

Figure S1 - The comparing enrichment analysis between apoptosis and autophagy

The figure shows the complete list of the comparing enrichment analysis, including GO Molecular Function, GO biological process and GO Cellular Component, KEGG pathway and Reactome pathway.

The colour represents the p-value while the number represents the number of proteins associated with each term.

The category with lowest p-value is indicated with a black rectangle around the fill colour.

The column T represents the total number of proteins in the reference set (whole genome) associated to this functional term.

The analysis was done with g:Cocoa in the g:Profiler package.

AUTOPHAGOSOMES			P-value	T	term ID		term domain and name
APOPTOSIS							
12	8	12	5.64e-04	37		GO:0042743	BP hydrogen peroxide metabolic process (1)
5	15	23	7.44e-06	103		GO:0000041	BP transition metal ion transport (1)
4	13	17	4.12e-06	55		GO:0006826	BP iron ion transport (2)
8	22		6.60e-03	88		GO:0018196	BP peptidyl-asparagine modification (1)
8	22	14	2.09e-02	94		GO:0006487	BP protein N-linked glycosylation (1)
8	22		5.38e-03	87		GO:0018279	BP protein N-linked glycosylation via asparagine (2)
2	9		1.92e-03	22		GO:0046466	BP membrane lipid catabolic process (1)
2	7		1.64e-03	12		GO:0019377	BP glycolipid catabolic process (2)
2	9		1.19e-03	21		GO:0030149	BP sphingolipid catabolic process (1)
2	6		3.63e-03	9		GO:0046479	BP glycosphingolipid catabolic process (1)
106	153	945	1.46e-43	15771		GO:0008150	BP biological_process (1)
46	45	367	2.79e-48	4194		GO:0071840	BP cellular component organization or biogenesis (2)
21	263	154	2.43e-22	1688		GO:0044085	BP cellular component biogenesis (3)
95	123	85	4.56e-11	746		GO:0070271	BP protein complex biogenesis (4)
44	59	367	9.88e-46	4077		GO:0016043	BP cellular component organization (3)
19	24	128	8.55e-39	1181		GO:0043933	BP macromolecular complex subunit organization (4)
21	38	10	5.14e-11	111		GO:0071826	BP ribonucleoprotein complex subunit organization (5)
14	19	116	2.11e-32	870		GO:0071822	BP protein complex subunit organization (5)
37	21	7	1.51e-07	184		GO:0071824	BP protein-DNA complex subunit organization (5)
72	126	104	2.20e-21	647		GO:0061024	BP membrane organization (4)
10	23	23	1.71e-08	78		GO:0061025	BP membrane fusion (5)
94	105	53	9.06e-41	289		GO:0022411	BP cellular component disassembly (4)
87	78	43	4.93e-30	195		GO:0032984	BP macromolecular complex disassembly (5)
61	73	40	8.53e-30	173		GO:0043241	BP protein complex disassembly (6)
18	23	144	7.56e-16	1544		GO:0022607	BP cellular component assembly (4)
145	179	97	5.58e-20	1014		GO:0065003	BP macromolecular complex assembly (5)

95	127	85	3.71e-11	744	BP	GO:0006461	BP	protein complex assembly (6)
32	56		7.21e-06	287	BP	GO:0051259	BP	protein oligomerization (7)
18	33		2.36e-03	158	BP	GO:0051260	BP	protein homooligomerization (8)
186	253	189	1.20e-16	1831	BP	GO:0016265	BP	death (2)
125	174	98	1.44e-04	1342	BP	GO:0000003	BP	reproduction (2)
508	653	547	5.75e-21	7394	BP	GO:0050896	BP	response to stimulus (2)
79	110	99	1.48e-08	913	BP	GO:0009719	BP	response to endogenous stimulus (3)
46	68	64	1.64e-05	564	BP	GO:0071495	BP	cellular response to endogenous stimulus (4)
100	119	114	1.75e-04	1308	BP	GO:0009605	BP	response to external stimulus (3)
24	131	284	7.51e-21	2970	BP	GO:0042221	BP	response to chemical stimulus (3)
159	218	178	1.59e-11	1889	BP	GO:0010033	BP	response to organic substance (4)
62	92	79	3.65e-06	736	BP	GO:0009725	BP	response to hormone stimulus (5)
38	65		6.57e-04	400	BP	GO:0043434	BP	response to peptide hormone stimulus (6)
24	49		1.85e-04	259	BP	GO:0032868	BP	response to insulin stimulus (7)
19	27	22	3.14e-02	150	BP	GO:0010243	BP	response to organic nitrogen (5)
33	49	40	4.24e-02	373	BP	GO:0042493	BP	response to drug (4)
11	17	18	4.90e-03	95	BP	GO:0001101	BP	response to acid (4)
48	51	48	1.71e-05	368	BP	GO:0010035	BP	response to inorganic substance (4)
24	33	33	2.39e-03	248	BP	GO:0010038	BP	response to metal ion (5)
282	336	276	5.30e-15	3189	BP	GO:0006950	BP	response to stress (3)
23	36	24	3.84e-05	154	BP	GO:0035966	BP	response to topologically incorrect protein (4)
21	35	23	1.70e-05	143	BP	GO:0006986	BP	response to unfolded protein (5)
88	85	124	7.06e-11	1161	BP	GO:0009611	BP	response to wounding (4)
62	60	91	3.01e-14	651	BP	GO:0042060	BP	wound healing (5)
37	33	34	4.81e-04	245	BP	GO:0006979	BP	response to oxidative stress (4)
23	17	19	9.55e-04	117	BP	GO:0000302	BP	response to reactive oxygen species (5)
18	15		3.93e-03	83	BP	GO:0042542	BP	response to hydrogen peroxide (6)
13	27	9	3.66e-05	96	BP	GO:0042594	BP	response to starvation (4)
67	82	597	1.18e-11	9059	BP	GO:0065007	BP	biological regulation (2)
177	217	171	1.34e-08	1931	BP	GO:0065009	BP	regulation of molecular function (3)
118	158	121	1.07e-09	1165	BP	GO:0044093	BP	positive regulation of molecular function (4)
68	86	86	7.41e-10	705	BP	GO:0044092	BP	negative regulation of molecular function (4)
207	238	238	4.84e-18	2472	BP	GO:0065008	BP	regulation of biological quality (3)
89	105	97	1.15e-02	1162	BP	GO:0042592	BP	homeostatic process (4)
29	23	20	4.76e-02	208	BP	GO:0060249	BP	anatomical structure homeostasis (5)
49	55	87	1.43e-03	961	BP	GO:0022610	BP	biological adhesion (2)
91	82	105	1.97e-05	1184	BP	GO:0040011	BP	locomotion (2)
54	51	60	3.10e-03	596	BP	GO:0042330	BP	taxis (3)
54	51	60	3.10e-03	596	BP	GO:0006935	BP	chemotaxis (4)
314	416	375	6.77e-16	4796	BP	GO:0023052	BP	signaling (2)
141	179	175	2.63e-10	1962	BP	GO:0002376	BP	immune system process (2)
19	52	56	2.60e-12	316	BP	GO:0019882	BP	antigen processing and presentation (3)
17	42	46	1.29e-16	176	BP	GO:0019884	BP	antigen processing and presentation of exogenous antigen (4)
18	50	52	2.62e-18	206	BP	GO:0048002	BP	antigen processing and presentation of peptide antigen (4)
16	40	46	7.76e-17	174	BP	GO:0002478	BP	antigen processing and presentation of exogenous peptide antigen (5)
18	50	52	1.18e-21	177	BP	GO:0002474	BP	antigen processing and presentation of peptide antigen via MHC class I (5)
16	40	46	8.80e-20	150	BP	GO:0042590	BP	antigen processing and presentation of exogenous peptide antigen via MHC cl... (6)
15	39	42	1.05e-16	146	BP	GO:0002479	BP	antigen processing and presentation of exogenous peptide antigen via MHC cl... (7)
243	118	625	9.09e-77	9718	BP	GO:0008152	BP	metabolic process (2)
789	105	564	1.82e-59	8915	BP	GO:0044238	BP	primary metabolic process (3)
57	117	70	9.63e-08	743	BP	GO:0005975	BP	carbohydrate metabolic process (4)
239	475	301	1.27e-46	2685	BP	GO:0044281	BP	small molecule metabolic process (3)
45	88	56	1.27e-04	578	BP	GO:0006066	BP	alcohol metabolic process (4)
67	87	416	6.49e-42	7363	BP	GO:0043170	BP	macromolecule metabolic process (3)
206	303	188	1.74e-07	2521	BP	GO:0043412	BP	macromolecule modification (4)
448	548	217	5.69e-33	4380	BP	GO:0010467	BP	gene expression (4)
368	547	321	7.92e-35	3849	BP	GO:0019538	BP	protein metabolic process (4)
85	124	101	5.38e-07	1000	BP	GO:0006508	BP	proteolysis (5)
467	604	280	1.41e-23	5092	BP	GO:0009058	BP	biosynthetic process (3)

48	76	42	1.22e-07	408	GO:0044283	BP	small molecule biosynthetic process (4)
17	27	20	4.30e-04	107	GO:0046165	BP	alcohol biosynthetic process (5)
385	460	187	4.40e-19	4125	GO:0009059	BP	macromolecule biosynthetic process (4)
23	38	24	8.25e-03	205	GO:0016051	BP	carbohydrate biosynthetic process (4)
71	15	68	5.50e-27	681	GO:0055114	BP	oxidation-reduction process (3)
262	315	277	5.94e-70	2023	GO:0009056	BP	catabolic process (3)
140	135	122	5.60e-35	892	GO:0009057	BP	macromolecule catabolic process (4)
64	93	71	1.74e-09	535	GO:0030163	BP	protein catabolic process (5)
39	75	27	9.58e-14	309	GO:0044282	BP	small molecule catabolic process (4)
18	36	19	1.21e-08	118	GO:0046164	BP	alcohol catabolic process (5)
20	43	31	5.99e-08	167	GO:0016052	BP	carbohydrate catabolic process (4)
582	780	360	8.52e-47	5813	GO:0006807	BP	nitrogen compound metabolic process (3)
59	13	92	8.73e-20	640	GO:0009308	BP	amine metabolic process (4)
11	27	7	8.04e-03	123	GO:0009310	BP	amine catabolic process (5)
102	14	275	1.44e-70	13431	GO:0009987	BP	cellular process (2)
5	6	12	8.80e-05	32	GO:0022406	BP	membrane docking (3)
387	512	276	4.31e-45	3307	GO:0071841	BP	cellular component organization or biogenesis at cellular level (3)
49	69	19	1.14e-15	250	GO:0071843	BP	cellular component biogenesis at cellular level (4)
49	69	19	4.56e-17	237	GO:0022613	BP	ribonucleoprotein complex biogenesis (5)
34	40	15	4.20e-08	152	GO:0042254	BP	ribosome biogenesis (6)
7	4	5	1.61e-02	14	GO:0042273	BP	ribosomal large subunit biogenesis (6)
8	10	7	1.81e-03	19	GO:0042274	BP	ribosomal small subunit biogenesis (6)
374	432	276	1.04e-41	3205	GO:0071842	BP	cellular component organization at cellular level (4)
94	145	53	2.03e-42	278	GO:0071845	BP	cellular component disassembly at cellular level (5)
152	174	82	1.06e-39	738	GO:0034621	BP	cellular macromolecular complex subunit organization (5)
67	78	43	2.33e-32	183	GO:0034623	BP	cellular macromolecular complex disassembly (6)
61	73	40	2.43e-32	161	GO:0043624	BP	cellular protein complex disassembly (7)
18	12	9	9.85e-06	58	GO:0051261	BP	protein depolymerization (8)
140	165	102	4.77e-13	1145	GO:0071844	BP	cellular component assembly at cellular level (5)
100	107	51	1.19e-18	582	GO:0034622	BP	cellular macromolecular complex assembly (6)
32	18	6	1.40e-05	169	GO:0065004	BP	protein-DNA complex assembly (7)
48	53	37	5.59e-06	315	GO:0043623	BP	cellular protein complex assembly (7)
27	26	21	3.48e-03	163	GO:0051258	BP	protein polymerization (8)
21	37	9	3.95e-11	105	GO:0022618	BP	ribonucleoprotein complex assembly (7)
256	332	168	9.48e-30	2055	GO:0006996	BP	organelle organization (5)
48	63	22	7.05e-04	384	GO:0048285	BP	organelle fission (6)
46	58	22	4.94e-03	369	GO:0000280	BP	nuclear division (7)
14	26	10	9.74e-05	94	GO:0070925	BP	organelle assembly (6)
2	19	12	6.33e-05	53	GO:0007033	BP	vacuole organization (6)
15	39	20	1.73e-15	90	GO:0016050	BP	vesicle organization (6)
95	94	20	8.84e-09	754	GO:0051276	BP	chromosome organization (6)
19	15	4	5.52e-04	81	GO:0032200	BP	telomere organization (7)
67	53	15	5.09e-04	582	GO:0006325	BP	chromatin organization (7)
34	18	5	2.67e-07	162	GO:0034728	BP	nucleosome organization (8)
34	18	6	2.73e-06	176	GO:0006333	BP	chromatin assembly or disassembly (8)
7	14	9	8.04e-03	41	GO:0048284	BP	organelle fusion (6)
13	45	15	2.42e-07	187	GO:0007005	BP	mitochondrion organization (6)
105	110	82	4.26e-14	767	GO:0007010	BP	cytoskeleton organization (6)
85	91	97	9.53e-09	880	GO:0030030	BP	cell projection organization (5)
18	34	6	1.49e-04	148	GO:0007059	BP	chromosome segregation (3)
66	54	86	6.34e-06	839	GO:0001775	BP	cell activation (3)
67	69	65	7.60e-11	436	GO:0030029	BP	actin filament-based process (3)
12	3		5.88e-03	40	GO:0070252	BP	actin-mediated cell contraction (4)
55	63	61	1.21e-10	397	GO:0030036	BP	actin cytoskeleton organization (4)
35	36	31	5.16e-05	206	GO:0007015	BP	actin filament organization (5)
17	12		3.97e-03	75	GO:0051017	BP	actin filament bundle assembly (6)
51	48	20	2.06e-04	385	GO:0007017	BP	microtubule-based process (3)
44	36	14	2.78e-06	269	GO:0000226	BP	microtubule cytoskeleton organization (4)

20	8	4	1.60e-06	65	GO:0031023	BP	microtubule organizing center organization (5)
17	8	4	1.22e-04	60	GO:0051297	BP	centrosome organization (6)
13	7	2	8.06e-03	48	GO:0031109	BP	microtubule polymerization or depolymerization (5)
17	20	28	1.16e-03	185	GO:0034330	BP	cell junction organization (3)
7	15	19	2.75e-02	117	GO:0045216	BP	cell-cell junction organization (4)
15	18	25	4.57e-03	165	GO:0034329	BP	cell junction assembly (4)
182	224	124	1.11e-19	1437	GO:0007049	BP	cell cycle (3)
118	137	77	7.79e-17	799	GO:0000278	BP	mitotic cell cycle (4)
321	433	387	2.72e-16	4905	GO:0007154	BP	cell communication (3)
65	58	35	8.10e-07	474	GO:0051301	BP	cell division (3)
98	93	102	2.69e-05	1090	GO:0006928	BP	cellular component movement (3)
18	9		3.75e-06	55	GO:0030048	BP	actin filament-based movement (4)
11	3		3.00e-02	39	GO:0033275	BP	actin-myosin filament sliding (5)
11	3		3.00e-02	39	GO:0030049	BP	muscle filament sliding (6)
389	503	399	1.09e-14	5209	GO:0051716	BP	cellular response to stimulus (3)
15	197	115	4.83e-18	1170	GO:0033554	BP	cellular response to stress (4)
13	25	15	9.59e-04	98	GO:0034976	BP	response to endoplasmic reticulum stress (5)
85	117	61	1.11e-12	632	GO:0006974	BP	response to DNA damage stimulus (5)
141	182	161	2.86e-12	1614	GO:0070887	BP	cellular response to chemical stimulus (4)
103	142	113	1.25e-07	1223	GO:0071310	BP	cellular response to organic substance (5)
33	58	46	4.47e-03	416	GO:0032870	BP	cellular response to hormone stimulus (6)
27	51		1.51e-03	293	GO:0071375	BP	cellular response to peptide hormone stimulus (7)
21	44		5.09e-05	212	GO:0032869	BP	cellular response to insulin stimulus (8)
5	6	12	5.64e-04	37	GO:0071377	BP	cellular response to glucagon stimulus (8)
14	23	14	4.86e-03	93	GO:0035967	BP	cellular response to topologically incorrect protein (6)
12	23	14	6.96e-04	84	GO:0034620	BP	cellular response to unfolded protein (7)
23	20		1.01e-05	93	GO:0034599	BP	cellular response to oxidative stress (5)
19	14		1.12e-05	65	GO:0034614	BP	cellular response to reactive oxygen species (6)
13	12		2.71e-03	44	GO:0070301	BP	cellular response to hydrogen peroxide (7)
13	20	17	2.79e-02	97	GO:0000910	BP	cytokinesis (3)
148	176	93	2.37e-16	1106	GO:0022402	BP	cell cycle process (3)
123	144	81	2.63e-17	905	GO:0022403	BP	cell cycle phase (4)
65	79	28	3.88e-04	554	GO:0000279	BP	M phase (5)
48	58	23	2.03e-03	380	GO:0000087	BP	M phase of mitotic cell cycle (6)
74	82	56	2.48e-12	446	GO:0051325	BP	interphase (5)
74	82	54	2.50e-13	428	GO:0051329	BP	interphase of mitotic cell cycle (6)
36	53	37	1.38e-14	166	GO:0051320	BP	S phase (5)
36	52	36	1.68e-16	147	GO:0000084	BP	S phase of mitotic cell cycle (6)
46	58	22	4.94e-03	369	GO:0007067	BP	mitosis (5)
14	21	4	4.14e-02	91	GO:0000236	BP	mitotic prometaphase (5)
21	44	33	1.26e-19	93	GO:0000216	BP	M/G1 transition of mitotic cell cycle (4)
41	57	42	1.46e-10	228	GO:0000082	BP	G1/S transition of mitotic cell cycle (4)
6	12	1	1.29e-02	32	GO:0007062	BP	sister chromatid cohesion (4)
7	16		1.78e-02	55	GO:0000819	BP	sister chromatid segregation (4)
49	55	87	1.43e-03	961	GO:0007155	BP	cell adhesion (3)
786	115	577	4.69e-79	8733	GO:0044237	BP	cellular metabolic process (3)
237	375	241	3.59e-69	1729	GO:0044248	BP	cellular catabolic process (4)
8	32	13	1.85e-10	84	GO:0006914	BP	autophagy (5)
635	821	372	1.07e-45	6658	GO:0044260	BP	cellular macromolecule metabolic process (4)
34	49	283	7.00e-43	3213	GO:0044267	BP	cellular protein metabolic process (5)
50	65	39	2.73e-14	239	GO:0006457	BP	protein folding (6)
14	22	16	4.62e-05	68	GO:0006458	BP	'de novo' protein folding (7)
13	21	15	3.85e-05	62	GO:0051084	BP	'de novo' posttranslational protein folding (8)
196	294	184	1.03e-07	2419	GO:0006464	BP	protein modification process (6)
57	104	59	4.09e-11	529	GO:0070647	BP	protein modification by small protein conjugation or removal (7)
53	87	55	3.82e-09	465	GO:0032446	BP	protein modification by small protein conjugation (8)
50	80	54	1.04e-07	438	GO:0016567	BP	protein ubiquitination (9)
23	46	41	1.75e-12	178	GO:0000209	BP	protein polyubiquitination (10)
13	47	101	2.26e-37	731	GO:0044265	BP	cellular macromolecule catabolic process (5)

