PROCESS_D4_10mM_DOWN

#term ID	term description.NIST	observed g	backgroun	strength.NI	false disco	observed g	backgroun	strength.DI	false discovery rate.DP12
GO:00099	Cellular process	140	15994	0.15	7.93E-13				
GO:00442	Cellular metabolic process	90	7040	0.32	1.27E-11				
GO:00081	Metabolic process	100	8581	0.28	1.47E-11				
GO:00346	Cellular nitrogen compound metabolic process	64	3820	0.43	1.47E-11				
GO:19013	Organic cyclic compound metabolic process	58	3212	0.47	1.48E-11				
GO:00464	Heterocycle metabolic process	54	2937	0.48	8.30E-11				
GO:00717	Organic substance metabolic process	95	8137	0.28	9.47E-11				
GO:00061	Nucleobase-containing compound metabolic process	52	2791	0.48	1.33E-10				
GO:00067	Cellular aromatic compound metabolic process	54	2992	0.47	1.33E-10				
GO:00440	Cellular component biogenesis	50	2815	0.46	2.44E-09				
GO:00718	Cellular component organization or biogenesis	75	5887	0.32	7.85E-09				
GO:00442	Primary metabolic process	88	7736	0.27	9.55E-09				
GO:00903	Nucleic acid metabolic process	43	2240	0.49	1.01E-08				
GO:00068	Nitrogen compound metabolic process	82	7145	0.27	6.87E-08				
GO:00104	Gene expression	42	2399	0.45	2.85E-07				
GO:00226	Ribonucleoprotein complex biogenesis	21	616	0.74	2.85E-07				
GO:00069	Organelle organization	53	3632	0.37	3.90E-07				
GO:00431	Macromolecule metabolic process	74	6322	0.28	5.03E-07				
GO:00422	Ribosome biogenesis	18	459	0.8	5.74E-07				
GO:00160	R- metabolic process	30	1558	0.5	1.67E-05				
GO:00469	Intracellular transport	27	1297	0.53	1.90E-05				
GO:00516	Nuclear pore localization	4	4	2.21	5.32E-05				
GO:00063	R- processing	22	941	0.58	5.61E-05				
GO:00436	Dicarboxylic acid metabolic process	8	93	1.15	0.00011				
GO:00160	Cellular component organization	62	5621	0.25	0.00026				
GO:00160	rR- metabolic process	12	320	0.78	0.00049				
GO:00069	Nuclear envelope organization	6	49	1.3	5.00E-04				
GO:00226	Cellular component assembly	36	2516	0.37	0.00057				
GO:00062	D- metabolic process	18	770	0.58	0.00071				
GO:00442	Small molecule metabolic process	28	1690	0.43	0.00071				
GO:00516	Establishment of localization in cell	28	1689	0.43	0.00071				
GO:00314	Chromatin assembly	9	181	0.91	0.001				
GO:00442	Cellular biosynthetic process	35	2480	0.36	0.001				
GO:00512	Chromosome organization	20	966	0.53	0.001				
GO:00063	rR- processing	11	296	0.78	0.0011				
GO:00070	Mitochondrion organization	13	439	0.68	0.0016				
GO:00330	Regulation of chromosome organization	10	249	0.81	0.0016				
GO:19015	Organic substance biosynthetic process	35	2581	0.34	0.002				
GO:00330	Macromolecule localization	33	2366	0.36	0.0022				

GO:000709	Nuclear migration	5	40	1.31	0.0025			
GO:00717(	Nitrogen compound transport	24	1456	0.43	0.0034			
GO:007082	Heterochromatin organization	6	80	1.09	0.0044			
GO:00442(	Cellular macromolecule metabolic process	36	2825	0.32	0.0048			
GO:004581	Negative regulation of gene expression, epigenetic	6	83	1.07	0.005			
GO:005112	Regulation of cellular component organization	33	2504	0.33	0.0057	12	2504	0.66	0.0319
GO:005123	Establishment of localization	44	3839	0.27	0.0057			
GO:00717(	Organic substance transport	27	1835	0.38	0.0057			
GO:00328(	Regulation of protein localization	18	939	0.49	0.0059			
GO:00083(	R- splicing	11	372	0.68	0.0061			
GO:001094	Regulation of cell death	26	1740	0.39	0.0061			
GO:00429(	Regulation of apoptotic process	24	1531	0.41	0.0061			
GO:19054(	Regulation of D- duplex unwinding	3	7	1.84	0.0061			
GO:006034	Regulation of cellular localization	19	1043	0.47	0.0062			
GO:00346(	ncR- metabolic process	14	605	0.57	0.0064			
GO:19013(	Organic cyclic compound biosynthetic process	18	957	0.48	0.0066			
GO:000000	Mitochondrial genome mainte-nce	4	26	1.4	0.0071			
GO:004427	Cellular nitrogen compound biosynthetic process	25	1662	0.39	0.0071			
GO:00451(	Establishment of protein localization	20	1173	0.44	0.0085			
GO:003447	ncR- processing	12	469	0.62	0.0086			
GO:000691	Nucleocytoplasmic transport	9	260	0.75	0.0087			
GO:190113	Carbohydrate derivative metabolic process	18	1002	0.47	0.0104			
GO:00069(	Nucleus organization	7	151	0.88	0.0105			
GO:00725(	Establishment of protein localization to organelle	10	344	0.67	0.0128			
GO:001813	Heterocycle biosynthetic process	16	836	0.49	0.0129			
GO:005164	Cellular localization	33	2661	0.3	0.0129			
GO:200124	Regulation of intrinsic apoptotic sig-ling pathway	7	157	0.86	0.0129			
GO:000681	Transport	41	3660	0.26	0.0136			
GO:00436(	Dicarboxylic acid biosynthetic process	3	11	1.65	0.0137			
GO:000632	Chromatin organization	13	584	0.56	0.014			
GO:00068(	Intracellular protein transport	14	669	0.53	0.014			
GO:00315(	Heterochromatin assembly	5	67	1.08	0.014			
GO:005117	Localization	47	4471	0.23	0.015			
GO:00069(	Response to stress	37	3187	0.28	0.0153			
GO:004533	Cellular respiration	7	166	0.84	0.0157			
GO:190169	Response to nitrogen compound	19	1149	0.43	0.0157			
GO:001407	Response to organic cyclic compound	17	964	0.46	0.0173			
GO:00092(	Purine ribonucleoside triphosphate metabolic process	8	232	0.75	0.0185			
GO:009043	Protein localization to nuclear envelope	3	13	1.57	0.0185			
GO:00081(	Protein localization	26	1924	0.34	0.0196			
GO:00432(	Positive regulation of cysteine-type endopeptidase activity involved in apoptotic proce	6	121	0.91	0.0201			

GO:00064(	R- localization	7	176	0.81	0.0203				
GO:005102	mR- transport	6	122	0.9	0.0203				
GO:19028E	Microtubule cytoskeleton organization involved in mitosis	6	122	0.9	0.0203				
GO:00439(	Protein-containing complex organization	22	1505	0.38	0.0214				
GO:00063(	mR- processing	11	462	0.59	0.0226				
GO:007252	Purine-containing compound metabolic process	11	465	0.58	0.0236				
GO:000691	Activation of cysteine-type endopeptidase activity involved in apoptotic process	5	80	1.01	0.0239				
GO:00109E	Positive regulation of peptidase activity	7	188	0.78	0.027				
GO:001827	Protein N-linked glycosylation via asparagine	3	16	1.48	0.027				
GO:00229(	Respiratory electron transport chain	5	84	0.99	0.0285				
GO:00333(	Protein localization to organelle	14	739	0.49	0.0285				
GO:00511(	Nuclear export	6	133	0.86	0.0285				
GO:006054	Negative regulation of cell death	18	1125	0.41	0.0285				
GO:00062(	D- replication	7	192	0.77	0.0287				
GO:001943	Aromatic compound biosynthetic process	15	838	0.46	0.0291				
GO:003204	Mitochondrial D- metabolic process	3	17	1.46	0.0291				
GO:004594	Positive regulation of transcription by R- polymerase III	3	17	1.46	0.0291				
GO:004333	Response to exogenous dsR-	4	46	1.15	0.0295				
GO:190227	Regulation of chromatin organization	4	48	1.13	0.0337				
GO:00003(	mR- splicing, via spliceosome	8	267	0.69	0.0344				
GO:00060(	Generation of precursor metabolites and energy	10	416	0.59	0.0344				
GO:00550E	Nucleobase-containing small molecule metabolic process	12	582	0.52	0.0344				
GO:19015(	Organonitrogen compound biosynthetic process	22	1579	0.35	0.0344				
GO:190382	Positive regulation of protein localization	11	498	0.55	0.0344				
GO:199054	Mitochondrial transmembrane transport	5	91	0.95	0.0344				
GO:00432E	Regulation of cysteine-type endopeptidase activity involved in apoptotic process	7	204	0.75	0.035				
GO:00150(	Protein transport	17	1062	0.41	0.0353				
GO:00460(	ATP metabolic process	7	205	0.74	0.0354				
GO:00469E	Ketone body catabolic process	2	3	2.03	0.0381				
GO:19054(	Negative regulation of D- duplex unwinding	2	3	2.03	0.0381				
GO:00090E	Macromolecule biosynthetic process	22	1615	0.34	0.041				
GO:00359(	Cellular response to topologically incorrect protein	5	97	0.92	0.041				
GO:00442E	Small molecule catabolic process	9	354	0.62	0.041				
GO:00510E	Negative regulation of D- metabolic process	6	150	0.81	0.041				
GO:00345(	Protein localization to nucleus	7	213	0.73	0.0415				
GO:00100(	Response to organic substance	32	2827	0.26	0.0461				
GO:00650(	Protein-containing complex assembly	19	1312	0.37	0.0472				
GO:000692	Substrate-dependent cell migration	-	-	-	-	2	28	2.01	0.0319

PROCESS_D4_10mM_UP

#term ID	term description.NIST	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DF	false discovery rate.DP12
GO:005508	Nucleobase-containing small mole	10	582	0.99	0.00073	-	-	-	-
GO:007252	Purine-containing compound meta	8	465	0.99	0.0091	-	-	-	-
GO:000911	Nucleotide metabolic process	8	516	0.95	0.013	-	-	-	-
GO:000915	Purine ribonucleotide metabolic pı	7	421	0.98	0.0191	-	-	-	-
GO:190113	Carbohydrate derivative metabolic	10	1002	0.75	0.0191	-	-	-	-
GO:000701	Cytoskeleton organization	11	1308	0.68	0.0199	-	-	-	-
GO:000998	Cellular process	40	15994	0.15	0.0199	60	15994	0.14	0.0061
GO:004428	Small molecule metabolic process	12	1690	0.61	0.0254	-	-	-	-
GO:000091	Cytokinesis	4	107	1.33	0.0418	-	-	-	-
GO:000608	acetyl-CoA metabolic process	3	37	1.66	0.0423	-	-	-	-
GO:000613	Nucleobase-containing compounc	15	2791	0.49	0.0423	-	-	-	-
GO:190136	Organic cyclic compound metabol	16	3212	0.45	0.0471	-	-	-	-
GO:005124	Regulation of protein metabolic pr	-	-	-	-	25	2708	0.53	0.00021
GO:003016	Regulation of proteolysis	-	-	-	-	12	724	0.78	0.0037

PROCESS_D4_30mM_DOWN

#term ID	term description.NIST	observed g	background gene count.NIST		strength.NI	false disco	observed g	backgroun	strength.DI	false discovery rate.DP12
GO:0044237	Cellular metabolic process	239	7040	0.33	6.87E-38	79	7040	0.29	7.23E-09	
GO:0008152	Metabolic process	263	8581	0.29	9.48E-37	88	8581	0.26	1.12E-08	
GO:0034641	Cellular nitrogen compound metabolic process	166	3820	0.44	9.67E-34	58	3820	0.43	1.23E-09	
GO:0071704	Organic substance metabolic process	247	8137	0.29	5.66E-32	86	8137	0.27	7.23E-09	
GO:0009987	Cellular process	350	15994	0.14	5.62E-31	128	15994	0.15	2.94E-10	
GO:0044238	Primary metabolic process	238	7736	0.29	6.00E-31	84	7736	0.28	5.27E-09	
GO:1901360	Organic cyclic compound metabolic process	140	3212	0.44	3.40E-27	50	3212	0.44	1.03E-08	
GO:0006139	Nucleobase-containing compound metabolic process	128	2791	0.47	2.77E-26	47	2791	0.47	6.05E-09	
GO:0006725	Cellular aromatic compound metabolic process	133	2992	0.45	2.77E-26	50	2992	0.47	2.71E-09	
GO:0046483	Heterocycle metabolic process	131	2937	0.45	5.26E-26	49	2937	0.47	3.30E-09	
GO:0006807	Nitrogen compound metabolic process	217	7145	0.29	1.20E-25	81	7145	0.3	3.02E-09	
GO:0010467	Gene expression	111	2399	0.47	2.32E-22	39	2399	0.46	1.12E-06	
GO:0090304	Nucleic acid metabolic process	105	2240	0.47	2.57E-21	37	2240	0.46	2.09E-06	
GO:0043170	Macromolecule metabolic process	190	6322	0.28	4.48E-20	72	6322	0.3	6.11E-08	
GO:0071840	Cellular component organization or biogenesis	177	5887	0.28	5.58E-18	71	5887	0.33	7.53E-09	
GO:0006396	R- processing	60	941	0.61	1.21E-16	20	941	0.57	0.00026	
GO:0016070	R- metabolic process	78	1558	0.5	1.74E-16	28	1558	0.5	4.31E-05	
GO:0006996	Organelle organization	123	3632	0.33	2.47E-14	46	3632	0.35	4.31E-05	
GO:0044085	Cellular component biogenesis	104	2815	0.37	6.49E-14	39	2815	0.39	6.20E-05	
GO:0022613	Ribonucleoprotein complex biogenesis	40	616	0.62	1.04E-10	18	616	0.71	1.54E-05	
GO:0016043	Cellular component organization	152	5621	0.24	2.19E-10	63	5621	0.29	4.64E-06	
GO:0034660	ncR- metabolic process	38	605	0.6	1.03E-09	-	-	-	-	
GO:0042254	Ribosome biogenesis	33	459	0.66	1.05E-09	11	459	0.62	0.0125	
GO:0044281	Small molecule metabolic process	67	1690	0.4	2.70E-09	-	-	-	-	
GO:0044271	Cellular nitrogen compound biosynthetic process	66	1662	0.4	3.59E-09	25	1662	0.42	0.0024	
GO:0044260	Cellular macromolecule metabolic process	92	2825	0.32	5.97E-09	38	2825	0.37	0.00018	
GO:0008380	R- splicing	28	372	0.68	1.68E-08	13	372	0.79	0.00018	
GO:0009058	Biosynthetic process	86	2636	0.32	2.95E-08	-	-	-	-	
GO:0051276	Chromosome organization	46	966	0.48	2.95E-08	17	966	0.49	0.0074	
GO:0045333	Cellular respiration	19	166	0.86	3.86E-08	-	-	-	-	
GO:1901576	Organic substance biosynthetic process	84	2581	0.32	5.36E-08	32	2581	0.34	0.0041	
GO:0016072	rR- metabolic process	25	320	0.7	7.93E-08	-	-	-	-	
GO:0034470	ncR- processing	30	469	0.61	1.11E-07	-	-	-	-	
GO:0009060	Aerobic respiration	17	139	0.89	1.33E-07	-	-	-	-	
GO:0043603	Cellular amide metabolic process	48	1102	0.44	1.55E-07	-	-	-	-	
GO:0019752	Carboxylic acid metabolic process	43	917	0.47	1.60E-07	-	-	-	-	
GO:0006397	mR- processing	29	462	0.6	2.90E-07	13	462	0.69	0.0012	
GO:0016071	mR- metabolic process	34	625	0.54	3.27E-07	16	625	0.65	0.00036	
GO:0006364	rR- processing	23	296	0.69	3.77E-07	-	-	-	-	
GO:0007005	Mitochondrion organization	28	439	0.61	3.77E-07	-	-	-	-	
GO:0046907	Intracellular transport	52	1297	0.41	3.77E-07	20	1297	0.43	0.0088	
GO:0044249	Cellular biosynthetic process	79	2480	0.31	4.21E-07	32	2480	0.36	0.0024	

GO:0048024	Regulation of mR- splicing, via spliceosome	15	116	0.92	5.53E-07	-	-	-	-	
GO:1901566	Organonitrogen compound biosynthetic process	58	1579	0.37	7.56E-07	-	-	-	-	
GO:0033043	Regulation of organelle organization	49	1214	0.41	8.42E-07	20	1214	0.46	0.0043	
GO:1903311	Regulation of mR- metabolic process	23	313	0.67	8.52E-07	11	313	0.79	0.001	
GO:0015980	Energy derivation by oxidation of organic compounds	20	235	0.73	9.03E-07	-	-	-	-	
GO:0007049	Cell cycle	46	1118	0.42	1.44E-06	17	1118	0.43	0.0282	
GO:0006091	Generation of precursor metabolites and energy	26	416	0.6	1.80E-06	-	-	-	-	
GO:0033044	Regulation of chromosome organization	20	249	0.71	2.12E-06	9	249	0.8	0.0038	
GO:0043648	Dicarboxylic acid metabolic process	13	93	0.95	2.44E-06	-	-	-	-	
GO:0010608	Post-transcriptio-l regulation of gene expression	32	623	0.51	2.76E-06	14	623	0.6	0.0037	
GO:0050684	Regulation of mR- processing	16	156	0.81	2.76E-06	-	-	-	-	
GO:0022607	Cellular component assembly	77	2516	0.29	3.04E-06	30	2516	0.32	0.0123	
GO:0006259	D- metabolic process	36	770	0.47	3.11E-06	-	-	-	-	
GO:1901564	Organonitrogen compound metabolic process	133	5394	0.2	3.11E-06	50	5394	0.21	0.0198	
GO:0006417	Regulation of translation	29	531	0.54	3.57E-06	13	531	0.63	0.0033	
GO:0043604	Amide biosynthetic process	37	830	0.45	5.95E-06	-	-	-	-	
GO:2000112	Regulation of cellular macromolecule biosynthetic process	31	613	0.51	5.95E-06	14	613	0.6	0.0033	
GO:0006260	D- replication	17	192	0.75	6.33E-06	-	-	-	-	
GO:0043484	Regulation of R- splicing	16	174	0.77	9.80E-06	-	-	-	-	
GO:0033554	Cellular response to stress	54	1609	0.33	3.61E-05	-	-	-	-	
GO:0051726	Regulation of cell cycle	41	1071	0.39	5.07E-05	-	-	-	-	
GO:0051649	Establishment of localization in cell	55	1689	0.32	6.77E-05	-	-	-	-	
GO:0006950	Response to stress	86	3187	0.24	7.41E-05	33	3187	0.26	0.0432	
GO:0045184	Establishment of protein localization	43	1173	0.37	7.51E-05	-	-	-	-	
GO:0006520	Cellular amino acid metabolic process	19	293	0.62	8.49E-05	-	-	-	-	
GO:0051128	Regulation of cellular component organization	72	2504	0.26	8.49E-05	32	2504	0.35	0.0028	
GO:0000398	mR- splicing, via spliceosome	18	267	0.63	9.75E-05	8	267	0.72	0.0242	
GO:0006886	Intracellular protein transport	30	669	0.46	9.75E-05	-	-	-	-	
GO:0071705	Nitrogen compound transport	49	1456	0.33	0.00011	-	-	-	-	
GO:0051641	Cellular localization	74	2661	0.25	0.00018	30	2661	0.3	0.0259	
GO:1903312	Negative regulation of mR- metabolic process	11	99	0.85	0.00018	-	-	-	-	
GO:0006412	Translation	30	700	0.44	0.00022	-	-	-	-	
GO:0010564	Regulation of cell cycle process	30	706	0.43	0.00025	-	-	-	-	
GO:0043933	Protein-containing complex organization	49	1505	0.32	0.00026	-	-	-	-	
GO:0022904	Respiratory electron transport chain	10	84	0.88	0.00031	-	-	-	-	
GO:0033036	Macromolecule localization	67	2366	0.26	0.00033	-	-	-	-	
GO:0019222	Regulation of metabolic process	146	6627	0.15	0.00034	63	6627	0.22	0.0012	
GO:0006974	Cellular response to D- damage stimulus	30	720	0.42	0.00035	-	-	-	-	
GO:0009059	Macromolecule biosynthetic process	51	1615	0.3	0.00035	21	1615	0.36	0.0372	
GO:0006281	D- repair	23	470	0.49	0.00044	-	-	-	-	
GO:0006518	Peptide metabolic process	33	850	0.39	0.00044	-	-	-	-	
GO:0006261	D--templated D- replication	12	135	0.75	0.00045	-	-	-	-	
GO:0006099	Tricarboxylic acid cycle	7	35	1.1	0.00047	-	-	-	-	
GO:0015031	Protein transport	38	1062	0.36	0.00048	-	-	-	-	

GO:0031323	Regulation of cellular metabolic process	127	5592	0.16	0.00049	54	5592	0.23	0.004
GO:0009411	Response to UV	12	137	0.75	5.00E-04	-	-	-	-
GO:0051664	Nuclear pore localization	4	4	1.8	5.00E-04	2	4	1.94	0.0455
GO:0009259	Ribonucleotide metabolic process	22	443	0.5	0.00053	-	-	-	-
GO:0070727	Cellular macromolecule localization	57	1929	0.27	0.00054	-	-	-	-
GO:0071103	D- conformation change	11	115	0.78	0.00056	-	-	-	-
GO:0072594	Establishment of protein localization to organelle	19	344	0.55	0.00056	-	-	-	-
GO:0006119	Oxidative phosphorylation	10	93	0.84	0.00058	-	-	-	-
GO:0010638	Positive regulation of organelle organization	25	557	0.46	0.00062	11	557	0.54	0.0405
GO:0060255	Regulation of macromolecule metabolic process	135	6089	0.15	0.00065	61	6089	0.25	0.00039
GO:0045934	Negative regulation of nucleobase-containing compound metabo	47	1480	0.31	0.00066	-	-	-	-
GO:0045727	Positive regulation of translation	13	169	0.69	0.00068	-	-	-	-
GO:0051171	Regulation of nitrogen compound metabolic process	126	5595	0.16	0.00075	57	5595	0.25	0.00067
GO:0044282	Small molecule catabolic process	19	354	0.53	0.00077	-	-	-	-
GO:0065003	Protein-containing complex assembly	43	1312	0.32	0.00078	-	-	-	-
GO:0006913	Nucleocytoplasmic transport	16	260	0.59	0.00082	-	-	-	-
GO:1901605	Alpha-amino acid metabolic process	14	201	0.65	0.00082	-	-	-	-
GO:0007097	Nuclear migration	7	40	1.05	0.00083	4	40	1.24	0.0169
GO:1902850	Microtubule cytoskeleton organization involved in mitosis	11	122	0.76	0.00083	-	-	-	-
GO:0000278	Mitotic cell cycle	27	648	0.42	0.00084	-	-	-	-
GO:0008104	Protein localization	56	1924	0.27	0.00087	-	-	-	-
GO:0060236	Regulation of mitotic spindle organization	7	41	1.04	0.00093	-	-	-	-
GO:0044248	Cellular catabolic process	48	1557	0.29	0.00098	-	-	-	-
GO:0006997	Nucleus organization	12	151	0.7	0.001	6	151	0.84	0.0322
GO:0033365	Protein localization to organelle	29	739	0.4	0.0011	13	739	0.49	0.0372
GO:0042775	Mitochondrial ATP synthesis coupled electron transport	8	61	0.92	0.0011	-	-	-	-
GO:0048519	Negative regulation of biological process	120	5319	0.16	0.0011	49	5319	0.21	0.0253
GO:0048523	Negative regulation of cellular process	110	4752	0.17	0.0011	47	4752	0.24	0.0085
GO:0055086	Nucleobase-containing small molecule metabolic process	25	582	0.44	0.0011	-	-	-	-
GO:0044242	Cellular lipid catabolic process	13	182	0.66	0.0012	-	-	-	-
GO:1901575	Organic substance catabolic process	51	1714	0.28	0.0012	-	-	-	-
GO:0009117	Nucleotide metabolic process	23	516	0.45	0.0013	-	-	-	-
GO:0022402	Cell cycle process	31	831	0.38	0.0013	-	-	-	-
GO:1901362	Organic cyclic compound biosynthetic process	34	957	0.35	0.0013	17	957	0.49	0.007
GO:0018130	Heterocycle biosynthetic process	31	836	0.37	0.0014	16	836	0.53	0.0053
GO:0051301	Cell division	20	412	0.49	0.0014	-	-	-	-
GO:1901135	Carbohydrate derivative metabolic process	35	1002	0.35	0.0014	-	-	-	-
GO:0000463	Maturation of LSU-rR- from tricistronic rR- transcript (SSU-rR-, 5.8	6	30	1.1	0.0016	-	-	-	-
GO:0031324	Negative regulation of cellular metabolic process	61	2234	0.24	0.0018	27	2234	0.33	0.0211
GO:0061024	Membrane organization	27	684	0.4	0.0018	-	-	-	-
GO:0080090	Regulation of primary metabolic process	127	5780	0.15	0.0018	57	5780	0.24	0.0015
GO:0048518	Positive regulation of biological process	137	6368	0.14	0.0019	60	6368	0.22	0.0026
GO:0051656	Establishment of organelle localization	19	387	0.49	0.0019	10	387	0.66	0.0143
GO:0009056	Catabolic process	56	1999	0.25	0.002	-	-	-	-

