999E-3	218	806	kinase activity
8104	2.3109E-3	146	511	protein localization
6974	2.3442E-3	70	212	response to DNA damage stimulus
4672	2.7091E-3	159	566	protein kinase activity
6281	3.4731E-3	64	192	DNA repair
9719	3.4756E-3	73	226	response to endogenous stimulus
43037	3.5227E-3	58	170	translation
8134	4.0054E-3	87	281	transcription factor binding
16879	4.0586E-3	122	420	ligase activity, forming carbon-nitrogen bonds
31090	4.0598E-3	114	388	organelle membrane
6366	4.1554E-3	133	465	transcription from RNA polymerase II promoter
51244	4.3644E-3	663	2776	regulation of cellular physiological process
16310	4.4423E-3	176	643	phosphorylation
3676	5.2019E-3	739	3124	nucleic acid binding
6446	5.4918E-3	16	30	regulation of translational initiation
278	7.2076E-3	78	251	mitotic cell cycle
16817	8.3121E-3	146	526	hydrolase activity, acting on acid anhydrides
17111	8.9413E-3	138	494	nucleoside-triphosphatase activity
16818	8.9413E-3	145	523	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
9889	8.9413E-3	43	121	regulation of biosynthesis
7001	8.9413E-3	78	253	chromosome organization and biogenesis (sensu Eukaryota)
8361	9.5810E-3	47	136	regulation of cell size
16049	9.5810E-3	47	136	cell growth
3712	9.6167E-3	76	246	transcription cofactor activity
46483	1.0079E-2	23	53	heterocycle metabolism
16462	1.0079E-2	144	521	pyrophosphatase activity
16787	1.0378E-2	473	1948	hydrolase activity
6325	1.0576E-2	68	216	establishment and/or maintenance of chromatin architecture
6323	1.0889E-2	70	224	DNA packaging
51169	1.0940E-2	37	101	nuclear transport

49	1.1024E-2	9	13	tRNA binding
30529	1.1216E-2	99	339	ribonucleoprotein complex
45182	1.1611E-2	38	105	translation regulator activity
6605	1.1611E-2	46	134	protein targeting
6454	1.1611E-2	24	57	translational initiation
8135	1.5979E-2	37	103	translation factor activity, nucleic acid binding
6417	1.6435E-2	40	114	regulation of protein biosynthesis
4177	1.7368E-2	16	33	aminopeptidase activity
3743	1.8571E-2	25	62	translation initiation factor activity
16569	1.9599E-2	11	19	covalent chromatin modification
16570	1.9599E-2	11	19	histone modification
43122	1.9977E-2	31	83	regulation of I-kappaB kinase/NF-kappaB cascade
6913	1.9977E-2	38	108	nucleocytoplasmic transport
43123	2.2158E-2	30	80	positive regulation of I-kappaB kinase/NF-kappaB cascade
6512	2.3560E-2	150	558	ubiquitin cycle
6091	2.3986E-2	158	592	generation of precursor metabolites and energy
9165	2.4297E-2	45	135	nucleotide biosynthesis
1558	2.6058E-2	37	106	regulation of cell growth
16779	2.6058E-2	40	117	nucleotidyltransferase activity
9260	2.6058E-2	30	81	ribonucleotide biosynthesis
6445	2.6058E-2	28	74	regulation of translation
51276	2.6058E-2	89	308	chromosome organization and biogenesis
15078	2.6058E-2	48	147	hydrogen ion transporter activity
8415	2.6450E-2	41	121	acyltransferase activity
16747	2.6450E-2	41	121	transferase activity, transferring groups other than amino-acyl groups
9967	2.7031E-2	33	92	positive regulation of signal transduction
16410	2.7031E-2	19	44	N-acyltransferase activity
5654	2.7546E-2	68	225	nucleoplasm
16881	2.8920E-2	108	387	acid-amino acid ligase activity
16485	3.2232E-2	12	23	protein processing
5525	3.2546E-2	94	331	GTP binding
12505	3.3221E-2	63	207	endomembrane system
6164	3.3881E-2	29	79	purine nucleotide biosynthesis
6732	3.5041E-2	45	138	coenzyme metabolism
40008	3.5974E-2	38	112	regulation of growth
16575	3.6758E-2	7	10	histone deacetylation
9966	3.6758E-2	54	173	regulation of signal transduction
129	3.6758E-2	18	42	DNA-directed RNA polymerase activity
7582	3.6758E-2	2367	10844	physiological process
6468	3.6758E-2	144	541	protein amino acid phosphorylation
6357	3.6758E-2	74	252	regulation of transcription from RNA polymerase II promoter
51246	3.7219E-2	49	154	regulation of protein metabolism
15077	3.7866E-2	50	158	monovalent inorganic cation transporter activity

502	3.8236E-2	17	39	proteasome complex (sensu Eukaryota)
16070	3.8236E-2	113	412	RNA metabolism
3713	3.8847E-2	46	143	transcription coactivator activity
9987	3.9150E-2	2445	11225	cellular process
19001	4.2426E-2	95	339	guanyl nucleotide binding
6394	4.8004E-2	92	328	RNA processing
42623	4.8376E-2	73	251	ATPase activity, coupled
3702	4.8376E-2	65	219	RNA polymerase II transcription factor activity
279	4.8376E-2	66	223	M phase
6473	4.8590E-2	8	13	protein amino acid acetylation
4842	4.9930E-2	102	370	ubiquitin-protein ligase activity