53	79	57	2.72e-08	419	BP	GO:0043632	BP	cellular macromolecule catabolic process (3)
56	82	61	1.30e-08	441	BP	GO:0044257	BP	modification-dependent macromolecule catabolic process (6)
56	81	60	1.49e-08	431	BP	GO:0051603	BP	cellular protein catabolic process (6)
36	57	52	8.25e-15	244	BP	GO:0010498	BP	proteolysis involved in cellular protein catabolic process (7)
53	77	57	9.57e-08	416	BP	GO:0019941	BP	proteasomal protein catabolic process (8)
52	75	56	1.61e-07	410	BP	GO:0006511	BP	modification-dependent protein catabolic process (8)
35	56	49	2.86e-13	237	BP	GO:0043161	BP	ubiquitin-dependent protein catabolic process (9)
17	39	34	3.68e-16	97	BP	GO:0031145	BP	proteasomal ubiquitin-dependent protein catabolic process (10)
27	65	24	1.40e-12	257	BP	GO:0051186	BP	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protei... (11)
24	54	20	2.13e-11	200	BP	GO:0006732	BP	cofactor metabolic process (4)
12	22	11	1.01e-06	57	BP	GO:0006733	BP	coenzyme metabolic process (5)
7	22	4	1.68e-08	48	BP	GO:0006084	BP	oxidoreduction coenzyme metabolic process (6)
9	18	4	6.80e-07	38	BP	GO:0051187	BP	acetyl-CoA metabolic process (6)
7	17	3	1.05e-07	31	BP	GO:0009109	BP	cofactor catabolic process (5)
6	17	3	1.87e-09	26	BP	GO:0046356	BP	coenzyme catabolic process (6)
60	114	64	9.16e-23	461	BP	GO:0006091	BP	acetyl-CoA catabolic process (7)
19	45	16	7.28e-11	151	BP	GO:0022900	BP	generation of precursor metabolites and energy (4)
43	89	41	2.87e-19	338	BP	GO:0015980	BP	electron transport chain (5)
20	29	26	7.16e-03	180	BP	GO:0006112	BP	energy derivation by oxidation of organic compounds (5)
21	59	15	4.70e-21	154	BP	GO:0045333	BP	energy reserve metabolic process (6)
8	23	5	9.77e-12	40	BP	GO:0009060	BP	cellular respiration (6)
6	17	3	1.87e-09	26	BP	GO:0006099	BP	aerobic respiration (7)
15	41	10	4.69e-13	113	BP	GO:0022904	BP	tricarboxylic acid cycle (8)
3	24	5	7.07e-07	66	BP	GO:0006119	BP	respiratory electron transport chain (7)
2	19	3	3.33e-04	58	BP	GO:0042773	BP	oxidative phosphorylation (5)
2	19	3	3.33e-04	58	BP	GO:0042775	BP	ATP synthesis coupled electron transport (6)
1	14	2	2.05e-02	44	BP	GO:0006120	BP	mitochondrial ATP synthesis coupled electron transport (7)
106	183	143	2.50e-23	1040	BP	GO:0046483	BP	mitochondrial electron transport, NADH to ubiquinone (8)
67	104	99	2.91e-22	580	BP	GO:0046700	BP	heterocycle metabolic process (4)
453	593	272	4.08e-23	4997	BP	GO:0044249	BP	heterocycle catabolic process (5)
4	11	4	4.04e-02	30	BP	GO:0043094	BP	cellular biosynthetic process (4)
30	60	42	7.72e-04	360	BP	GO:0018130	BP	cellular metabolic compound salvage (5)
7	32	11	2.84e-04	138	BP	GO:0051188	BP	heterocycle biosynthetic process (5)
6	23	10	2.15e-02	101	BP	GO:0009108	BP	cofactor biosynthetic process (5)
378	452	179	1.01e-18	4043	BP	GO:0034645	BP	coenzyme biosynthetic process (6)
103	107	74	2.25e-50	511	BP	GO:0006412	BP	cellular macromolecule biosynthetic process (5)
43	60	30	2.63e-35	100	BP	GO:0006415	BP	translation (6)
49	66	35	4.81e-36	119	BP	GO:0006414	BP	translational termination (7)
58	75	352	2.44e-49	5706	BP	GO:0034641	BP	translational elongation (6)
81	132	121	1.44e-23	787	BP	GO:0072521	BP	cellular nitrogen compound metabolic process (4)
68	107	101	2.70e-23	583	BP	GO:0044270	BP	purine-containing compound metabolic process (5)
63	99	88	1.09e-25	517	BP	GO:0072523	BP	cellular nitrogen compound catabolic process (5)
58	130	83	3.36e-24	551	BP	GO:0044106	BP	purine-containing compound catabolic process (6)
12	22	11	1.68e-08	48	BP	GO:0072524	BP	cellular amine metabolic process (5)
51	86	56	4.84e-05	549	BP	GO:0044271	BP	pyridine-containing compound metabolic process (5)
22	36	33	6.87e-03	260	BP	GO:0072522	BP	cellular nitrogen compound biosynthetic process (5)
55	65	319	4.61e-49	5279	BP	GO:0006139	BP	purine-containing compound biosynthetic process (6)
46	549	197	2.05e-37	4463	BP	GO:0090304	BP	nucleobase-containing compound metabolic process (5)
17	17	6	3.87e-05	56	BP	GO:0090305	BP	nucleic acid metabolic process (6)
125	130	44	9.48e-15	925	BP	GO:0006259	BP	nucleic acid phosphodiester bond hydrolysis (7)
42	38	6	9.61e-08	225	BP	GO:0071103	BP	DNA metabolic process (7)
8	11	2	4.04e-02	30	BP	GO:0032392	BP	DNA conformation change (8)
8	11	2	2.77e-02	29	BP	GO:0032508	BP	DNA geometric change (9)
35	27	5	6.77e-06	191	BP	GO:0006323	BP	DNA duplex unwinding (10)
29	14	5	8.20e-05	154	BP	GO:0031497	BP	DNA packaging (9)
28	13	4	5.85e-05	143	BP	GO:0006334	BP	chromatin assembly (10)
33	38	9	2.82e-03	221	BP	GO:0006310	BP	nucleosome assembly (11)
11	11	2	1.71e-02	37	BP	GO:0006312	BP	DNA recombination (8)
								mitotic recombination (9)

15	13	2	1.09e-06	35	GO:0022616	BP	DNA strand elongation (8)
46	51	14	2.55e-07	269	GO:0006260	BP	DNA replication (8)
18	22	2	8.07e-03	89	GO:0006261	BP	DNA-dependent DNA replication (9)
15	13	2	2.26e-07	32	GO:0006271	BP	DNA strand elongation involved in DNA replication (10)
5	6		1.85e-02	8	GO:0006268	BP	DNA unwinding involved in replication (10)
56	64	18	7.11e-06	401	GO:0006281	BP	DNA repair (8)
19	15	4	4.47e-04	80	GO:0000723	BP	telomere maintenance (8)
12	10	3	7.86e-03	41	GO:0010833	BP	telomere maintenance via telomere lengthening (9)
9	7		1.39e-02	24	GO:0032201	BP	telomere maintenance via semi-conservative replication (10)
9	7	2	4.22e-02	27	GO:0000722	BP	telomere maintenance via recombination (9)
394	475	173	3.91e-27	3890	GO:0016070	BP	RNA metabolic process (7)
283	291	115	5.78e-11	3193	GO:0032774	BP	RNA biosynthetic process (8)
25	237	90	4.58e-04	3100	GO:0006351	BP	transcription, DNA-dependent (9)
12	115	34	4.05e-03	1310	GO:0006366	BP	transcription from RNA polymerase II promoter (10)
17	21	1	1.34e-02	85	GO:0006353	BP	transcription termination, DNA-dependent (9)
14	18	1	8.14e-06	43	GO:0006369	BP	termination of RNA polymerase II transcription (10)
37	83	25	3.90e-18	312	GO:0034660	BP	ncRNA metabolic process (8)
23	34	10	9.32e-08	114	GO:0016072	BP	rRNA metabolic process (9)
11	35	13	3.65e-05	147	GO:0006399	BP	tRNA metabolic process (9)
174	243	84	1.08e-89	671	GO:0016071	BP	mRNA metabolic process (8)
135	175	31	4.25e-39	679	GO:0006396	BP	RNA processing (8)
29	48	13	1.30e-06	217	GO:0034470	BP	ncRNA processing (9)
23	34	10	1.74e-08	108	GO:0006364	BP	rRNA processing (10)
27	27	8	1.31e-09	87	GO:0031123	BP	RNA 3'-end processing (9)
87	111	13	5.15e-33	341	GO:0008380	BP	RNA splicing (9)
71	91	7	6.96e-36	225	GO:0000375	BP	RNA splicing, via transesterification reactions (10)
68	90	7	6.08e-36	220	GO:0000377	BP	RNA splicing, via transesterification reactions with bulged adenosine as nu... (11)
101	121	14	2.21e-31	418	GO:0006397	BP	mRNA processing (9)
25	24	6	7.64e-10	73	GO:0031124	BP	mRNA 3'-end processing (10)
68	90	7	6.08e-36	220	GO:0000398	BP	nuclear mRNA splicing, via spliceosome (10)
9	8		9.15e-03	23	GO:0000380	BP	alternative nuclear mRNA splicing, via spliceosome (11)
4	14	2	3.59e-04	33	GO:0000387	BP	spliceosomal snRNP assembly (11)
10	15	1	7.06e-03	46	GO:0000245	BP	spliceosome assembly (11)
61	88	36	6.53e-33	227	GO:0006401	BP	RNA catabolic process (8)
57	83	35	1.59e-33	200	GO:0006402	BP	mRNA catabolic process (9)
57	81	35	1.33e-35	181	GO:0000956	BP	nuclear-transcribed mRNA catabolic process (10)
50	68	32	7.19e-36	127	GO:0000184	BP	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (11)
31	49	39	1.12e-03	310	GO:0034654	BP	nucleobase-containing compound biosynthetic process (6)
65	103	101	1.70e-24	554	GO:0034655	BP	nucleobase-containing compound catabolic process (6)
104	169	141	1.08e-27	913	GO:0055086	BP	nucleobase-containing small molecule metabolic process (6)
97	159	133	3.40e-26	866	GO:0006753	BP	nucleoside phosphate metabolic process (7)
97	159	133	3.40e-26	866	GO:0009117	BP	nucleotide metabolic process (8)
70	117	107	2.39e-29	550	GO:0009259	BP	ribonucleotide metabolic process (9)
64	109	101	6.70e-27	528	GO:0009141	BP	nucleoside triphosphate metabolic process (9)
62	105	101	4.35e-27	516	GO:0009199	BP	ribonucleoside triphosphate metabolic process (10)
12	22	11	1.68e-08	48	GO:0019362	BP	pyridine nucleotide metabolic process (9)
12	22	11	3.26e-09	45	GO:0046496	BP	nicotinamide nucleotide metabolic process (10)
6	11	7	1.75e-03	23	GO:0006739	BP	NADP metabolic process (11)
6	9	6	2.47e-04	13	GO:0006740	BP	NADPH regeneration (12)
6	11	4	2.99e-03	24	GO:0019674	BP	NAD metabolic process (11)
77	126	118	6.41e-24	748	GO:0006163	BP	purine nucleotide metabolic process (9)
70	114	104	4.75e-28	540	GO:0009150	BP	purine ribonucleotide metabolic process (10)
62	106	99	3.30e-26	519	GO:0009144	BP	purine nucleoside triphosphate metabolic process (10)
62	104	99	1.72e-26	515	GO:0009205	BP	purine ribonucleoside triphosphate metabolic process (11)
35	59	64	3.05e-13	380	GO:0046039	BP	GTP metabolic process (12)
27	45	35	1.28e-12	137	GO:0046034	BP	ATP metabolic process (12)
28	45	37	1.99e-03	293	GO:0009165	BP	nucleotide biosynthetic process (9)
15	28	21	2.82e-06	92	GO:0009260	BP	ribonucleotide biosynthetic process (10)
8	18	14	1.37e-02	66	GO:0009142	BP	nucleoside triphosphate biosynthetic process (10)

8	18	14	1.37e-02	66	GO:0009142	BP	nucleoside triphosphate biosynthetic process (10)
8	17	14	1.14e-02	64	GO:0009201	BP	ribonucleoside triphosphate biosynthetic process (11)
20	32	30	4.54e-02	247	GO:0006164	BP	purine nucleotide biosynthetic process (10)
8	17	13	3.58e-02	64	GO:0009145	BP	purine nucleoside triphosphate biosynthetic process (11)
15	26	18	7.25e-06	84	GO:0009152	BP	purine ribonucleotide biosynthetic process (11)
8	16	13	4.83e-02	63	GO:0009206	BP	purine ribonucleoside triphosphate biosynthetic process (12)
8	15	12	2.43e-02	51	GO:0006754	BP	ATP biosynthetic process (13)
64	102	100	4.95e-26	531	GO:0009166	BP	nucleotide catabolic process (9)
60	95	91	1.65e-24	468	GO:0009261	BP	ribonucleotide catabolic process (10)
59	95	90	5.53e-24	466	GO:0009143	BP	nucleoside triphosphate catabolic process (10)
58	93	89	1.13e-23	461	GO:0009203	BP	ribonucleoside triphosphate catabolic process (11)
63	99	98	4.88e-26	512	GO:0006195	BP	purine nucleotide catabolic process (10)
60	94	91	1.18e-24	466	GO:0009154	BP	purine ribonucleotide catabolic process (11)
58	94	89	1.33e-23	462	GO:0009146	BP	purine nucleoside triphosphate catabolic process (11)
58	93	89	1.13e-23	461	GO:0009207	BP	purine ribonucleoside triphosphate catabolic process (12)
23	35	25	2.91e-11	94	GO:0006200	BP	ATP catabolic process (13)
35	58	64	6.81e-14	369	GO:0006184	BP	GTP catabolic process (13)
88	139	110	2.87e-29	908	GO:0042180	BP	cellular ketone metabolic process (4)
87	138	112	1.41e-29	896	GO:0006082	BP	organic acid metabolic process (4)
87	137	109	9.76e-30	879	GO:0043436	BP	oxoacid metabolic process (5)
87	137	109	9.76e-30	879	GO:0019752	BP	carboxylic acid metabolic process (6)
8	19	6	9.31e-06	48	GO:0043648	BP	dicarboxylic acid metabolic process (7)
4	7	2	1.59e-02	11	GO:0006107	BP	oxaloacetate metabolic process (8)
53	126	78	8.42e-30	463	GO:0006520	BP	cellular amino acid metabolic process (7)
7	25	12	3.25e-08	63	GO:0043038	BP	amino acid activation (8)
7	25	12	3.25e-08	63	GO:0043039	BP	tRNA aminoacylation (9)
7	25	12	5.64e-09	59	GO:0006418	BP	tRNA aminoacylation for protein translation (10)
10	18	9	6.61e-03	63	GO:0009064	BP	glutamine family amino acid metabolic process (8)
19	39	8	2.01e-04	185	GO:0016054	BP	organic acid catabolic process (5)
19	39	8	2.01e-04	185	GO:0046395	BP	carboxylic acid catabolic process (6)
11	26	6	4.78e-03	113	GO:0009063	BP	cellular amino acid catabolic process (7)
31	45	22	3.43e-02	275	GO:0016053	BP	organic acid biosynthetic process (5)
31	45	22	3.43e-02	275	GO:0046394	BP	carboxylic acid biosynthetic process (6)
14	22	9	2.99e-02	96	GO:0008652	BP	cellular amino acid biosynthetic process (7)
44	98	58	6.04e-08	578	GO:0044262	BP	cellular carbohydrate metabolic process (4)
20	40	23	6.60e-09	139	GO:0044275	BP	cellular carbohydrate catabolic process (5)
20	37	22	5.08e-07	139	GO:0034637	BP	cellular carbohydrate biosynthetic process (5)
29	66	39	9.62e-09	314	GO:0005996	BP	monosaccharide metabolic process (5)
18	33	18	1.12e-08	101	GO:0046365	BP	monosaccharide catabolic process (6)
17	25	18	2.04e-05	82	GO:0046364	BP	monosaccharide biosynthetic process (6)
29	62	35	4.34e-10	267	GO:0019318	BP	hexose metabolic process (6)
18	31	17	9.31e-08	97	GO:0019320	BP	hexose catabolic process (7)
26	59	28	3.41e-12	223	GO:0006006	BP	glucose metabolic process (7)
17	29	16	1.64e-08	81	GO:0006007	BP	glucose catabolic process (8)
13	22	13	4.62e-05	68	GO:0006096	BP	glycolysis (9)
6	8	5	2.02e-03	12	GO:0006098	BP	pentose-phosphate shunt (9)
13	19	12	8.25e-03	70	GO:0019319	BP	hexose biosynthetic process (7)
12	18	12	3.95e-03	61	GO:0006094	BP	gluconeogenesis (8)
186	253	185	1.06e-16	1829	GO:0008219	BP	cell death (3)
175	234	172	9.85e-15	1669	GO:0012501	BP	programmed cell death (4)
173	231	168	1.20e-13	1656	GO:0006915	BP	apoptotic process (5)
29	25	12	5.10e-13	77	GO:0006921	BP	cellular component disassembly involved in apoptosis (6)
72	126	103	6.38e-21	645	GO:0016044	BP	cellular membrane organization (3)
42	51	48	3.59e-06	351	GO:0010324	BP	membrane invagination (4)
10	23	22	7.31e-08	76	GO:0006944	BP	cellular membrane fusion (4)
2	12	3	1.29e-02	32	GO:0007006	BP	mitochondrial membrane organization (4)
45	62	70	2.65e-05	649	GO:0019725	BP	cellular homeostasis (3)
60	92	41	1.76e-37	177	GO:0006413	BP	translational initiation (3)
98	155	85	2.24e-43	515	GO:0016032	BP	viral reproduction (2)