GO:0006998	Nuclear envelope organization	7	49	0.96	0.0021	-	-	-	-	
GO:0033119	Negative regulation of R- splicing	6	32	1.08	0.0021	-	-	-	-	
GO:0072521	Purine-containing compound metabolic process	21	465	0.46	0.0022	-	-	-	-	
GO:1990542	Mitochondrial transmembrane transport	9	91	0.8	0.0022	-	-	-	-	
GO:0006103	2-oxoglutarate metabolic process	5	19	1.22	0.0024	-	-	-	-	
GO:0006325	Chromatin organization	24	584	0.42	0.0025	-	-	-	-	
GO:1903047	Mitotic cell cycle process	23	544	0.43	0.0025	-	-	-	-	
GO:0051640	Organelle localization	23	547	0.43	0.0026	11	547	0.55	0.0366	
GO:0034645	Cellular macromolecule biosynthetic process	36	1089	0.32	0.0027	-	-	-	-	
GO:0006839	Mitochondrial transport	10	120	0.72	0.0029	-	-	-	-	
GO:0009260	Ribonucleotide biosynthetic process	12	175	0.64	0.003	-	-	-	-	
GO:0009636	Response to toxic substance	13	204	0.61	0.003	-	-	-	-	
GO:0006403	R- localization	12	176	0.64	0.0031	-	-	-	-	
GO:0019438	Aromatic compound biosynthetic process	30	838	0.36	0.0031	16	838	0.53	0.0054	
GO:0010629	Negative regulation of gene expression	31	890	0.35	0.0037	-	-	-	-	
GO:0034654	Nucleobase-containing compound biosynthetic process	28	765	0.37	0.0038	14	765	0.51	0.0201	
GO:0000470	Maturation of LSU-rR-	8	77	0.82	0.004	-	-	-	-	
GO:0031497	Chromatin assembly	12	181	0.63	0.004	-	-	-	-	
GO:0006626	Protein targeting to mitochondrion	7	57	0.89	0.0045	-	-	-	-	
GO:0010468	Regulation of gene expression	106	4725	0.15	0.0045	49	4725	0.26	0.0024	
GO:0046395	Carboxylic acid catabolic process	13	214	0.59	0.0045	-	-	-	-	
GO:0140694	Non-membrane-bounded organelle assembly	19	418	0.46	0.0045	-	-	-	-	
GO:0034644	Cellular response to UV	8	79	0.81	0.0046	-	-	-	-	
GO:0009150	Purine ribonucleotide metabolic process	19	421	0.46	0.0048	-	-	-	-	
GO:0048522	Positive regulation of cellular process	124	5758	0.14	0.0048	55	5758	0.22	0.0042	
GO:0070828	Heterochromatin organization	8	80	0.8	0.0049	-	-	-	-	
GO:0071702	Organic substance transport	51	1835	0.25	0.005	-	-	-	-	
GO:0060341	Regulation of cellular localization	34	1043	0.32	0.0052	16	1043	0.43	0.0358	
GO:0016042	Lipid catabolic process	15	285	0.53	0.0054	-	-	-	-	
GO:0009892	Negative regulation of metabolic process	72	2911	0.2	0.0056	31	2911	0.27	0.0426	
GO:0051052	Regulation of D- metabolic process	22	543	0.41	0.0056	11	543	0.55	0.0354	
GO:0051168	Nuclear export	10	133	0.68	0.0057	-	-	-	-	
GO:0032392	D- geometric change	9	107	0.73	0.0058	-	-	-	-	
GO:0051246	Regulation of protein metabolic process	68	2708	0.2	0.0058	34	2708	0.34	0.0023	
GO:0006107	Oxaloacetate metabolic process	4	12	1.33	0.0062	-	-	-	-	
GO:0048025	Negative regulation of mR- splicing, via spliceosome	5	25	1.1	0.0062	-	-	-	-	
GO:0000002	Mitochondrial genome mainte-nce	5	26	1.09	0.0072	-	-	-	-	
GO:0034063	Stress granule assembly	5	26	1.09	0.0072	-	-	-	-	
GO:0009165	Nucleotide biosynthetic process	13	229	0.56	0.0075	-	-	-	-	
GO:0006739	DP metabolic process	6	44	0.94	0.008	-	-	-	-	
GO:0006790	Sulfur compound metabolic process	16	333	0.49	0.0081	-	-	-	-	
GO:2001234	Negative regulation of apoptotic sig-ling pathway	13	231	0.55	0.0081	-	-	-	-	
GO:0019538	Protein metabolic process	98	4367	0.15	0.0082	-	-	-	-	
GO:0006605	Protein targeting	13	234	0.55	0.0089	-	-	-	-	

GO:0043254	Regulation of protein-containing complex assembly	18	416	0.44	0.0106	-	-	-	-		
GO:0007059	Chromosome segregation	15	307	0.49	0.0107	-	-	-	-		
GO:0010033	Response to organic substance	69	2827	0.19	0.0107		35	2827	0.34	0.0022	
GO:1902275	Regulation of chromatin organization	6	48	0.9	0.0117		4	48	1.17	0.027	
GO:0042273	Ribosomal large subunit biogenesis	12	210	0.56	0.0121	-	-	-	-		
GO:0072522	Purine-containing compound biosynthetic process	11	179	0.59	0.0123	-	-	-	-		
GO:0051053	Negative regulation of D- metabolic process	10	150	0.63	0.0128	-	-	-	-		
GO:0051028	mR- transport	9	122	0.67	0.013	-	-	-	-		
GO:0042981	Regulation of apoptotic process	43	1531	0.25	0.0133	-	-	-	-		
GO:0032271	Regulation of protein polymerization	12	213	0.55	0.0134	-	-	-	-		
GO:2001252	Positive regulation of chromosome organization	9	123	0.67	0.0136	-	-	-	-		
GO:0050658	R- transport	10	152	0.62	0.0138	-	-	-	-		
GO:0051253	Negative regulation of R- metabolic process	39	1344	0.27	0.0138	-	-	-	-		
GO:0032273	Positive regulation of protein polymerization	8	97	0.72	0.014	-	-	-	-		
GO:0010822	Positive regulation of mitochondrion organization	7	73	0.79	0.0146	-	-	-	-		
GO:0065007	Biological regulation	232	12586	0.07	0.0146	-	-	-	-		
GO:0019637	Organophosphate metabolic process	30	934	0.31	0.0147	-	-	-	-		
GO:0032880	Regulation of protein localization	30	939	0.31	0.0158	-	-	-	-		
GO:0045945	Positive regulation of transcription by R- polymerase III	4	17	1.18	0.0162	-	-	-	-		
GO:1901978	Positive regulation of cell cycle checkpoint	4	17	1.18	0.0162	-	-	-	-		
GO:0019646	Aerobic electron transport chain	6	53	0.86	0.0173	-	-	-	-		
GO:0009141	Nucleoside triphosphate metabolic process	13	256	0.51	0.018	-	-	-	-		
GO:0010605	Negative regulation of macromolecule metabolic process	65	2682	0.19	0.0184		30	2682	0.29	0.028	
GO:0032508	D- duplex unwinding	8	103	0.69	0.0192	-	-	-	-		
GO:0009152	Purine ribonucleotide biosynthetic process	10	161	0.6	0.0197	-	-	-	-		
GO:0009062	Fatty acid catabolic process	7	79	0.75	0.0214	-	-	-	-		
GO:0006399	tR- metabolic process	11	195	0.56	0.0217	-	-	-	-		
GO:0051234	Establishment of localization	86	3839	0.15	0.022	-	-	-	-		
GO:0006338	Chromatin remodeling	14	300	0.47	0.0233	-	-	-	-		
GO:0051172	Negative regulation of nitrogen compound metabolic process	58	2342	0.2	0.0233		27	2342	0.31	0.0352	
GO:0000132	Establishment of mitotic spindle orientation	5	37	0.93	0.0253	-	-	-	-		
GO:0006734	DH metabolic process	5	37	0.93	0.0253	-	-	-	-		
GO:0009416	Response to light stimulus	14	304	0.47	0.0259	-	-	-	-		
GO:0042063	Gliogenesis	13	269	0.49	0.0265	-	-	-	-		
GO:0045814	Negative regulation of gene expression, epigenetic	7	83	0.73	0.027	-	-	-	-		
GO:0006635	Fatty acid beta-oxidation	6	59	0.81	0.0272	-	-	-	-		
GO:2001233	Regulation of apoptotic sig-ling pathway	16	381	0.43	0.0272	-	-	-	-		
GO:0009408	Response to heat	9	139	0.62	0.0274	-	-	-	-		
GO:0009144	Purine nucleoside triphosphate metabolic process	12	237	0.51	0.0286	-	-	-	-		
GO:0016139	Glycoside catabolic process	3	8	1.38	0.0291	-	-	-	-		
GO:0001889	Liver development	10	172	0.57	0.0296	-	-	-	-		
GO:0009893	Positive regulation of metabolic process	87	3939	0.15	0.0296		43	3939	0.28	0.0029	
GO:0032543	Mitochondrial translation	6	61	0.8	0.0308	-	-	-	-		
GO:0007052	Mitotic spindle organization	7	86	0.71	0.031	-	-	-	-		

GO:0009199	Ribonucleoside triphosphate metabolic process	12	240	0.5	0.031	-	-	-	-	
GO:0019219	Regulation of nucleobase-containing compound metabolic proce	85	3835	0.15	0.031	43	3835	0.29	0.0018	
GO:0031326	Regulation of cellular biosynthetic process	88	4002	0.15	0.031	45	4002	0.3	0.0011	
GO:0044283	Small molecule biosynthetic process	17	428	0.4	0.0317	-	-	-	-	
GO:0044087	Regulation of cellular component biogenesis	31	1038	0.28	0.0322	-	-	-	-	
GO:0031503	Protein-containing complex localization	10	176	0.56	0.0336	-	-	-	-	
GO:0050789	Regulation of biological process	218	11860	0.07	0.034	-	-	-	-	
GO:0051179	Localization	96	4471	0.14	0.0346	-	-	-	-	
GO:0046477	Glycosylceramide catabolic process	3	9	1.33	0.0361	-	-	-	-	
GO:0051247	Positive regulation of protein metabolic process	41	1529	0.23	0.0361	-	-	-	-	
GO:0090063	Positive regulation of microtubule nucleation	3	9	1.33	0.0361	-	-	-	-	
GO:0006270	D- replication initiation	4	23	1.04	0.0365	-	-	-	-	
GO:0006999	Nuclear pore organization	4	23	1.04	0.0365	-	-	-	-	
GO:0009628	Response to abiotic stimulus	34	1190	0.26	0.0365	-	-	-	-	
GO:0140374	Antiviral in-te immune response	4	23	1.04	0.0365	-	-	-	-	
GO:0009889	Regulation of biosynthetic process	89	4090	0.14	0.0371	46	4090	0.3	0.00086	
GO:0015931	Nucleobase-containing compound transport	11	213	0.52	0.0374	-	-	-	-	
GO:0031100	Animal organ regeneration	7	90	0.69	0.0374	-	-	-	-	
GO:0034504	Protein localization to nucleus	11	213	0.52	0.0374	7	213	0.76	0.031	
GO:0050794	Regulation of cellular process	208	11253	0.07	0.0385	-	-	-	-	
GO:1901698	Response to nitrogen compound	33	1149	0.26	0.0388	23	1149	0.55	0.00011	
GO:0007006	Mitochondrial membrane organization	7	91	0.69	0.0391	-	-	-	-	
GO:0010941	Regulation of cell death	45	1740	0.22	0.0391	24	1740	0.38	0.0088	
GO:0090150	Establishment of protein localization to membrane	11	215	0.51	0.0391	-	-	-	-	
GO:0140053	Mitochondrial gene expression	7	91	0.69	0.0391	-	-	-	-	
GO:1901606	Alpha-amino acid catabolic process	7	91	0.69	0.0391	-	-	-	-	
GO:0006268	D- unwinding involved in D- replication	4	24	1.03	0.0397	-	-	-	-	
GO:0009064	Glutamine family amino acid metabolic process	6	66	0.76	0.04	-	-	-	-	
GO:1904377	Positive regulation of protein localization to cell periphery	6	66	0.76	0.04	-	-	-	-	
GO:0006629	Lipid metabolic process	34	1202	0.26	0.0402	-	-	-	-	
GO:0016032	Viral process	9	151	0.58	0.0405	-	-	-	-	
GO:0043066	Negative regulation of apoptotic process	29	967	0.28	0.0405	-	-	-	-	
GO:0051129	Negative regulation of cellular component organization	24	740	0.31	0.0405	-	-	-	-	
GO:0043280	Positive regulation of cysteine-type endopeptidase activity involve	8	121	0.62	0.0411	-	-	-	-	
GO:0044419	Biological process involved in interspecies interaction between or	37	1351	0.24	0.0416	-	-	-	-	
GO:0009112	Nucleobase metabolic process	5	44	0.86	0.0418	-	-	-	-	
GO:0031507	Heterochromatin assembly	6	67	0.76	0.0418	-	-	-	-	
GO:0051096	Positive regulation of helicase activity	3	10	1.28	0.0418	-	-	-	-	
GO:0010639	Negative regulation of organelle organization	15	367	0.42	0.0432	-	-	-	-	
GO:0033260	Nuclear D- replication	4	25	1.01	0.0434	-	-	-	-	
GO:0032787	Monocarboxylic acid metabolic process	21	615	0.34	0.0439	-	-	-	-	
GO:0051130	Positive regulation of cellular component organization	34	1212	0.25	0.0442	-	-	-	-	
GO:0051170	Import into nucleus	8	124	0.61	0.0462	-	-	-	-	
GO:0007051	Spindle organization	9	155	0.57	0.0463	-	-	-	-	

GO:0030490	Maturation of SSU-rR-		6		69	0.74	0.0467	-	-	-	-		
GO:0097305	Response to alcohol		13		297	0.45	0.0499	-	-	-	-		
GO:0032386	Regulation of intracellular transport	-	-		-	-			12	334	0.8	0.00034	
GO:0010556	Regulation of macromolecule biosynthetic process	-	-		-	-			45	3816	0.32	0.00036	
GO:0010604	Positive regulation of macromolecule metabolic process	-	-		-	-			42	3592	0.31	0.001	
GO:0048856	A-tomical structure development	-	-		-	-			53	5157	0.26	0.0013	
GO:0007275	Multicellular organism development	-	-		-	-			47	4353	0.28	0.0016	
GO:0032502	Developmental process	-	-		-	-			55	5590	0.24	0.0024	
GO:0010243	Response to organonitrogen compound	-	-		-	-			19	1056	0.5	0.0028	
GO:0014070	Response to organic cyclic compound	-	-		-	-			18	964	0.52	0.0029	
GO:0070887	Cellular response to chemical stimulus	-	-		-	-			33	2646	0.34	0.003	
GO:0046719	Regulation by virus of viral protein levels in host cell	-	-		-	-			3	6	1.94	0.0034	
GO:0045070	Positive regulation of viral genome replication	-	-		-	-			4	24	1.47	0.004	
GO:0009891	Positive regulation of biosynthetic process	-	-		-	-			28	2100	0.37	0.0042	
GO:0042221	Response to chemical	-	-		-	-			46	4477	0.26	0.0047	
GO:0031328	Positive regulation of cellular biosynthetic process	-	-		-	-			27	2046	0.36	0.0065	
GO:0051173	Positive regulation of nitrogen compound metabolic process	-	-		-	-			36	3188	0.3	0.007	
GO:0010557	Positive regulation of macromolecule biosynthetic process	-	-		-	-			26	1945	0.37	0.0072	
GO:0048731	System development	-	-		-	-			41	3916	0.26	0.0088	
GO:0030154	Cell differentiation	-	-		-	-			37	3418	0.28	0.0114	
GO:0022618	Ribonucleoprotein complex assembly	-	-		-	-			9	314	0.7	0.0149	
GO:0048468	Cell development	-	-		-	-			24	1825	0.36	0.0163	
GO:0051252	Regulation of R- metabolic process	-	-		-	-			37	3508	0.27	0.0178	
GO:0045069	Regulation of viral genome replication	-	-		-	-			5	83	1.02	0.0207	
GO:0031453	Positive regulation of heterochromatin assembly	-	-		-	-			3	16	1.52	0.0224	
GO:0031325	Positive regulation of cellular metabolic process	-	-		-	-			34	3172	0.27	0.0242	
GO:0032388	Positive regulation of intracellular transport	-	-		-	-			7	202	0.78	0.0253	
GO:0032535	Regulation of cellular component size	-	-		-	-			10	433	0.61	0.027	
GO:0045646	Regulation of erythrocyte differentiation	-	-		-	-			4	48	1.17	0.027	
GO:0001732	Formation of cytoplasmic translation initiation complex	-	-		-	-			3	20	1.42	0.0331	
GO:0043331	Response to dsR-	-	-		-	-			4	52	1.13	0.0331	
GO:0046500	S-adenosylmethionine metabolic process	-	-		-	-			3	20	1.42	0.0331	
GO:0099563	Modification of sy-ptic structure	-	-		-	-			3	20	1.42	0.0331	
GO:0032387	Negative regulation of intracellular transport	-	-		-	-			4	53	1.12	0.0342	
GO:2000278	Regulation of D- biosynthetic process	-	-		-	-			6	156	0.83	0.0355	
GO:0033157	Regulation of intracellular protein transport	-	-		-	-			7	225	0.74	0.0375	
GO:0050792	Regulation of viral process	-	-		-	-			6	159	0.82	0.0375	
GO:2000573	Positive regulation of D- biosynthetic process	-	-		-	-			5	104	0.93	0.0403	
GO:0051017	Actin filament bundle assembly	-	-		-	-			4	58	1.08	0.0426	
GO:0120035	Regulation of plasma membrane bounded cell projection organiz	-	-		-	-			13	760	0.48	0.0451	
GO:1901700	Response to oxygen-containing compound	-	-		-	-			21	1648	0.35	0.0451	
GO:0046726	Positive regulation by virus of viral protein levels in host cell	-	-		-	-			2	4	1.94	0.0455	
GO:0009894	Regulation of catabolic process	-	-		-	-			15	973	0.43	0.0464	
GO:0061162	Establishment of monopolar cell polarity	-	-		-	-			3	25	1.32	0.0492	

PROCESS_D4_30mM_UP

#term ID	term description.NIST	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DF	false discovery rate.DP12
GO:000998	Cellular process	148	15994	0.15	4.77E-14	60	15994	0.14	0.0061
GO:000645	Protein folding	13	243	0.92	7.93E-05	-	-	-	-
GO:000681	Transport	52	3660	0.34	7.93E-05	-	-	-	-
GO:004428	Small molecule metabolic pr	33	1690	0.48	7.93E-05	-	-	-	-
GO:000905	Catabolic process	35	1999	0.43	0.00011	-	-	-	-
GO:003287	Regulation of localization	38	2276	0.41	0.00011	-	-	-	-
GO:005117	Localization	58	4471	0.3	0.00011	-	-	-	-
GO:000815	Metabolic process	87	8581	0.19	0.00038	-	-	-	-
GO:007170	Organic substance metabolic	83	8137	0.2	0.00071	-	-	-	-
GO:005104	Regulation of transport	32	1906	0.41	0.00076	-	-	-	-
GO:190157	Organic substance catabolic	30	1714	0.43	0.00076	-	-	-	-
GO:004851	Positive regulation of biologic	69	6368	0.22	0.0014	-	-	-	-
GO:005105	Positive regulation of transpo	22	1045	0.51	0.0014	-	-	-	-
GO:005508	Nucleobase-containing small	16	582	0.63	0.0015	-	-	-	-
GO:007088	Cellular response to chemica	38	2646	0.34	0.0017	-	-	-	-
GO:000679	Sulfur compound metabolic p	12	333	0.74	0.002	-	-	-	-
GO:004423	Cellular metabolic process	73	7040	0.2	0.0022	-	-	-	-
GO:190161	Organic hydroxy compound m	14	473	0.66	0.0022	-	-	-	-
GO:190265	Secondary alcohol metabolic	8	129	0.98	0.0022	-	-	-	-
GO:001003	Response to organic substan	39	2827	0.33	0.0024	-	-	-	-
GO:001619	Vesicle-mediated transport	23	1231	0.46	0.0033	-	-	-	-
GO:004428	Small molecule biosynthetic p	13	428	0.67	0.0033	-	-	-	-
GO:003303	Macromolecule localization	34	2366	0.35	0.0044	-	-	-	-
GO:004852	Positive regulation of cellular	62	5758	0.22	0.0048	-	-	-	-
GO:005124	Regulation of protein metabol	37	2708	0.32	0.0048	25	2708	0.53	0.00021
GO:005112	Regulation of cellular compor	35	2504	0.33	0.0051	-	-	-	-
GO:190156	Organonitrogen compound m	59	5394	0.23	0.0051	-	-	-	-
GO:000606	Alcohol metabolic process	11	325	0.72	0.0053	-	-	-	-

GO:000820	Cholesterol metabolic proces	7	113	0.98	0.0055	-	-	-	-
GO:004423	Primary metabolic process	76	7736	0.18	0.0055	-	-	-	-
GO:005113	Positive regulation of cellular	22	1212	0.45	0.0055	-	-	-	-
GO:006500	Biological regulation	108	12586	0.12	0.0055	-	-	-	-
GO:190136	Organic cyclic compound me	41	3212	0.29	0.0055	-	-	-	-
GO:005124	Negative regulation of protein	20	1035	0.47	0.0057	-	-	-	-
GO:000810	Protein localization	29	1924	0.37	0.0062	-	-	-	-
GO:003002	Actin filament-based process	15	625	0.57	0.0062	-	-	-	-
GO:006107	Chaperone-mediated protein	6	78	1.07	0.0062	-	-	-	-
GO:006500	Regulation of biological qualit	46	3854	0.26	0.0064	-	-	-	-
GO:001605	Carbohydrate biosynthetic pr	7	124	0.94	0.007	-	-	-	-
GO:006500	Regulation of molecular funct	38	2956	0.3	0.008	-	-	-	-
GO:004424	Cellular catabolic process	25	1557	0.39	0.0081	-	-	-	-
GO:190382	Positive regulation of protein	13	498	0.6	0.0081	-	-	-	-
GO:004636	Monosaccharide biosynthetic	5	51	1.18	0.0084	-	-	-	-
GO:005078	Regulation of biological proce	102	11860	0.12	0.0104	-	-	-	-
GO:005164	Cellular localization	35	2661	0.31	0.0104	-	-	-	-
GO:003288	Regulation of protein localizat	18	939	0.47	0.0123	-	-	-	-
GO:000641	Regulation of translation	13	531	0.58	0.0138	-	-	-	-
GO:006034	Regulation of cellular localiza	19	1043	0.45	0.0141	-	-	-	-
GO:190136	Organic cyclic compound bio	18	957	0.46	0.0147	-	-	-	-
GO:001094	Regulation of cell death	26	1740	0.36	0.0149	-	-	-	-
GO:000657	Cellular modified amino acid	8	201	0.79	0.0155	-	-	-	-
GO:000905	Macromolecule catabolic pro	18	967	0.46	0.0158	-	-	-	-
GO:003226	Regulation of cellular protein	3	10	1.66	0.0158	-	-	-	-
GO:003250	Developmental process	58	5590	0.2	0.0158	-	-	-	-
GO:007131	Cellular response to organic s	29	2069	0.33	0.0158	-	-	-	-
GO:000922	Nucleotide-sugar metabolic p	4	31	1.3	0.016	-	-	-	-
GO:003464	Cellular nitrogen compound r	44	3820	0.25	0.016	-	-	-	-
GO:005160	Proteolysis involved in protein	14	635	0.53	0.0172	-	-	-	-