36343571	3.90e-04	5609	BP	G0:0032501	BP	multicellular organismal process (2)
54 55 82	2.29e-15	528	BP	G0:0050817	BP	coagulation (3)
60 60 87	1.42e-13	621	BP	G0:0050878	BP	regulation of body fluid levels (3)
56 56 82	2.29e-15	528	BP	G0:0007599	BP	hemostasis (4)
53 54 80	1.75e-14	524	BP	G0:0007596	BP	blood coagulation (5)
31 23 44	6.14e-11	223	BP	G0:0030168	BP	platelet activation (6)
299380500	1.29e-03	4421	BP	G0:0032502	BP	developmental process (2)
265323267	3.74e-04	3799	BP	G0:0048856	BP	anatomical structure development (3)
236283235	3.43e-03	3352	BP	G0:0048731	BP	system development (4)
143161155	8.34e-04	1984	BP	G0:0009653	BP	anatomical structure morphogenesis (3)
386568455	1.11e-53	4383	BP	G0:0051179	BP	localization (2)
244574265	3.40e-59	1818	BP	G0:0033036	BP	macromolecule localization (3)
209322245	4.89e-55	1555	BP	G0:0008104	BP	protein localization (4)
35 45 7	4.33e-12	141	BP	G0:0006403	BP	RNA localization (4)
58 55 75	1.32e-02	838	BP	G0:0051674	BP	localization of cell (3)
58 55 75	1.32e-02	838	BP	G0:0048870	BP	cell motility (4)
51 51 72	7.24e-03	781	BP	G0:0016477	BP	cell migration (5)
15 17 32	3.98e-03	242	BP	G0:0050900	BP	leukocyte migration (6)
241573254	2.60e-55	1950	BP	G0:0051641	BP	cellular localization (3)
25 44 18	1.18e-10	147	BP	G0:0051640	BP	organelle localization (4)
10 28 13	1.04e-10	64	BP	G0:0051648	BP	vesicle localization (5)
138223134	6.45e-49	868	BP	G0:0070727	BP	cellular macromolecule localization (4)
137213134	1.12e-48	864	BP	G0:0034613	BP	cellular protein localization (5)
89 135 68	1.92e-32	493	BP	G0:0033365	BP	protein localization to organelle (6)
46 70 37	9.64e-39	125	BP	G0:0070972	BP	protein localization in endoplasmic reticulum (7)
4 17 5	1.67e-05	40	BP	G0:0070585	BP	protein localization in mitochondrion (7)
33 36 27	3.25e-02	247	BP	G0:0034504	BP	protein localization to nucleus (7)
118137117	1.85e-09	1120	BP	G0:0051704	BP	multi-organism process (2)
73 81 64	1.04e-10	468	BP	G0:0044419	BP	interspecies interaction between organisms (3)
333513134	2.88e-52	3671	BP	G0:0051234	BP	establishment of localization (2)
34 44 7	3.72e-12	135	BP	G0:0051236	BP	establishment of RNA localization (3)
21 37 16	2.78e-11	104	BP	G0:0051656	BP	establishment of organelle localization (3)
327513295	7.87e-52	3612	BP	G0:0006810	BP	transport (3)
36 47 11	9.46e-12	155	BP	G0:0015931	BP	nucleobase-containing compound transport (4)
34 44 7	3.72e-12	135	BP	G0:0050657	BP	nucleic acid transport (5)
34 44 7	3.72e-12	135	BP	G0:0050658	BP	RNA transport (6)
1 5 1	9.04e-03	5	BP	G0:0051029	BP	rRNA transport (7)
29 37 5	3.24e-09	119	BP	G0:0051028	BP	mRNA transport (7)
10 22 20	1.26e-04	92	BP	G0:0006818	BP	hydrogen transport (4)
10 22 20	8.53e-05	90	BP	G0:0015992	BP	proton transport (5)
41 74 99	2.85e-06	1003	BP	G0:0006811	BP	ion transport (4)
29 53 66	2.81e-02	725	BP	G0:0006812	BP	cation transport (5)
57 78 88	2.40e-08	777	BP	G0:0046903	BP	secretion (4)
102166154	3.80e-35	926	BP	G0:0016192	BP	vesicle-mediated transport (4)
2 6 10	1.40e-03	27	BP	G0:0048278	BP	vesicle docking (5)
42 51 48	3.59e-06	351	BP	G0:0006897	BP	endocytosis (5)
9 27 9	2.77e-19	35	BP	G0:0006900	BP	membrane budding (5)
9 26 9	6.51e-19	33	BP	G0:0006901	BP	vesicle coating (6)
6 11 9	4.93e-03	25	BP	G0:0006906	BP	vesicle fusion (5)
51 88 92	4.24e-04	1006	BP	G0:0055085	BP	transmembrane transport (4)
18 31 41	1.40e-03	337	BP	G0:0034220	BP	ion transmembrane transport (5)
174287215	1.19e-52	1303	BP	G0:0045184	BP	establishment of protein localization (3)
48 91 40	3.44e-42	195	BP	G0:0072594	BP	establishment of protein localization to organelle (4)
44 83 34	6.29e-41	115	BP	G0:0072599	BP	establishment of protein localization in endoplasmic reticulum (5)
4 17 5	1.04e-05	39	BP	G0:0072655	BP	establishment of protein localization in mitochondrion (5)
173253215	5.19e-54	1270	BP	G0:0015031	BP	protein transport (4)
32 50 28	3.50e-04	272	BP	G0:0017038	BP	protein import (5)
221355235	7.16e-56	1760	BP	G0:0051649	BP	establishment of localization in cell (3)
10 54 10	5.28e-10	50	BP	G0:0051650	BP	establishment of vesicle localization (4)

10	24	12	5.28e-10	50	GO:0051650	BP	establishment of vesicle localization (4)
8	24	10	1.77e-14	36	GO:0006903	BP	vesicle targeting (5)
18	30	17	3.73e-74	1131	GO:0046907	BP	intracellular transport (4)
56	73	33	2.54e-09	356	GO:0051169	BP	nuclear transport (5)
56	73	33	1.64e-09	353	GO:0006913	BP	nucleocytoplasmic transport (6)
25	37	10	1.35e-09	116	GO:0051168	BP	nuclear export (7)
17	24	4	2.46e-05	77	GO:0006405	BP	RNA export from nucleus (8)
13	20	2	1.14e-03	68	GO:0006406	BP	mRNA export from nucleus (9)
9	37	12	1.74e-13	91	GO:0006839	BP	mitochondrial transport (5)
5	8		3.83e-02	16	GO:0042776	BP	mitochondrial ATP synthesis coupled proton transport (6)
16	30	29	6.94e-08	130	GO:0016197	BP	endosome transport (5)
24	61	41	5.11e-19	177	GO:0048193	BP	Golgi vesicle transport (5)
12	21	21	9.65e-08	70	GO:0006892	BP	post-Golgi vesicle-mediated transport (6)
5	22	11	1.19e-07	52	GO:0006888	BP	ER to Golgi vesicle-mediated transport (6)
1	10	4	2.92e-05	14	GO:0090114	BP	COPII-coated vesicle budding (7)
6	13	6	2.70e-04	28	GO:0006890	BP	retrograde vesicle-mediated transport, Golgi to ER (6)
6	21		2.80e-15	26	GO:0048199	BP	vesicle targeting, to, from or within Golgi (6)
1	10	4	2.92e-05	14	GO:0048207	BP	vesicle targeting, rough ER to cis-Golgi (7)
1	10	4	2.92e-05	14	GO:0048208	BP	COPII vesicle coating (8)
5	14		2.09e-12	14	GO:0048194	BP	Golgi vesicle budding (6)
5	13		2.46e-11	13	GO:0035964	BP	COPI-coated vesicle budding (7)
5	13	5	2.46e-11	13	GO:0048200	BP	Golgi transport vesicle coating (7)
5	13	5	2.46e-11	13	GO:0048205	BP	COPI coating of Golgi vesicle (8)
124	130	116	6.45e-53	695	GO:0006886	BP	intracellular protein transport (5)
89	147	77	6.63e-37	488	GO:0006605	BP	protein targeting (6)
46	30	36	2.81e-41	154	GO:0006612	BP	protein targeting to membrane (7)
43	69	33	2.74e-41	114	GO:0006613	BP	cotranslational protein targeting to membrane (8)
10	15	8	2.70e-04	37	GO:0006611	BP	protein export from nucleus (7)
44	69	34	6.29e-41	115	GO:0045047	BP	protein targeting to ER (7)
43	69	33	4.99e-42	112	GO:0006614	BP	SRP-dependent cotranslational protein targeting to membrane (8)
4	17	5	2.25e-06	36	GO:0006626	BP	protein targeting to mitochondrion (7)
52	69	83	3.05e-09	686	GO:0032940	BP	secretion by cell (4)
27	44	53	4.35e-14	262	GO:0006887	BP	exocytosis (5)
15	13	20	2.43e-05	84	GO:0002576	BP	platelet degranulation (6)
2	6	9	6.83e-03	25	GO:0006904	BP	vesicle docking involved in exocytosis (6)
128	170	97	1.06e-04	1336	GO:0022414	BP	reproductive process (2)
84	115	45	1.44e-15	566	GO:0048610	BP	cellular process involved in reproduction (3)
65	90	42	7.77e-24	301	GO:0022415	BP	viral reproductive process (3)
6	4		2.88e-03	8	GO:0030069	BP	lysogeny (4)
64	86		1.04e-28	253	GO:0019058	BP	viral infectious cycle (4)
52	70		4.59e-28	168	GO:0019080	BP	viral genome expression (5)
52	70		4.59e-28	168	GO:0019083	BP	viral transcription (6)
6	4		2.88e-03	8	GO:0019047	BP	provirus integration (4)
645	795	559	1.40e-12	8570	GO:0050789	BP	regulation of biological process (2)
282	351	257	4.83e-06	3463	GO:0048518	BP	positive regulation of biological process (3)
42	39	41	1.73e-04	312	GO:0044087	BP	regulation of cellular component biogenesis (3)
115	120	111	2.09e-04	1253	GO:0032879	BP	regulation of localization (3)
425	485	282	6.26e-14	4998	GO:0019222	BP	regulation of metabolic process (3)
275	275	130	1.76e-04	3496	GO:0009889	BP	regulation of biosynthetic process (4)
360	398	229	8.55e-11	4231	GO:0060255	BP	regulation of macromolecule metabolic process (4)
266	257	114	6.90e-05	3269	GO:0010556	BP	regulation of macromolecule biosynthetic process (5)
294	275	125	7.42e-09	3393	GO:0010468	BP	regulation of gene expression (5)
58	67	35	4.01e-09	351	GO:0010608	BP	posttranscriptional regulation of gene expression (6)
364	410	235	8.99e-09	4430	GO:0080090	BP	regulation of primary metabolic process (4)
132	180	147	4.30e-13	1389	GO:0051246	BP	regulation of protein metabolic process (5)
148	184	126	2.06e-02	1749	GO:0009893	BP	positive regulation of metabolic process (4)
135	164	108	3.24e-02	1579	GO:0010604	BP	positive regulation of macromolecule metabolic process (5)
52	82	77	1.11e-10	575	GO:0051247	BP	positive regulation of protein metabolic process (6)
299	313	153	5.38e-07	3594	GO:0051171	BP	regulation of nitrogen compound metabolic process (4)

148	189	152	1.27e-10	1557	GO:0050790	BP	regulation of catalytic activity (4)
81	91	61	5.24e-03	798	GO:0051336	BP	regulation of hydrolase activity (5)
12	19	14	1.61e-02	73	GO:0032069	BP	regulation of nuclease activity (6)
36	30	24	2.50e-03	251	GO:0052547	BP	regulation of peptidase activity (6)
35	30	24	3.52e-03	244	GO:0052548	BP	regulation of endopeptidase activity (7)
30	24	16	2.51e-04	171	GO:2000116	BP	regulation of cysteine-type endopeptidase activity (8)
29	21	16	4.48e-04	166	GO:0043281	BP	regulation of cysteine-type endopeptidase activity involved in apoptotic pr... (9)
19	42	37	9.45e-17	112	GO:0051340	BP	regulation of ligase activity (5)
57	72	78	1.42e-11	565	GO:0043086	BP	negative regulation of catalytic activity (5)
15	35	34	6.24e-18	87	GO:0051352	BP	negative regulation of ligase activity (6)
92	139	105	7.60e-09	982	GO:0043085	BP	positive regulation of catalytic activity (5)
16	41	36	3.33e-18	97	GO:0051351	BP	positive regulation of ligase activity (6)
613	758	526	9.17e-12	8106	GO:0050794	BP	regulation of cellular process (3)
265	334	244	9.26e-07	3128	GO:0048522	BP	positive regulation of cellular process (4)
27	25		6.33e-03	168	GO:0032970	BP	regulation of actin filament-based process (4)
94	123	70	1.96e-09	751	GO:0051726	BP	regulation of cell cycle (4)
66	90	55	8.26e-11	458	GO:0010564	BP	regulation of cell cycle process (5)
24	41	40	2.78e-12	172	GO:0090068	BP	positive regulation of cell cycle process (6)
45	62	45	2.34e-05	343	GO:0007346	BP	regulation of mitotic cell cycle (5)
29	44	38	5.63e-11	170	GO:2000602	BP	regulation of interphase of mitotic cell cycle (6)
20	39	38	2.18e-16	121	GO:2000045	BP	regulation of G1/S transition of mitotic cell cycle (7)
22	15	7	3.43e-05	91	GO:0032886	BP	regulation of microtubule-based process (4)
100	119	112	4.14e-03	1362	GO:0010646	BP	regulation of cell communication (4)
141	189	141	4.57e-12	1346	GO:0010941	BP	regulation of cell death (4)
139	186	137	2.00e-11	1316	GO:0043067	BP	regulation of programmed cell death (5)
139	186	136	2.49e-11	1306	GO:0042981	BP	regulation of apoptotic process (6)
373	432	246	3.46e-09	4535	GO:0031323	BP	regulation of cellular metabolic process (4)
20	54	38	8.68e-15	170	GO:0010565	BP	regulation of cellular ketone metabolic process (5)
15	38	36	3.98e-20	87	GO:0033238	BP	regulation of cellular amine metabolic process (5)
13	36	33	5.14e-20	72	GO:0006521	BP	regulation of cellular amino acid metabolic process (6)
273	270	127	9.08e-04	3469	GO:0031326	BP	regulation of cellular biosynthetic process (5)
262	252	109	5.49e-05	3202	GO:2000112	BP	regulation of cellular macromolecule biosynthetic process (6)
283	276	117	2.78e-05	3489	GO:0019219	BP	regulation of nucleobase-containing compound metabolic process (5)
25	42	29	1.03e-04	3047	GO:0051252	BP	regulation of RNA metabolic process (6)
232	209	88	1.98e-02	2979	GO:2001141	BP	regulation of RNA biosynthetic process (7)
23	104	88	1.89e-02	2962	GO:0006355	BP	regulation of transcription, DNA-dependent (8)
14	9	3	4.41e-05	38	GO:0043487	BP	regulation of RNA stability (7)
11	7	2	2.85e-04	26	GO:0043489	BP	RNA stabilization (8)
14	9	3	1.94e-05	36	GO:0043488	BP	regulation of mRNA stability (8)
11	7	2	2.85e-04	26	GO:0048255	BP	mRNA stabilization (9)
5	1		1.91e-03	5	GO:0070934	BP	CRD-mediated mRNA stabilization (10)
124	170	135	8.59e-13	1239	GO:0032268	BP	regulation of cellular protein metabolic process (5)
86	127	113	1.28e-11	991	GO:0031399	BP	regulation of protein modification process (6)
29	50	42	3.06e-13	178	GO:0031396	BP	regulation of protein ubiquitination (7)
19	41	37	2.27e-17	108	GO:0051438	BP	regulation of ubiquitin-protein ligase activity (8)
16	39	34	5.18e-17	92	GO:0051439	BP	regulation of ubiquitin-protein ligase activity involved in mitotic cell cy... (9)
35	43	21	4.54e-05	205	GO:0006417	BP	regulation of translation (6)
12	18	7	3.03e-03	60	GO:0006446	BP	regulation of translational initiation (7)
291	383	344	5.00e-14	4333	GO:0007165	BP	signal transduction (4)
14	8	4	9.59e-03	56	GO:0097190	BP	apoptotic signaling pathway (5)
12	26	15	2.44e-04	98	GO:0006984	BP	ER-nucleus signaling pathway (5)
12	23	14	6.96e-04	84	GO:0030968	BP	endoplasmic reticulum unfolded protein response (6)
153	211	183	1.39e-11	1959	GO:0035556	BP	intracellular signal transduction (5)
20	46	40	1.89e-15	142	GO:0072331	BP	signal transduction by p53 class mediator (6)
8	6	2	2.67e-02	20	GO:0097193	BP	intrinsic apoptotic signaling pathway (6)
56	82	81	4.96e-11	613	GO:0007264	BP	small GTPase mediated signal transduction (6)
25	49	42	4.54e-15	160	GO:0042770	BP	signal transduction in response to DNA damage (6)
20	45	40	4.54e-16	137	GO:0030330	BP	DNA damage response, signal transduction by p53 class mediator (7)
10	11	11	6.80e-05	100	GO:0066007	BP	regulation of cell cycle process (4)

19	24	31	6.30e-05	192	BP	regulation of vesicle-mediated transport (4)
139	163	144	8.80e-03	1888	BP	regulation of signaling (3)
122	126	114	1.25e-07	1153	BP	regulation of cellular component organization (3)
67	65	46	1.45e-08	453	BP	regulation of organelle organization (4)
44	41	35	3.24e-07	252	BP	regulation of cytoskeleton organization (5)
20	13	7	5.31e-05	78	BP	regulation of microtubule cytoskeleton organization (6)
25	25		3.80e-02	164	BP	regulation of actin cytoskeleton organization (6)
45	48	45	2.04e-02	427	BP	positive regulation of cellular component organization (4)
19	15	10	4.34e-05	70	BP	regulation of protein complex disassembly (4)
33	29	26	1.05e-05	176	BP	regulation of protein complex assembly (4)
22	20		1.76e-04	99	BP	regulation of protein polymerization (5)
292	365	238	1.97e-13	3101	BP	negative regulation of biological process (2)
46	36	34	1.22e-05	302	BP	negative regulation of cellular component organization (3)
17	10	7	1.81e-06	47	BP	negative regulation of protein complex disassembly (4)
16	14	13	9.70e-04	61	BP	negative regulation of protein complex assembly (4)
137	164	95	7.55e-07	1341	BP	negative regulation of metabolic process (3)
88	81	35	1.92e-02	918	BP	negative regulation of nitrogen compound metabolic process (4)
123	151	87	1.85e-07	1212	BP	negative regulation of macromolecule metabolic process (4)
85	80	33	3.30e-02	891	BP	negative regulation of macromolecule biosynthetic process (5)
84	79	30	1.75e-02	863	BP	negative regulation of cellular macromolecule biosynthetic process (6)
44	63	60	5.94e-14	329	BP	negative regulation of protein metabolic process (5)
28	34	22	4.39e-16	2822	BP	negative regulation of cellular process (3)
33	23	17	4.03e-07	156	BP	negative regulation of organelle organization (4)
22	17	14	1.46e-06	78	BP	negative regulation of cytoskeleton organization (5)
10	6	2	4.72e-03	27	BP	negative regulation of microtubule polymerization or depolymerization (6)
13	11		2.02e-03	43	BP	negative regulation of protein polymerization (4)
63	94	48	8.14e-12	471	BP	negative regulation of cell cycle (4)
54	91	46	1.83e-14	409	BP	cell cycle arrest (5)
43	71	41	7.27e-13	293	BP	regulation of cell cycle arrest (6)
40	67	39	1.71e-12	271	BP	cell cycle checkpoint (6)
19	38	36	1.06e-16	106	BP	G1/S transition checkpoint (7)
20	44	35	1.17e-09	160	BP	DNA integrity checkpoint (7)
19	44	35	2.86e-10	153	BP	DNA damage checkpoint (8)
17	35	34	1.01e-18	83	BP	signal transduction involved in cell cycle checkpoint (7)
17	35	34	6.26e-19	82	BP	signal transduction involved in DNA integrity checkpoint (8)
17	35	34	6.26e-19	82	BP	signal transduction involved in DNA damage checkpoint (9)
17	35	34	6.26e-19	82	BP	signal transduction involved in G1/S transition checkpoint (8)
26	45	36	1.79e-10	159	BP	mitotic cell cycle checkpoint (7)
17	35	34	3.85e-19	81	BP	signal transduction involved in mitotic cell cycle checkpoint (8)
19	38	36	2.40e-17	102	BP	mitotic cell cycle G1/S transition checkpoint (8)
17	35	34	3.85e-19	81	BP	signal transduction involved in mitotic cell cycle G1/S checkpoint (9)
17	36	34	1.48e-17	89	BP	mitotic cell cycle G1/S transition DNA damage checkpoint (9)
17	35	34	3.85e-19	81	BP	signal transduction involved in mitotic cell cycle G1/S transition DNA dama... (10)
17	36	35	1.61e-17	95	BP	positive regulation of cell cycle arrest (6)
17	35	34	3.85e-19	81	BP	DNA damage response, signal transduction by p53 class mediator resulting in... (7)
71	93	59	1.60e-03	657	BP	negative regulation of cell death (4)
69	88	54	2.86e-03	635	BP	negative regulation of programmed cell death (5)
69	87	53	2.03e-03	629	BP	negative regulation of apoptotic process (6)
13	144	92	2.11e-07	1227	BP	negative regulation of cellular metabolic process (4)
88	80	33	1.36e-02	910	BP	negative regulation of nucleobase-containing compound metabolic process (5)
81	67	28	5.50e-03	799	BP	negative regulation of RNA metabolic process (6)
7	5		2.86e-02	15	BP	negative regulation of RNA splicing (7)
43	62	57	8.97e-15	289	BP	negative regulation of cellular protein metabolic process (5)
29	48	49	1.45e-17	190	BP	negative regulation of protein modification process (6)
22	38		4.46e-12	104	BP	negative regulation of protein ubiquitination (7)
15	35	34	6.24e-18	87	BP	negative regulation of ubiquitin-protein ligase activity (8)
15	35	33	5.05e-18	81	BP	negative regulation of ubiquitin-protein ligase activity involved in mitoti... (9)
14	30	2	7.49e-03	144	BP	lipid modification (1)
10	23	2	1.38e-03	87	BP	lipid oxidation (2)

7	12	7	8.76e-03	31	GO:0009161	BP	ribonucleoside monophosphate metabolic process (1)
7	11	6	1.23e-02	27	GO:0009156	BP	ribonucleoside monophosphate biosynthetic process (2)
7	11	5	2.99e-03	24	GO:0009126	BP	purine nucleoside monophosphate metabolic process (1)
7	11	5	2.99e-03	24	GO:0009167	BP	purine ribonucleoside monophosphate metabolic process (2)
7	10	4	3.34e-03	20	GO:0009127	BP	purine nucleoside monophosphate biosynthetic process (2)
7	10	4	3.34e-03	20	GO:0009168	BP	purine ribonucleoside monophosphate biosynthetic process (3)
82	94	93	8.36e-06	940	GO:0032989	BP	cellular component morphogenesis (1)
80	89	88	2.73e-05	893	GO:0000902	BP	cell morphogenesis (2)
61	70	67	3.70e-04	653	GO:0032990	BP	cell part morphogenesis (2)
61	67	66	4.79e-04	644	GO:0048858	BP	cell projection morphogenesis (3)
59	62	62	3.93e-02	675	GO:0048585	BP	negative regulation of response to stimulus (1)
14	18	10	8.47e-03	64	GO:0009112	BP	nucleobase metabolic process (1)
9	13	9	1.74e-02	38	GO:0006144	BP	purine base metabolic process (2)
34	50	57	2.43e-02	594	GO:0050801	BP	ion homeostasis (1)
20	34	46	3.92e-03	414	GO:0055080	BP	cation homeostasis (2)
7	18	20	4.62e-05	87	GO:0055072	BP	iron ion homeostasis (3)
16	29	40	6.98e-03	346	GO:0055065	BP	metal ion homeostasis (3)
36	47	59	1.22e-03	566	GO:0055082	BP	cellular chemical homeostasis (1)
32	46	55	4.28e-03	534	GO:0006873	BP	cellular ion homeostasis (2)
18	30	44	3.79e-04	357	GO:0030003	BP	cellular cation homeostasis (3)
15	27	38	6.00e-03	319	GO:0006875	BP	cellular metal ion homeostasis (4)
6	16	20	2.21e-06	74	GO:0006879	BP	cellular iron ion homeostasis (5)
97	95	95	1.55e-03	1080	GO:0022008	BP	neurogenesis (1)
90	91	92	8.21e-04	1021	GO:0048699	BP	generation of neurons (2)
78	86	87	8.01e-04	948	GO:0030182	BP	neuron differentiation (3)
67	86	84	4.25e-05	846	GO:0007167	BP	enzyme linked receptor protein signaling pathway (1)
54	77	72	8.13e-07	623	GO:0007169	BP	transmembrane receptor protein tyrosine kinase signaling pathway (2)
25	27	21	4.22e-02	165	GO:0007173	BP	epidermal growth factor receptor signaling pathway (3)
16	39		1.75e-05	170	GO:0008286	BP	insulin receptor signaling pathway (3)
20	16	9	4.89e-02	117	GO:0010952	BP	positive regulation of peptidase activity (1)
11	19	13	4.02e-03	67	GO:0032075	BP	positive regulation of nuclease activity (1)
10	17	12	4.46e-02	65	GO:0006987	BP	activation of signaling protein activity involved in unfolded protein respo... (2)
65	70	70	6.67e-05	664	GO:0000904	BP	cell morphogenesis involved in differentiation (1)
4	2	3	3.20e-02	4	GO:0046796	BP	viral genome transport in host cell (1)
62	78	76	1.13e-02	849	GO:0042325	BP	regulation of phosphorylation (1)
60	75	73	8.15e-03	798	GO:0001932	BP	regulation of protein phosphorylation (2)
73	78	82	2.12e-06	767	GO:0048666	BP	neuron development (1)
67	73	77	3.34e-07	674	GO:0031175	BP	neuron projection development (2)
58	63	63	3.00e-05	560	GO:0048812	BP	neuron projection morphogenesis (3)
60	60	64	8.72e-06	555	GO:0048667	BP	cell morphogenesis involved in neuron differentiation (2)
54	53	55	1.15e-03	512	GO:0007409	BP	axonogenesis (3)
44	38	44	3.23e-04	355	GO:0007411	BP	axon guidance (4)
8	21	8	1.33e-04	66	GO:0009267	BP	cellular response to starvation (1)
5	16	4	1.45e-08	25	GO:0016236	BP	macroautophagy (2)
2	13	2	1.40e-07	18	GO:0000045	BP	autophagic vacuole assembly (3)
3	12	1	5.82e-03	30	GO:0010506	BP	regulation of autophagy (1)
20	21	22	4.32e-02	153	GO:0042176	BP	regulation of protein catabolic process (1)
10	23	2	6.96e-04	84	GO:0019395	BP	fatty acid oxidation (1)
5	13		8.71e-03	36	GO:0046320	BP	regulation of fatty acid oxidation (2)
17	18		4.58e-02	89	GO:0030832	BP	regulation of actin filament length (1)
17	18		3.93e-02	88	GO:0008064	BP	regulation of actin polymerization or depolymerization (2)
1	7		1.59e-02	11	GO:0010508	BP	positive regulation of autophagy (1)
10	8		1.99e-02	31	GO:0030042	BP	actin filament depolymerization (1)
10	8		1.43e-02	30	GO:0030834	BP	regulation of actin filament depolymerization (2)
10	7		3.14e-03	26	GO:0030835	BP	negative regulation of actin filament depolymerization (2)
9	6	7	1.39e-02	24	GO:0051693	BP	actin filament capping (3)
47	77	73	5.20e-12	499	GO:0032270	BP	positive regulation of cellular protein metabolic process (1)
36	67	63	5.17e-11	411	GO:0031401	BP	positive regulation of protein modification process (2)

19	45	38	8.29e-15	133		GO:0031398	BP	positive regulation of protein ubiquitination (3)
16	49	36	6.15e-19	93		GO:0051443	BP	positive regulation of ubiquitin-protein ligase activity (4)
13	38	34	4.00e-18	86		GO:0051437	BP	positive regulation of ubiquitin-protein ligase activity involved in mitoti... (5)
9	15	12	1.32e-03	41		GO:0042059	BP	negative regulation of epidermal growth factor receptor signaling pathway (1)
16	16		3.14e-02	78		GO:0030833	BP	regulation of actin filament polymerization (1)
6	4	1	4.06e-02	11		GO:0048025	BP	negative regulation of nuclear mRNA splicing, via spliceosome (1)
20	19		7.73e-03	104		GO:0030518	BP	intracellular steroid hormone receptor signaling pathway (1)
5	7		6.24e-03	10		GO:0031958	BP	corticosteroid receptor signaling pathway (2)
5	7		2.02e-03	9		GO:0042921	BP	glucocorticoid receptor signaling pathway (3)

			P-value	T		term ID	term domain and name
9	10	28	4.20e-03	197		GO:0045121	CC membrane raft (1)
109	153	995	9.91e-10	17930		GO:0005575	CC cellular_component (1)
48	17	351	2.14e-101	4046		GO:0032991	CC macromolecular complex (2)
27	14	2	2.29e-04	143		GO:0032993	CC protein-DNA complex (3)
34	15	303	2.06e-47	3353		GO:0043234	CC protein complex (3)
27	15	158	9.83e-69	2750		GO:0031974	CC membrane-enclosed lumen (2)
109	153	981	6.81e-42	16623		GO:0005623	CC cell (2)
93	134	731	3.37e-121	10938		GO:0043226	CC organelle (2)
40	45	241	2.32e-53	3164		GO:0043228	CC non-membrane-bounded organelle (3)
94	123	635	1.65e-102	9866		GO:0043227	CC membrane-bounded organelle (3)
99	151	163	1.62e-41	975		GO:0031982	CC vesicle (3)
95	138	152	2.47e-35	902		GO:0031988	CC membrane-bounded vesicle (4)
109	153	981	6.30e-42	16622		GO:0044464	CC cell part (2)
11	7	11	6.39e-03	38		GO:0032153	CC cell division site (3)
103	134	63	2.10e-35	851		GO:0031975	CC envelope (3)
11	7	11	6.39e-03	38		GO:0032155	CC cell division site part (3)
11	7		1.27e-02	36		GO:0032154	CC cleavage furrow (4)
127	121	147	3.17e-04	1828		GO:0012505	CC endomembrane system (3)
378	245	566	6.09e-14	8233		GO:0016020	CC membrane (3)
12	27		1.66e-08	71		GO:0048475	CC coated membrane (4)
13	36	14	1.62e-06	138		GO:0019867	CC outer membrane (4)
14	23		3.93e-05	73		GO:0030496	CC midbody (3)
98	118	113	3.78e-07	1160		GO:0042995	CC cell projection (3)
52	51	57	2.56e-02	595		GO:0044463	CC cell projection part (4)
106	157	672	6.95e-166	12958		GO:0005622	CC intracellular (3)
38	38	41	6.08e-08	240		GO:0031252	CC cell leading edge (3)
21	22	25	4.14e-06	117		GO:0001726	CC ruffle (4)
231	303	376	8.28e-17	4691		GO:0071944	CC cell periphery (3)
219	295	368	6.89e-16	4614		GO:0005886	CC plasma membrane (4)
102	124	195	1.47e-10	2247		GO:0044459	CC plasma membrane part (5)
11	12	21	7.71e-05	98		GO:0009898	CC internal side of plasma membrane (6)
31	27	39	1.93e-04	290		GO:0016323	CC basolateral plasma membrane (6)
113	169	166	2.26e-23	1315		GO:0000267	CC cell fraction (3)
64	89	72	5.60e-16	414		GO:0005625	CC soluble fraction (4)
71	102	113	3.92e-11	1007		GO:0005626	CC insoluble fraction (4)
63	93	105	1.34e-10	973		GO:0005624	CC membrane fraction (5)
106	153	966	2.79e-174	12631		GO:0044424	CC intracellular part (3)
85	133	321	6.82e-178	9357		GO:0005737	CC cytoplasm (4)
139	209	50	2.12e-69	606		GO:0030529	CC ribonucleoprotein complex (4)
93	134	731	6.15e-122	10921		GO:0043229	CC intracellular organelle (4)
40	45	241	2.32e-53	3164		GO:0043232	CC intracellular non-membrane-bounded organelle (5)
105	93	14	4.19e-19	661		GO:0005694	CC chromosome (6)
29	32	1	3.92e-04	165		GO:0000793	CC condensed chromosome (7)
205	240	178	1.34e-17	1778		GO:0005856	CC cytoskeleton (6)
62	73	61	4.66e-14	337		GO:0015629	CC actin cytoskeleton (7)
103	121	69	5.50e-09	840		GO:0015630	CC microtubule cytoskeleton (7)