GO:190495	Positive regulation of establis	10	334	0.66	0.0172	-	-	-	-
GO:001063	Positive regulation of organell	13	557	0.56	0.0175	-	-	-	-
GO:004222	Response to chemical	49	4477	0.23	0.0182	-	-	-	-
GO:005076	Regulation of phagocytosis	6	108	0.93	0.0191	-	-	-	-
GO:003003	Actin cytoskeleton organizati	13	566	0.55	0.0195	-	-	-	-
GO:190113	Carbohydrate derivative meta	18	1002	0.44	0.0202	-	-	-	-
GO:007020	Regulation of establishment o	13	570	0.55	0.0203	-	-	-	-
GO:004885	A-tomical structure developm	54	5157	0.21	0.0205	-	-	-	-
GO:003016	Protein catabolic process	15	741	0.49	0.0212	-	-	-	-
GO:003245	Endocytic recycling	5	69	1.05	0.0212	-	-	-	-
GO:001003	Response to inorganic substa	13	577	0.54	0.0215	-	-	-	-
GO:001972	Cellular homeostasis	14	666	0.51	0.0236	-	-	-	-
GO:003304	Regulation of organelle organ	20	1214	0.4	0.0236	-	-	-	-
GO:000674	Glutathione metabolic proces	5	72	1.03	0.024	-	-	-	-
GO:000688	Intracellular protein transport	14	669	0.51	0.024	-	-	-	-
GO:000803	Cell recognition	6	117	0.9	0.0245	-	-	-	-
GO:005079	Regulation of cellular process	96	11253	0.12	0.0254	-	-	-	-
GO:004327	Apoptotic cell clearance	4	39	1.2	0.0267	-	-	-	-
GO:000680	Nitrogen compound metaboli	68	7145	0.17	0.0273	-	-	-	-
GO:000687	Cellular ion homeostasis	11	447	0.58	0.0305	-	-	-	-
GO:000597	Carbohydrate metabolic proc	12	527	0.54	0.0311	-	-	-	-
GO:001503	Protein transport	18	1062	0.42	0.0321	-	-	-	-
GO:004851	Animal organ development	39	3378	0.25	0.0321	-	-	-	-
GO:190156	Organonitrogen compound ca	18	1061	0.42	0.0321	-	-	-	-
GO:005172	Regulation of cell cycle	18	1071	0.41	0.0344	-	-	-	-
GO:001003	Response to metal ion	10	384	0.6	0.0355	-	-	-	-
GO:000673	NADP metabolic process	4	44	1.15	0.0358	-	-	-	-
GO:004851	Negative regulation of biologi	54	5319	0.19	0.0358	-	-	-	-
GO:190157	Organic substance biosynthe	32	2581	0.28	0.036	-	-	-	-
GO:000691	Phagocytosis, recognition	3	17	1.43	0.037	-	-	-	-

GO:000922	Nucleotide-sugar biosynthetic	3	17	1.43	0.037	-	-	-	-	
GO:007252	Purine-containing compound	11	465	0.56	0.037	-	-	-	-	
GO:000650	Proteolysis	19	1197	0.39	0.0422	-	-	-	-	
GO:190121	Regulation of neuron death	10	397	0.59	0.0422	-	-	-	-	
GO:004360	Cellular amide metabolic pro	18	1102	0.4	0.0429	-	-	-	-	
GO:008009	Regulation of primary metabo	57	5780	0.18	0.043	-	-	-	-	
GO:000701	Cytoskeleton organization	20	1308	0.37	0.0451	-	-	-	-	
GO:007170	Organic substance transport	25	1835	0.32	0.0451	-	-	-	-	
GO:002260	Cellular component assembly	31	2516	0.28	0.0461	-	-	-	-	
GO:005508	Cellular chemical homeostas	12	566	0.51	0.0467	-	-	-	-	
GO:001081	Positive regulation of cell-sub	6	143	0.81	0.0484	-	-	-	-	
GO:001648	Cytosolic transport	6	142	0.81	0.0484	-	-	-	-	
GO:006135	Positive regulation of Wnt pro	2	3	2.01	0.0484	-	-	-	-	
GO:007238	Plus-end-directed vesicle tra	2	3	2.01	0.0484	-	-	-	-	
GO:003016	Regulation of proteolysis	-	-	-	-	12	724	0.78	0.0037	

FUNCTION_D4_10mM_DOWN

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
GO:19013	Heterocycli	94	6088	0.4	5.93E-19	-	-	-	-
GO:00971	Organic cyc	94	6155	0.39	6.77E-19	-	-	-	-
GO:00054	Binding	136	13754	0.21	3.89E-18	-	-	-	-
GO:00037	R- binding	45	1541	0.68	7.02E-16	-	-	-	-
GO:00036	Nucleic aci	64	3725	0.45	6.94E-13	-	-	-	-
GO:00360	Small mole	53	2793	0.49	1.18E-11	-	-	-	-
GO:00001	Nucleotide	49	2478	0.51	3.08E-11	-	-	-	-
GO:00431	Anion bindi	51	2671	0.49	3.08E-11	-	-	-	-
GO:00973	Carbohydra	47	2440	0.5	2.27E-10	-	-	-	-
GO:01406	ATP-depen	24	652	0.78	1.09E-09	-	-	-	-
GO:00325	Purine ribo	42	2130	0.51	2.32E-09	-	-	-	-
GO:00168	ATP hydroly	17	343	0.91	1.88E-08	-	-	-	-
GO:00325	Adenyl ribo	36	1731	0.53	1.92E-08	-	-	-	-
GO:00038	Catalytic ac	73	6043	0.29	4.30E-08	-	-	-	-
GO:00356	Purine ribo	38	2054	0.48	1.16E-07	-	-	-	-
GO:00164	Pyrophosph	22	721	0.7	1.60E-07	-	-	-	-
GO:00171	Nucleoside	21	670	0.71	2.19E-07	-	-	-	-
GO:00037	R- helicase	9	79	1.27	4.89E-07	-	-	-	-
GO:00055	ATP binding	32	1663	0.49	1.05E-06	-	-	-	-
GO:00167	Hydrolase a	40	2470	0.42	1.14E-06	-	-	-	-
GO:00043	Helicase ac	11	174	1.01	2.35E-06	-	-	-	-
GO:00431	Ion binding	65	5669	0.27	5.17E-06	-	-	-	-
GO:00055	Protein bin	78	7697	0.22	1.78E-05	-	-	-	-
GO:01406	Catalytic ac	17	618	0.65	4.00E-05	-	-	-	-
GO:00198	Enzyme bin	36	2431	0.38	5.79E-05	-	-	-	-
GO:00469	Protein dim	21	1036	0.52	2.00E-04	-	-	-	-

GO:000372	Double-stra	7	95	1.08	0.00031	4	95	1.6	0.0108
GO:000368	Chromatin	16	686	0.58	0.00063	-	-	-	
GO:000519	Structural r	20	1060	0.49	0.00091	-	-	-	
GO:014066	ATP-depen	5	49	1.22	0.0018	-	-	-	
GO:004280	Identical pr	30	2174	0.35	0.002	-	-	-	
GO:004487	Protein-cor	25	1625	0.4	0.002	-	-	-	
GO:014009	Catalytic ac	11	377	0.68	0.0023	-	-	-	
GO:000520	Structural c	6	100	0.99	0.0039	-	-	-	
GO:014029	D--binding	12	517	0.58	0.0082	-	-	-	
GO:001692	Nuclear rec	7	171	0.82	0.0089	-	-	-	
GO:000372	mR- binding	10	385	0.63	0.0124	-	-	-	
GO:003052	Structural c	5	79	1.01	0.0124	-	-	-	
GO:004698	Protein het	9	314	0.67	0.0125	-	-	-	
GO:000813	Transcriptic	13	638	0.52	0.0133	-	-	-	
GO:003051	snoR- bindi	4	44	1.17	0.0143	-	-	-	
GO:000817	Succi-te de	2	2	2.21	0.0146	-	-	-	
GO:005066	Flavin aden	5	95	0.93	0.0237	-	-	-	
GO:004280	Protein hon	13	712	0.47	0.0323	-	-	-	
GO:000508	Protein ki-s	4	59	1.04	0.0363	-	-	-	
GO:006162	R- polymera	9	381	0.58	0.0405	-	-	-	
GO:009710	Supercoiled	2	5	1.81	0.0443	-	-	-	

FUNCTION_D4_10mM_UP

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
GO:00001€	Nucleotide	15	2478	0.54	0.0111	-	-	-	-
GO:00054€	Binding	38	13754	0.2	0.0111	60	13754	0.2	1.86E-06
GO:000551	Protein bin	28	7697	0.32	0.0111	45	7697	0.33	1.95E-06
GO:001641	S-acetyltra	2	2	2.75	0.0111	-	-	-	-
GO:00164€	Pyrophospl	8	721	0.8	0.0111	-	-	-	-
GO:001707	Purine nucl	14	2148	0.57	0.0111	-	-	-	-
GO:00360€	Small mole	16	2793	0.51	0.0111	-	-	-	-
GO:00973€	Carbohydra	15	2440	0.54	0.0111	-	-	-	-
GO:01406E	ATP-depen	8	652	0.84	0.0111	-	-	-	-
GO:00167€	Hydrolase a	14	2470	0.51	0.0125	-	-	-	-
GO:00325E	Purine ribo	13	2130	0.54	0.0125	-	-	-	-
GO:00431€	Ion binding	22	5669	0.34	0.0125	-	-	-	-
GO:005101	Actin filame	5	245	1.06	0.0144	-	-	-	-
GO:00431€	Anion bindi	14	2671	0.47	0.0222	-	-	-	-
GO:000517	Integrin bin	4	145	1.2	0.0234	-	-	-	-
GO:001711	Nucleoside	7	670	0.77	0.0261	-	-	-	-
GO:00305E	Adenyl nucl	11	1743	0.55	0.0261	-	-	-	-
GO:00356E	Purine ribo	12	2054	0.52	0.0261	-	-	-	-
GO:00080E	Cytoskeleta	9	1184	0.64	0.0267	-	-	-	-
GO:00199C	Ki-se bindir	8	929	0.69	0.0267	-	-	-	-
GO:00198E	Enzyme bin	-	-	-	-	19	2431	0.46	0.019
GO:00199C	Protein don	-	-	-	-	11	883	0.66	0.0216

FUNCTION_D4_30mM_DOWN

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
GO:00971	Organic cyc	231	6155	0.38	8.41E-44	82	6155	0.37	4.91E-14
GO:19013	Heterocycli	229	6088	0.38	1.22E-43	82	6088	0.37	4.91E-14
GO:00054	Binding	335	13754	0.19	4.08E-38	120	13754	0.19	4.82E-12
GO:00001	Nucleotide	120	2478	0.49	1.64E-26	36	2478	0.41	4.16E-05
GO:00036	Nucleic aci	150	3725	0.41	1.64E-26	61	3725	0.46	7.23E-13
GO:00037	R- binding	93	1541	0.58	3.35E-26	41	1541	0.67	5.63E-14
GO:00360	Small mole	127	2793	0.46	3.35E-26	42	2793	0.42	1.29E-06
GO:00431	Anion bindi	112	2671	0.43	1.05E-19	37	2671	0.39	6.51E-05
GO:00038	Catalytic ac	181	6043	0.28	7.63E-19	56	6043	0.21	0.0047
GO:00325	Ribonucleo	91	2149	0.43	1.36E-15	-	-	-	-
GO:00325	Purine ribo	90	2130	0.43	2.29E-15	31	2130	0.41	0.00023
GO:00973	Carbohydra	97	2440	0.4	3.59E-15	36	2440	0.41	3.19E-05
GO:00356	Purine ribo	86	2054	0.43	2.06E-14	31	2054	0.42	0.00012
GO:00325	Adenyl ribo	76	1731	0.45	1.62E-13	-	-	-	-
GO:00055	ATP binding	72	1663	0.44	1.94E-12	24	1663	0.4	0.0033
GO:00431	Ion binding	157	5669	0.25	2.27E-12	52	5669	0.21	0.0121
GO:01406	ATP-depen	42	652	0.61	8.26E-12	13	652	0.54	0.0111
GO:00448	Protein-cor	68	1625	0.43	4.94E-11	24	1625	0.41	0.0029
GO:00167	Hydrolase a	87	2470	0.35	1.38E-10	-	-	-	-
GO:00055	Protein bin	185	7697	0.18	1.09E-09	73	7697	0.22	6.51E-05
GO:00037	R- helicase	15	79	1.08	2.21E-09	-	-	-	-
GO:01406	Catalytic ac	36	618	0.57	6.71E-09	13	618	0.57	0.007
GO:00043	Helicase ac	19	174	0.84	2.32E-08	7	174	0.85	0.0084
GO:00168	Ligase activ	18	179	0.81	2.27E-07	-	-	-	-
GO:01400	Catalytic ac	25	377	0.63	5.32E-07	-	-	-	-
GO:00037	mR- bindin	25	385	0.62	7.63E-07	15	385	0.84	4.24E-06

GO:00164	Oxidoreduc	39	858	0.46	7.63E-07	-	-	-	-
GO:00428	Identical pr	70	2174	0.31	1.05E-06	30	2174	0.38	0.00093
GO:00171	Nucleoside	32	670	0.48	5.88E-06	15	670	0.59	0.0015
GO:00430	Ribonucleo	17	203	0.73	6.38E-06	7	203	0.78	0.0193
GO:00168	ATP hydroly	22	343	0.61	6.55E-06	10	343	0.71	0.0042
GO:00164	Pyrophospl	33	721	0.46	8.59E-06	-	-	-	-
GO:00036	Chromatin	30	686	0.44	7.71E-05	15	686	0.58	0.0019
GO:00198	Enzyme bin	69	2431	0.26	0.00011	28	2431	0.31	0.022
GO:00512	#NAME?	12	138	0.74	0.00032	-	-	-	-
GO:00900	Translation	11	122	0.76	0.00057	-	-	-	-
GO:00051	Structural r	37	1060	0.35	0.00062	16	1060	0.42	0.032
GO:00451	Translation	12	158	0.68	0.0011	-	-	-	-
GO:00037	Double-stra	9	95	0.78	0.0025	5	95	0.97	0.023
GO:00506	Flavin aden	9	95	0.78	0.0025	-	-	-	-
GO:00052	Structural c	9	100	0.76	0.0035	6	100	1.02	0.004
GO:00000	tR- binding	8	77	0.82	0.0036	-	-	-	-
GO:00469	Protein dim	34	1036	0.32	0.0042	-	-	-	-
GO:00166	Oxidoreduc	7	59	0.88	0.0047	-	-	-	-
GO:00081	Translation	9	107	0.73	0.0053	-	-	-	-
GO:00166	Oxidoreduc	8	83	0.79	0.0053	-	-	-	-
GO:01400	Catalytic ac	14	259	0.54	0.0062	-	-	-	-
GO:00036	D- binding	57	2178	0.22	0.0073	-	-	-	-
GO:00469	Protein het	15	314	0.48	0.0124	-	-	-	-
GO:00166	Oxidoreduc	10	152	0.62	0.0132	-	-	-	-
GO:00010	Regulatory	3	6	1.5	0.0166	-	-	-	-
GO:00166	Oxidoreduc	4	18	1.15	0.0188	-	-	-	-
GO:00080	ATP-depen	9	132	0.64	0.02	-	-	-	-
GO:00351	miR- bindin	5	35	0.96	0.02	-	-	-	-

GO:00036	Single-stra	9	133	0.63	0.0204	-	-	-	-	
GO:00305	Structural c	7	79	0.75	0.0204	-	-	-	-	
GO:00038	3-hydroxya	3	7	1.44	0.0212	-	-	-	-	
GO:00480	mR- 5-UTR	5	36	0.95	0.0212	-	-	-	-	
GO:00037	Translation	5	37	0.93	0.0232	-	-	-	-	
GO:00199	Protein don	28	883	0.31	0.0238	-	-	-	-	
GO:00616	R- polymera	16	381	0.43	0.0249	-	-	-	-	
GO:00037	mR- 3-UTR	8	111	0.66	0.026	-	-	-	-	
GO:00039	acetyl-CoA	3	8	1.38	0.026	-	-	-	-	
GO:00044	Isocitrate d	3	8	1.38	0.026	-	-	-	-	
GO:00168	Ligase activ	3	8	1.38	0.026	-	-	-	-	
GO:00169	Nuclear rec	10	171	0.57	0.026	-	-	-	-	
GO:00314	Nucleosom	6	60	0.8	0.026	-	-	-	-	
GO:00166	Oxidoreduc	9	144	0.6	0.0289	-	-	-	-	
GO:00081	Transcriptic	22	638	0.34	0.0296	-	-	-	-	
GO:00421	Telomeric D	5	43	0.87	0.037	-	-	-	-	
GO:00305	snoR- bindi	5	44	0.86	0.0402	-	-	-	-	
GO:00045	Hydrolase a	7	94	0.68	0.0418	-	-	-	-	
GO:00150	Disulfide ox	5	45	0.85	0.043	-	-	-	-	
GO:00170	Purine nucl	-	-	-	-	32	2148	0.42	1.00E-04	
GO:00305	Adenyl nucl	-	-	-	-	25	1743	0.4	0.0029	
GO:00435	ADP bindin	-	-	-	-	4	47	1.17	0.0193	
GO:00055	GTP bindin	-	-	-	-	10	437	0.6	0.0218	
GO:00037	Translation	-	-	-	-	4	60	1.07	0.0377	

FUNCTION_D4_30mM_UP

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
GO:000551	Protein bin	101	7697	0.31	2.07E-13	45	7697	0.33	1.95E-06
GO:00054	Binding	134	13754	0.18	1.40E-11	60	13754	0.2	1.86E-06
GO:01406	ATP-depen	19	652	0.65	7.90E-05	-	-	-	-
GO:00198	Enzyme bin	38	2431	0.38	0.00022	19	2431	0.46	0.019
GO:00428	Identical pr	35	2174	0.39	3.00E-04	-	-	-	-
GO:000382	Catalytic ac	67	6043	0.23	0.00055	-	-	-	-
GO:01406	ATP-depen	6	49	1.28	0.00069	-	-	-	-
GO:00001	Nucleotide	36	2478	0.35	0.001	-	-	-	-
GO:00051	Sig-ling rec	26	1451	0.44	0.001	-	-	-	-
GO:001982	ATPase-cou	6	54	1.23	0.001	-	-	-	-
GO:00510	Unfolded p	8	126	0.99	0.001	-	-	-	-
GO:00431	Ion binding	62	5669	0.23	0.0014	-	-	-	-
GO:004487	Protein-cor	27	1625	0.41	0.0015	-	-	-	-
GO:00973	Carbohydra	35	2440	0.34	0.0015	-	-	-	-
GO:00080	Cytoskeleta	22	1184	0.46	0.0021	-	-	-	-
GO:00360	Small mole	37	2793	0.31	0.0036	-	-	-	-
GO:00199	Protein dor	18	883	0.5	0.004	11	883	0.66	0.0216
GO:00469	Proton-tran	4	25	1.39	0.0057	-	-	-	-
GO:005101	Actin filame	9	245	0.75	0.006	-	-	-	-
GO:00167	Hydrolase a	33	2470	0.31	0.0067	-	-	-	-
GO:00168	Isomerase	8	198	0.79	0.0076	-	-	-	-
GO:00305	Adenyl nucl	26	1743	0.36	0.0079	-	-	-	-
GO:00451	Translation	7	158	0.83	0.0116	-	-	-	-
GO:00168	Intramolec	3	12	1.59	0.0124	-	-	-	-
GO:001707	Purine nucl	29	2148	0.32	0.0141	-	-	-	-
GO:00325	Ribonucleo	29	2149	0.32	0.0141	-	-	-	-

GO:00325E	Adenyl ribo	25	1731	0.35	0.0149	-	-	-	-
GO:000552	ATP binding	24	1663	0.35	0.0202	-	-	-	-
GO:00431E	Anion bindi	33	2671	0.28	0.0209	-	-	-	-
GO:004454	S100 protei	3	16	1.46	0.0216	-	-	-	-
GO:00082E	Lipid bindir	15	794	0.46	0.0218	-	-	-	-
GO:00325E	Purine ribor	28	2130	0.31	0.0236	-	-	-	-
GO:00356E	Purine ribor	27	2054	0.31	0.0301	-	-	-	-
GO:00199C	Ki-se bindir	16	929	0.42	0.0342	-	-	-	-
GO:000517	Integrin bin	6	145	0.8	0.0363	-	-	-	-
GO:00168E	ATP hydroly	9	343	0.61	0.038	-	-	-	-
GO:003162	Ubiquitin pr	9	355	0.59	0.0472	-	-	-	-

KEGG_D4_10mM_DOWN

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DF	false discovery rate.DP12
cge01100	Metabolic p	25	1132	0.55	1.09E-05	-	-	-	-
cge01200	Carbon me	9	104	1.15	1.09E-05	-	-	-	-
cge05014	Amyotrophi	12	278	0.85	2.66E-05	-	-	-	-
cge00020	Citrate cycl	5	27	1.48	0.00012	-	-	-	-
cge04141	Protein pro	8	128	1.01	0.00013	-	-	-	-
cge05012	Parkinson c	9	183	0.9	0.00016	-	-	-	-
cge05020	Prion disea	9	198	0.87	0.00026	-	-	-	-
cge00280	Valine, leuc	5	42	1.29	0.00041	-	-	-	-
cge00620	Pyruvate m	4	27	1.38	0.0014	-	-	-	-
cge05016	Huntington	8	230	0.75	0.0037	-	-	-	-
cge04217	Necroptosi	6	125	0.89	0.0046	-	-	-	-
cge04714	Thermogen	7	179	0.8	0.0046	-	-	-	-
cge00510	N-Glycan b	4	45	1.16	0.0059	-	-	-	-
cge00650	Butanoate r	3	19	1.41	0.0075	-	-	-	-
cge04210	Apoptosis	5	92	0.95	0.0075	3	92	1.49	0.0436
cge05010	Alzheimer c	8	273	0.68	0.0075	-	-	-	-
cge03008	Ribosome b	4	58	1.05	0.0111	-	-	-	-
cge00190	Oxidative p	5	112	0.86	0.0143	-	-	-	-
cge00630	Glyoxylate a	3	27	1.26	0.0143	-	-	-	-
cge00640	Propanoate	3	28	1.24	0.0143	-	-	-	-
cge03040	Spliceosom	5	114	0.85	0.0143	-	-	-	-
cge01230	Biosynthes	4	67	0.99	0.0144	-	-	-	-
cge05322	Systemic lu	4	69	0.97	0.0152	-	-	-	-
cge00380	Tryptophan	3	31	1.2	0.0162	-	-	-	-
cge00071	Fatty acid d	3	36	1.13	0.0229	-	-	-	-
cge00072	Synthesis a	2	9	1.56	0.0229	-	-	-	-

cge00330	Arginine an	3	36	1.13	0.0229	-	-	-	-	
cge00513	Various typ	3	36	1.13	0.0229	-	-	-	-	
cge03013	R- transpor	5	135	0.78	0.0229	-	-	-	-	
cge00310	Lysine degr	3	41	1.07	0.0274	-	-	-	-	
cge01212	Fatty acid n	3	46	1.02	0.0361	-	-	-	-	
cge05017	Spinocereb	4	105	0.79	0.0473	-	-	-	-	
cge03060	Protein exp	2	15	1.34	0.0476	-	-	-	-	
cge05034	Alcoholism	4	107	0.78	0.0476	-	-	-	-	
cge05132	Salmonella	5	172	0.67	0.0476	-	-	-	-	
cge00010	Glycolysis /	3	55	0.95	0.0492	-	-	-	-	
cge00670	One carbor	2	16	1.31	0.0492	-	-	-	-	
cge04530	Tight junctio	-	-	-	-		3	105	1.44	0.0436

KEGG_D4_10mM_UP

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	term descri	observed g	backgrounc	strength.DI	false discovery rate.DP12
cge00010	Glycolysis /	3	55	1.49	0.0442	-	-	-	-	-
cge01100	Metabolic p	9	1132	0.66	0.0442	-	-	-	-	-
cge04721	Sy-ptic vesi	3	60	1.45	0.0442	-	-	-	-	-
cge05132	Salmonella	4	172	1.12	0.0442	-	-	-	-	-
cge04966	Collecting c	2	20	1.75	0.0452	-	-	-	-	-
cge01200	Carbon me	3	104	1.21	0.0487	-	-	-	-	-
cge04145	Phagosome	3	106	1.21	0.0487	-	-	-	-	-
cge00620	Pyruvate m	2	27	1.62	0.0492	-	-	-	-	-
cge00030	Pentose ph	-	-	-	-	3	28	1.59	0.027	

KEGG_D4_30mM_DOWN

#term ID	term description.NIST	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
cge01100	Metabolic pathways	65	1132	0.56	2.06E-16	18	1132	0.45	0.0027
cge05014	Amyotrophic lateral scle	28	278	0.81	9.02E-12	9	278	0.75	0.0022
cge05012	Parkinson disease	21	183	0.86	9.77E-10	7	183	0.83	0.0027
cge01200	Carbon metabolism	16	104	0.99	4.65E-09	6	104	1.01	0.0022
cge00020	Citrate cycle (TCA cycle)	9	27	1.33	1.99E-07	3	27	1.29	0.0107
cge00280	Valine, leucine and isole	10	42	1.18	3.41E-07	-	-	-	-
cge05016	Huntington disease	19	230	0.72	6.43E-07	6	230	0.66	0.0283
cge05010	Alzheimer disease	20	273	0.67	1.52E-06	8	273	0.71	0.0043
cge05020	Prion disease	17	198	0.74	1.74E-06	8	198	0.85	0.0022
cge04210	Apoptosis	12	92	0.92	2.51E-06	6	92	1.06	0.0022
cge04714	Thermogenesis	15	179	0.73	1.17E-05	-	-	-	-
cge03040	Spliceosome	12	114	0.83	1.74E-05	6	114	0.97	0.0022
cge03030	DNA replication	7	27	1.22	1.92E-05	-	-	-	-
cge00380	Tryptophan metabolism	7	31	1.16	3.96E-05	-	-	-	-
cge01230	Biosynthesis of amino ac	9	67	0.93	5.82E-05	-	-	-	-
cge00190	Oxidative phosphorylatic	11	112	0.8	6.71E-05	-	-	-	-
cge03013	RNA transport	12	135	0.75	6.71E-05	7	135	0.96	0.0022
cge00620	Pyruvate metabolism	6	27	1.15	0.00019	-	-	-	-
cge04932	Non-alcoholic fatty liver	10	118	0.73	0.00055	-	-	-	-
cge00071	Fatty acid degradation	6	36	1.03	0.00072	-	-	-	-
cge00630	Glyoxylate and dicarboxy	5	27	1.07	0.0019	-	-	-	-
cge00640	Propanoate metabolism	5	28	1.06	0.0022	-	-	-	-
cge04260	Cardiac muscle contract	6	46	0.92	0.0022	-	-	-	-
cge01210	2-Oxocarboxylic acid me	4	16	1.2	0.0031	-	-	-	-
cge04217	Necroptosis	9	125	0.66	0.0033	-	-	-	-
cge04141	Protein processing in en	9	128	0.65	0.0037	5	128	0.84	0.0141
cge03430	Mismatch repair	4	18	1.15	0.004	-	-	-	-

cge05164	Influenza A	9	130	0.64	0.004	-	-	-	-	
cge00330	Arginine and proline met	5	36	0.95	0.0047	-	-	-	-	
cge03008	Ribosome biogenesis in	6	58	0.82	0.0051	3	58	0.96	0.0464	
cge05203	Viral carcinogenesis	9	143	0.6	0.0066	10	143	1.09	5.83E-06	
cge00310	Lysine degradation	5	41	0.89	0.0073	-	-	-	-	
cge00052	Galactose metabolism	4	26	0.99	0.0113	-	-	-	-	
cge04142	Lysosome	7	101	0.64	0.0143	-	-	-	-	
cge05169	Epstein-Barr virus infecti	9	163	0.55	0.0143	7	163	0.88	0.0022	
cge00010	Glycolysis / Gluconeoge	5	55	0.76	0.0216	3	55	0.98	0.0453	
cge00053	Ascorbate and aldarate r	3	15	1.1	0.0226	-	-	-	-	
cge00603	Glycosphingolipid biosyr	3	15	1.1	0.0226	-	-	-	-	
cge03060	Protein export	3	15	1.1	0.0226	-	-	-	-	
cge00670	One carbon pool by folat	3	16	1.08	0.0245	2	16	1.34	0.0461	
cge04979	Cholesterol metabolism	4	35	0.86	0.0245	-	-	-	-	
cge00970	Aminoacyl-tR- biosynthe	4	36	0.85	0.0256	-	-	-	-	
cge03010	Ribosome	9	184	0.49	0.0256	-	-	-	-	
cge04146	Peroxisome	5	60	0.72	0.0256	-	-	-	-	
cge00040	Pentose and glucuro-te i	3	19	1	0.0335	-	-	-	-	
cge00270	Cysteine and methionine	4	40	0.8	0.0335	3	40	1.12	0.0237	
cge00650	Butanoate metabolism	3	19	1	0.0335	-	-	-	-	
cge04110	Cell cycle	6	99	0.59	0.0404	5	99	0.95	0.0059	
cge04215	Apoptosis - multiple spe	3	21	0.96	0.0404	-	-	-	-	
cge01212	Fatty acid metabolism	4	46	0.74	0.0492	-	-	-	-	
cge04530	Tight junction	-	-	-	-	6	105	1	0.0022	
cge05161	Hepatitis B	-	-	-	-	7	130	0.98	0.0022	
cge05200	Pathways in cancer	-	-	-	-	10	391	0.65	0.0027	
cge05165	Human papillomavirus ir	-	-	-	-	8	251	0.75	0.0028	
cge05160	Hepatitis C	-	-	-	-	6	140	0.88	0.0041	
cge04810	Regulation of actin cytos	-	-	-	-	6	153	0.84	0.0058	

cge05162	Measles	-	-	-	-	5	111	0.9	0.0092
cge05206	MicroR-s in cancer	-	-	-	-	5	117	0.88	0.0107
cge05216	Thyroid cancer	-	-	-	-	3	29	1.26	0.0118
cge04933	AGE-RAGE sig-ling pathv	-	-	-	-	4	77	0.96	0.0162
cge05145	Toxoplasmosis	-	-	-	-	4	84	0.92	0.0211
cge05167	Kaposi sarcoma-associa	-	-	-	-	5	157	0.75	0.0283
cge05214	Glioma	-	-	-	-	3	50	1.02	0.0388
cge05223	Non-small cell lung canc	-	-	-	-	3	50	1.02	0.0388
cge05230	Central carbon metaboli	-	-	-	-	3	53	1	0.0424
cge04917	Prolactin sig-ling pathwa	-	-	-	-	3	56	0.97	0.0461
cge05212	Pancreatic cancer	-	-	-	-	3	57	0.97	0.0461

KEGG_D4_30mM_UP

#term ID	term description.NIST	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
cge01100	Metabolic pathways	23	1132	0.5	0.00049	20	1132	0.49	0.0016
cge04510	Focal adhesion	8	136	0.96	0.00074	-	-	-	-
cge03013	R- transport	7	135	0.9	0.0043	-	-	-	-
cge01200	Carbon metabolism	6	104	0.95	0.0067	-	-	-	-
cge04145	Phagosome	6	106	0.94	0.0067	7	106	1.06	0.0014
cge04530	Tight junction	6	105	0.94	0.0067	-	-	-	-
cge04810	Regulation of actin cytos	7	153	0.85	0.0067	-	-	-	-
cge05146	Amoebiasis	5	67	1.06	0.0067	-	-	-	-
cge00520	Amino sugar and nucleot	4	41	1.18	0.0075	-	-	-	-
cge04144	Endocytosis	7	183	0.77	0.008	6	183	0.75	0.0295
cge05165	Human papillomavirus ir	8	251	0.69	0.0087	-	-	-	-
cge04966	Collecting duct acid sec	3	20	1.36	0.0117	-	-	-	-
cge00480	Glutathione metabolism	4	52	1.07	0.012	-	-	-	-
cge04512	ECM-receptor interactio	4	57	1.03	0.0155	-	-	-	-
cge05100	Bacterial invasion of epit	4	61	1	0.0184	-	-	-	-
cge05132	Salmonella infection	6	172	0.73	0.0221	6	172	0.78	0.0271
cge00970	Aminoacyl-tR- biosynthe	3	36	1.11	0.0396	-	-	-	-
cge03050	Proteasome	3	37	1.1	0.0403	-	-	-	-
cge04141	Protein processing in en	-	-	-	-	6	128	0.91	0.014
cge04260	Cardiac muscle contract	-	-	-	-	4	46	1.18	0.015
cge04612	Antigen processing and p	-	-	-	-	4	45	1.19	0.015
cge05014	Amyotrophic lateral scle	-	-	-	-	8	278	0.7	0.015
cge03018	R- degradation	-	-	-	-	4	62	1.05	0.0271
cge03015	mR- surveillance pathwa	-	-	-	-	4	73	0.98	0.0339
cge05010	Alzheimer disease	-	-	-	-	7	273	0.65	0.0363
cge05205	Proteoglycans in cancer	-	-	-	-	5	140	0.79	0.0422
cge04962	Vasopressin-regulated w	-	-	-	-	3	38	1.14	0.0431

KEGG_D7_10mM_UP

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
cge01100	Metabolic p	55	1132	0.5	5.51E-11	32	1132	0.56	1.27E-07
cge05205	Proteoglyca	15	140	0.84	2.70E-06	-	-	-	
cge01200	Carbon me	12	104	0.87	2.38E-05	9	104	1.05	4.03E-05
cge04141	Protein pro	13	128	0.82	2.38E-05	-	-	-	
cge04145	Phagosome	12	106	0.86	2.38E-05	-	-	-	
cge05146	Amoebiasis	10	67	0.98	2.38E-05	-	-	-	
cge04512	ECM-recep	9	57	1.01	3.25E-05	-	-	-	
cge04918	Thyroid hor	8	54	0.98	0.00018	-	-	-	
cge05418	Fluid shear	10	100	0.81	0.00027	-	-	-	
cge04114	Oocyte mei	9	82	0.85	0.00035	-	-	-	
cge04144	Endocytosi	13	183	0.66	0.00035	-	-	-	
cge04510	Focal adhe	11	136	0.72	0.00043	-	-	-	
cge05165	Human pap	15	251	0.59	0.00043	-	-	-	
cge05200	Pathways ir	19	391	0.5	0.00047	-	-	-	
cge04971	Gastric acic	7	51	0.95	0.00061	-	-	-	
cge00480	Glutathione	7	52	0.94	0.00064	-	-	-	
cge04810	Regulation	11	153	0.67	0.00088	-	-	-	
cge04976	Bile secreti	7	59	0.89	0.0012	-	-	-	
cge00520	Amino suga	6	41	0.98	0.0013	-	-	-	
cge00620	Pyruvate m	5	27	1.08	0.0019	3	27	1.15	0.0478
cge00980	Metabolism	6	45	0.94	0.0019	-	-	-	
cge04142	Lysosome	8	101	0.71	0.004	-	-	-	
cge05204	Chemical c	6	53	0.86	0.004	-	-	-	
cge04216	Ferroptosis	5	34	0.98	0.0041	-	-	-	
cge00010	Glycolysis /	6	55	0.85	0.0043	-	-	-	
cge04530	Tight junctio	8	105	0.69	0.0043	5	105	0.79	0.0478

cge04961	Endocrine a	5	35	0.97	0.0043	-	-	-	-
cge00071	Fatty acid d	5	36	0.95	0.0045	-	-	-	-
cge05414	Dilated car	6	57	0.83	0.0045	-	-	-	-
cge00983	Drug metab	6	58	0.83	0.0047	-	-	-	-
cge04966	Collecting d	4	20	1.11	0.0047	-	-	-	-
cge04261	Adrenergic	7	85	0.73	0.0049	-	-	-	-
cge04611	Platelet act	7	84	0.73	0.0049	-	-	-	-
cge04720	Long-term p	5	38	0.93	0.0049	-	-	-	-
cge04925	Aldosteron	6	60	0.81	0.0049	-	-	-	-
cge04978	Mineral abs	5	39	0.92	0.0049	-	-	-	-
cge05100	Bacterial in	6	61	0.8	0.0049	-	-	-	-
cge05203	Viral carcin	9	143	0.61	0.0049	7	143	0.8	0.0071
cge05323	Rheumatoi	6	64	0.78	0.0059	-	-	-	-
cge00280	Valine, leuc	5	42	0.89	0.006	-	-	-	-
cge05012	Parkinson d	10	183	0.55	0.0064	-	-	-	-
cge00630	Glyoxylate a	4	27	0.98	0.0095	-	-	-	-
cge04137	Mitophagy -	5	51	0.8	0.0124	-	-	-	-
cge04970	Salivary sec	5	51	0.8	0.0124	-	-	-	-
cge05014	Amyotrophi	12	278	0.45	0.0128	-	-	-	-
cge05132	Salmonella	9	172	0.53	0.0136	-	-	-	-
cge04964	Proximal tu	3	14	1.14	0.0143	-	-	-	-
cge05170	Human imr	9	174	0.52	0.0143	-	-	-	-
cge04911	Insulin secr	5	55	0.77	0.0148	-	-	-	-
cge04934	Cushing syr	7	115	0.6	0.0178	-	-	-	-
cge00100	Steroid bios	3	16	1.08	0.0184	-	-	-	-
cge00970	Aminoacyl-	4	36	0.86	0.0199	-	-	-	-
cge04146	Peroxisome	5	60	0.73	0.0199	6	60	1.11	0.001
cge04150	mTOR sig-li	7	120	0.58	0.0199	-	-	-	-

cge04151	PI3K-Akt sig	11	261	0.44	0.0199	-	-	-	-
cge04721	Sy-ptic vesi	5	60	0.73	0.0199	-	-	-	-
cge00982	Drug metab	4	37	0.84	0.02	-	-	-	-
cge04962	Vasopressi	4	38	0.83	0.0214	-	-	-	-
cge01230	Biosynthes	5	67	0.68	0.0271	6	67	1.06	0.0014
cge04070	Phosphatid	5	67	0.68	0.0271	-	-	-	-
cge04913	Ovarian ste	4	42	0.79	0.0271	-	-	-	-
cge04924	Renin secre	4	41	0.8	0.0271	-	-	-	-
cge04972	Pancreatic	5	67	0.68	0.0271	-	-	-	-
cge05135	Yersinia inf	6	97	0.6	0.0271	-	-	-	-
cge05225	Hepatocell	7	131	0.54	0.0271	-	-	-	-
cge04750	Inflammato	5	69	0.67	0.0273	-	-	-	-
cge05222	Small cell l	5	69	0.67	0.0273	-	-	-	-
cge04140	Autophagy	6	103	0.58	0.0318	-	-	-	-
cge01212	Fatty acid n	4	46	0.75	0.0337	5	46	1.14	0.0022
cge04024	cAMP sig-li	7	140	0.51	0.0351	-	-	-	-
cge04730	Long-term	4	48	0.73	0.0376	-	-	-	-
cge04927	Cortisol syr	4	49	0.72	0.0397	-	-	-	-
cge00052	Galactose r	3	26	0.87	0.043	-	-	-	-
cge00190	Oxidative p	6	112	0.54	0.043	-	-	-	-
cge00020	Citrate cycl	3	27	0.86	0.0464	-	-	-	-
cge04722	Neurotroph	5	82	0.6	0.0464	-	-	-	-
cge04726	Serotonergi	5	82	0.6	0.0464	-	-	-	-
cge00072	Synthesis a	2	9	1.16	0.0471	-	-	-	-
cge00640	Propanoate	3	28	0.84	0.0471	3	28	1.14	0.0478
cge01524	Platinum dr	4	53	0.69	0.0471	-	-	-	-
cge04670	Leukocyte t	5	83	0.59	0.0471	-	-	-	-
cge05230	Central car	4	53	0.69	0.0471	-	-	-	-

cge05410	Hypertroph	4	53	0.69	0.0471	-	-	-	-	
cge00051	Fructose ar	3	29	0.83	0.0492	-	-	-	-	
cge00562	Inositol pho	4	55	0.67	0.0492	-	-	-	-	
cge04973	Carbohydra	3	29	0.83	0.0492	-	-	-	-	
cge00900	Terpenoid b	-	-	-	-		4	21	1.39	0.0021
cge00240	Pyrimidine	-	-	-	-		6	41	1.27	0.00018
cge01040	Biosynthes	-	-	-	-		3	24	1.21	0.0385
cge03320	PPAR sig-lir	-	-	-	-		4	63	0.91	0.0478
cge00230	Purine meta	-	-	-	-		5	90	0.85	0.0319
cge00750	Vitamin B6	-	-	-	-		2	6	1.63	0.0478

PROCESS_D7_10mM_UP

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
GO:00099	Cellular pro	332	15994	0.13	9.27E-21	165	15994	0.12	4.20E-08
GO:00330	Macromole	102	2366	0.45	1.06E-17	35	2366	0.28	0.0143
GO:00707	Cellular ma	90	1929	0.48	2.36E-17	-	-	-	-
GO:00511	Localizatio	147	4471	0.33	2.73E-17	54	4471	0.19	0.029
GO:00512	Establishm	134	3839	0.35	2.73E-17	47	3839	0.2	0.0474
GO:00081	Protein loc	89	1924	0.48	3.56E-17	-	-	-	-
GO:00516	Cellular loc	107	2661	0.42	3.63E-17	41	2661	0.3	0.0024
GO:00068	Transport	129	3660	0.36	4.87E-17	-	-	-	-
GO:00451	Establishm	67	1173	0.57	1.24E-16	-	-	-	-
GO:00469	Intracellula	69	1297	0.54	1.07E-15	24	1297	0.38	0.0087
GO:00150	Protein trar	62	1062	0.58	1.08E-15	-	-	-	-
GO:00717	Nitrogen co	71	1456	0.5	2.18E-14	-	-	-	-
GO:00717	Organic sul	80	1835	0.45	6.16E-14	-	-	-	-
GO:00161	Vesicle-me	63	1231	0.52	1.87E-13	-	-	-	-
GO:00516	Establishm	74	1689	0.45	7.98E-13	26	1689	0.3	0.0411
GO:00328	Regulation	86	2276	0.39	9.02E-12	-	-	-	-
GO:00068	Intracellula	43	669	0.62	1.11E-11	-	-	-	-
GO:00442	Small mole	71	1690	0.43	2.16E-11	46	1690	0.54	1.03E-09
GO:00081	Metabolic p	203	8581	0.18	7.15E-11	105	8581	0.2	8.76E-06
GO:00511	Regulation	88	2504	0.36	1.81E-10	42	2504	0.33	0.00039
GO:00717	Organic sul	192	8137	0.18	1.02E-09	101	8137	0.2	9.15E-06
GO:00603	Regulation	50	1043	0.49	2.21E-09	25	1043	0.49	0.00023
GO:00650	Biological r	259	12586	0.12	4.59E-09	135	12586	0.14	1.43E-05
GO:00442	Cellular me	171	7040	0.2	5.12E-09	89	7040	0.21	4.33E-05
GO:00485	Positive reg	159	6368	0.21	5.92E-09	84	6368	0.23	2.61E-05
GO:00161	Endosomal	22	215	0.82	7.85E-09	-	-	-	-

GO:00650(	Regulation	111	3854	0.27	1.32E-08	53	3854	0.25	0.0024
GO:004852	Positive reg	146	5758	0.21	2.43E-08	82	5758	0.26	5.91E-06
GO:00708E	Cellular res	85	2646	0.32	3.46E-08	38	2646	0.27	0.0132
GO:00164E	Cytosolic tr	17	142	0.89	1.59E-07	-	-	-	-
GO:005104	Regulation	67	1906	0.36	1.59E-07	-	-	-	-
GO:00328E	Regulation	43	939	0.47	2.19E-07	20	939	0.44	0.0061
GO:005124	Regulation	84	2708	0.3	2.19E-07	49	2708	0.37	9.15E-06
GO:00650(	Regulation	89	2956	0.29	2.40E-07	39	2956	0.23	0.0389
GO:00060E	Alcohol me	24	325	0.68	3.51E-07	15	325	0.77	2.94E-05
GO:00090E	Catabolic p	68	1999	0.34	3.61E-07	-	-	-	-
GO:00481E	Golgi vesicl	22	276	0.71	4.52E-07	-	-	-	-
GO:001604	Cellular co	138	5621	0.2	8.28E-07	83	5621	0.28	1.14E-06
GO:00461E	Alcohol bio	14	101	0.95	8.28E-07	8	101	1.01	5.00E-04
GO:19026E	Secondary	15	129	0.88	1.87E-06	11	129	1.04	8.79E-06
GO:00442E	Primary me	173	7736	0.16	2.12E-06	99	7736	0.22	6.85E-06
GO:00507E	Regulation	229	11253	0.12	2.33E-06	122	11253	0.14	0.00011
GO:00507E	Regulation	238	11860	0.11	2.57E-06	124	11860	0.13	5.00E-04
GO:19015E	Organonitro	132	5394	0.2	2.57E-06	-	-	-	-
GO:004214	Retrograde	12	77	1	3.01E-06	-	-	-	-
GO:190161	Organic hyc	27	473	0.57	4.40E-06	19	473	0.71	8.76E-06
GO:006062	Regulation	32	647	0.51	5.06E-06	-	-	-	-
GO:00100E	Response t	82	2827	0.27	5.18E-06	44	2827	0.3	0.0011
GO:00060E	Organic aci	40	956	0.43	6.61E-06	-	-	-	-
GO:00197E	Carboxylic	39	917	0.44	6.61E-06	23	917	0.51	0.00029
GO:00324E	Endocytic r	11	69	1.01	8.90E-06	-	-	-	-
GO:00507E	Regulation	68	2223	0.3	1.47E-05	-	-	-	-
GO:00082(	Cholestero	13	113	0.87	1.59E-05	10	113	1.06	2.13E-05
GO:00508E	Response t	174	8055	0.15	1.96E-05	-	-	-	-

GO:00069[illegible]	Response t	87	3187	0.25	2.08E-05	-	-	-	-
GO:000971	Response t	50	1425	0.36	2.08E-05	-	-	-	-
GO:001094	Regulation	57	1740	0.33	2.08E-05	32	1740	0.37	0.0011
GO:003304	Regulation	45	1214	0.38	2.08E-05	24	1214	0.4	0.0039
GO:004424	Cellular cat	53	1557	0.34	2.08E-05	-	-	-	-
GO:00487[illegible]	System dev	101	3916	0.22	2.08E-05	49	3916	0.21	0.0269
GO:00511[illegible]	Positive reg	45	1212	0.38	2.08E-05	22	1212	0.37	0.0178
GO:004217	Regulation	22	363	0.59	2.64E-05	-	-	-	-
GO:004222	Response t	111	4477	0.21	2.64E-05	-	-	-	-
GO:00325[illegible]	Developme	131	5590	0.18	2.66E-05	70	5590	0.21	0.0017
GO:00514[illegible]	Regulation	28	564	0.51	2.66E-05	-	-	-	-
GO:190161	Organic hy	15	167	0.76	2.66E-05	10	167	0.89	0.00033
GO:004851	Negative re	125	5319	0.18	5.21E-05	72	5319	0.24	0.00012
GO:009887	Vesicle-me	13	130	0.81	5.48E-05	-	-	-	-
GO:00098[illegible]	Regulation	38	973	0.4	5.50E-05	19	973	0.4	0.019
GO:004852	Negative re	114	4752	0.19	8.06E-05	68	4752	0.26	4.33E-05
GO:00068[illegible]	Endoplasm	12	113	0.84	8.33E-05	-	-	-	-
GO:00442[illegible]	Small mole	23	428	0.54	8.73E-05	18	428	0.73	8.79E-06
GO:00440[illegible]	Regulation	39	1038	0.39	9.07E-05	22	1038	0.43	0.0032
GO:00488[illegible]	A-tomical s	121	5157	0.18	9.07E-05	66	5157	0.22	0.0017
GO:00513[illegible]	Regulation	38	996	0.39	9.07E-05	-	-	-	-
GO:00323[illegible]	Regulation	20	334	0.59	9.56E-05	10	334	0.58	0.0239
GO:00510[illegible]	Positive reg	39	1045	0.38	1.00E-04	-	-	-	-
GO:00068[illegible]	Nitrogen co	155	7145	0.15	0.00011	-	-	-	-
GO:000727	Multicellula	106	4353	0.2	0.00011	57	4353	0.23	0.0038
GO:00327[illegible]	Monocarbo	28	615	0.47	0.00011	16	615	0.52	0.0041
GO:190157	Organic sul	54	1714	0.31	0.00011	-	-	-	-
GO:001922	Regulation	146	6627	0.15	0.00012	86	6627	0.22	2.94E-05

GO:00333€	Protein loca	31	739	0.43	0.00014	-	-	-	-
GO:00974(	Supramole	26	549	0.49	0.00014	-	-	-	-
GO:00069(	Organelle o	92	3632	0.21	0.00015	56	3632	0.3	8.38E-05
GO:005171	Cellular res	143	6532	0.15	0.00023	-	-	-	-
GO:00102(	Endomemb	24	498	0.49	0.00026	-	-	-	-
GO:00097(	Response t	32	809	0.41	3.00E-04	-	-	-	-
GO:00100(	Response t	26	577	0.46	3.00E-04	-	-	-	-
GO:00800(	Regulation	129	5780	0.16	0.00039	81	5780	0.25	8.76E-06
GO:00516€	Localizatio	25	550	0.47	0.00041	-	-	-	-
GO:004001	Regulation	38	1080	0.36	0.00047	-	-	-	-
GO:00725(	Establishm	19	344	0.55	0.00047	-	-	-	-
GO:00226(	Regulation	19	347	0.55	0.00052	-	-	-	-
GO:00100(	Response t	20	384	0.53	0.00058	-	-	-	-
GO:001407	Response t	35	964	0.37	0.00058	18	964	0.38	0.0362
GO:007131	Cellular res	59	2069	0.27	0.00061	31	2069	0.28	0.0233
GO:00190(	Viral life cy	11	119	0.78	0.00063	-	-	-	-
GO:190547	Regulation	14	198	0.66	0.00063	-	-	-	-
GO:00301€	Regulation	29	724	0.41	0.00064	-	-	-	-
GO:006102	Membrane	28	684	0.42	0.00064	-	-	-	-
GO:19017(	Response t	50	1648	0.29	0.00068	28	1648	0.34	0.009
GO:00015(	Regulation	21	426	0.5	7.00E-04	-	-	-	-
GO:00430€	Regulation	48	1557	0.3	7.00E-04	-	-	-	-
GO:00066(	Cholestero	7	40	1.05	0.00078	5	40	1.21	0.0032
GO:00444(	Biological p	14	203	0.65	0.00078	-	-	-	-
GO:003134	Regulation	30	776	0.4	0.00081	-	-	-	-
GO:00073(	Nervous sy	60	2147	0.26	0.00083	-	-	-	-
GO:00160(	Viral proce	12	151	0.71	9.00E-04	-	-	-	-
GO:005164	Organelle l	24	547	0.45	0.00093	-	-	-	-