13	21	29	3.60e-02	232	GO:0045111	CC	intermediate filament cytoskeleton (7)
13	17	5	6.38e-06	38	GO:0009295	CC	nucleoid (6)
845	128	634	1.65e-102	9853	GO:0043231	CC	intracellular membrane-bounded organelle (5)
614	742	284	3.05e-51	6129	GO:0005634	CC	nucleus (6)
674	105	705	3.33e-149	6867	GO:0044444	CC	cytoplasmic part (4)
53	81		3.27e-07	456	GO:0048471	CC	perinuclear region of cytoplasm (5)
391	545	582	6.65e-119	2361	GO:0005829	CC	cytosol (5)
1	8		2.02e-03	12	GO:0000407	CC	pre-autophagosomal structure (5)
58	38	47	2.20e-40	190	GO:0044445	CC	cytosolic part (5)
6	7	6	6.55e-05	7	GO:0005832	CC	chaperonin-containing T-complex (6)
36	28	25	1.39e-07	175	GO:0005938	CC	cell cortex (5)
19	16	14	2.90e-04	78	GO:0044448	CC	cell cortex part (5)
16	11		2.26e-05	48	GO:0030863	CC	cortical cytoskeleton (6)
6	5		8.19e-03	9	GO:0016281	CC	eukaryotic translation initiation factor 4F complex (5)
5	1		1.91e-03	5	GO:0070937	CC	CRD-mediated mRNA stability complex (5)
6	8	3	2.07e-02	15	GO:0005852	CC	eukaryotic translation initiation factor 3 complex (5)
95	146	164	7.79e-41	935	GO:0031410	CC	cytoplasmic vesicle (5)
92	136	151	2.34e-35	881	GO:0016023	CC	cytoplasmic membrane-bounded vesicle (6)
32	46		3.10e-18	108	GO:0048770	CC	pigment granule (7)
32	46		3.10e-18	108	GO:0042470	CC	melanosome (8)
19	23	44	1.67e-09	244	GO:0030141	CC	secretory granule (7)
5	21	23	2.29e-02	158	GO:0030133	CC	transport vesicle (7)
21	47	36	1.17e-03	275	GO:0030135	CC	coated vesicle (7)
16	27	26	1.61e-02	188	GO:0030136	CC	clathrin-coated vesicle (8)
9	19	10	8.99e-05	54	GO:0005793	CC	endoplasmic reticulum-Golgi intermediate compartment (5)
14	64	105	1.15e-35	455	GO:0005773	CC	vacuole (5)
13	49	82	1.16e-30	401	GO:0000323	CC	lytic vacuole (6)
13	49	82	1.16e-30	401	GO:0005764	CC	lysosome (7)
1	13	5	8.84e-05	26	GO:0005776	CC	autophagic vacuole (6)
145	33	119	3.21e-60	1560	GO:0005739	CC	mitochondrion (5)
28	26	22	6.85e-05	144	GO:0043292	CC	contractile fiber (5)
25	23	22	8.62e-04	134	GO:0030016	CC	myofibril (6)
44	76	103	8.09e-20	666	GO:0005768	CC	endosome (5)
22	29	34	1.44e-04	231	GO:0005769	CC	early endosome (6)
3	10	17	4.33e-04	73	GO:0055037	CC	recycling endosome (6)
9	26	33	1.67e-06	185	GO:0005770	CC	late endosome (6)
67	143	126	2.93e-09	1251	GO:0005794	CC	Golgi apparatus (5)
12	27		1.66e-08	71	GO:0030117	CC	membrane coat (5)
50	83	31	1.70e-27	235	GO:0005840	CC	ribosome (5)
41	58		3.05e-33	99	GO:0022626	CC	cytosolic ribosome (6)
16	39	37	1.27e-23	77	GO:0000502	CC	proteasome complex (4)
5	10	7	4.09e-07	11	GO:0022624	CC	proteasome accessory complex (5)
1	6		4.99e-03	7	GO:0031588	CC	AMP-activated protein kinase complex (4)
3	11	14	1.47e-06	34	GO:0005839	CC	proteasome core complex (4)
3	7	5	4.85e-04	8	GO:0005838	CC	proteasome regulatory particle (4)
3	7		4.85e-04	8	GO:0019773	CC	proteasome core complex, alpha-subunit complex (4)
665	956	496	1.78e-113	6470	GO:0044422	CC	organelle part (2)
365	63	154	5.60e-64	2699	GO:0043233	CC	organelle lumen (3)
24	23	21	9.89e-04	126	GO:0044449	CC	contractile fiber part (3)
22	21	20	1.47e-03	111	GO:0030017	CC	sarcomere (4)
164	342	225	6.10e-19	2445	GO:0031090	CC	organelle membrane (3)
25	51	52	5.99e-07	378	GO:0012506	CC	vesicle membrane (4)
685	975	487	3.61e-113	6391	GO:0044446	CC	intracellular organelle part (3)
97	80	13	3.23e-18	561	GO:0044427	CC	chromosomal part (4)
10	9	2	3.72e-02	33	GO:0005657	CC	replication fork (5)
49	35	4	1.02e-05	331	GO:0000785	CC	chromatin (5)
24	23	6	4.77e-02	156	GO:0000775	CC	chromosome, centromeric region (5)
5	3	2	1.09e-02	6	GO:0005663	CC	DNA replication factor C complex (5)

36	48	149	1.35e-64	2654	GO:0070013	CC	intracellular organelle lumen (4)
42	66	29	1.03e-28	147	GO:0044391	CC	ribosomal subunit (4)
23	40	68	7.28e-13	428	GO:0044440	CC	endosomal part (4)
22	39	66	3.97e-12	421	GO:0010008	CC	endosome membrane (5)
1	4	10	4.32e-03	30	GO:0055038	CC	recycling endosome membrane (6)
3	33	58	4.66e-16	281	GO:0044437	CC	vacuolar part (4)
3	27	47	1.01e-10	254	GO:0005774	CC	vacuolar membrane (5)
3	18	35	6.49e-06	215	GO:0005765	CC	lysosomal membrane (6)
1	6	15	7.34e-07	38	GO:0005775	CC	vacuolar lumen (5)
103	134	63	9.80e-37	834	GO:0031967	CC	organelle envelope (4)
7	19	5	4.52e-04	59	GO:0031970	CC	organelle envelope lumen (5)
13	36	14	4.22e-07	132	GO:0031968	CC	organelle outer membrane (5)
51	111	28	6.20e-28	389	GO:0019866	CC	organelle inner membrane (5)
151	172	126	2.12e-13	1264	GO:0044430	CC	cytoskeletal part (4)
36	40	17	1.80e-04	226	GO:0005819	CC	spindle (5)
16	13	10	5.24e-06	44	GO:0032432	CC	actin filament bundle (5)
16	15	11	4.40e-05	50	GO:0042641	CC	actomyosin (5)
15	13	10	1.52e-05	41	GO:0001725	CC	stress fiber (6)
54	61	34	9.33e-03	472	GO:0005815	CC	microtubule organizing center (5)
44	47	27	2.42e-02	368	GO:0005813	CC	centrosome (6)
10	15	26	3.43e-02	196	GO:0005882	CC	intermediate filament (5)
10	9	12	3.70e-02	53	GO:0005884	CC	actin filament (5)
9	7		4.22e-02	27	GO:0030864	CC	cortical actin cytoskeleton (5)
4	1	2	3.20e-02	4	GO:0005862	CC	muscle thin filament tropomyosin (5)
341	422	133	6.87e-49	2528	GO:0044428	CC	nuclear part (4)
42	60	5	1.94e-22	151	GO:0005681	CC	spliceosomal complex (5)
30	40	1	8.51e-18	84	GO:0071013	CC	catalytic step 2 spliceosome (6)
2	12	1	2.96e-04	24	GO:0005689	CC	U12-type spliceosomal complex (6)
16	14		8.50e-15	18	GO:0030530	CC	heterogeneous nuclear ribonucleoprotein complex (5)
3	17		1.05e-07	31	GO:0030532	CC	small nuclear ribonucleoprotein complex (5)
20	18	3	1.05e-02	106	GO:0016585	CC	chromatin remodeling complex (5)
46	55	25	1.68e-05	305	GO:0005635	CC	nuclear envelope (5)
235	361	105	1.23e-43	2166	GO:0031981	CC	nuclear lumen (5)
234	266	74	2.75e-39	1543	GO:0005654	CC	nucleoplasm (5)
21	27	13	3.41e-06	87	GO:0034399	CC	nuclear periphery (5)
106	103	15	8.38e-11	820	GO:0044451	CC	nucleoplasm part (5)
56	50	4	5.18e-12	285	GO:0016604	CC	nuclear body (6)
30	30		3.36e-05	157	GO:0016607	CC	nuclear speck (7)
6	5		1.14e-04	6	GO:0042382	CC	paraspeckles (7)
14	9		7.61e-03	55	GO:0017053	CC	transcriptional repressor complex (6)
18	24		2.46e-05	77	GO:0016363	CC	nuclear matrix (5)
84	107	32	1.37e-09	615	GO:0005730	CC	nucleolus (5)
43	45	4	7.03e-05	288	GO:0000228	CC	nuclear chromosome (5)
39	38	4	3.73e-05	242	GO:0044454	CC	nuclear chromosome part (6)
6	6		1.14e-04	6	GO:0042555	CC	MCM complex (7)
26	55	55	1.54e-06	423	GO:0044433	CC	cytoplasmic vesicle part (4)
22	50	50	1.69e-06	366	GO:0030659	CC	cytoplasmic vesicle membrane (5)
12	32	22	4.82e-02	173	GO:0030662	CC	coated vesicle membrane (6)
8	20		1.98e-08	40	GO:0030120	CC	vesicle coat (7)
1	5	13	3.97e-03	51	GO:0030667	CC	secretory granule membrane (6)
79	270	48	1.11e-47	751	GO:0044429	CC	mitochondrial part (4)
57	134	40	1.33e-30	537	GO:0005740	CC	mitochondrial envelope (5)
45	91	15	1.62e-26	285	GO:0005759	CC	mitochondrial matrix (5)
55	133	37	3.95e-30	510	GO:0031966	CC	mitochondrial membrane (5)
9	43	10	2.49e-10	144	GO:0044455	CC	mitochondrial membrane part (6)
43	104	27	3.46e-27	354	GO:0005743	CC	mitochondrial inner membrane (6)
10	31	13	3.98e-06	111	GO:0005741	CC	mitochondrial outer membrane (6)
6	17	4	1.37e-04	45	GO:0005758	CC	mitochondrial intermembrane space (5)
43	47	5	2.25e-06	36	GO:0042645	CC	mitochondrial nucleoid (5)

13	17	5	2.23e-06	36			GO:0042643	CC	mitochondrial nucleoid (5)
18	32	17	2.47e-12	74			GO:0015935	CC	small ribosomal subunit (4)
17	28		8.31e-17	43			GO:0022627	CC	cytosolic small ribosomal subunit (5)
24	34	12	3.15e-14	74			GO:0015934	CC	large ribosomal subunit (4)
24	30		1.22e-15	53			GO:0022625	CC	cytosolic large ribosomal subunit (5)
1	15	2	1.70e-02	49			GO:0030964	CC	NADH dehydrogenase complex (1)
28	25	23	1.53e-02	186			GO:0005912	CC	adherens junction (1)
6	27	4	1.05e-06	83			GO:0070469	CC	respiratory chain (1)
1	15	2	1.70e-02	49			GO:0045271	CC	respiratory chain complex I (2)
3	23	3	9.18e-05	76			GO:0005746	CC	mitochondrial respiratory chain (2)
1	15	2	1.70e-02	49			GO:0005747	CC	mitochondrial respiratory chain complex I (3)
14	14	28	1.02e-08	113			GO:0019898	CC	extrinsic to membrane (1)
8	11	23	5.00e-09	74			GO:0019897	CC	extrinsic to plasma membrane (2)
4	4	13	1.43e-03	47			GO:0031234	CC	extrinsic to internal side of plasma membrane (3)
3	2	12	1.94e-04	34			GO:0005834	CC	heterotrimeric G-protein complex (4)
7	18	17	4.12e-06	55			GO:0016469	CC	proton-transporting two-sector ATPase complex (1)
2	7	10	1.40e-03	27			GO:0033176	CC	proton-transporting V-type ATPase complex (2)
5	10	10	2.27e-05	19			GO:0033178	CC	proton-transporting two-sector ATPase complex, catalytic domain (2)
2	5	6	8.67e-03	10			GO:0033180	CC	proton-transporting V-type ATPase, V1 domain (3)
15	26	10	8.67e-07	77			GO:0046930	CC	pore complex (1)
13	21	7	1.97e-05	60			GO:0005643	CC	nuclear pore (2)
22	17	17	2.56e-02	131			GO:0030055	CC	cell-substrate junction (1)
21	16	16	4.56e-02	126			GO:0005924	CC	cell-substrate adherens junction (2)
4	7		1.59e-02	11			GO:0030132	CC	clathrin coat of coated pit (1)
7	19	14	6.08e-04	60			GO:0005798	CC	Golgi-associated vesicle (1)
3	11		2.78e-04	20			GO:0030137	CC	COPI-coated vesicle (2)
6	13	7	6.03e-03	35			GO:0030660	CC	Golgi-associated vesicle membrane (1)
3	9		3.11e-03	16			GO:0030663	CC	COPI coated vesicle membrane (2)
5	9	4	3.33e-02	20			GO:0005753	CC	mitochondrial proton-transporting ATP synthase complex (1)
	7		2.02e-03	9			GO:0030127	CC	COPII vesicle coat (1)
19	35	32	2.74e-02	265			GO:0005911	CC	cell-cell junction (1)

			P-value	T		term ID	term domain and name
1	6	1	4.99e-03	7		GO:0004679	MF AMP-activated protein kinase activity (1)
17	33	16	4.37e-02	180		GO:0000287	MF magnesium ion binding (1)
21	16		1.21e-02	116		GO:0035257	MF nuclear hormone receptor binding (1)
16	13		7.12e-03	70		GO:0035258	MF steroid hormone receptor binding (2)
108	154	929	7.20e-31	16378		GO:0003674	MF molecular_function (1)
15	11	15	5.20e-04	58		GO:0016209	MF antioxidant activity (2)
61	113	107	1.74e-03	1262		GO:0005215	MF transporter activity (2)
55	92	96	1.20e-04	1036		GO:0022892	MF substrate-specific transporter activity (3)
19	29	12	5.66e-07	92		GO:0008565	MF protein transporter activity (4)
31	66	86	8.16e-03	988		GO:0022857	MF transmembrane transporter activity (3)
13	31	54	1.44e-08	364		GO:0022804	MF active transmembrane transporter activity (4)
8	21	32	9.11e-10	134		GO:0015399	MF primary active transmembrane transporter activity (5)
8	21	32	9.11e-10	134		GO:0015405	MF P-P-bond-hydrolysis-driven transmembrane transporter activity (6)
30	62	81	2.20e-03	884		GO:0022891	MF substrate-specific transmembrane transporter activity (4)
96	126	85	2.06e-15	667		GO:0005198	MF structural molecule activity (2)
12	11	21	1.00e-05	88		GO:0005200	MF structural constituent of cytoskeleton (3)
44	71	28	4.71e-27	178		GO:0003735	MF structural constituent of ribosome (3)
994	138	796	1.14e-71	12549		GO:0005488	MF binding (2)
3104	5246		3.97e-53	2699		GO:0036094	MF small molecule binding (3)
2994	43236		1.45e-52	2529		GO:0000166	MF nucleotide binding (4)
1983	24203		3.11e-28	1986		GO:0032553	MF ribonucleotide binding (5)
2013	3202		9.82e-28	1998		GO:0017076	MF purine nucleotide binding (5)
17	424	127	1.81e-21	1627		GO:0030554	MF adenylyl nucleotide binding (6)