GO:000701	Cytoskelet	42	1308	0.32	0.001	27	1308	0.42	0.00089
GO:00226(	Cellular co	67	2516	0.24	0.001	43	2516	0.34	0.00021
GO:00066	Fatty acid n	19	375	0.52	0.0012	11	375	0.58	0.0172
GO:00436(	Cellular am	37	1102	0.34	0.0014	-	-	-	-
GO:00300	Actin cytos	24	566	0.44	0.0015	13	566	0.47	0.0351
GO:00432	Regulation	20	416	0.49	0.0015	12	416	0.57	0.0117
GO:190307	Regulation	10	109	0.77	0.0015	-	-	-	-
GO:00440	Positive reg	47	1571	0.29	0.0016	-	-	-	-
GO:00507	Regulation	67	2555	0.23	0.0016	35	2555	0.25	0.0397
GO:005124	Positive reg	46	1529	0.29	0.0017	27	1529	0.36	0.007
GO:00429	Regulation	46	1531	0.29	0.0018	26	1531	0.34	0.0141
GO:005124	Negative re	35	1035	0.34	0.002	25	1035	0.49	0.00021
GO:00510	Positive reg	43	1402	0.3	0.0021	-	-	-	-
GO:190437	Regulation	11	140	0.71	0.0021	-	-	-	-
GO:00082(	Steroid met	14	229	0.6	0.0023	13	229	0.86	2.62E-05
GO:00195	Protein met	100	4367	0.17	0.0023	-	-	-	-
GO:003002	Actin filame	25	625	0.41	0.0023	-	-	-	-
GO:00300	Cell project	40	1269	0.31	0.0023	-	-	-	-
GO:00705(	Regulation	12	170	0.66	0.0023	-	-	-	-
GO:000657	Cellular mc	13	201	0.62	0.0025	-	-	-	-
GO:004324	Regulation	11	144	0.69	0.0025	-	-	-	-
GO:000962	Response t	38	1190	0.32	0.0026	-	-	-	-
GO:00335	Cellular res	47	1609	0.28	0.0026	-	-	-	-
GO:000674	Glutathione	8	72	0.86	0.0027	-	-	-	-
GO:000963	Response t	13	204	0.62	0.0028	-	-	-	-
GO:012003	Regulation	28	760	0.38	0.0029	-	-	-	-
GO:00009(	Cell morph	29	803	0.37	0.003	-	-	-	-
GO:00160	Vesicle org	15	269	0.56	0.003	-	-	-	-

GO:00440E	Positive reg	23	560	0.42	0.003	-	-	-	-
GO:00726E	Protein loca	21	482	0.45	0.003	-	-	-	-
GO:19029C	Regulation	19	408	0.48	0.003	11	408	0.54	0.0283
GO:003134	Positive reg	20	448	0.46	0.0032	-	-	-	-
GO:00400C	Regulation	26	683	0.39	0.0032	-	-	-	-
GO:00096E	A-tomical s	62	2377	0.23	0.0033	-	-	-	-
GO:00602E	Regulation	129	6089	0.14	0.0034	80	6089	0.23	6.26E-05
GO:00508C	Regulation	15	275	0.55	0.0036	-	-	-	-
GO:00064E	Protein fold	14	243	0.57	0.0037	9	243	0.68	0.0132
GO:00702C	Regulation	23	570	0.42	0.0037	-	-	-	-
GO:00066E	Steroid bios	9	101	0.76	0.0038	8	101	1.01	5.00E-04
GO:00322E	Regulation	4	10	1.41	0.0038	-	-	-	-
GO:003227	Regulation	13	213	0.6	0.0038	-	-	-	-
GO:00339E	Response t	30	861	0.35	0.0038	-	-	-	-
GO:00714E	Cellular res	36	1127	0.32	0.0038	-	-	-	-
GO:00068E	Endocytosi	19	422	0.46	0.004	13	422	0.6	0.0043
GO:00303C	Positive reg	12	184	0.63	0.004	-	-	-	-
GO:00328E	Regulation	15	280	0.54	0.004	-	-	-	-
GO:005117	Regulation	120	5595	0.14	0.004	78	5595	0.25	1.22E-05
GO:00726E	Protein loca	13	215	0.59	0.004	-	-	-	-
GO:00901E	Establishm	13	215	0.59	0.004	-	-	-	-
GO:012003	Plasma me	38	1222	0.3	0.004	-	-	-	-
GO:00301E	Protein cata	27	741	0.37	0.0041	-	-	-	-
GO:005254	Regulation	19	423	0.46	0.0041	-	-	-	-
GO:190382	Positive reg	21	498	0.44	0.0041	-	-	-	-
GO:00516E	Establishm	18	387	0.48	0.0042	-	-	-	-
GO:005104	Regulation	27	746	0.37	0.0045	-	-	-	-
GO:003164	Regulation	18	393	0.47	0.0049	-	-	-	-

GO:19016(	Response t	36	1149	0.31	0.005	-	-	-	-
GO:005254	Regulation	18	395	0.47	0.0052	-	-	-	-
GO:000697	Response t	17	360	0.49	0.0053	-	-	-	-
GO:00458(	Negative re	16	324	0.5	0.0053	-	-	-	-
GO:200014	Regulation	33	1017	0.32	0.0053	-	-	-	-
GO:000662	Lipid metat	37	1202	0.3	0.0055	28	1202	0.48	9.57E-05
GO:00510(	Negative re	20	474	0.44	0.0056	-	-	-	-
GO:000691	Autophagy	15	292	0.52	0.0057	-	-	-	-
GO:00440(	Movement	8	84	0.79	0.0057	-	-	-	-
GO:00486(	Regulation	18	399	0.47	0.0057	-	-	-	-
GO:00516(	Establishm	11	164	0.64	0.0057	-	-	-	-
GO:000651	Peptide me	29	850	0.34	0.0061	-	-	-	-
GO:00067(	Sulfur com	16	333	0.49	0.0068	-	-	-	-
GO:000941	Response t	20	483	0.43	0.0069	12	483	0.5	0.0304
GO:002241	Cellular co	15	300	0.51	0.0072	-	-	-	-
GO:00226(	Regulation	32	993	0.32	0.0072	-	-	-	-
GO:19013(	Organic cyc	76	3212	0.18	0.0074	54	3212	0.33	1.43E-05
GO:00323(	Positive reg	12	202	0.58	0.0077	-	-	-	-
GO:001647	Cell migrati	30	909	0.33	0.0078	-	-	-	-
GO:003464	Cellular nit	87	3820	0.17	0.0078	49	3820	0.22	0.0178
GO:19018(	Regulation	13	235	0.55	0.0078	8	235	0.64	0.0361
GO:001081	Positive reg	10	143	0.66	0.008	-	-	-	-
GO:199077	Protein loca	14	269	0.53	0.008	-	-	-	-
GO:19017(	Cellular res	34	1095	0.3	0.0083	-	-	-	-
GO:005112	Negative re	26	740	0.36	0.0084	17	740	0.47	0.0086
GO:003287	Cellular res	20	494	0.42	0.0086	-	-	-	-
GO:00329(	Regulation	17	379	0.46	0.0086	-	-	-	-
GO:00362(	Cellular res	4	14	1.27	0.0086	-	-	-	-

GO:00301E	Neuron diff	35	1149	0.29	0.0092	-	-	-	-	
GO:005122	Regulation	21	537	0.4	0.0092	-	-	-	-	
GO:00068E	Retrograde	6	47	0.92	0.0093	-	-	-	-	
GO:000741	Central ner	33	1060	0.3	0.0095	-	-	-	-	
GO:00440E	Cellular co	68	2815	0.19	0.0095	-	-	-	-	
GO:00517C	Biological p	9	119	0.69	0.0095	-	-	-	-	
GO:19015E	Organonitro	33	1061	0.3	0.0096	-	-	-	-	
GO:00162E	Macroautop	11	178	0.6	0.0097	-	-	-	-	
GO:004887	Chemical h	31	972	0.31	0.0098	-	-	-	-	
GO:001972	Cellular ho	24	666	0.37	0.0099	-	-	-	-	
GO:00067E	Phosphorus	51	1940	0.23	0.0102	36	1940	0.38	0.00029	
GO:00109E	Negative re	12	211	0.57	0.0102	-	-	-	-	
GO:003051	Regulation	9	121	0.68	0.0102	-	-	-	-	
GO:004592	Negative re	5	30	1.03	0.0104	-	-	-	-	
GO:003297	Regulation	18	428	0.43	0.0109	-	-	-	-	
GO:199074	Cellular det	8	96	0.73	0.0112	-	-	-	-	
GO:00220C	Neurogene	40	1408	0.26	0.0118	-	-	-	-	
GO:00308E	Negative re	6	50	0.89	0.0118	-	-	-	-	
GO:00325C	Multicellula	136	6725	0.12	0.0118	-	-	-	-	
GO:004617	Polyol biosy	6	50	0.89	0.0118	-	-	-	-	
GO:005117	Import into	9	124	0.67	0.0118	6	124	0.79	0.0319	
GO:005134	Negative re	15	319	0.48	0.0118	-	-	-	-	
GO:00325E	Regulation	18	433	0.43	0.012	-	-	-	-	
GO:00508C	Sy-pse orga	16	357	0.46	0.012	-	-	-	-	
GO:190157	Organic sul	63	2581	0.2	0.012	41	2581	0.31	0.0014	
GO:00090E	Biosyntheti	64	2636	0.2	0.0121	43	2636	0.32	5.00E-04	
GO:003117	Neuron pro	26	765	0.34	0.0121	-	-	-	-	
GO:001967	#NAME?	5	32	1	0.0127	-	-	-	-	

GO:00106(	Positive reg	21	557	0.39	0.0129	-	-	-	-
GO:00070(	Vacuolar tr	10	157	0.61	0.0136	-	-	-	-
GO:00093(	Protein sec	8	100	0.71	0.0136	-	-	-	-
GO:00459	Positive reg	14	290	0.49	0.0138	-	-	-	-
GO:00430	Positive reg	34	1139	0.29	0.014	-	-	-	-
GO:19018	Regulation	8	101	0.71	0.0142	-	-	-	-
GO:00484	Cell develo	48	1825	0.23	0.0143	28	1825	0.29	0.0302
GO:00301	Cell differe	78	3418	0.17	0.0146	50	3418	0.27	0.0012
GO:00303	Regulation	30	961	0.31	0.0156	-	-	-	-
GO:00109	Regulation	21	568	0.38	0.0158	-	-	-	-
GO:00485	Response t	14	295	0.49	0.0158	-	-	-	-
GO:00065(	Proteolysis	35	1197	0.28	0.016	-	-	-	-
GO:00102	Response t	32	1056	0.29	0.016	-	-	-	-
GO:00507	Positive reg	14	296	0.49	0.016	-	-	-	-
GO:00996	Endosome	4	18	1.16	0.016	-	-	-	-
GO:00457	Positive reg	6	55	0.85	0.0166	-	-	-	-
GO:00400	Positive reg	22	615	0.36	0.0172	-	-	-	-
GO:00512	Positive reg	43	1593	0.24	0.0172	-	-	-	-
GO:00513(	Cell divisio	17	412	0.43	0.0173	-	-	-	-
GO:00300(	Cellular mc	8	106	0.69	0.018	-	-	-	-
GO:00107	Positive reg	16	376	0.44	0.0182	-	-	-	-
GO:00425	Homeostat	40	1451	0.25	0.0182	-	-	-	-
GO:00455	Positive reg	29	928	0.31	0.0182	-	-	-	-
GO:00902(	Positive reg	4	19	1.13	0.0182	-	-	-	-
GO:00343	Cell junctio	21	578	0.37	0.0184	-	-	-	-
GO:00486	Neuron dev	29	932	0.3	0.019	-	-	-	-
GO:00704	Response t	15	341	0.45	0.0194	-	-	-	-
GO:00197	Polyol meta	8	108	0.68	0.0195	-	-	-	-

GO:00420€	Gliogenesis	13	269	0.5	0.0199	-	-	-	-
GO:19035:	Negative re	10	168	0.59	0.0199	-	-	-	-
GO:000673	#NAME?	5	37	0.94	0.0201	-	-	-	-
GO:005101	Actin filame	6	58	0.83	0.0201	5	58	1.04	0.0116
GO:00067ᵹ	Phosphate-	49	1919	0.22	0.0209	35	1919	0.37	5.00E-04
GO:005082	Protein stal	13	271	0.49	0.0209	-	-	-	-
GO:00320ᵹ	Positive reg	8	110	0.67	0.0212	-	-	-	-
GO:190547	Positive reg	8	110	0.67	0.0212	-	-	-	-
GO:00619ᵹ	Establishm	6	59	0.82	0.0213	-	-	-	-
GO:001081	Regulation	12	237	0.52	0.0214	-	-	-	-
GO:00508(	Modulation	20	546	0.37	0.0215	-	-	-	-
GO:000007	Mitotic sist	9	140	0.62	0.0218	-	-	-	-
GO:005507	Transition r	9	140	0.62	0.0218	-	-	-	-
GO:19018ᵹ	Negative re	7	84	0.73	0.0218	-	-	-	-
GO:19035:	Regulation	23	676	0.34	0.022	-	-	-	-
GO:00108ᵹ	Regulation	6	60	0.81	0.0225	-	-	-	-
GO:004691	Cellular tra	8	112	0.66	0.0225	-	-	-	-
GO:007124	Cellular res	11	205	0.54	0.0225	-	-	-	-
GO:190307	Positive reg	6	60	0.81	0.0225	-	-	-	-
GO:00516(	Proteolysis	22	635	0.35	0.0226	-	-	-	-
GO:00098ᵹ	Positive reg	86	3939	0.15	0.0227	60	3939	0.29	4.32E-05
GO:00300(	Cellular cat	17	428	0.41	0.0228	-	-	-	-
GO:004327	Apoptotic c	5	39	0.92	0.023	-	-	-	-
GO:001064	Regulation	75	3331	0.16	0.0238	-	-	-	-
GO:00083€	Regulation	12	242	0.51	0.0241	-	-	-	-
GO:007124	Cellular res	12	243	0.5	0.0248	-	-	-	-
GO:000687	Cellular me	15	355	0.44	0.0251	-	-	-	-
GO:00070:	Vacuole org	10	176	0.57	0.0251	-	-	-	-

GO:000704	Lysosome c	7	87	0.72	0.0251	-	-	-	-
GO:000861	Lipid biosyr	19	515	0.38	0.0251	13	515	0.51	0.0185
GO:00301E	Regulation	25	775	0.32	0.0251	-	-	-	-
GO:003111	Positive reg	5	40	0.91	0.0251	-	-	-	-
GO:00442E	Small mole	15	354	0.44	0.0251	10	354	0.56	0.0335
GO:00510S	Regulation	16	394	0.42	0.0251	11	394	0.55	0.0225
GO:00714E	Cellular res	9	145	0.6	0.0251	-	-	-	-
GO:19013E	Organic cyc	29	957	0.29	0.0251	28	957	0.57	5.91E-06
GO:19033C	Negative re	4	22	1.07	0.0251	-	-	-	-
GO:000701	Actin filame	13	281	0.48	0.0254	-	-	-	-
GO:000821	Cell death	28	914	0.3	0.0256	-	-	-	-
GO:00230E	Regulation	75	3347	0.16	0.0257	-	-	-	-
GO:00060E	Cellular ald	6	63	0.79	0.026	-	-	-	-
GO:190121	Regulation	16	397	0.42	0.0264	-	-	-	-
GO:00420E	Wound hea	13	283	0.47	0.0267	-	-	-	-
GO:00125C	Programme	27	872	0.3	0.0269	17	872	0.4	0.0335
GO:00904C	Organopho	18	479	0.39	0.0271	21	479	0.75	1.14E-06
GO:004352	Regulation	13	284	0.47	0.0273	-	-	-	-
GO:009917	Regulation	8	118	0.64	0.0281	-	-	-	-
GO:00550E	Cellular ch	20	566	0.36	0.0287	-	-	-	-
GO:004317	Macromole	126	6322	0.11	0.0297	-	-	-	-
GO:19029C	Negative re	10	182	0.55	0.0298	-	-	-	-
GO:00016E	Ameboidal-	11	216	0.52	0.0299	-	-	-	-
GO:003112	Cytoplasmi	6	66	0.77	0.0314	-	-	-	-
GO:00517C	Biological p	7	92	0.69	0.0314	-	-	-	-
GO:00106E	Negative re	15	367	0.42	0.0322	12	367	0.62	0.0049
GO:00515S	Response t	9	152	0.58	0.0322	-	-	-	-
GO:00519E	Positive reg	15	367	0.42	0.0322	-	-	-	-

GO:01100E	Regulation	13	291	0.46	0.0323	-	-	-	-
GO:004364	Dicarboxyli	7	93	0.69	0.0325	-	-	-	-
GO:00329E	Cellular co	22	661	0.33	0.0326	-	-	-	-
GO:003432	Cell junctio	13	292	0.46	0.0329	-	-	-	-
GO:19028E	Microtubul	8	122	0.63	0.0329	8	122	0.93	0.0014
GO:006054	Negative re	32	1125	0.26	0.033	-	-	-	-
GO:015011	Cell-substr	5	44	0.87	0.033	-	-	-	-
GO:00301E	Extracellula	12	256	0.48	0.0332	9	256	0.65	0.0178
GO:00457E	Positive reg	10	186	0.54	0.0332	-	-	-	-
GO:19029C	Positive reg	10	187	0.54	0.0342	-	-	-	-
GO:00108E	Regulation	4	25	1.02	0.0343	-	-	-	-
GO:003431	Diol biosyn	4	25	1.02	0.0343	-	-	-	-
GO:00307C	Cytoskelet	10	188	0.54	0.0351	-	-	-	-
GO:00512E	Regulation	65	2847	0.17	0.0357	-	-	-	-
GO:01200E	Plasma me	19	538	0.36	0.0358	-	-	-	-
GO:00442E	Cellular lipi	28	944	0.28	0.0365	21	944	0.46	0.0027
GO:005077	Regulation	8	125	0.62	0.0365	-	-	-	-
GO:00550E	Nucleobas	20	582	0.35	0.0365	21	582	0.67	8.76E-06
GO:00714C	Cellular res	19	541	0.36	0.0376	-	-	-	-
GO:003227	Positive reg	7	97	0.67	0.0384	-	-	-	-
GO:00433E	Regulation	11	226	0.5	0.0386	-	-	-	-
GO:190304	Mitotic cell	19	544	0.35	0.0396	14	544	0.52	0.0108
GO:001611	Terpenoid b	3	11	1.25	0.0397	-	-	-	-
GO:00457E	Positive reg	17	460	0.38	0.0397	-	-	-	-
GO:19016E	Cellular res	22	676	0.32	0.0399	-	-	-	-
GO:00313E	Positive reg	10	193	0.53	0.0406	8	193	0.73	0.0144
GO:00091E	Nucleotide	11	229	0.49	0.0419	13	229	0.86	2.62E-05
GO:001812	Protein hyd	4	27	0.98	0.0419	-	-	-	-

GO:005507	Iron ion hor	7	99	0.66	0.0419	-	-	-	-
GO:005165	Spindle loc	6	72	0.73	0.0424	-	-	-	-
GO:007030	Cellular res	6	72	0.73	0.0424	-	-	-	-
GO:009951	Vesicle cyt	6	72	0.73	0.0424	-	-	-	-
GO:004689	Regulation	10	195	0.52	0.0429	-	-	-	-
GO:014001	Mitotic nuc	10	195	0.52	0.0429	-	-	-	-
GO:000752	Neuromusc	5	48	0.83	0.043	-	-	-	-
GO:009030	Mitotic spir	5	48	0.83	0.043	-	-	-	-
GO:004851	Animal orga	74	3378	0.15	0.0435	-	-	-	-
GO:000651	Ubiquitin-d	19	552	0.35	0.0442	-	-	-	-
GO:200014	Positive reg	20	597	0.34	0.0454	-	-	-	-
GO:000699	Nuclear env	5	49	0.82	0.0455	-	-	-	-
GO:000717	Epidermal g	2	2	1.81	0.0455	-	-	-	-
GO:003612	Cellular res	4	28	0.97	0.0455	-	-	-	-
GO:014035	Export from	16	427	0.38	0.0455	-	-	-	-
GO:190423	Positive reg	2	2	1.81	0.0455	-	-	-	-
GO:200110	Regulation	2	2	1.81	0.0455	-	-	-	-
GO:000601	Mannose m	3	12	1.21	0.0458	-	-	-	-
GO:000687	Cellular iro	6	74	0.72	0.0458	-	-	-	-
GO:003637	Sodium ion	3	12	1.21	0.0458	-	-	-	-
GO:004645	Short-chair	3	12	1.21	0.0458	-	-	-	-
GO:000660	Protein targ	11	234	0.48	0.046	-	-	-	-
GO:000905	Macromole	28	967	0.27	0.0462	-	-	-	-
GO:000689	post-Golgi v	7	103	0.64	0.0481	-	-	-	-
GO:005081	Regulation	6	75	0.71	0.0481	-	-	-	-
GO:000027	Mitotic cell	21	648	0.32	0.0492	16	648	0.5	0.0066
GO:004316	Ubiquitin-d	4	29	0.95	0.0492	-	-	-	-
GO:000030	Response t	9	167	0.54	0.0499	-	-	-	-

GO:000672	Cellular arc	-	-	-	-	45	2992	0.29	0.0017
GO:004648	Heterocycl	-	-	-	-	44	2937	0.28	0.0022
GO:000613	Nucleobas	-	-	-	-	43	2791	0.3	0.0016
GO:001607	mR- metab	-	-	-	-	14	625	0.46	0.0296
GO:004424	Cellular bio	-	-	-	-	40	2480	0.32	0.0014
GO:000911	Nucleotide	-	-	-	-	20	516	0.7	8.76E-06
GO:190113	Carbohydra	-	-	-	-	20	1002	0.41	0.0117
GO:004424	Cellular lipi	-	-	-	-	7	182	0.69	0.0387
GO:001060	Positive reg	-	-	-	-	51	3592	0.26	0.0017
GO:003132	Regulation	-	-	-	-	79	5592	0.26	8.76E-06
GO:005065	R- transpor	-	-	-	-	-	-	-	-
GO:190113	Carbohydra	-	-	-	-	-	-	-	-
GO:000704	Cell cycle	-	-	-	-	21	1118	0.38	0.0163
GO:007182	Ribonucleo	-	-	-	-	-	-	-	-
GO:000926	Ribonucleo	-	-	-	-	8	175	0.77	0.009
GO:001813	Heterocycl	-	-	-	-	20	836	0.49	0.0017
GO:000915	Purine ribo	-	-	-	-	13	421	0.6	0.0042
GO:001943	Aromatic c	-	-	-	-	20	838	0.49	0.0017
GO:000608	acetyl-CoA	-	-	-	-	5	37	1.24	0.0024
GO:000915	Purine ribo	-	-	-	-	-	-	-	-
GO:000989	Positive reg	-	-	-	-	12	502	0.49	0.0387
GO:004593	Positive reg	-	-	-	-	32	2047	0.3	0.0116
GO:190485	Positive reg	-	-	-	-	-	-	-	-
GO:000705	Mitotic spir	-	-	-	-	7	86	1.02	0.0014
GO:001943	Aromatic c	-	-	-	-	-	-	-	-
GO:003132	Positive reg	-	-	-	-	55	3172	0.35	8.76E-06
GO:190331	Regulation	-	-	-	-	13	313	0.73	0.00041
GO:003387	Ribonucleo	-	-	-	-	6	114	0.83	0.0233