198313202	6.55e-28	1985	MF	G0:0032555	MF	purine ribonucleotide binding (6)
169259127	1.60e-21	1617	MF	G0:0032559	MF	adenyl ribonucleotide binding (7)
197315198	8.73e-28	1953	MF	G0:0035639	MF	purine ribonucleoside triphosphate binding (7)
168255123	3.62e-21	1591	MF	G0:0005524	MF	ATP binding (8)
34 69 79	1.34e-20	411	MF	G0:0019001	MF	guanyl nucleotide binding (6)
34 69 79	1.34e-20	411	MF	G0:0032561	MF	guanyl ribonucleotide binding (7)
3 11	2.77e-02	29	MF	G0:0019003	MF	GDP binding (8)
33 69 79	1.82e-21	399	MF	G0:0005525	MF	GTP binding (8)
9 19 8	1.08e-03	62	MF	G0:0043021	MF	ribonucleoprotein complex binding (3)
853370101	9.60e-23	3509	MF	G0:0003676	MF	nucleic acid binding (3)
204 24 68	2.68e-62	903	MF	G0:0003723	MF	RNA binding (4)
27 31 17	2.77e-07	107	MF	G0:0008135	MF	translation factor activity, nucleic acid binding (5)
11 9 6	4.84e-03	33	MF	G0:0003746	MF	translation elongation factor activity (6)
14 19 11	1.26e-04	55	MF	G0:0003743	MF	translation initiation factor activity (6)
4 12 5	5.82e-03	30	MF	G0:0000049	MF	tRNA binding (5)
29 32 10	2.19e-11	87	MF	G0:0003729	MF	mRNA binding (5)
12 5 1	2.22e-05	26	MF	G0:0003730	MF	mRNA 3'-UTR binding (6)
12 11 3	1.65e-03	36	MF	G0:0003727	MF	single-stranded RNA binding (5)
6 5	4.06e-02	11	MF	G0:0070717	MF	poly-purine tract binding (6)
6 4	8.19e-03	9	MF	G0:0008143	MF	poly(A) RNA binding (7)
7 13	1.24e-02	37	MF	G0:0019843	MF	rRNA binding (5)
16 37 46	1.58e-02	436	MF	G0:0030246	MF	carbohydrate binding (3)
11 28 30	4.82e-03	221	MF	G0:0005529	MF	sugar binding (4)
7 18 17	7.63e-06	57	MF	G0:0048029	MF	monosaccharide binding (5)
37 67 26	3.08e-12	274	MF	G0:0048037	MF	cofactor binding (3)
28 54 21	5.22e-12	194	MF	G0:0050662	MF	coenzyme binding (4)
14 26 7	2.30e-12	49	MF	G0:0051287	MF	NAD binding (5)
8 6 1	2.67e-02	20	MF	G0:0000062	MF	fatty-acyl-CoA binding (5)
723107 605	3.54e-93	7186	MF	G0:0005515	MF	protein binding (3)
80 121	9.12e-06	836	MF	G0:0042802	MF	identical protein binding (4)
133160 96	1.70e-13	1050	MF	G0:0019899	MF	enzyme binding (4)
53 53 38	3.11e-05	385	MF	G0:0019900	MF	kinase binding (5)
47 49 32	1.27e-04	336	MF	G0:0019901	MF	protein kinase binding (6)
15 11 9	4.65e-05	44	MF	G0:0005080	MF	protein kinase C binding (7)
23 25	4.79e-02	146	MF	G0:0051020	MF	GTPase binding (5)
28 23 19	7.00e-04	160	MF	G0:0005516	MF	calmodulin binding (4)
68 61	6.44e-05	563	MF	G0:0019904	MF	protein domain specific binding (4)
33 41 29	5.20e-09	144	MF	G0:0051082	MF	unfolded protein binding (4)
10 16 10	5.97e-03	51	MF	G0:0051087	MF	chaperone binding (4)
95 100 72	4.42e-15	600	MF	G0:0008092	MF	cytoskeletal protein binding (4)
66 62 53	8.71e-14	347	MF	G0:0003779	MF	actin binding (5)
18 15 12	4.08e-04	72	MF	G0:0051015	MF	actin filament binding (6)
5 7 18	1.41e-02	102	MF	G0:0019838	MF	growth factor binding (4)
95 100 65	1.54e-02	1006	MF	G0:0030234	MF	enzyme regulator activity (2)
21 36	4.60e-03	185	MF	G0:0009055	MF	electron carrier activity (2)
53 51 22	2.51e-02	476	MF	G0:0000988	MF	protein binding transcription factor activity (2)
53 51 22	1.28e-02	465	MF	G0:0000989	MF	transcription factor binding transcription factor activity (3)
53 50 22	5.91e-03	453	MF	G0:0003712	MF	transcription cofactor activity (4)
42 7 95 439	1.09e-32	5640	MF	G0:0003824	MF	catalytic activity (2)
27 38 17	9.10e-07	148	MF	G0:0016853	MF	isomerase activity (3)
8 16 10	2.90e-04	42	MF	G0:0016860	MF	intramolecular oxidoreductase activity (4)
4 7 5	3.53e-02	12	MF	G0:0016862	MF	intramolecular oxidoreductase activity, interconverting keto- and enol-grou... (5)
188322274	1.01e-30	2512	MF	G0:0016787	MF	hydrolase activity (3)
37 66 60	9.92e-03	618	MF	G0:0008233	MF	peptidase activity (4)
95 162134	1.96e-27	853	MF	G0:0016817	MF	hydrolase activity, acting on acid anhydrides (4)
95 162134	5.71e-28	843	MF	G0:0016818	MF	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anh... (5)
95 161134	3.93e-28	840	MF	G0:0016462	MF	pyrophosphatase activity (6)
92 156131	7.21e-28	813	MF	G0:0017111	MF	nucleoside-triphosphatase activity (7)
68 161 5	4.25e-02	455	MF	G0:0004286	MF	helicase activity (8)

28	34	5	1.35e-03	165		GU:0004386	MF	helicase activity (8)
24	47	67	7.85e-27	242		GO:0003924	MF	GTPase activity (8)
50	79	53	5.10e-10	389		GO:0016887	MF	ATPase activity (8)
37	61	41	2.57e-06	317		GO:0042623	MF	ATPase activity, coupled (9)
7	19	81	5.64e-10	124		GO:0043492	MF	ATPase activity, coupled to movement of substances (10)
7	19	31	2.75e-09	131		GO:0016820	MF	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane mov... (5)
7	19	31	4.45e-10	123		GO:0042626	MF	ATPase activity, coupled to transmembrane movement of substances (6)
6	12	21	8.22e-03	128		GO:0016798	MF	hydrolase activity, acting on glycosyl bonds (4)
4	9	19	5.32e-03	105		GO:0004553	MF	hydrolase activity, hydrolyzing O-glycosyl compounds (5)
44	74	34	2.45e-03	493		GO:0016874	MF	ligase activity (3)
8	20	10	2.07e-05	55		GO:0016875	MF	ligase activity, forming carbon-oxygen bonds (4)
8	20	10	2.07e-05	55		GO:0016876	MF	ligase activity, forming aminoacyl-tRNA and related compounds (5)
8	20	10	2.07e-05	55		GO:0004812	MF	aminoacyl-tRNA ligase activity (6)
67	136	62	1.56e-14	746		GO:0016491	MF	oxidoreductase activity (3)
10	9	10	4.61e-02	38		GO:0016684	MF	oxidoreductase activity, acting on peroxide as acceptor (4)
10	9	10	4.61e-02	38		GO:0004601	MF	peroxidase activity (5)
5	26	9	3.05e-04	99		GO:0016651	MF	oxidoreductase activity, acting on NADH or NADPH (4)
2	18	4	3.95e-03	61		GO:0016655	MF	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compou... (5)
1	14	2	4.78e-02	47		GO:0003954	MF	NADH dehydrogenase activity (5)
1	14		4.78e-02	47		GO:0050136	MF	NADH dehydrogenase (quinone) activity (6)
1	14		4.78e-02	47		GO:0008137	MF	NADH dehydrogenase (ubiquinone) activity (7)
19	42	16	1.00e-10	135		GO:0016614	MF	oxidoreductase activity, acting on CH-OH group of donors (4)
19	42	16	1.79e-12	122		GO:0016616	MF	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP a... (5)
10	20	13	2.07e-05	55		GO:0016667	MF	oxidoreductase activity, acting on a sulfur group of donors (4)
7	12	10	1.15e-02	33		GO:0015036	MF	disulfide oxidoreductase activity (5)
6	11	8	1.87e-02	28		GO:0015035	MF	protein disulfide oxidoreductase activity (6)
44	75		4.66e-02	544		GO:0042803	MF	protein homodimerization activity (1)
12	31	22	1.90e-06	108		GO:0015078	MF	hydrogen ion transmembrane transporter activity (1)
5	10	7	8.10e-05	15		GO:0046933	MF	hydrogen ion transporting ATP synthase activity, rotational mechanism (2)
6	16	27	7.65e-14	69		GO:0042625	MF	ATPase activity, coupled to transmembrane movement of ions (1)
3	9	19	1.60e-08	52		GO:0015662	MF	ATPase activity, coupled to transmembrane movement of ions, phosphorylative... (2)
6	11	16	2.11e-09	32		GO:0019829	MF	cation-transporting ATPase activity (1)
5	10	11	2.15e-06	20		GO:0046961	MF	proton-transporting ATPase activity, rotational mechanism (2)
37	39	8	5.68e-05	226		GO:0043566	MF	structure-specific DNA binding (1)
22	20	5	1.84e-09	58		GO:0003697	MF	single-stranded DNA binding (2)
2	3	8	3.30e-02	23		GO:0015175	MF	neutral amino acid transmembrane transporter activity (1)
3	11	14	2.34e-06	35		GO:0070003	MF	threonine-type peptidase activity (1)
3	11	14	2.34e-06	35		GO:0004298	MF	threonine-type endopeptidase activity (2)
7	7		5.16e-05	8		GO:0051920	MF	peroxiredoxin activity (1)
23	33	31	2.62e-03	226		GO:0005543	MF	phospholipid binding (1)
8	10	9	6.83e-03	25		GO:0005544	MF	calcium-dependent phospholipid binding (2)

P-value T

term ID

term domain and name

798134 697 6.44e-123 6392

BIOGRID:000000

bi BioGRID interaction data (1)

P-value T

term ID

term domain and name

6 21 2 7.66e-06 51

HP:0001427

hp Mitochondrial inheritance (1)

7 18 27 6.84e-04 123

HP:0003468

hp Abnormality of the vertebrae (1)

6 15 24 2.32e-04 96

HP:0003312

hp Abnormal form of the vertebral bodies (2)

4 8 1.01e-02 16

HP:0003300

hp Ovoid vertebral bodies (3)

2 4 3.40e-02 4

HP:0003309

hp Ovoid thoracolumbar vertebrae (4)

5 6 13 4.69e-02 47

HP:0000926

hp Platyspondyly (1)

15 24 28 3.50e-02 158

HP:0100763

hp Abnormality of the lymphatic system (1)

15 24 28 3.50e-02 158

HP:0000000

hp Abnormality of the lymphatic system (1)

19	34	33	4.26e-02	203	HP:0003271	hp	Visceromegaly (1)
14	21	27	8.47e-03	139	HP:0001743	hp	Abnormality of the spleen (1)
13	21	27	1.87e-03	129	HP:0001744	hp	Splenomegaly (2)
4	10		2.35e-03	22	HP:0000943	hp	Dysostosis multiplex (1)
2	6		5.38e-03	8	HP:0011012	hp	Abnormality of polysaccharide metabolism (1)
3	6		3.50e-02	10	HP:0004367	hp	Abnormality of glycoprotein metabolism (1)
2	6		5.38e-03	8	HP:0004355	hp	Abnormality of proteoglycan metabolism (2)
2	4		3.40e-02	4	HP:0002159	hp	Heparan sulfate excretion in urine (3)
18	39	6	1.21e-04	159	HP:0004360	hp	Abnormality of acid-base homeostasis (1)
17	38	4	2.13e-05	144	HP:0001941	hp	Acidosis (2)
9	22	2	3.48e-03	75	HP:0003128	hp	Lactic acidosis (3)
7	17	2	2.81e-04	42	HP:0002151	hp	Increased serum lactate (3)
19	32	14	4.81e-03	136	HP:0001637	hp	Abnormality of the myocardium (1)
19	31	14	9.89e-03	134	HP:0001638	hp	Cardiomyopathy (2)
3	4	8	1.01e-02	16	HP:0001387	hp	Joint stiffness (1)
2	4		3.40e-02	4	HP:0003033	hp	Mild joint stiffness (2)
10	24	3	1.20e-02	92	HP:0001943	hp	Hypoglycemia (1)
3	12	1	3.81e-02	32	HP:0002490	hp	Increased CSF lactate (1)
12	25	7	1.77e-02	100	HP:0004372	hp	Reduced consciousness/confusion (1)
7	4	2	4.21e-02	15	HP:0000424	hp	Broad nasal root (1)
26	47	40	6.78e-03	248	HP:0001276	hp	Hypertonia (1)
18	37	31	1.09e-02	174	HP:0001257	hp	Spasticity (2)
3	12	20	3.33e-05	63	HP:0000280	hp	Coarse facial features (1)
27	44	24	1.05e-02	222	HP:0002795	hp	Functional respiratory abnormality (1)
2	4		3.40e-02	4	HP:0000900	hp	Thickened ribs (1)
2	5	12	1.06e-04	25	HP:0008518	hp	Aplasia/Hypoplasia involving the vertebral column (1)
73	115	81	8.49e-03	794	HP:0003011	hp	Abnormality of musculature (1)
8	8	2	1.10e-02	17	HP:0003201	hp	Rhabdomyolysis (2)
12	31	7	1.17e-03	122	HP:0004354	hp	Abnormality of carboxylic acid metabolism (1)
9	28	7	4.61e-03	111	HP:0004337	hp	Abnormality of amino acid metabolism (2)
4	11	23	4.28e-03	104	HP:0001268	hp	Mental deterioration (1)
71	103	74	6.26e-03	667	HP:0000004	hp	Onset and clinical course (1)
26	44	28	9.43e-04	204	HP:0003679	hp	Pace of progression (2)
5	9	4	6.39e-03	16	HP:0001432	hp	Early death (3)

		P-value	T	term ID	term domain and name
11	22	111	1.24e-06	1187	KEGG:01100 ke Metabolic pathways (1)
5	11	9	1.77e-02	27	KEGG:00030 ke Pentose phosphate pathway (1)
8	17	21	4.05e-07	60	KEGG:05110 ke Vibrio cholerae infection (1)
17	14	14	2.91e-03	63	KEGG:05130 ke Pathogenic Escherichia coli infection (1)
6	20	7	7.78e-06	42	KEGG:00620 ke Pyruvate metabolism (1)
3	8	11	3.47e-03	33	KEGG:04966 ke Collecting duct acid secretion (1)
4	10		5.55e-05	19	KEGG:00531 ke Glycosaminoglycan degradation (1)
29	56	20	4.87e-08	181	KEGG:05016 ke Huntington's disease (1)
3	9		6.18e-03	24	KEGG:00511 ke Other glycan degradation (1)

11	32	29	5.22e-15	58
8	19	20	4.33e-05	70
43	59	4	1.32e-12	157
4	10	5	3.60e-02	23
28	26	9	4.38e-04	124
36	35	33	1.47e-02	211
7	10	10	3.27e-02	35
6	20	10	1.13e-04	48
14	48	25	7.41e-09	137
14	18	15	4.12e-02	70
14	14	2	8.38e-05	35
16	14	22	1.28e-02	115
27	48	23	4.37e-05	174
27	24	23	9.56e-03	138
10	13	18	4.92e-03	79
8	20	3	2.04e-05	44
8	10	2	3.60e-02	23
8	14	18	1.92e-03	74
11	15	8	4.63e-02	45
22	44	16	1.23e-07	129
27	55	32	4.39e-07	186
24	27	4	3.20e-04	96
13	23	16	5.32e-04	65
4	15	3	4.19e-04	32
41	57	18	7.16e-10	169
15	29	48	9.38e-05	285
7	19	5	6.19e-08	31
15	18	12	2.58e-02	61
3	14	2	5.28e-03	34
42	57	28	6.45e-25	94
5	23	51	4.48e-20	135

P-value T

74	96	36	2.49e-03	754
66	114	76	1.23e-05	810
75	87	50	2.04e-03	763
61	104	50	6.65e-03	821
70	99	50	2.83e-03	757
73	102	56	1.23e-03	771
63	96	56	4.86e-03	738

KEGG:03050	ke	Proteasome (1)
KEGG:04721	ke	Synaptic vesicle cycle (1)
KEGG:03040	ke	Spliceosome (1)
KEGG:03060	ke	Protein export (1)
KEGG:04110	ke	Cell cycle (1)
KEGG:04810	ke	Regulation of actin cytoskeleton (1)
KEGG:04130	ke	SNARE interactions in vesicular transport (1)
KEGG:00970	ke	Aminoacyl-tRNA biosynthesis (1)
KEGG:00190	ke	Oxidative phosphorylation (1)
KEGG:05100	ke	Bacterial invasion of epithelial cells (1)
KEGG:03030	ke	DNA replication (1)
KEGG:04670	ke	Leukocyte transendothelial migration (1)
KEGG:05010	ke	Alzheimer's disease (1)
KEGG:04530	ke	Tight junction (1)
KEGG:04520	ke	Adherens junction (1)
KEGG:00280	ke	Valine, leucine and isoleucine degradation (1)
KEGG:03430	ke	Mismatch repair (1)
KEGG:05120	ke	Epithelial cell signaling in Helicobacter pylori infection (1)
KEGG:00480	ke	Glutathione metabolism (1)
KEGG:05012	ke	Parkinson's disease (1)
KEGG:04141	ke	Protein processing in endoplasmic reticulum (1)
KEGG:03015	ke	mRNA surveillance pathway (1)
KEGG:00010	ke	Glycolysis / Gluconeogenesis (1)
KEGG:00640	ke	Propanoate metabolism (1)
KEGG:03013	ke	RNA transport (1)
KEGG:04145	ke	Phagosome (1)
KEGG:00020	ke	Citrate cycle (TCA cycle) (1)
KEGG:05131	ke	Shigellosis (1)
KEGG:04140	ke	Regulation of autophagy (1)
KEGG:03010	ke	Ribosome (1)
KEGG:04142	ke	Lysosome (1)

term ID term domain and name

MI:hsa-miR-429	mi	MI:hsa-miR-429 (1)
MI:hsa-miR-582-3p	mi	MI:hsa-miR-582-3p (1)
MI:hsa-miR-451	mi	MI:hsa-miR-451 (1)
MI:hsa-let-7g*	mi	MI:hsa-let-7g* (1)
MI:hsa-miR-548d-5p	mi	MI:hsa-miR-548d-5p (1)
MI:hsa-miR-548c-5p	mi	MI:hsa-miR-548c-5p (1)
MI:hsa-miR-548a-5p	mi	MI:hsa-miR-548a-5p (1)