GO:00340	Purine nucl	-	-	-	-	6	114	0.83	0.0233
GO:00463	Carboxylic	-	-	-	-	8	247	0.62	0.0464
GO:00506	Regulation	-	-	-	-	9	156	0.87	0.0011
GO:20006	Regulation	-	-	-	-	-	-	-	-
GO:00346	Nucleobas	-	-	-	-	19	765	0.5	0.0017
GO:00171	Negative re	-	-	-	-	8	160	0.81	0.0056
GO:00517	Regulation	-	-	-	-	20	1071	0.38	0.022
GO:00105	Regulation	-	-	-	-	15	706	0.44	0.0309
GO:00313	Regulation	-	-	-	-	16	745	0.44	0.0206
GO:00070	Microtubul	-	-	-	-	17	902	0.38	0.0444
GO:00098	Negative re	-	-	-	-	47	2911	0.32	0.00025
GO:00091	Nucleoside	-	-	-	-	9	256	0.65	0.0178
GO:00104	Regulation	-	-	-	-	62	4725	0.23	0.0017
GO:00480	Regulation	-	-	-	-	7	116	0.89	0.0056
GO:00224	Cell cycle p	-	-	-	-	18	831	0.44	0.0103
GO:00062	Pyrimidine	-	-	-	-	4	28	1.26	0.01
GO:00091	Nucleobas	-	-	-	-	4	44	1.07	0.0312
GO:00106	Negative re	-	-	-	-	45	2682	0.33	0.00018
GO:00511	Negative re	-	-	-	-	41	2342	0.35	0.00021
GO:00098	Regulation	-	-	-	-	58	4090	0.26	5.00E-04
GO:00313	Regulation	-	-	-	-	57	4002	0.26	5.00E-04
GO:00106	Negative re	-	-	-	-	21	890	0.48	0.0014
GO:00192	Regulation	-	-	-	-	28	1434	0.4	0.0014
GO:00302	Chromosor	-	-	-	-	5	39	1.22	0.003
GO:00313	Negative re	-	-	-	-	36	2234	0.32	0.0032
GO:00091	Pyrimidine	-	-	-	-	4	19	1.43	0.0035
GO:00105	Regulation	-	-	-	-	52	3816	0.24	0.0035
GO:00313	Regulation	-	-	-	-	28	1588	0.35	0.0056

GO:001921	Regulation	-	-	-	-	51	3835	0.23	0.0069
GO:00082	Isoprenoid	-	-	-	-	4	25	1.31	0.0073
GO:00900	Positive reg	-	-	-	-	10	273	0.67	0.0077
GO:000914	Nucleoside	-	-	-	-	6	86	0.95	0.0082
GO:00340	Stress gran	-	-	-	-	4	26	1.3	0.0082
GO:00098	Positive reg	-	-	-	-	33	2100	0.3	0.009
GO:00031	Endotheliu	-	-	-	-	6	91	0.93	0.0103
GO:00713	Cellular res	-	-	-	-	13	472	0.55	0.0103
GO:003132	Negative re	-	-	-	-	26	1505	0.35	0.0116
GO:003132	Positive reg	-	-	-	-	32	2046	0.3	0.0116
GO:00308	Epithelial c	-	-	-	-	15	626	0.49	0.0126
GO:00457	Positive reg	-	-	-	-	11	359	0.59	0.0129
GO:00020	Colum-r/cu	-	-	-	-	6	100	0.89	0.0144
GO:006102	Establishm	-	-	-	-	4	34	1.18	0.0163
GO:00512	Regulation	-	-	-	-	46	3508	0.23	0.0178
GO:00905	Establishm	-	-	-	-	3	13	1.47	0.0178
GO:00071	Establishm	-	-	-	-	9	259	0.65	0.0185
GO:00092	Ribonucleo	-	-	-	-	5	69	0.97	0.0198
GO:000624	CTP biosyn	-	-	-	-	3	14	1.44	0.0203
GO:00300	Hemopoies	-	-	-	-	15	667	0.46	0.0203
GO:003252	Microvillus	-	-	-	-	3	14	1.44	0.0203
GO:00020	Epithelial c	-	-	-	-	8	211	0.69	0.022
GO:00310	Actomyosir	-	-	-	-	6	112	0.84	0.022
GO:00440	Negative re	-	-	-	-	20	1072	0.38	0.022
GO:19001	Regulation	-	-	-	-	7	161	0.75	0.0231
GO:00105	Negative re	-	-	-	-	24	1438	0.33	0.0262
GO:004544	Endothelial	-	-	-	-	5	77	0.92	0.0283
GO:000022	Microtubul	-	-	-	-	14	624	0.46	0.0294

GO:012017	Steroid hor	-	-	-	-	3	17	1.36	0.0296
GO:000193	Regulation	-	-	-	-	20	1109	0.36	0.0302
GO:004421	De novo CT	-	-	-	-	2	3	1.93	0.0344
GO:00105	Positive reg	-	-	-	-	29	1945	0.28	0.0351
GO:00346(	Cellular res	-	-	-	-	5	83	0.89	0.0354
GO:19019	Positive reg	-	-	-	-	6	128	0.78	0.036
GO:190331	Positive reg	-	-	-	-	6	128	0.78	0.036
GO:00020	Colum-r/cu	-	-	-	-	4	47	1.04	0.0367
GO:00512	Chromosor	-	-	-	-	18	966	0.38	0.0367
GO:00091	Ribonucleo	-	-	-	-	8	240	0.63	0.0397
GO:00065	Glutamine	-	-	-	-	3	21	1.26	0.0444
GO:00065	L-serine bic	-	-	-	-	2	4	1.81	0.0464
GO:00329	Inositol tris	-	-	-	-	2	4	1.81	0.0464
GO:00423	Regulation	-	-	-	-	21	1251	0.33	0.0464
GO:19035	Positive reg	-	-	-	-	2	4	1.81	0.0464
GO:00062(	Pyrimidine	-	-	-	-	3	22	1.24	0.0474
GO:00459	Positive reg	-	-	-	-	6	138	0.75	0.0474
GO:00094(	Response t	-	-	-	-	6	139	0.74	0.0481

KEGG_D7_10mM_DOWN

#term ID	term descri	observed g	backgrounc	strength.K1	false disco	observed g	backgrounc	strength.DF	false discovery rate.DP12
cge01100	Metabolic p	59	1132	0.52	7.83E-13	53	1132	0.69	5.77E-19
cge04142	Lysosome	18	101	1.05	6.60E-11	13	101	1.13	5.95E-09
cge00511	Other glyca	6	16	1.38	8.94E-05	5	16	1.51	3.47E-05
cge01200	Carbon me	11	104	0.83	0.00015	19	104	1.28	1.30E-15
cge03040	Spliceosom	11	114	0.79	0.00024	5	114	0.66	0.0443
cge04510	Focal adhe	12	136	0.75	0.00024	-	-	-	-
cge00531	Glycosamir	5	13	1.39	3.00E-04	4	13	1.5	0.00039
cge05100	Bacterial in	8	61	0.92	0.00047	-	-	-	-
cge03320	PPAR sig-lir	8	63	0.91	0.00052	4	63	0.82	0.0329
cge00280	Valine, leuc	6	42	0.96	0.0031	8	42	1.3	8.53E-07
cge04611	Platelet act	8	84	0.78	0.0031	-	-	-	-
cge00480	Glutathione	6	52	0.86	0.0076	-	-	-	-
cge00982	Drug metab	5	37	0.93	0.011	3	37	0.93	0.0471
cge00983	Drug metab	6	58	0.82	0.011	4	58	0.85	0.0262
cge04512	ECM-recep	6	57	0.83	0.011	-	-	-	-
cge05020	Prion disea	11	198	0.55	0.011	15	198	0.9	1.27E-07
cge00270	Cysteine ar	5	40	0.9	0.0125	-	-	-	-
cge00860	Porphyrin a	4	23	1.04	0.0139	-	-	-	-
cge01230	Biosynthes	6	67	0.75	0.0158	8	67	1.09	1.79E-05
cge05012	Parkinson d	10	183	0.54	0.0158	16	183	0.96	6.18E-09
cge00980	Metabolism	5	45	0.85	0.0165	-	-	-	-
cge00052	Galactose r	4	26	0.99	0.0171	3	26	1.08	0.0247
cge04915	Estrogen sig	7	97	0.66	0.0172	-	-	-	-
cge00630	Glyoxylate a	4	27	0.97	0.0178	4	27	1.19	0.0036
cge04141	Protein pro	8	128	0.6	0.0178	6	128	0.69	0.0197
cge00640	Propanoate	4	28	0.96	0.018	6	28	1.35	2.10E-05

cge05418	Fluid shear	7	100	0.65	0.018	6	100	0.79	0.0082
cge05200	Pathways ir	15	391	0.39	0.0216	10	391	0.42	0.0425
cge00604	Glycosphin	3	14	1.13	0.0233	-	-	-	-
cge01524	Platinum dı	5	53	0.78	0.0233	-	-	-	-
cge05204	Chemical c	5	53	0.78	0.0233	-	-	-	-
cge05205	Proteoglyca	8	140	0.56	0.0233	6	140	0.65	0.0261
cge00603	Glycosphin	3	15	1.1	0.0255	-	-	-	-
cge00513	Various typ	4	36	0.85	0.0327	3	36	0.94	0.0449
cge04614	Renin-angi(	3	17	1.05	0.0329	-	-	-	-
cge04810	Regulation	8	153	0.52	0.0344	6	153	0.61	0.0357
cge05016	Huntington	10	230	0.44	0.0399	15	230	0.83	6.36E-07
cge00040	Pentose an	3	19	1	0.04	-	-	-	-
cge00650	Butanoate ı	3	19	1	0.04	3	19	1.21	0.0132
cge05010	Alzheimer c	11	273	0.41	0.0418	17	273	0.81	1.50E-07
cge04270	Vascular sr	6	97	0.59	0.0438	-	-	-	-
cge00020	Citrate cycl	-	-	-		11	27	1.63	4.99E-12
cge05014	Amyotrophi	-	-	-		16	278	0.78	8.78E-07
cge04714	Thermogen	-	-	-		10	179	0.76	0.00035
cge00190	Oxidative p	-	-	-		8	112	0.87	0.00042
cge00062	Fatty acid e	-	-	-		4	21	1.3	0.0017
cge05017	Spinocereb	-	-	-		7	105	0.84	0.0019
cge00620	Pyruvate m	-	-	-		4	27	1.19	0.0036
cge03030	D- replicati	-	-	-		4	27	1.19	0.0036
cge00071	Fatty acid d	-	-	-		4	36	1.06	0.0082
cge00330	Arginine an	-	-	-		4	36	1.06	0.0082
cge00970	Aminoacyl-	-	-	-		4	36	1.06	0.0082
cge03050	Proteasom	-	-	-		4	37	1.05	0.0082
cge01210	2-Oxocarbo	-	-	-		3	16	1.29	0.0091

cge03015	mR- surveil	-	-	-	-	5	73	0.85	0.0108
cge01212	Fatty acid n	-	-	-	-	4	46	0.96	0.0146
cge00410	beta-Alanin	-	-	-	-	3	24	1.11	0.022
cge00010	Glycolysis /	-	-	-	-	4	55	0.88	0.0241
cge04210	Apoptosis	-	-	-	-	5	92	0.75	0.0241
cge04110	Cell cycle	-	-	-	-	5	99	0.72	0.0283
cge00072	Synthesis a	-	-	-	-	2	9	1.36	0.0381
cge05169	Epstein-Ba	-	-	-	-	6	163	0.58	0.0443
cge04932	Non-alcoho	-	-	-	-	5	118	0.64	0.0471

FUNCTION_D7_10mM_UP

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
GO:00054	Binding	320	13754	0.18	4.92E-30	172	13754	0.21	8.47E-23
GO:00055	Protein bin	224	7697	0.27	1.62E-25	126	7697	0.32	1.03E-19
GO:00038	Catalytic ac	159	6043	0.23	1.51E-10	-	-	-	-
GO:00360	Small mole	94	2793	0.34	2.94E-10	47	2793	0.33	8.36E-05
GO:00431	Ion binding	151	5669	0.24	2.94E-10	76	5669	0.24	6.64E-05
GO:00198	Enzyme bin	85	2431	0.35	5.91E-10	44	2431	0.37	4.78E-05
GO:00448	Protein-cor	66	1625	0.42	6.08E-10	38	1625	0.48	1.07E-06
GO:00428	Identical pr	78	2174	0.37	1.43E-09	50	2174	0.47	2.90E-09
GO:00001	Nucleotide	83	2478	0.34	6.80E-09	39	2478	0.31	0.0036
GO:00431	Anion bindi	87	2671	0.32	6.80E-09	38	2671	0.26	0.0228
GO:00973	Carbohydra	78	2440	0.32	2.05E-07	38	2440	0.3	0.0053
GO:00080	Cytoskeleta	48	1184	0.42	6.05E-07	31	1184	0.53	2.90E-06
GO:00325	Ribonucleo	69	2149	0.32	1.79E-06	-	-	-	-
GO:00170	Purine nucl	68	2148	0.31	3.69E-06	-	-	-	-
GO:00356	Purine ribo	66	2054	0.32	3.69E-06	-	-	-	-
GO:00325	Purine ribo	67	2130	0.31	5.53E-06	-	-	-	-
GO:00164	Oxidoreduc	36	858	0.43	2.30E-05	-	-	-	-
GO:00167	Hydrolase a	72	2470	0.28	2.57E-05	-	-	-	-
GO:00468	Metal ion bi	94	3580	0.23	2.57E-05	49	3580	0.24	0.0081
GO:00431	Cation binc	95	3679	0.22	4.18E-05	-	-	-	-
GO:00037	Actin bindir	25	481	0.53	4.45E-05	-	-	-	-
GO:00171	Nucleoside	30	670	0.46	5.85E-05	-	-	-	-
GO:00198	ATPase-cou	9	54	1.03	6.27E-05	-	-	-	-
GO:01406	ATP-depen	28	652	0.44	0.00028	-	-	-	-
GO:00510	Actin filame	16	245	0.63	0.00032	-	-	-	-
GO:00055	ATP binding	51	1663	0.3	0.00037	-	-	-	-

GO:00325E	Adenyl ribo	52	1731	0.29	5.00E-04	28	1731	0.32	0.0228
GO:19013E	Heterocycli	131	6088	0.14	0.0015	81	6088	0.23	4.31E-05
GO:00469E	Protein dim	35	1036	0.34	0.0019	-	-	-	-
GO:00051C	Sig-ling rec	44	1451	0.29	0.0021	29	1451	0.41	0.00084
GO:00168E	Isomerase	13	198	0.63	0.0021	-	-	-	-
GO:00428C	Protein hon	27	712	0.39	0.0024	16	712	0.46	0.0219
GO:00971E	Organic cyc	131	6155	0.14	0.0024	81	6155	0.23	5.32E-05
GO:000417	Aminopepti	6	39	1	0.005	-	-	-	-
GO:004802	Monosacch	8	83	0.79	0.0062	-	-	-	-
GO:00433E	Proteoglyca	6	43	0.96	0.0065	4	43	1.08	0.0456
GO:004691	Transition r	34	1072	0.31	0.0065	-	-	-	-
GO:00469E	Proton-tran	5	25	1.11	0.0065	-	-	-	-
GO:00507E	Low-densit	5	25	1.11	0.0065	-	-	-	-
GO:005102	GTPase bin	17	364	0.48	0.0065	-	-	-	-
GO:00611E	Endopeptid	11	165	0.63	0.0065	-	-	-	-
GO:00055C	Calcium ior	25	686	0.37	0.0067	-	-	-	-
GO:00611E	Peptidase r	12	199	0.59	0.0067	-	-	-	-
GO:00700C	Metalloami	5	27	1.08	0.0072	-	-	-	-
GO:000517	Integrin bin	10	145	0.65	0.0082	-	-	-	-
GO:00168E	ATP hydroly	16	343	0.48	0.0082	-	-	-	-
GO:005084	Extracellula	7	68	0.82	0.0084	-	-	-	-
GO:00199C	Protein dor	29	883	0.33	0.0094	24	883	0.54	5.61E-05
GO:00043E	Glutathione	5	30	1.03	0.0099	-	-	-	-
GO:001661	Oxidoreduc	10	152	0.63	0.0108	-	-	-	-
GO:000551	Collagen bi	7	72	0.8	0.0109	-	-	-	-
GO:00312E	Small GTPa	15	330	0.47	0.0154	-	-	-	-
GO:00082E	Lipid bindir	26	794	0.33	0.0197	17	794	0.44	0.0228
GO:00053E	P-type sodi	3	7	1.44	0.02	-	-	-	-

GO:00190C	GDP bindin	7	81	0.75	0.02	-	-	-	-
GO:007234	Modified ar	7	84	0.73	0.0234	-	-	-	-
GO:00043C	Epoxide hyc	3	8	1.38	0.0252	-	-	-	-
GO:000823	Metalloexo	6	61	0.8	0.0253	-	-	-	-
GO:003024	Carbohydra	12	241	0.51	0.0253	-	-	-	-
GO:000554	Phospholip	19	512	0.38	0.0255	-	-	-	-
GO:00048E	Endopeptid	9	144	0.61	0.0262	-	-	-	-
GO:00156E	P-type ion t	4	22	1.07	0.027	-	-	-	-
GO:000552	GTP binding	17	437	0.4	0.0287	-	-	-	-
GO:001687	Ligase activ	10	179	0.56	0.0287	-	-	-	-
GO:004323	Laminin bir	5	41	0.9	0.0287	-	-	-	-
GO:004323	laminin-1 b	3	9	1.33	0.0294	-	-	-	-
GO:000392	GTPase act	14	325	0.45	0.0316	-	-	-	-
GO:00199C	Ki-se bindir	28	929	0.29	0.0328	-	-	-	-
GO:00167E	Transferase	6	67	0.76	0.0351	-	-	-	-
GO:00199C	Protein ki-s	26	845	0.3	0.0363	-	-	-	-
GO:000823	Exopeptida	7	95	0.68	0.0376	-	-	-	-
GO:005083	Cell adhesi	14	335	0.43	0.0389	11	335	0.62	0.0133
GO:000372	R- binding	-	-	-	-	30	1541	0.4	0.00087
GO:003055	Adenyl nucl	-	-	-	-	29	1743	0.33	0.0142
GO:000367	Nucleic aci	-	-	-	-	47	3725	0.21	0.0456
GO:000372	mR- binding	-	-	-	-	14	385	0.67	0.00075
GO:001563	Tubulin bin	-	-	-	-	12	459	0.53	0.0327
GO:000398	acetyl-CoA	-	-	-	-	3	8	1.68	0.0118
GO:001984	Vitamin bin	-	-	-	-	9	136	0.93	0.00055
GO:00314C	Carboxylic	-	-	-	-	7	159	0.75	0.0327
GO:004317	Organic aci	-	-	-	-	7	143	0.8	0.0217
GO:000372	Double-stra	-	-	-	-	6	95	0.91	0.0186

GO:00335	R- strand a	-	-	-	-	3	11	1.54	0.0205
GO:00080	Protein C-t	-	-	-	-	9	252	0.66	0.0228

FUNCTION_D7_10mM_DOWN

#term ID	term descri	observed g	backgrounc	strength.K1	false disco	observed g	backgrounc	strength.DF	false discovery rate.DP12
GO:000382	Catalytic ac	195	6043	0.31	3.56E-24	136	6043	0.37	1.42E-23
GO:000548	Binding	315	13754	0.16	4.69E-24	194	13754	0.17	6.26E-15
GO:000551	Protein bin	201	7697	0.22	3.58E-14	110	7697	0.17	7.55E-05
GO:001678	Hydrolase a	96	2470	0.39	9.77E-14	72	2470	0.48	6.30E-15
GO:003609	Small mole	94	2793	0.33	8.45E-10	77	2793	0.46	6.30E-15
GO:000016	Nucleotide	85	2478	0.34	4.53E-09	71	2478	0.47	1.44E-14
GO:004487	Protein-cor	65	1625	0.4	4.53E-09	45	1625	0.46	2.93E-08
GO:009736	Carbohydra	80	2440	0.32	1.22E-07	68	2440	0.46	2.29E-13
GO:009715	Organic cyc	152	6155	0.2	1.90E-07	105	6155	0.25	1.34E-08
GO:001989	Enzyme bin	79	2431	0.31	1.99E-07	52	2431	0.35	4.21E-06
GO:001707	Purine nucl	72	2148	0.33	3.52E-07	62	2148	0.48	1.28E-12
GO:190136	Heterocycli	148	6088	0.19	9.12E-07	105	6088	0.25	7.13E-09
GO:004316	Anion bindi	82	2671	0.29	9.17E-07	75	2671	0.46	6.30E-15
GO:003255	Purine ribo	70	2130	0.32	1.11E-06	61	2130	0.47	2.95E-12
GO:004316	Ion binding	138	5669	0.19	3.28E-06	112	5669	0.31	1.11E-13
GO:004280	Identical pr	68	2174	0.3	1.05E-05	50	2174	0.38	9.82E-07
GO:003563	Purine ribo	65	2054	0.3	1.37E-05	59	2054	0.47	6.89E-12
GO:000372	R- binding	53	1541	0.34	2.08E-05	44	1541	0.47	1.98E-08
GO:001711	Nucleoside	31	670	0.47	3.10E-05	26	670	0.61	4.65E-07
GO:003055	Adenyl nucl	57	1743	0.32	3.10E-05	52	1743	0.49	7.36E-11
GO:001646	Pyrophosph	32	721	0.45	4.34E-05	-	-	-	-
GO:014064	Catalytic ac	29	618	0.47	5.17E-05	22	618	0.57	2.62E-05
GO:003321	Amide bind	23	417	0.54	5.68E-05	-	-	-	-
GO:000455	Hydrolase a	11	94	0.87	8.58E-05	7	94	0.89	0.0039
GO:003255	Adenyl ribo	55	1731	0.3	9.35E-05	51	1731	0.49	1.95E-10
GO:014009	Catalytic ac	21	377	0.55	0.00014	12	377	0.52	0.0219

GO:00167	Hydrolase a	12	128	0.77	0.00021	8	128	0.81	0.0038
GO:00469	Protein dim	38	1036	0.37	0.00022	-	-	-	-
GO:00164	Oxidoreduc	33	858	0.39	4.00E-04	20	858	0.38	0.0178
GO:00043	Helicase ac	13	174	0.68	0.00075	14	174	0.92	5.11E-07
GO:01406	ATP-depen	27	652	0.42	0.00083	32	652	0.71	2.73E-11
GO:00055	ATP binding	50	1663	0.28	0.0011	49	1663	0.49	5.68E-10
GO:00167	Transferase	8	67	0.88	0.0019	5	67	0.89	0.0301
GO:00428	Protein hon	27	712	0.38	0.0034	18	712	0.42	0.015
GO:00199	Protein don	31	883	0.35	0.0036	-	-	-	-
GO:00037	R- helicase	8	79	0.81	0.0051	7	79	0.96	0.0015
GO:00168	ATP hydroly	16	343	0.47	0.0134	20	343	0.78	5.22E-08
GO:00080	Cytoskeleta	36	1184	0.29	0.0135	24	1184	0.32	0.0281
GO:00043	Glutathione	5	30	1.02	0.0145	4	30	1.14	0.0177
GO:00055	FK506 bind	3	5	1.58	0.0145	-	-	-	-
GO:00167	Transferase	61	2430	0.2	0.0157	-	-	-	-
GO:00039	GTPase act	15	325	0.47	0.0212	-	-	-	-
GO:00431	Cation binc	83	3679	0.16	0.0307	63	3679	0.25	0.00027
GO:00166	Oxidoreduc	7	83	0.73	0.034	-	-	-	-
GO:00037	mR- binding	16	385	0.42	0.0356	-	-	-	-
GO:00037	mR- 3-UTR	8	111	0.66	0.0356	-	-	-	-
GO:00199	Protein ki-s	27	845	0.31	0.0356	-	-	-	-
GO:00483	Calcium-de	7	84	0.72	0.0356	-	-	-	-
GO:00045	beta-N-ace	3	9	1.33	0.0439	-	-	-	-
GO:00038	D--directed	4	23	1.04	0.0443	-	-	-	-
GO:00055	Calcium ion	23	686	0.33	0.0444	17	686	0.41	0.0238
GO:00468	Metal ion bi	80	3580	0.15	0.0444	61	3580	0.25	0.00046
GO:00055	GTP binding	17	437	0.39	0.0448	-	-	-	-
GO:00168	Ligase activ	-	-	-	-	17	179	0.99	1.29E-09

GO:000367	D- helicase	-	-	-	-	8	80	1.02	2.00E-04
GO:005101	Actin filam	-	-	-	-	12	245	0.71	0.00067
GO:00080	ATP-depen	-	-	-	-	9	132	0.85	0.00078
GO:00435	ADP bindin	-	-	-	-	6	47	1.12	0.00097
GO:01400	Catalytic a	-	-	-	-	12	259	0.68	0.0011
GO:00001	Succi-te de	-	-	-	-	3	3	2.02	0.0014
GO:00082	Peptidase a	-	-	-	-	18	613	0.48	0.003
GO:00036	Single-stra	-	-	-	-	8	133	0.8	0.0046
GO:00526	Carboxylic	-	-	-	-	9	180	0.72	0.0062
GO:00168	Ligase acti	-	-	-	-	3	8	1.59	0.0092
GO:000004	tR- binding	-	-	-	-	6	77	0.91	0.0097
GO:000481	aminoacyl-	-	-	-	-	5	51	1.01	0.0128
GO:001662	Oxidoreduc	-	-	-	-	5	53	0.99	0.0146
GO:00510	Chaperone	-	-	-	-	7	124	0.77	0.0164
GO:00510	Unfolded p	-	-	-	-	7	126	0.76	0.0177
GO:000367	Nucleic aci	-	-	-	-	56	3725	0.19	0.0226
GO:001681	Hydrolase a	-	-	-	-	5	61	0.93	0.0232
GO:00469	Proton-tran	-	-	-	-	3	13	1.38	0.0237
GO:0000513	3-sulfino-L-	-	-	-	-	2	2	2.02	0.0281
GO:000051	Aspartate:g	-	-	-	-	2	2	2.02	0.0281
GO:00046	propionyl-C	-	-	-	-	2	2	2.02	0.0281
GO:000817	Succi-te de	-	-	-	-	2	2	2.02	0.0281
GO:003024	Carbohydra	-	-	-	-	9	241	0.59	0.033
GO:00021	aminoacyl-	-	-	-	-	3	16	1.29	0.0344
GO:00082	Metallopep	-	-	-	-	8	196	0.63	0.0359
GO:001687	Ligase acti	-	-	-	-	4	40	1.02	0.0362
GO:00041	Carboxype	-	-	-	-	4	41	1.01	0.0389
GO:00041	Serine-type	-	-	-	-	2	3	1.84	0.0389

GO:000482	isoleucine-	-	-	-	-	2	3	1.84	0.0389
GO:003612	Double-stra	-	-	-	-	2	3	1.84	0.0389
GO:000377	Actin bindir	-	-	-	-	13	481	0.45	0.0395
GO:000417	Endopeptid	-	-	-	-	12	420	0.47	0.0395
GO:001690	Oxidoreduc	-	-	-	-	6	112	0.75	0.0395
GO:000422	Metalloend	-	-	-	-	6	116	0.73	0.0452

PROCESS_D7_10mM_DOWN

#term ID	term descri	observed g	backgrounc	strength.K1	false disco	observed g	backgrounc	strength.DF	false discovery rate.DP12
GO:00081	Metabolic p	237	8581	0.24	4.78E-22	165	8581	0.3	3.30E-24
GO:00717	Organic sul	224	8137	0.24	8.50E-20	162	8137	0.32	7.22E-25
GO:00099	Cellular pro	333	15994	0.12	1.82E-18	204	15994	0.12	3.42E-11
GO:00442	Primary me	206	7736	0.23	2.15E-15	154	7736	0.32	6.80E-23
GO:00442	Cellular me	192	7040	0.24	8.45E-15	137	7040	0.31	1.62E-17
GO:00068	Nitrogen co	193	7145	0.23	1.54E-14	135	7145	0.29	6.16E-16
GO:00346	Cellular nit	121	3820	0.3	2.22E-11	85	3820	0.36	2.70E-11
GO:19015	Organonitro	149	5394	0.24	2.70E-10	107	5394	0.31	3.18E-12
GO:19015	Organic sul	67	1714	0.39	1.48E-08	51	1714	0.49	8.34E-10
GO:00330	Macromole	81	2366	0.34	4.10E-08	NA	NA	NA	NA
GO:00090	Catabolic p	72	1999	0.36	6.82E-08	55	1999	0.46	1.61E-09
GO:00718	Cellular co	148	5887	0.2	3.42E-07	90	5887	0.2	0.00026
GO:00707	Cellular ma	68	1929	0.35	5.32E-07	NA	NA	NA	NA
GO:00511	Localizatio	120	4471	0.23	8.67E-07	NA	NA	NA	NA
GO:00081	Protein loc	67	1924	0.34	1.03E-06	NA	NA	NA	NA
GO:00464	Heterocycl	89	2937	0.28	1.03E-06	66	2937	0.37	2.14E-08
GO:00431	Macromole	151	6322	0.18	5.40E-06	104	6322	0.23	4.06E-07
GO:00516	Cellular loc	81	2661	0.29	5.40E-06	NA	NA	NA	NA
GO:19013	Organic cyc	92	3212	0.26	6.41E-06	71	3212	0.36	8.43E-09
GO:00061	Nucleobas	83	2791	0.28	8.01E-06	65	2791	0.38	9.31E-09
GO:00333	Protein loc	35	739	0.48	1.07E-05	NA	NA	NA	NA
GO:00440	Cellular co	83	2815	0.27	1.07E-05	51	2815	0.27	0.0013
GO:00725	Establishm	23	344	0.63	1.07E-05	NA	NA	NA	NA
GO:00469	Intracellula	49	1297	0.38	1.36E-05	NA	NA	NA	NA
GO:00067	Cellular arc	86	2992	0.26	1.49E-05	69	2992	0.38	3.23E-09
GO:00160	Cellular co	136	5621	0.19	1.66E-05	84	5621	0.19	0.0013

GO:00068E	Intracellula	32	669	0.48	2.84E-05	NA	NA	NA	NA	
GO:00451E	Establishm	45	1173	0.39	3.01E-05	24	1173	0.33	0.0398	
GO:00436C	Cellular am	43	1102	0.39	3.66E-05	32	1102	0.48	1.52E-05	
GO:19015E	Organonitrc	42	1061	0.4	3.66E-05	26	1061	0.41	0.0028	
GO:00717C	Nitrogen co	51	1456	0.35	5.35E-05	30	1456	0.33	0.01	
GO:00442E	Small mole	56	1690	0.32	6.89E-05	60	1690	0.57	2.40E-15	
GO:19011E	Carbohydra	14	150	0.77	0.00011	NA	NA	NA	NA	
GO:00069E	Organelle o	95	3632	0.22	0.00014	58	3632	0.22	0.0077	
GO:004424	Cellular cat	52	1557	0.33	0.00015	39	1557	0.41	1.84E-05	
GO:00512E	Establishm	98	3839	0.21	0.00024	58	3839	0.2	0.025	
GO:000681	Transport	94	3660	0.21	0.00033	NA	NA	NA	NA	
GO:00226C	Cellular cor	71	2516	0.25	0.00042	45	2516	0.27	0.0054	
GO:001604	Lipid catab	18	285	0.6	0.00045	10	285	0.56	0.0425	
GO:004647	Glycosphin	6	18	1.33	0.00045	NA	NA	NA	NA	
GO:00150E	Protein trar	39	1062	0.37	0.00047	NA	NA	NA	NA	
GO:004851	Negative re	124	5319	0.17	0.00047	NA	NA	NA	NA	
GO:005164	Establishm	53	1689	0.3	0.00055	NA	NA	NA	NA	
GO:004424	Cellular lipi	14	182	0.69	0.00071	8	182	0.66	0.0397	
GO:19011E	Carbohydra	37	1002	0.37	0.00071	35	1002	0.56	4.57E-08	
GO:00104E	Gene expre	67	2399	0.25	0.001	44	2399	0.28	0.0041	
GO:004852	Negative re	112	4752	0.18	0.001	NA	NA	NA	NA	
GO:001094	Regulation	53	1740	0.29	0.0011	NA	NA	NA	NA	
GO:001607	RNA metab	49	1558	0.3	0.0012	29	1558	0.29	0.0436	
GO:00717C	Organic sul	55	1835	0.28	0.0012	NA	NA	NA	NA	
GO:004651	Ceramide c	6	24	1.2	0.0014	NA	NA	NA	NA	
GO:00903C	Nucleic aci	63	2240	0.25	0.0015	40	2240	0.27	0.013	
GO:000657	Cellular mc	14	201	0.65	0.0017	9	201	0.67	0.0191	
GO:005112	Regulation	68	2504	0.24	0.0018	NA	NA	NA	NA	

GO:00100З	Response t	25	577	0.44	0.0021	18	577	0.51	0.003
GO:000905	Biosyntheti	70	2636	0.23	0.0025	NA	NA	NA	NA
GO:006164	Cytoskelet	10	104	0.79	0.0025	NA	NA	NA	NA
GO:190157	Organic sul	69	2581	0.23	0.0025	50	2581	0.3	0.00034
GO:004298	Regulation	47	1531	0.29	0.0029	NA	NA	NA	NA
GO:000941	Response t	22	483	0.46	0.0031	17	483	0.56	0.0012
GO:000905	Macromole	34	967	0.35	0.0035	24	967	0.41	0.0044
GO:001024	Response t	36	1056	0.34	0.0037	NA	NA	NA	NA
GO:001953	Protein met	102	4367	0.17	0.0037	72	4367	0.23	0.00037
GO:003250	Developme	123	5590	0.15	0.0057	NA	NA	NA	NA
GO:006054	Negative re	37	1125	0.32	0.0057	NA	NA	NA	NA
GO:000674	Glutathione	8	72	0.85	0.0061	NA	NA	NA	NA
GO:001003	Response t	72	2827	0.21	0.0061	49	2827	0.26	0.0052
GO:000660	Protein targ	14	234	0.58	0.0064	NA	NA	NA	NA
GO:000668	Ganglioside	4	9	1.45	0.0064	NA	NA	NA	NA
GO:000679	Sulfur comp	17	333	0.51	0.0064	17	333	0.72	1.73E-05
GO:190169	Response t	37	1149	0.31	0.0077	NA	NA	NA	NA
GO:000639	RNA proces	32	941	0.33	0.0095	NA	NA	NA	NA
GO:005124	Negative re	34	1035	0.32	0.0106	22	1035	0.34	0.0415
GO:003287	Regulation	60	2276	0.22	0.0109	NA	NA	NA	NA
GO:004424	Cellular bio	64	2480	0.21	0.0109	47	2480	0.29	0.001
GO:002261	Ribonucleo	24	616	0.39	0.011	NA	NA	NA	NA
GO:000639	mRNA proc	20	462	0.44	0.0112	NA	NA	NA	NA
GO:003016	Protein cata	27	741	0.36	0.0112	19	741	0.43	0.0143
GO:005112	Negative re	27	740	0.36	0.0112	18	740	0.4	0.0326
GO:001975	Carboxylic	31	917	0.33	0.0125	35	917	0.6	7.36E-09
GO:001619	Vesicle-me	38	1231	0.29	0.0126	NA	NA	NA	NA
GO:006500	Regulation	89	3854	0.17	0.0171	59	3854	0.2	0.0163

GO:00516€	Nuclear po	3	4	1.68	0.0176	NA	NA	NA	NA	
GO:00066€	Glycolipid r	8	89	0.76	0.019	NA	NA	NA	NA	
GO:00003ᵹ	mRNA splic	14	267	0.52	0.0192	NA	NA	NA	NA	
GO:199054	Mitochondı	8	91	0.75	0.0207	8	91	0.96	0.00092	
GO:00196ᵹ	Ribose pho	19	456	0.42	0.023	23	456	0.72	1.32E-07	
GO:000931	Oligosacch	4	15	1.23	0.0237	NA	NA	NA	NA	
GO:00100ᵹ	Response t	17	384	0.45	0.025	14	384	0.58	0.0046	
GO:00071€	Cell-matrix	9	121	0.67	0.0252	NA	NA	NA	NA	
GO:00430€	Negative re	31	967	0.31	0.0261	NA	NA	NA	NA	
GO:00430ᵹ	Negative re	25	707	0.35	0.0265	NA	NA	NA	NA	
GO:007252	Purine-con	19	465	0.41	0.0275	24	465	0.73	3.83E-08	
GO:19029(	Negative re	11	182	0.58	0.0275	NA	NA	NA	NA	
GO:000662	Lipid metat	36	1202	0.28	0.0279	26	1202	0.35	0.0133	
GO:00508(	Synapse or	16	357	0.45	0.0311	NA	NA	NA	NA	
GO:000651	Peptide me	28	850	0.32	0.0325	21	850	0.41	0.0114	
GO:000701	Cytoskelet	38	1308	0.27	0.0325	NA	NA	NA	NA	
GO:19016ᵹ	Glycosyl co	7	75	0.77	0.0328	NA	NA	NA	NA	
GO:00061€	Purine nucl	18	436	0.42	0.033	23	436	0.74	5.94E-08	
GO:19017(	Response t	45	1648	0.24	0.033	33	1648	0.32	0.008	
GO:000727	Multicellula	96	4353	0.15	0.0341	NA	NA	NA	NA	
GO:00335ᵹ	Cellular res	44	1609	0.24	0.0364	NA	NA	NA	NA	
GO:00488ᵹ	Anatomical	110	5157	0.13	0.0371	NA	NA	NA	NA	
GO:00092ᵹ	Ribonucleo	18	443	0.41	0.0375	NA	NA	NA	NA	
GO:003134	Regulation	26	776	0.33	0.0383	NA	NA	NA	NA	
GO:19013€	Organic cyc	30	957	0.3	0.0403	21	957	0.36	0.0383	
GO:000962	Response t	35	1190	0.27	0.0416	NA	NA	NA	NA	
GO:00616ᵹ	Chaperone	3	7	1.43	0.0425	NA	NA	NA	NA	
GO:00708ᵹ	Cellular res	64	2646	0.19	0.0425	NA	NA	NA	NA	

GO:00065(	Proteolysis	35	1197	0.27	0.045		31	1197	0.43	0.00021		
GO:00224(	Cell cycle p	27	831	0.31	0.045	NA	NA	NA	NA			
GO:00995(	Modificatio	4	20	1.1	0.0478	NA	NA	NA	NA			
GO:00181(	Heterocycl	27	836	0.31	0.048		19	836	0.37	0.0435		
GO:004851	Positive reg	130	6368	0.11	0.049	NA	NA	NA	NA			
GO:00060(	Tricarboxyli	NA	NA	NA	NA		10	35	1.47	9.69E-09		
GO:00453(	Cellular res	NA	NA	NA	NA		16	166	1	1.62E-08		
GO:00060(	Generation	NA	NA	NA	NA		22	416	0.74	1.32E-07		
GO:00090(	Aerobic res	NA	NA	NA	NA		14	139	1.02	1.32E-07		
GO:00091(	Purine ribo	NA	NA	NA	NA		22	421	0.73	1.56E-07		
GO:00159(	Energy deri	NA	NA	NA	NA		17	235	0.88	1.68E-07		
GO:00550(	Nucleobas(	NA	NA	NA	NA		25	582	0.65	4.06E-07		
GO:00725(	Purine-con	NA	NA	NA	NA		13	179	0.88	1.59E-05		
GO:00196(	Organopho	NA	NA	NA	NA		29	934	0.51	1.67E-05		
GO:00436(	Dicarboxyli	NA	NA	NA	NA		10	93	1.05	1.84E-05		
GO:00091(	Purine nucl	NA	NA	NA	NA		14	237	0.79	4.69E-05		
GO:00512(	Regulation	NA	NA	NA	NA		54	2708	0.32	5.88E-05		
GO:00061(	Purine nucl	NA	NA	NA	NA		12	171	0.86	6.25E-05		
GO:00342(	Regulation	NA	NA	NA	NA		21	592	0.57	0.00014		
GO:00463(	Ribose pho	NA	NA	NA	NA		12	186	0.83	0.00014		
GO:00092(	Purine ribo	NA	NA	NA	NA		13	232	0.76	2.00E-04		
GO:00091(	Purine ribo	NA	NA	NA	NA		11	161	0.85	0.00023		
GO:00325(	DNA duple>	NA	NA	NA	NA		9	103	0.96	0.00032		
GO:00460(	ATP metab(	NA	NA	NA	NA		12	205	0.78	0.00032		
GO:00064(	Regulation	NA	NA	NA	NA		19	531	0.57	0.00037		
GO:19015(	Organonitr(	NA	NA	NA	NA		36	1579	0.37	0.00038		
GO:00069(	Response t	NA	NA	NA	NA		57	3187	0.27	0.00055		
GO:00442(	Small mole	NA	NA	NA	NA		15	354	0.64	0.00061		

GO:200011	Regulation	NA	NA	NA	NA	20	613	0.53	0.00064
GO:00106(	Post-transc	NA	NA	NA	NA	20	623	0.52	0.00079
GO:000914	Purine nucl	NA	NA	NA	NA	7	63	1.06	0.00089
GO:004277	Proton mot	NA	NA	NA	NA	5	22	1.37	0.00094
GO:00458(	Positive reg	NA	NA	NA	NA	14	361	0.6	0.0028
GO:000072	Double-stra	NA	NA	NA	NA	4	13	1.5	0.0029
GO:00067!	ATP biosyn	NA	NA	NA	NA	6	53	1.07	0.0034
GO:003387	Ribonucleo	NA	NA	NA	NA	8	114	0.86	0.0037
GO:003403	Purine nucl	NA	NA	NA	NA	8	114	0.86	0.0037
GO:00067!	Phosphoru	NA	NA	NA	NA	38	1940	0.31	0.0041
GO:004427	Cellular nit	NA	NA	NA	NA	34	1662	0.33	0.0046
GO:00442(	Cellular ma	NA	NA	NA	NA	49	2825	0.26	0.0051
GO:000652	Cellular am	NA	NA	NA	NA	12	293	0.63	0.0055
GO:000663	acyl-CoA m	NA	NA	NA	NA	7	90	0.91	0.0055
GO:00327(	Monocarbo	NA	NA	NA	NA	18	615	0.48	0.0055
GO:00067!	Phosphate-	NA	NA	NA	NA	37	1919	0.3	0.0062
GO:001931	Hexose me	NA	NA	NA	NA	10	208	0.7	0.0064
GO:004393	Protein-cor	NA	NA	NA	NA	31	1505	0.33	0.0081
GO:190297	Mitotic DN/	NA	NA	NA	NA	3	6	1.72	0.0086
GO:000597	Carbohydra	NA	NA	NA	NA	16	527	0.5	0.0087
GO:00650(	Protein-cor	NA	NA	NA	NA	28	1312	0.35	0.01
GO:00904(	Organopho	NA	NA	NA	NA	15	479	0.51	0.0102
GO:00061(	Succinate r	NA	NA	NA	NA	3	7	1.65	0.0113
GO:00301(	Regulation	NA	NA	NA	NA	19	724	0.44	0.0115
GO:000627	DNA replica	NA	NA	NA	NA	4	23	1.26	0.013
GO:190113	Carbohydra	NA	NA	NA	NA	16	550	0.48	0.013
GO:00109!	Positive reg	NA	NA	NA	NA	9	188	0.7	0.0132
GO:00070(	Mitochondr	NA	NA	NA	NA	14	439	0.52	0.0133

GO:00062E	DNA unwin	NA	NA	NA	NA	4	24	1.24	0.0144
GO:00515E	Mitochondı	NA	NA	NA	NA	4	24	1.24	0.0144
GO:00160E	Carbohydra	NA	NA	NA	NA	9	192	0.69	0.0146
GO:006102	Membrane	NA	NA	NA	NA	18	684	0.44	0.0153
GO:00063E	tRNA metal	NA	NA	NA	NA	9	195	0.68	0.016
GO:00332E	Nuclear DN	NA	NA	NA	NA	4	25	1.22	0.016
GO:000641	tRNA amin	NA	NA	NA	NA	5	49	1.02	0.0163
GO:001581	Aspartate t	NA	NA	NA	NA	3	9	1.54	0.0174
GO:00229C	Respiratory	NA	NA	NA	NA	6	84	0.87	0.0218
GO:00061C	succinyl-C	NA	NA	NA	NA	3	10	1.49	0.0219
GO:00070C	Inner mitoc	NA	NA	NA	NA	4	28	1.17	0.0224
GO:200011	Regulation	NA	NA	NA	NA	4	29	1.16	0.0247
GO:190331	Regulation	NA	NA	NA	NA	11	313	0.56	0.0275
GO:00463E	Carboxylic	NA	NA	NA	NA	9	214	0.64	0.0277
GO:004441	Biological p	NA	NA	NA	NA	27	1351	0.32	0.0286
GO:00327E	Positive reg	NA	NA	NA	NA	6	91	0.84	0.0302
GO:00434E	Regulation	NA	NA	NA	NA	7	129	0.75	0.0302
GO:00517C	Biological p	NA	NA	NA	NA	6	92	0.83	0.0313
GO:00420E	Gliogenesis	NA	NA	NA	NA	10	269	0.59	0.032
GO:000611	Oxidative p	NA	NA	NA	NA	6	93	0.83	0.0326
GO:00447E	Modulation	NA	NA	NA	NA	4	33	1.1	0.0351
GO:007061	Regulation	NA	NA	NA	NA	5	61	0.93	0.0351
GO:003004	Actin filam	NA	NA	NA	NA	6	96	0.81	0.0362
GO:00447E	Positive reg	NA	NA	NA	NA	3	13	1.38	0.0362
GO:190372	Regulation	NA	NA	NA	NA	3	13	1.38	0.0362
GO:003002	Actin filam	NA	NA	NA	NA	16	625	0.42	0.038
GO:000642	isoleucyl-tF	NA	NA	NA	NA	2	2	2.02	0.0417
GO:004222	Response t	NA	NA	NA	NA	64	4477	0.17	0.0417

GO:190392	Positive reg	NA	NA	NA	NA	2	2	2.02	0.0417
GO:190402	Negative re	NA	NA	NA	NA	2	2	2.02	0.0417
GO:200037	Negative re	NA	NA	NA	NA	5	65	0.9	0.0417
GO:004306	Positive reg	NA	NA	NA	NA	15	577	0.43	0.0441
GO:010607	aminoacyl-	NA	NA	NA	NA	3	15	1.32	0.0458
GO:002260	Regulation	NA	NA	NA	NA	11	347	0.52	0.0499

KEGG_D7_30mM_UP

#term ID	term description.NIST	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DF	false discovery rate.DP12
cge01100	Metabolic pathways	102	1132	0.58	5.49E-27	56	1132	0.57	1.65E-14
cge04144	Endocytosis	33	183	0.88	1.64E-15	11	183	0.66	0.001
cge04145	Phagosome	23	106	0.96	3.44E-12	9	106	0.81	0.00058
cge03050	Proteasome	14	37	1.2	5.83E-10	6	37	1.09	0.00058
cge01200	Carbon metabolism	20	104	0.91	6.82E-10	10	104	0.86	0.00012
cge04810	Regulation of actin cytoske	23	153	0.8	1.41E-09	NA	NA	NA	NA
cge00480	Glutathione metabolism	15	52	1.08	1.47E-09	5	52	0.86	0.0098
cge05020	Prion disease	25	198	0.72	4.25E-09	15	198	0.76	8.33E-06
cge05012	Parkinson disease	24	183	0.74	4.44E-09	15	183	0.79	4.79E-06
cge04141	Protein processing in endo	20	128	0.82	8.47E-09	16	128	0.98	8.32E-09
cge05170	Human immunodeficiency	23	174	0.74	8.47E-09	NA	NA	NA	NA
cge05010	Alzheimer disease	28	273	0.63	1.71E-08	13	273	0.56	0.002
cge05132	Salmonella infection	22	172	0.73	2.79E-08	8	172	0.55	0.0211
cge05205	Proteoglycans in cancer	20	140	0.78	2.79E-08	NA	NA	NA	NA
cge05016	Huntington disease	25	230	0.66	3.87E-08	13	230	0.63	0.00058
cge05200	Pathways in cancer	33	391	0.55	3.87E-08	NA	NA	NA	NA
cge05146	Amoebiasis	14	67	0.94	1.02E-07	NA	NA	NA	NA
cge00983	Drug metabolism - other e	13	58	0.97	1.64E-07	NA	NA	NA	NA
cge05418	Fluid shear stress and athe	16	100	0.83	2.19E-07	NA	NA	NA	NA
cge04142	Lysosome	16	101	0.82	2.36E-07	NA	NA	NA	NA
cge05017	Spinocerebellar ataxia	16	105	0.8	3.66E-07	NA	NA	NA	NA
cge00980	Metabolism of xenobiotics	11	45	1.01	8.48E-07	NA	NA	NA	NA
cge05014	Amyotrophic lateral sclero	25	278	0.58	8.48E-07	23	278	0.8	2.20E-09
cge04140	Autophagy - animal	15	103	0.79	1.50E-06	NA	NA	NA	NA
cge05165	Human papillomavirus infe	23	251	0.58	1.86E-06	9	251	0.43	0.0472
cge01524	Platinum drug resistance	11	53	0.94	3.12E-06	NA	NA	NA	NA
cge05204	Chemical carcinogenesis	11	53	0.94	3.12E-06	NA	NA	NA	NA
cge00010	Glycolysis / Gluconeogene	11	55	0.92	4.02E-06	6	55	0.92	0.0025