85	10452	1.31e-02	943		MI:hsa-miR-519c-3p	MI:hsa-miR-519c-3p (1)
58	85	3.18e-02	667		MI:hsa-miR-142-5p	MI:hsa-miR-142-5p (1)
67	78	3.00e-02	716		MI:hsa-miR-195	MI:hsa-miR-195 (1)
96	11061	6.74e-05	970		MI:hsa-miR-548d-3p	MI:hsa-miR-548d-3p (1)
80	98	2.47e-03	834		MI:hsa-miR-200b	MI:hsa-miR-200b (1)
74	96	1.23e-02	790		MI:hsa-miR-548b-5p	MI:hsa-miR-548b-5p (1)
55	85	1.07e-02	647		MI:hsa-miR-561	MI:hsa-miR-561 (1)
60	90	1.20e-02	697		MI:hsa-miR-191	MI:hsa-miR-191 (1)
		P-value	T		term ID	term domain and name
3	2	10	4.49e-02	25	REAC:167433	re G-protein beta-gamma subunits rebind the alpha-GDP subunit (1)
13	29	16	6.33e-11	41	REAC:199991	re Membrane Trafficking (1)
5	10	4	1.21e-05	10	REAC:199983	re Golgi to ER Retrograde Transport (2)
5	10	4	1.21e-05	10	REAC:199997	re COPI Mediated Transport (3)
4	9	4	6.70e-05	9	REAC:200461	re GAP Recruitment to the Coatome:Arf1-GTP Complex (4)
4	9	4	6.70e-05	9	REAC:200456	re Hydrolysis of Arf1-GTP to Arf1-GDP (4)
4	9	4	6.70e-05	9	REAC:200462	re Coatome:Arf1-GTP:GAP lattice formation on golgi membrane (4)
4	9	4	6.70e-05	9	REAC:200459	re Diffusion of inactive Arf1-GDP from membrane (4)
3	8	4	3.69e-04	8	REAC:199990	re Coat Complex Formation (4)
4	8	3	3.69e-04	8	REAC:200516	re Sculpting and pinching-off of Golgi vessicle (4)
4	8	3	3.69e-04	8	REAC:200604	re Golgi vesicle lattice disassociation (4)
9	14	10	4.06e-03	24	REAC:199992	re trans-Golgi Network Vesicle Budding (2)
9	13	10	6.90e-03	22	REAC:375433	re Vamp7 associated clathrin derived vesicle budding (3)
	7	3	1.37e-02	8	REAC:203996	re Vesicle Uncoating (1)
7	6	2	4.98e-02	11	REAC:110306	re Repair synthesis for gap-filling by DNA pol epsilon in TC-NER (1)
4	3	9	6.46e-03	17	REAC:163624	re Glucagon:GCCR mediates GTP-GDP exchange (1)
29	46	34	4.79e-08	101	REAC:69306	re DNA Replication (1)
21	43	32	5.13e-10	82	REAC:69002	re DNA Replication Pre-Initiation (2)
20	40	32	6.66e-11	74	REAC:69304	re Regulation of DNA replication (2)
20	40	32	6.66e-11	74	REAC:69300	re Removal of licensing factors from origins (3)
60	81	48	4.24e-02	306	REAC:69278	re Cell Cycle, Mitotic (1)
31	47	35	5.05e-08	106	REAC:69242	re S Phase (2)
29	46	34	5.34e-09	96	REAC:69239	re Synthesis of DNA (3)
20	40	32	2.58e-11	72	REAC:69052	re Switching of origins to a post-replicative state (4)
20	40	32	2.58e-11	72	REAC:68949	re Orc1 removal from chromatin (5)
12	34	32	1.90e-15	56	REAC:68948	re Ubiquitinated Orc1 is degraded by the proteasome (6)
12	34	32	7.92e-15	58	REAC:69017	re CDK-mediated phosphorylation and removal of Cdc6 (5)
12	34	32	3.92e-15	57	REAC:69016	re Ubiquitinated Cdc6 is degraded by the proteasome (6)
6	6		1.87e-03	6	REAC:69019	re Mcm4,6,7 trimer forms and associates with the replication fork (5)
15	12	2	2.53e-04	29	REAC:69190	re DNA strand elongation (4)
7	6		2.04e-02	10	REAC:176974	re Unwinding of DNA (5)
6	6		1.87e-03	6	REAC:169468	re MCM2-7 mediated fork unwinding (6)
7	6		6.91e-03	9	REAC:176942	re Multiple proteins are localized at replication fork (6)
13	34	32	7.92e-15	58	REAC:75815	re Ubiquitin-dependent degradation of Cyclin D (3)
13	34	32	7.92e-15	58	REAC:69229	re Ubiquitin-dependent degradation of Cyclin D1 (4)
12	34	32	3.92e-15	57	REAC:75825	re Proteasome mediated degradation of Cyclin D1 (5)
15	35	33	6.85e-13	69	REAC:69656	re Cyclin A:Cdk2-associated events at S phase entry (3)
28	45	34	1.29e-07	104	REAC:69206	re G1/S Transition (2)
15	35	33	1.18e-12	70	REAC:69202	re Cyclin E associated events during G1/S transition (3)
13	35	33	1.05e-14	62	REAC:187577	re SCF(Skp2)-mediated degradation of p27/p21 (4)
13	35	33	1.05e-14	62	REAC:187574	re Degradation of ubiquitinated p27/p21 by the 26S proteasome (5)
18	40	32	3.40e-12	68	REAC:68874	re M/G1 Transition (2)

18	40	32	3.40e-12	68	REAC:68867	re	Assembly of the pre-replicative complex (3)
12	34	32	1.09e-13	62	REAC:68827	re	CDT1 association with the CDC6:ORC:origin complex (4)
12	34	32	3.92e-15	57	REAC:68825	re	Ubiquitinated geminin is degraded by the proteasome (5)
14	37	33	1.08e-09	85	REAC:174143	re	APC/C-mediated degradation of cell cycle proteins (2)
14	37	33	3.25e-10	82	REAC:176408	re	Regulation of APC/C activators between G1/S and early anaphase (3)
12	35	33	1.05e-14	62	REAC:174113	re	SCF-beta-TrCP mediated degradation of Emi1 (4)
12	35	33	1.05e-14	62	REAC:174203	re	SCF-mediated degradation of Emi1 (5)
12	34	32	1.58e-11	71	REAC:174084	re	Autodegradation of Cdh1 by Cdh1:APC/C (3)
12	34	32	1.58e-11	71	REAC:174058	re	Degradation of multiubiquitinated Cdh1 (4)
12	35	32	1.65e-10	76	REAC:174178	re	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted prot... (3)
12	35	32	1.65e-10	76	REAC:174105	re	Degradation of multiubiquitinated cell cycle proteins (4)
14	36	32	2.56e-10	77	REAC:176814	re	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic protein... (3)
14	35	32	1.65e-10	76	REAC:176409	re	APC/C:Cdc20 mediated degradation of mitotic proteins (4)
12	34	32	2.58e-11	72	REAC:174154	re	APC/C:Cdc20 mediated degradation of Securin (5)
12	34	32	2.58e-11	72	REAC:174202	re	Degradation of multiubiquitinated Securin (6)
6	7	6	3.39e-02	9	REAC:390450	re	Folding of actin by CCT/TriC (1)
6	7	6	3.39e-02	9	REAC:390459	re	Exchange of ADP for ATP in CCT/TriC:actin complex (2)
6	7	6	3.39e-02	9	REAC:390453	re	Hydrolysis of ATP and release of folded actin from CCT/TriC (2)
19	29	19	4.76e-02	82	REAC:15869	re	Metablism of nucleotides (1)
16	23	13	1.72e-03	50	REAC:73847	re	Purine metabolism (2)
6	6		4.13e-02	8	REAC:68954	re	Mcm2-7 is phosphorylated by DDK (1)
5	6	11	4.19e-03	24	REAC:195146	re	Dissociation of Rho GTP:GDP from GDI complex (1)
53	67	37	4.01e-21	111	REAC:157279	re	3' -UTR-mediated translational regulation (1)
53	67	37	4.01e-21	111	REAC:156827	re	L13a-mediated translational silencing of Ceruloplasmin expression (2)
24	29	12	1.00e-07	50	REAC:156826	re	Dissociation of L13a from the 60s ribosomal subunit (3)
30	39	25	1.70e-12	62	REAC:156823	re	Association of phospho-L13a with GAIT element of Ceruloplasmin mRNA (3)
13	35	32	3.92e-15	57	REAC:212919	re	Regulation of activated PAK-2p34 by proteasome mediated degradation (1)
13	35	32	3.92e-15	57	REAC:212917	re	Proteasome mediated degradation of PAK-2p34 (2)
27	62	45	1.67e-06	177	REAC:71291	re	Metabolism of amino acids (1)
15	38	33	1.99e-12	71	REAC:70694	re	Ornithine and proline metabolism (2)
14	37	33	3.94e-13	68	REAC:70693	re	Ornithine metabolism (3)
13	34	32	5.82e-14	61	REAC:350562	re	Regulation of ornithine decarboxylase (ODC) (4)
12	33	31	1.69e-13	59	REAC:353125	re	26S proteasome degrades ODC holoenzyme complex (5)
27	47	33	6.66e-06	118	REAC:69620	re	Cell Cycle Checkpoints (1)
13	34	32	6.50e-13	65	REAC:69615	re	G1/S DNA Damage Checkpoints (2)
12	34	32	3.92e-15	57	REAC:69613	re	p53-Independent G1/S DNA damage checkpoint (3)
12	34	32	3.92e-15	57	REAC:69610	re	p53-Independent DNA Damage Response (4)
12	34	32	3.92e-15	57	REAC:69601	re	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A (5)
12	34	32	3.92e-15	57	REAC:69600	re	Proteolytic degradation of ubiquitinated-Cdc25A (6)
	7	3	1.37e-02	8	REAC:204008	re	Cargo, Sec31p:Sec13p, and v-SNARE recruitment (1)
5	3		1.43e-02	5	REAC:175174	re	Association of Ku heterodimer with viral DNA ends (1)
75	95	33	3.99e-30	160	REAC:168254	re	Influenza Infection (1)
74	93	33	6.05e-30	155	REAC:168255	re	Influenza Life Cycle (2)
70	91	30	1.88e-29	151	REAC:168273	re	Influenza Viral RNA Transcription and Replication (3)
41	56	28	2.86e-18	90	REAC:192823	re	Viral mRNA Translation (4)
41	56	28	2.86e-18	90	REAC:192841	re	Viral Protein Synthesis (5)
41	56	28	2.86e-18	90	REAC:192704	re	Synthesis of PB1-F2 (5)
29	35	2	4.02e-09	62	REAC:168325	re	Viral Messenger RNA Synthesis (4)
29	35	2	2.11e-09	61	REAC:192781	re	Viral mRNA Splicing (M, NS segments) (5)
13	37	34	3.62e-15	64	REAC:195721	re	Signaling by Wnt (1)
13	37	34	3.62e-15	64	REAC:195253	re	Degradation of beta-catenin by the destruction complex (2)
13	37	34	3.62e-15	64	REAC:195298	re	Degradation of ubiquitinated -beta catenin by the proteasome (3)

33	80	39	5.33e-09	217	REAC:381150	re	Diabetes pathways (1)
8	15	5	7.98e-03	28	REAC:71406	re	Pyruvate metabolism and TCA cycle (1)
21	36	25	1.27e-03	95	REAC:71387	re	Metabolism of carbohydrates (1)
16	31	21	1.39e-03	77	REAC:70326	re	Glucose metabolism (2)
12	17	11	4.55e-03	33	REAC:70263	re	Gluconeogenesis (3)
36	82	41	1.93e-09	221	REAC:163685	re	Integration of energy metabolism (1)
1	11	2	9.21e-03	17	REAC:200409	re	Activated AMPK stimulates fatty-acid oxidation in muscle (2)
1	10	2	5.60e-04	12	REAC:200421	re	Activation of cytosolic AMPK by phosphorylation (3)
27	62	25	1.32e-08	153	REAC:265764	re	Glucose Regulation of Insulin Secretion (2)
8	30	6	5.82e-03	78	REAC:163200	re	Electron Transport Chain (3)
3	8	1	1.17e-02	10	REAC:164651	re	Electron transfer from ubiquinol to cytochrome c of complex III (4)
9	9	10	1.18e-02	22	REAC:70171	re	Glycolysis (3)
5	11	1	9.21e-03	17	REAC:71403	re	Citric acid cycle (TCA cycle) (3)
40	60	2	2.07e-15	111	REAC:72203	re	Processing of Capped Intron-Containing Pre-mRNA (1)
118	162	57	1.94e-25	407	REAC:74160	re	Gene Expression (1)
47	64	3	2.32e-08	162	REAC:75983	re	Formation and Maturation of mRNA Transcript (2)
46	63	3	1.46e-10	144	REAC:112295	re	Elongation and Processing of Capped Transcripts (3)
46	63	3	1.46e-10	144	REAC:76043	re	Elongation of Intron-Containing Transcripts and co-transcriptional mRNA spl... (4)
19	19	2	1.41e-06	34	REAC:72103	re	Formation of pre-mRNPs (5)
40	59	2	1.10e-15	107	REAC:72172	re	mRNA Splicing (5)
40	59	2	1.10e-15	107	REAC:72163	re	mRNA Splicing - Major Pathway (6)
39	58	2	1.92e-15	105	REAC:156661	re	Formation of Exon Junction Complex (7)
35	53	2	4.55e-15	92	REAC:72127	re	Formation of the Spliceosomal B Complex (7)
39	58	2	5.50e-16	103	REAC:72143	re	Lariat Formation and 5'-Splice Site Cleavage (7)
39	58	2	1.92e-15	105	REAC:72160	re	Cleavage at the 3'-Splice Site and Exon Ligation (7)
29	35	2	2.11e-09	61	REAC:72107	re	Formation of the Spliceosomal E complex (7)
40	59	2	1.66e-16	104	REAC:72130	re	Formation of an intermediate Spliceosomal C complex (7)
33	46	2	9.89e-14	77	REAC:72124	re	Formation of the Spliceosomal A Complex (7)
39	58	2	2.89e-16	102	REAC:72139	re	Formation of the active Spliceosomal C complex (7)
6	23		9.77e-05	44	REAC:72165	re	mRNA Splicing - Minor Pathway (6)
6	23		9.77e-05	44	REAC:75081	re	Formation of AT-AC B Complex (7)
6	23		9.77e-05	44	REAC:75079	re	Formation of AT-AC C complex (7)
4	17		8.12e-04	30	REAC:75080	re	Formation of AT-AC A complex (7)
6	23		9.77e-05	44	REAC:75083	re	ATAC spliceosome mediated 3' splice site cleavage, exon ligation (7)
6	23		9.77e-05	44	REAC:75082	re	ATAC spliceosome mediated Lariat formation, 5' splice site cleavage (7)
6	21	11	1.65e-02	49	REAC:379724	re	tRNA Aminoacylation (2)
6	18	11	1.19e-05	27	REAC:379716	re	Cytosolic tRNA aminoacylation (3)
3	8	5	2.79e-03	9	REAC:380008	re	lysine + tRNA(Lys) + ATP => Lys-tRNA(Lys) + AMP + pyrophosphate (4)
3	8	5	2.79e-03	9	REAC:379861	re	glutamate + tRNA(Glu) + ATP => Glu-tRNA(Glu) + AMP + pyrophosphate (4)
3	8	5	2.79e-03	9	REAC:379893	re	isoleucine + tRNA(Ile) + ATP => Ile-tRNA(Ile) + AMP + pyrophosphate (4)
3	8	5	2.79e-03	9	REAC:379993	re	arginine + tRNA(Arg) + ATP => Arg-tRNA(Arg) + AMP + pyrophosphate (4)
3	8	5	2.79e-03	9	REAC:379982	re	glutamine + tRNA(Gln) + ATP => Gln-tRNA(Gln) + AMP + pyrophosphate (4)
3	8	5	2.79e-03	9	REAC:379865	re	proline + tRNA(Pro) + ATP => Pro-tRNA(Pro) + AMP + pyrophosphate (4)
3	8	5	2.79e-03	9	REAC:379974	re	leucine + tRNA(Leu) + ATP => Leu-tRNA(Leu) + AMP + pyrophosphate (4)
3	8	5	2.79e-03	9	REAC:379867	re	aspartate + tRNA(Asp) + ATP => Asp-tRNA(Asp) + AMP + pyrophosphate (4)
3	8	5	2.79e-03	9	REAC:379994	re	methionine + tRNA(Met) + ATP => Met-tRNA(Met) + AMP + pyrophosphate (4)
72	91	55	1.98e-16	206	REAC:392499	re	Metabolism of proteins (1)
61	75	43	2.42e-23	126	REAC:72766	re	Translation (2)
46	60	33	1.51e-20	94	REAC:156842	re	Eukaryotic Translation Elongation (3)
43	58	30	9.36e-20	91	REAC:156902	re	Peptide chain elongation (4)
41	56	28	1.30e-18	89	REAC:156912	re	Peptide transfer from P-site tRNA to the A-site tRNA (5)
42	57	29	3.50e-19	90	REAC:156907	re	Aminoacyl-tRNA binds to the ribosome at the A-site (5)
43	58	30	9.36e-20	91	REAC:156915	re	Translocation of ribosome by 3 bases in the 3' direction (5)
42	57	29	3.50e-19	90	REAC:156923	re	Hydrolysis of eEF1A:GTP (5)
4	3	4	5.00e-02	4	REAC:156913	re	Regeneration of eEF1A:GTP by eEF1B activity (4)
41	57	28	7.79e-19	91	REAC:72764	re	Eukaryotic Translation Termination (3)
41	57	28	7.79e-19	91	REAC:141671	re	Polypeptide release from the eRF3-GDP:eRF1:mRNA:80S Ribosome complex (4)
41	57	28	7.79e-19	91	REAC:141691	re	GTP bound eRF3:eRF1 complex binds the peptidyl tRNA:mRNA:80S Ribosome compl... (4)

41	57	28	7.79e-19	91	REAC:141673	re	GTP Hydrolysis by eRF3 bound to the eRF1:mRNA:polypeptide:80S Ribosome comp... (4)
56	70	38	3.26e-21	119	REAC:72613	re	Eukaryotic Translation Initiation (3)
56	70	38	3.26e-21	119	REAC:72737	re	Cap-dependent Translation Initiation (4)
47	62	32	5.80e-20	101	REAC:72689	re	Formation of a pool of free 40S subunits (5)
41	56	29	2.86e-18	90	REAC:72673	re	Release of 40S and 60S subunits from the 80S ribosome (6)
23	33	20	7.00e-11	51	REAC:72676	re	eIF3 and eIF1A bind to the 40S subunit (6)
23	35	22	1.18e-11	54	REAC:72695	re	Formation of the ternary complex, and subsequently, the 43S complex (5)
23	35	22	1.18e-11	54	REAC:72691	re	Formation of the 43S pre-initiation complex (6)
30	38	25	1.31e-11	62	REAC:72662	re	Activation of the mRNA upon binding of the cap-binding complex and eIFs, an... (7)
29	38	25	6.12e-12	61	REAC:72649	re	Translation initiation complex formation (6)
29	38	25	6.12e-12	61	REAC:156808	re	Formation of translation initiation complexes yielding circularized Cerulop... (7)
28	38	24	2.78e-12	60	REAC:157849	re	Formation of translation initiation complexes containing mRNA that does not... (7)
28	39	25	7.59e-13	61	REAC:72702	re	Ribosomal scanning and start codon recognition (5)
28	38	24	2.78e-12	60	REAC:72621	re	Ribosomal scanning (6)
28	39	25	7.59e-13	61	REAC:72697	re	Start codon recognition (6)
53	69	37	1.43e-22	112	REAC:72706	re	GTP hydrolysis and joining of the 60S ribosomal subunit (5)
28	39	25	7.59e-13	61	REAC:72619	re	eIF2:GTP is hydrolyzed, eIFs are released (6)
42	57	28	3.50e-19	90	REAC:72672	re	The 60S subunit joins the translation initiation complex (6)
42	57	28	3.50e-19	90	REAC:72671	re	eIF5B:GTP is hydrolyzed and released (6)
14	35	32	6.66e-11	74	REAC:174184	re	Cdc20:Phospho-APC/C mediated degradation of Cyclin A (1)
14	35	32	6.66e-11	74	REAC:174255	re	Degradation multiubiquitinated Cyclin A (2)
46	78	48	3.25e-08	216	REAC:162906	re	HIV Infection (1)
37	66	48	3.60e-12	145	REAC:162909	re	Host Interactions of HIV factors (2)
12	35	33	1.36e-15	59	REAC:180534	re	Vpu mediated degradation of CD4 (3)
12	35	33	1.36e-15	59	REAC:180573	re	Degradation of ubiquitinated CD4 (4)
11	15	4	3.70e-02	31	REAC:177243	re	Interactions of Rev with host cellular proteins (3)
14	36	33	5.43e-15	61	REAC:180585	re	Vif-mediated degradation of APOBEC3G (3)
14	36	33	5.43e-15	61	REAC:180603	re	Proteasome-mediated degradation of APOBEC3G (4)
2	1	4	5.00e-02	4	REAC:114592	re	Collagen adhesion via alpha 2 beta 1 glycoprotein (1)
2	1	4	5.00e-02	4	REAC:114563	re	Adhesion via alpha 2 beta 1 glycoprotein (2)
30	28	56	1.99e-07	234	REAC:109582	re	Hemostasis (1)
11	9	11	2.50e-03	23	REAC:350701	re	Further platelet releasate (2)
14	12	29	2.50e-03	118	REAC:75178	re	Formation of Platelet plug (2)
14	8	24	2.96e-02	101	REAC:76002	re	Platelet Activation (3)
9	3	14	7.76e-04	33	REAC:114509	re	Platelet activation triggers (4)
6	3	11	1.07e-02	26	REAC:114696	re	Thrombin signalling through PARs (5)
5	3	11	6.79e-03	25	REAC:114665	re	Thrombin signalling G-protein cascades (6)
4	3	10	2.96e-02	24	REAC:114664	re	Proteinase activated receptor G alpha (12/13) cascade (7)
6	7	6	1.24e-02	8	REAC:390471	re	Association of TriC/CCT with target proteins during biosynthesis (1)
6	7	6	1.24e-02	8	REAC:391266	re	Association of CCT/TriC with sphingosine kinase 1 (2)
6	7	6	2.03e-03	7	REAC:390470	re	Association of CCT/TriC with other substrates during biosynthesis (unknown ... (2)
6	4	1	4.13e-02	8	REAC:162592	re	Integration of provirus (1)
7	6	2	4.98e-02	11	REAC:109968	re	Repair synthesis of ~27-30 bases long patch by DNA Pol Epsilon (1)
42	59	45	7.86e-10	144	REAC:109581	re	Apoptosis (1)
13	35	32	7.92e-15	58	REAC:169911	re	Regulation of Apoptosis (2)
13	35	32	3.92e-15	57	REAC:211733	re	Regulation of activated PAK-2p34 by proteasome mediated degradation (3)
13	35	32	3.92e-15	57	REAC:211715	re	Proteasome mediated degradation of PAK-2p34 (4)
23	17	9	3.30e-07	45	REAC:75153	re	Apoptotic execution phase (2)
18	14	8	1.72e-04	39	REAC:111465	re	Apoptotic cleavage of cellular proteins (3)
9	1	3	1.81e-03	13	REAC:264870	re	Caspase-mediated cleavage of cytoskeletal proteins (4)
5	6	11	4.19e-03	24	REAC:194854	re	GDI blocks activation of Rho GTPase:GDP (1)
2	14	7	1.39e-02	26	REAC:265088	re	Translocation of Preproinsulin to Endoplasmic Reticulum (1)
12	34	32	1.58e-11	71	REAC:188191	re	APC/C:Cdh1-mediated degradation of Skp2 (1)

7	3	1.37e-02	8	REAC:203973	re	Vesicle Budding (1)
		P-value	T	term ID		term domain and name
557835	548	1.34e-18	6723	TF:M00931_4	tf	Factor: Sp1; motif: GGGGCGGGGC; match class: 4 (1)
534782	518	2.24e-15	6375	TF:M00931_3	tf	Factor: Sp1; motif: GGGGCGGGGC; match class: 3 (2)
492703	468	3.54e-15	5645	TF:M00931_2	tf	Factor: Sp1; motif: GGGGCGGGGC; match class: 2 (3)
4236134	18	7.66e-12	5025	TF:M00931_1	tf	Factor: Sp1; motif: GGGGCGGGGC; match class: 1 (4)
275407	288	2.95e-14	3020	TF:M00931_0	tf	Factor: Sp1; motif: GGGGCGGGGC; match class: 0 (5)
41	62	6.33e-03	366	TF:M00920_4	tf	Factor: E2F; motif: NKCGCGCSAAN; match class: 4 (1)
308484	275	1.21e-04	4083	TF:M00623_4	tf	Factor: Crx; motif: YNNNTAATCYSMN; match class: 4 (1)
278433	253	2.94e-04	3680	TF:M00623_3	tf	Factor: Crx; motif: YNNNTAATCYSMN; match class: 3 (2)
197311	159	1.44e-03	2521	TF:M00327_4	tf	Factor: Pax-3; motif: NNNNNCGTCACGSTYNNNNN; match class: 4 (1)
111	68	9.43e-03	1124	TF:M00426_4	tf	Factor: E2F; motif: TTTSGCGS; match class: 4 (1)
27	55	2.37e-02	327	TF:M00187_1	tf	Factor: USF; motif: GYCACGTGNC; match class: 1 (1)
21	42	4.18e-02	234	TF:M00187_0	tf	Factor: USF; motif: GYCACGTGNC; match class: 0 (2)
259391	196	5.30e-18	2607	TF:M00025_4	tf	Factor: Elk-1; motif: NNNNCCGGGAARTNN; match class: 4 (1)
216334	166	7.82e-18	2130	TF:M00025_3	tf	Factor: Elk-1; motif: NNNNCCGGGAARTNN; match class: 3 (2)
133213	100	5.13e-16	1252	TF:M00025_2	tf	Factor: Elk-1; motif: NNNNCCGGGAARTNN; match class: 2 (3)
438621	114	6.07e-03	5773	TF:M00189_4	tf	Factor: AP-2; motif: MKCCSCNGGCG; match class: 4 (1)
73211	657	3.23e-47	8691	TF:M00803_0	tf	Factor: E2F; motif: GGCGSG; match class: 0 (1)
204313	172	3.07e-05	2485	TF:M01035_4	tf	Factor: YY1; motif: NYNKCCATNTT; match class: 4 (1)
184283	147	7.32e-07	2087	TF:M01035_3	tf	Factor: YY1; motif: NYNKCCATNTT; match class: 3 (2)
116193	97	9.24e-09	1242	TF:M01035_2	tf	Factor: YY1; motif: NYNKCCATNTT; match class: 2 (3)
101125	67	9.22e-03	989	TF:M00916_4	tf	Factor: CREB; motif: NNTKACGTCANNNS; match class: 4 (1)
87	104	4.25e-02	856	TF:M00916_3	tf	Factor: CREB; motif: NNTKACGTCANNNS; match class: 3 (2)
183293	179	1.47e-03	2401	TF:M00796_3	tf	Factor: USF; motif: NRCCACGTGASN; match class: 3 (1)
567807	534	1.49e-10	6969	TF:M00933_4	tf	Factor: Sp1; motif: CCCCCCCCCN; match class: 4 (1)
500724	476	1.92e-10	6053	TF:M00933_3	tf	Factor: Sp1; motif: CCCCCCCCCN; match class: 3 (2)
4236134	18	2.09e-12	5018	TF:M00933_2	tf	Factor: Sp1; motif: CCCCCCCCCN; match class: 2 (3)
391562	378	3.14e-09	4601	TF:M00933_1	tf	Factor: Sp1; motif: CCCCCCCCCN; match class: 1 (4)
219311	207	1.63e-02	2633	TF:M00933_0	tf	Factor: Sp1; motif: CCCCCCCCCN; match class: 0 (5)
219362	209	2.85e-03	3020	TF:M00122_3	tf	Factor: USF; motif: NNRNCACGTGNYNN; match class: 3 (1)
184303	176	3.65e-04	2465	TF:M00122_2	tf	Factor: USF; motif: NNRNCACGTGNYNN; match class: 2 (2)
85	143	1.50e-02	1056	TF:M00122_1	tf	Factor: USF; motif: NNRNCACGTGNYNN; match class: 1 (3)
224372	216	2.71e-03	3113	TF:M00726_0	tf	Factor: USF2; motif: CASGYG; match class: 0 (1)
512744	482	3.90e-03	6839	TF:M00915_4	tf	Factor: AP-2; motif: SNNCCNCAGGCN; match class: 4 (1)
452644	415	3.95e-02	5894	TF:M00915_3	tf	Factor: AP-2; motif: SNNCCNCAGGCN; match class: 3 (2)
809127	807	3.74e-02	12686	TF:M01100_3	tf	Factor: LRF; motif: VNNRMCCCC; match class: 3 (1)
311443	228	2.92e-13	3275	TF:M00431_4	tf	Factor: E2F-1; motif: TTTSGCGS; match class: 4 (1)
284142	202	3.52e-12	3023	TF:M00431_3	tf	Factor: E2F-1; motif: TTTSGCGS; match class: 3 (2)
125	70	1.02e-03	1277	TF:M00431_2	tf	Factor: E2F-1; motif: TTTSGCGS; match class: 2 (3)
83	106	1.14e-02	778	TF:M00431_1	tf	Factor: E2F-1; motif: TTTSGCGS; match class: 1 (4)
35	46	4.96e-02	266	TF:M00652_0	tf	Factor: NrF-1; motif: CGCATGCGCR; match class: 0 (1)
79	92	2.12e-02	744	TF:M00041_0	tf	Factor: ATF2:c-Jun; motif: TGACGTYA; match class: 0 (1)
121175	80	1.52e-06	1167	TF:M00940_4	tf	Factor: E2F-1; motif: NTTTCGCGCS; match class: 4 (1)
93	124	1.58e-02	905	TF:M00940_3	tf	Factor: E2F-1; motif: NTTTCGCGCS; match class: 3 (2)
253393	210	2.24e-02	3405	TF:M00793_4	tf	Factor: YY1; motif: GCCATNTTN; match class: 4 (1)
212394	168	2.91e-04	2644	TF:M00793_3	tf	Factor: YY1; motif: GCCATNTTN; match class: 3 (2)

21423100	2.91e-04	2044	TF:M00793_1	tf	Factor: YY1; motif: GCGHNTIN; match class: 1 (2)
733105594	1.65e-28	8550	TF:M00428_4	tf	Factor: E2F-1; motif: NKTSSCGC; match class: 4 (1)
623919493	1.91e-25	7274	TF:M00428_3	tf	Factor: E2F-1; motif: NKTSSCGC; match class: 3 (2)
400585301	7.65e-14	4523	TF:M00428_2	tf	Factor: E2F-1; motif: NKTSSCGC; match class: 2 (3)
216160	1.60e-03	2398	TF:M00428_1	tf	Factor: E2F-1; motif: NKTSSCGC; match class: 1 (4)
8310642	1.14e-02	778	TF:M00428_0	tf	Factor: E2F-1; motif: NKTSSCGC; match class: 0 (5)
639943589	4.87e-04	8762	TF:M00800_4	tf	Factor: AP-2; motif: GSCCSCRGCCNRNRNN; match class: 4 (1)
576866564	1.54e-17	7083	TF:M00932_4	tf	Factor: Sp1; motif: NNGGGCGGGGNN; match class: 4 (1)
548622530	2.90e-18	6609	TF:M00932_3	tf	Factor: Sp1; motif: NNGGGCGGGGNN; match class: 3 (2)
489703464	2.69e-13	5680	TF:M00932_2	tf	Factor: Sp1; motif: NNGGGCGGGGNN; match class: 2 (3)
361515346	2.54e-10	4077	TF:M00932_1	tf	Factor: Sp1; motif: NNGGGCGGGGNN; match class: 1 (4)
124185120	1.11e-02	1422	TF:M00932_0	tf	Factor: Sp1; motif: NNGGGCGGGGNN; match class: 0 (5)
588663566	9.27e-22	6923	TF:M00196_4	tf	Factor: Sp1; motif: NGGGGCGGGGYN; match class: 4 (1)
543795520	3.98e-18	6348	TF:M00196_3	tf	Factor: Sp1; motif: NGGGGCGGGGYN; match class: 3 (2)
442626425	2.61e-13	5066	TF:M00196_2	tf	Factor: Sp1; motif: NGGGGCGGGGYN; match class: 2 (3)
318454326	2.51e-14	3578	TF:M00196_1	tf	Factor: Sp1; motif: NGGGGCGGGGYN; match class: 1 (4)
125183121	4.58e-03	1437	TF:M00196_0	tf	Factor: Sp1; motif: NGGGGCGGGGYN; match class: 0 (5)
287422204	3.62e-13	3054	TF:M00427_4	tf	Factor: E2F; motif: TTTSGCGS; match class: 4 (1)
195128	2.16e-04	2063	TF:M00427_3	tf	Factor: E2F; motif: TTTSGCGS; match class: 3 (2)
138222132	2.68e-05	1620	TF:M00187_4	tf	Factor: USF; motif: GYCACGTGNC; match class: 4 (1)
108191112	1.13e-05	1335	TF:M00187_3	tf	Factor: USF; motif: GYCACGTGNC; match class: 3 (2)
11115171	1.35e-02	1124	TF:M00938_4	tf	Factor: E2F-1; motif: TTGGCGCGRAANNM; match class: 4 (1)
442635357	5.56e-09	5257	TF:M00695_0	tf	Factor: ETF; motif: GVGGMGG; match class: 0 (1)
198270151	2.89e-04	2110	TF:M00801_0	tf	Factor: CREB; motif: CGTCAN; match class: 0 (1)
714103671	2.42e-17	8876	TF:M00008_4	tf	Factor: Sp1; motif: GGGGCGGGGT; match class: 4 (1)
664979636	6.18e-18	8219	TF:M00008_3	tf	Factor: Sp1; motif: GGGGCGGGGT; match class: 3 (2)
457654429	4.98e-15	5151	TF:M00008_2	tf	Factor: Sp1; motif: GGGGCGGGGT; match class: 2 (3)
115126	9.92e-04	1380	TF:M00008_1	tf	Factor: Sp1; motif: GGGGCGGGGT; match class: 1 (4)
6369	4.20e-02	712	TF:M00008_0	tf	Factor: Sp1; motif: GGGGCGGGGT; match class: 0 (5)