cge04510	Focal adhesion	16	136	0.69	6.53E-06	NA	NA	NA	NA	
cge04961	Endocrine and other factor	9	35	1.03	7.26E-06	5	35	1.03	0.0028	
cge00982	Drug metabolism - cytochr	9	37	1.01	1.05E-05	NA	NA	NA	NA	
cge04910	Insulin signaling pathway	13	101	0.73	2.75E-05	NA	NA	NA	NA	
cge04666	Fc gamma R-mediated pha	11	70	0.82	2.81E-05	NA	NA	NA	NA	
cge04512	ECM-receptor interaction	10	57	0.87	3.22E-05	NA	NA	NA	NA	
cge04120	Ubiquitin mediated proteo	13	104	0.72	3.37E-05	7	104	0.71	0.008	
cge04919	Thyroid hormone signaling	12	89	0.75	3.84E-05	6	89	0.71	0.0152	
cge04721	Synaptic vesicle cycle	10	60	0.84	4.45E-05	NA	NA	NA	NA	
cge04540	Gap junction	10	63	0.82	6.38E-05	NA	NA	NA	NA	
cge05225	Hepatocellular carcinoma	14	131	0.65	6.78E-05	NA	NA	NA	NA	
cge04915	Estrogen signaling pathwa	12	97	0.71	7.67E-05	NA	NA	NA	NA	
cge04962	Vasopressin-regulated wat	8	38	0.95	8.06E-05	4	38	0.9	0.0184	
cge04151	PI3K-Akt signaling pathway	20	261	0.51	8.82E-05	NA	NA	NA	NA	
cge05211	Renal cell carcinoma	9	52	0.86	8.82E-05	NA	NA	NA	NA	
cge01230	Biosynthesis of amino acid	10	67	0.8	8.95E-05	8	67	0.96	0.00025	
cge05163	Human cytomegalovirus in	16	177	0.58	9.56E-05	NA	NA	NA	NA	
cge04261	Adrenergic signaling in car	11	85	0.73	0.00011	6	85	0.73	0.0133	
cge04966	Collecting duct acid secret	6	20	1.1	0.00017	NA	NA	NA	NA	
cge04612	Antigen processing and pre	8	45	0.87	2.00E-04	NA	NA	NA	NA	
cge05100	Bacterial invasion of epithe	9	61	0.79	0.00024	NA	NA	NA	NA	
cge04216	Ferroptosis	7	34	0.94	0.00027	6	34	1.12	0.00046	
cge04730	Long-term depression	8	48	0.84	0.00029	NA	NA	NA	NA	
cge05323	Rheumatoid arthritis	9	64	0.77	0.00031	NA	NA	NA	NA	
cge00071	Fatty acid degradation	7	36	0.91	0.00035	4	36	0.92	0.0171	
cge04114	Oocyte meiosis	10	82	0.71	0.00035	NA	NA	NA	NA	
cge04150	mTOR signaling pathway	12	120	0.62	0.00038	NA	NA	NA	NA	
cge04971	Gastric acid secretion	8	51	0.82	0.00038	5	51	0.87	0.0093	
cge04720	Long-term potentiation	7	38	0.89	0.00044	NA	NA	NA	NA	
cge05203	Viral carcinogenesis	13	143	0.58	0.00045	NA	NA	NA	NA	

cge00052	Galactose metabolism	6	26	0.99	0.00047	3	26	0.94	0.0417
cge05230	Central carbon metabolisr	8	53	0.8	0.00047	4	53	0.76	0.0427
cge04918	Thyroid hormone synthesis	8	54	0.79	0.00051	7	54	0.99	0.00048
cge04014	Ras signaling pathway	14	170	0.54	6.00E-04	NA	NA	NA	NA
cge00520	Amino sugar and nucleotic	7	41	0.85	0.00061	NA	NA	NA	NA
cge00030	Pentose phosphate pathw	6	28	0.95	0.00063	3	28	0.91	0.0472
cge04071	Sphingolipid signaling pat	10	92	0.66	7.00E-04	NA	NA	NA	NA
cge04935	Growth hormone synthesis	10	93	0.65	0.00075	NA	NA	NA	NA
cge04976	Bile secretion	8	59	0.75	8.00E-04	5	59	0.81	0.0151
cge03013	RNA transport	12	135	0.57	0.00087	10	135	0.75	0.00058
cge01212	Fatty acid metabolism	7	46	0.8	0.0011	5	46	0.91	0.0073
cge03320	PPAR signaling pathway	8	63	0.73	0.0011	NA	NA	NA	NA
cge04012	ErbB signaling pathway	8	62	0.73	0.0011	NA	NA	NA	NA
cge04921	Oxytocin signaling pathwa	10	98	0.63	0.0011	7	98	0.73	0.007
cge04726	Serotonergic synapse	9	82	0.66	0.0012	NA	NA	NA	NA
cge05169	Epstein-Barr virus infectio	13	163	0.52	0.0012	NA	NA	NA	NA
cge00900	Terpenoid backbone biosy	5	21	1	0.0013	5	21	1.25	0.00058
cge00061	Fatty acid biosynthesis	4	11	1.18	0.0014	NA	NA	NA	NA
cge05152	Tuberculosis	11	124	0.57	0.0014	NA	NA	NA	NA
cge00500	Starch and sucrose metab	5	22	0.98	0.0015	NA	NA	NA	NA
cge04922	Glucagon signaling pathwa	8	72	0.67	0.0023	6	72	0.8	0.0073
cge00562	Inositol phosphate metabo	7	55	0.73	0.0024	NA	NA	NA	NA
cge04152	AMPK signaling pathway	9	92	0.61	0.0024	6	92	0.69	0.0171
cge04934	Cushing syndrome	10	115	0.56	0.0029	NA	NA	NA	NA
cge05414	Dilated cardiomyopathy	7	57	0.71	0.0029	4	57	0.72	0.05
cge00240	Pyrimidine metabolism	6	41	0.79	0.003	NA	NA	NA	NA
cge04062	Chemokine signaling path	11	138	0.52	0.003	NA	NA	NA	NA
cge04912	GnRH signaling pathway	7	58	0.7	0.003	NA	NA	NA	NA
cge00620	Pyruvate metabolism	5	27	0.89	0.0031	4	27	1.05	0.0081
cge05142	Chagas disease	8	77	0.64	0.0031	NA	NA	NA	NA

cge04146	Peroxisome	7	60	0.69	0.0035	7	60	0.95	0.00058
cge04925	Aldosterone synthesis and	7	60	0.69	0.0035	6	60	0.88	0.0035
cge00051	Fructose and mannose me	5	29	0.86	0.0039	3	29	0.89	0.05
cge05134	Legionellosis	6	45	0.75	0.0042	5	45	0.92	0.007
cge04022	cGMP-PKG signaling pathv	9	103	0.56	0.0045	NA	NA	NA	NA
cge04670	Leukocyte transendothelia	8	83	0.61	0.0046	NA	NA	NA	NA
cge04530	Tight junction	9	105	0.56	0.0049	NA	NA	NA	NA
cge04611	Platelet activation	8	84	0.6	0.0049	NA	NA	NA	NA
cge04066	HIF-1 signaling pathway	8	86	0.59	0.0055	6	86	0.72	0.0137
cge04360	Axon guidance	10	129	0.51	0.0055	NA	NA	NA	NA
cge04927	Cortisol synthesis and sec	6	49	0.71	0.0057	NA	NA	NA	NA
cge04972	Pancreatic secretion	7	67	0.64	0.0057	NA	NA	NA	NA
cge04660	T cell receptor signaling pa	7	69	0.63	0.0065	NA	NA	NA	NA
cge04916	Melanogenesis	7	69	0.63	0.0065	NA	NA	NA	NA
cge00230	Purine metabolism	8	90	0.57	0.0067	NA	NA	NA	NA
cge04137	Mitophagy - animal	6	51	0.69	0.0067	NA	NA	NA	NA
cge00190	Oxidative phosphorylation	9	112	0.53	0.0068	NA	NA	NA	NA
cge04728	Dopaminergic synapse	8	91	0.57	0.007	NA	NA	NA	NA
cge04210	Apoptosis	8	92	0.56	0.0074	NA	NA	NA	NA
cge04650	Natural killer cell mediatec	7	72	0.61	0.0076	NA	NA	NA	NA
cge04024	cAMP signaling pathway	10	140	0.48	0.0085	7	140	0.58	0.0252
cge05160	Hepatitis C	10	140	0.48	0.0085	NA	NA	NA	NA
cge05206	MicroRNAs in cancer	9	117	0.51	0.0085	NA	NA	NA	NA
cge04911	Insulin secretion	6	55	0.66	0.0087	4	55	0.74	0.0472
cge04371	Apelin signaling pathway	8	96	0.54	0.0089	NA	NA	NA	NA
cge04270	Vascular smooth muscle c	8	97	0.54	0.0094	NA	NA	NA	NA
cge04015	Rap1 signaling pathway	10	144	0.46	0.0098	NA	NA	NA	NA
cge04926	Relaxin signaling pathway	8	99	0.53	0.0103	NA	NA	NA	NA
cge00270	Cysteine and methionine r	5	40	0.72	0.0109	NA	NA	NA	NA
cge04924	Renin secretion	5	41	0.71	0.0119	NA	NA	NA	NA

cge04928	Parathyroid hormone syntl	7	80	0.56	0.0119	NA	NA	NA	NA	
cge04913	Ovarian steroidogenesis	5	42	0.7	0.0128	4	42	0.86	0.0239	
cge04072	Phospholipase D signaling	8	104	0.51	0.0131	NA	NA	NA	NA	
cge04722	Neurotrophin signaling pat	7	82	0.55	0.0131	NA	NA	NA	NA	
cge04714	Thermogenesis	11	179	0.41	0.014	8	179	0.53	0.0252	
cge05145	Toxoplasmosis	7	84	0.54	0.0145	NA	NA	NA	NA	
cge05161	Hepatitis B	9	130	0.46	0.0145	NA	NA	NA	NA	
cge00630	Glyoxylate and dicarboxyla	4	27	0.79	0.0146	NA	NA	NA	NA	
cge05034	Alcoholism	8	107	0.5	0.0146	NA	NA	NA	NA	
cge05412	Arrhythmogenic right ventr	5	44	0.68	0.0146	NA	NA	NA	NA	
cge04713	Circadian entrainment	6	64	0.59	0.015	NA	NA	NA	NA	
cge04010	MAPK signaling pathway	12	209	0.38	0.0152	NA	NA	NA	NA	
cge04725	Cholinergic synapse	7	86	0.53	0.0154	NA	NA	NA	NA	
cge04260	Cardiac muscle contractio	5	46	0.66	0.0166	4	46	0.82	0.0296	
cge05133	Pertussis	5	46	0.66	0.0166	NA	NA	NA	NA	
cge04964	Proximal tubule bicarbona	3	14	0.95	0.0167	NA	NA	NA	NA	
cge00250	Alanine, aspartate and glu	4	29	0.76	0.0172	NA	NA	NA	NA	
cge04973	Carbohydrate digestion an	4	29	0.76	0.0172	NA	NA	NA	NA	
cge04070	Phosphatidylinositol signa	6	67	0.57	0.0173	NA	NA	NA	NA	
cge04929	GnRH secretion	5	47	0.65	0.0173	NA	NA	NA	NA	
cge05215	Prostate cancer	6	68	0.57	0.0182	NA	NA	NA	NA	
cge00380	Tryptophan metabolism	4	31	0.73	0.0205	NA	NA	NA	NA	
cge00100	Steroid biosynthesis	3	16	0.9	0.0218	3	16	1.15	0.0171	
cge04970	Salivary secretion	5	51	0.61	0.0228	4	51	0.77	0.0391	
cge05416	Viral myocarditis	5	51	0.61	0.0228	NA	NA	NA	NA	
cge03015	mRNA surveillance pathwa	6	73	0.54	0.0239	6	73	0.79	0.0076	
cge05135	Yersinia infection	7	97	0.48	0.0252	NA	NA	NA	NA	
cge05410	Hypertrophic cardiomyopa	5	53	0.6	0.0256	NA	NA	NA	NA	
cge04213	Longevity regulating pathw	5	54	0.59	0.0272	NA	NA	NA	NA	
cge04933	AGE-RAGE signaling pathw	6	77	0.51	0.0292	NA	NA	NA	NA	

cge00040	Pentose and glucuronate i		3		19		0.82		0.0307	NA		NA		NA		NA	
cge00330	Arginine and proline metal		4		36		0.67		0.0307	NA		NA		NA		NA	
cge00650	Butanoate metabolism		3		19		0.82		0.0307	NA		NA		NA		NA	
cge00970	Aminoacyl-tRNA biosynthe		4		36		0.67		0.0307	NA		NA		NA		NA	
cge04020	Calcium signaling pathway		8		129		0.41		0.0329	NA		NA		NA		NA	
cge04724	Glutamatergic synapse		6		81		0.49		0.0348	NA		NA		NA		NA	
cge05167	Kaposi sarcoma-associate		9		157		0.38		0.0348	NA		NA		NA		NA	
cge00062	Fatty acid elongation		3		21		0.78		0.0375	NA		NA		NA		NA	
cge04978	Mineral absorption		4		39		0.63		0.0375		4		39		0.89		0.0196
cge03018	RNA degradation		5		62		0.53		0.0421	NA		NA		NA		NA	
cge04914	Progesterone-mediated oc		5		62		0.53		0.0421	NA		NA		NA		NA	
cge00280	Valine, leucine and isoleuc		4		42		0.6		0.0458	NA		NA		NA		NA	
cge04370	VEGF signaling pathway		4		42		0.6		0.0458	NA		NA		NA		NA	
cge01040	Biosynthesis of unsaturate		3		24		0.72		0.0499		3		24		0.98		0.0354
cge03040	Spliceosome	NA		NA		NA		NA			12		114		0.9		6.87E-06
cge00513	Various types of N-glycan I	NA		NA		NA		NA			4		36		0.92		0.0171
cge00510	N-Glycan biosynthesis	NA		NA		NA		NA			4		45		0.83		0.0281
cge00860	Porphyrin and chlorophyll	NA		NA		NA		NA			3		23		0.99		0.0325

KEGG_D7_30mM_DOWN

#term ID	term description.NIST	observed g	backgroun	strength.NI	false disco	observed g	backgroun	strength.DI	false discovery rate.DP12
cge03008	Ribosome biogenesis in eukaryotes	11	58	1.02	1.08E-05	NA	NA	NA	NA
cge03040	Spliceosome	14	114	0.84	1.08E-05	7	114	0.59	0.0282
cge03013	RNA transport	13	135	0.73	0.00026	NA	NA	NA	NA
cge01100	Metabolic pathways	41	1132	0.31	0.0018	64	1132	0.56	6.34E-16
cge03030	DNA replication	6	27	1.09	0.0018	NA	NA	NA	NA
cge05014	Amyotrophic lateral sclerosis	17	278	0.53	0.0018	13	278	0.48	0.0094
cge03010	Ribosome	13	184	0.6	0.0024	NA	NA	NA	NA
cge00970	Aminoacyl-tRNA biosynthesis	6	36	0.97	0.0037	6	36	1.03	0.00099
cge04714	Thermogenesis	11	179	0.54	0.0214	NA	NA	NA	NA
cge00270	Cysteine and methionine metabolisn	5	40	0.84	0.0376	NA	NA	NA	NA
cge00280	Valine, leucine and isoleucine degra	5	42	0.82	0.0417	12	42	1.26	2.35E-09
cge04142	Lysosome	NA	NA	NA	NA	10	101	0.8	0.00032
cge01200	Carbon metabolism	NA	NA	NA	NA	18	104	1.04	8.97E-11
cge00020	Citrate cycle (TCA cycle)	NA	NA	NA	NA	11	27	1.42	9.05E-10
cge00640	Propanoate metabolism	NA	NA	NA	NA	8	28	1.26	3.34E-06
cge00071	Fatty acid degradation	NA	NA	NA	NA	9	36	1.2	1.58E-06
cge00531	Glycosaminoglycan degradation	NA	NA	NA	NA	3	13	1.17	0.0199
cge01212	Fatty acid metabolism	NA	NA	NA	NA	6	46	0.92	0.0028
cge00650	Butanoate metabolism	NA	NA	NA	NA	5	19	1.23	0.00084
cge00380	Tryptophan metabolism	NA	NA	NA	NA	5	31	1.01	0.0039
cge00980	Metabolism of xenobiotics by cytoch	NA	NA	NA	NA	5	45	0.85	0.0124
cge00620	Pyruvate metabolism	NA	NA	NA	NA	6	27	1.15	0.00033
cge05012	Parkinson disease	NA	NA	NA	NA	12	183	0.62	0.0012
cge00630	Glyoxylate and dicarboxylate metab	NA	NA	NA	NA	7	27	1.22	3.44E-05
cge01230	Biosynthesis of amino acids	NA	NA	NA	NA	6	67	0.76	0.0117
cge04210	Apoptosis	NA	NA	NA	NA	7	92	0.69	0.0117
cge04979	Cholesterol metabolism	NA	NA	NA	NA	6	35	1.04	0.00093
cge00410	beta-Alanine metabolism	NA	NA	NA	NA	4	24	1.03	0.0117
cge00983	Drug metabolism - other enzymes	NA	NA	NA	NA	6	58	0.82	0.0071
cge00310	Lysine degradation	NA	NA	NA	NA	5	41	0.89	0.0099

cge05205	Proteoglycans in cancer	NA	NA	NA	NA	8	140	0.56	0.0235
cge04510	Focal adhesion	NA	NA	NA	NA	10	136	0.67	0.0019
cge05016	Huntington disease	NA	NA	NA	NA	14	230	0.59	0.00084
cge05200	Pathways in cancer	NA	NA	NA	NA	14	391	0.36	0.0408
cge04810	Regulation of actin cytoskeleton	NA	NA	NA	NA	13	153	0.74	7.89E-05
cge04217	Necroptosis	NA	NA	NA	NA	9	125	0.66	0.0041
cge04530	Tight junction	NA	NA	NA	NA	8	105	0.69	0.0061
cge05322	Systemic lupus erythematosus	NA	NA	NA	NA	6	69	0.75	0.0124
cge04670	Leukocyte transendothelial migratio	NA	NA	NA	NA	6	83	0.67	0.0271
cge00670	One carbon pool by folate	NA	NA	NA	NA	3	16	1.08	0.0293
cge04962	Vasopressin-regulated water reabso	NA	NA	NA	NA	4	38	0.83	0.038
cge05146	Amoebiasis	NA	NA	NA	NA	5	67	0.68	0.0466

PROCESS_D7_30mM_DOWN

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
GO:00464	Heterocycl	180	2937	0.53	4.65E-48	98	2937	0.33	4.03E-10
GO:19013	Organic cy	187	3212	0.51	1.25E-47	102	3212	0.31	1.26E-09
GO:00067	Cellular arc	180	2992	0.53	2.08E-47	98	2992	0.32	7.28E-10
GO:00061	Nucleobas	173	2791	0.54	7.37E-47	94	2791	0.33	5.95E-10
GO:00346	Cellular nit	201	3820	0.47	3.99E-46	126	3820	0.32	9.08E-14
GO:00903	Nucleic aci	154	2240	0.58	6.61E-46	71	2240	0.31	3.50E-06
GO:00160	RNA metab	124	1558	0.65	1.97E-41	58	1558	0.38	5.24E-07
GO:00104	Gene expre	145	2399	0.53	1.72E-36	81	2399	0.33	2.23E-08
GO:00063	RNA proces	90	941	0.73	2.85E-34	39	941	0.42	1.77E-05
GO:00442	Cellular me	254	7040	0.3	1.02E-33	201	7040	0.26	5.78E-19
GO:00718	Cellular co	224	5887	0.33	6.79E-31	169	5887	0.26	1.28E-14
GO:00068	Nitrogen co	249	7145	0.29	4.35E-30	197	7145	0.25	1.24E-16
GO:00081	Metabolic p	277	8581	0.26	5.07E-30	234	8581	0.24	1.25E-21
GO:00717	Organic sul	268	8137	0.26	8.52E-30	226	8137	0.25	1.55E-21
GO:00442	Primary me	258	7736	0.27	9.39E-29	211	7736	0.24	4.17E-18
GO:00422	Ribosome b	60	459	0.86	1.65E-28	23	459	0.51	3.00E-04
GO:00346	ncRNA met	67	605	0.79	2.98E-28	30	605	0.5	1.76E-05
GO:00226	Ribonucleo	67	616	0.78	7.48E-28	32	616	0.52	2.55E-06
GO:00099	Cellular pro	387	15994	0.13	6.01E-27	338	15994	0.13	1.41E-22
GO:00440	Cellular co	139	2815	0.44	4.08E-26	95	2815	0.33	4.37E-10
GO:00160	rRNA metal	49	320	0.93	9.97E-26	21	320	0.62	2.24E-05
GO:00431	Macromole	220	6322	0.29	1.19E-24	164	6322	0.22	4.27E-10
GO:00063	rRNA proce	45	296	0.93	2.21E-23	20	296	0.64	2.76E-05
GO:00344	ncRNA proc	53	469	0.8	2.47E-22	23	469	0.5	0.00041
GO:00069	Organelle o	147	3632	0.35	1.53E-19	112	3632	0.3	5.25E-10
GO:00512	Chromosor	61	966	0.55	3.67E-14	NA	NA	NA	NA

GO:001604	Cellular co	175	5621	0.24	1.30E-12	152	5621	0.24	2.78E-10	
GO:001607	mRNA met	45	625	0.6	7.31E-12	NA	NA	NA	NA	
GO:190331	Regulation	30	313	0.73	2.86E-10	NA	NA	NA	NA	
GO:00083	RNA splicin	32	372	0.68	6.79E-10	15	372	0.41	0.0476	
GO:00516	Establishm	32	387	0.66	1.74E-09	22	387	0.56	8.46E-05	
GO:001921	Regulation	125	3835	0.26	4.55E-09	NA	NA	NA	NA	
GO:00512	Regulation	117	3508	0.27	6.52E-09	NA	NA	NA	NA	
GO:00063	mRNA proc	34	462	0.61	6.59E-09	NA	NA	NA	NA	
GO:005164	Organelle l	37	547	0.58	7.88E-09	23	547	0.43	0.0027	
GO:01406	Non-memb	32	418	0.63	9.71E-09	NA	NA	NA	NA	
GO:004227	Ribosomal	23	210	0.79	1.02E-08	12	210	0.56	0.012	
GO:00104	Regulation	143	4725	0.23	1.35E-08	110	4725	0.17	0.00072	
GO:014001	Mitotic nuc	22	195	0.8	1.55E-08	NA	NA	NA	NA	
GO:00106	Negative re	94	2682	0.29	8.55E-08	67	2682	0.2	0.0069	
GO:00313	Negative re	83	2234	0.32	8.55E-08	56	2234	0.21	0.0206	
GO:000704	Cell cycle	53	1118	0.42	9.67E-08	NA	NA	NA	NA	
GO:00459	Negative re	63	1480	0.38	1.13E-07	NA	NA	NA	NA	
GO:005117	Negative re	84	2342	0.3	3.12E-07	58	2342	0.2	0.0215	
GO:00226	Cellular co	88	2516	0.29	3.67E-07	75	2516	0.28	1.44E-05	
GO:00434	Regulation	19	174	0.78	4.58E-07	NA	NA	NA	NA	
GO:000027	Mitotic cell	37	648	0.5	5.05E-07	NA	NA	NA	NA	
GO:00459	Positive reg	76	2047	0.32	5.05E-07	NA	NA	NA	NA	
GO:00506	Regulation	18	156	0.81	5.23E-07	NA	NA	NA	NA	
GO:00003	mRNA splic	23	267	0.68	5.79E-07	NA	NA	NA	NA	
GO:00602	Regulation	165	6089	0.18	7.04E-07	133	6089	0.15	0.0012	
GO:00098	Negative re	96	2911	0.26	8.64E-07	75	2911	0.22	0.0012	
GO:004427	Cellular nit	65	1662	0.34	1.17E-06	54	1662	0.32	8.43E-05	
GO:005117	Regulation	154	5595	0.19	1.17E-06	118	5595	0.13	0.0132	

GO:00105E	Negative re	59	1438	0.36	1.23E-06	NA	NA	NA	NA	
GO:00513C	Cell divisio	28	412	0.58	1.28E-06	18	412	0.45	0.0094	
GO:000047	Maturation	13	77	0.97	1.35E-06	10	77	0.92	0.00016	
GO:003132	Negative re	60	1505	0.35	2.34E-06	NA	NA	NA	NA	
GO:00512E	Positive reg	68	1816	0.32	2.37E-06	NA	NA	NA	NA	
GO:190304	Mitotic cell	32	544	0.52	2.57E-06	NA	NA	NA	NA	
GO:00442E	Cellular ma	92	2825	0.26	3.14E-06	74	2825	0.22	0.00086	
GO:003132	Regulation	152	5592	0.18	3.20E-06	118	5592	0.13	0.013	
GO:000632	Chromatin	33	584	0.5	3.60E-06	NA	NA	NA	NA	
GO:00105E	Regulation	114	3816	0.22	3.83E-06	NA	NA	NA	NA	
GO:19028E	Microtubul	15	122	0.84	3.95E-06	NA	NA	NA	NA	
GO:004393	Protein-cor	59	1505	0.34	4.93E-06	NA	NA	NA	NA	
GO:00800E	Regulation	155	5780	0.17	4.93E-06	123	5780	0.13	0.007	
GO:001062	Negative re	42	890	0.42	5.16E-06	36	890	0.41	7.88E-05	
GO:003132	Positive reg	99	3172	0.24	5.34E-06	72	3172	0.16	0.0391	
GO:005117	Positive reg	99	3188	0.24	6.72E-06	73	3188	0.17	0.03	
GO:00105E	Regulation	36	706	0.45	8.37E-06	NA	NA	NA	NA	
GO:000652	Cellular am	22	293	0.62	8.58E-06	20	293	0.64	2.41E-05	
GO:00512E	Negative re	54	1344	0.35	8.58E-06	NA	NA	NA	NA	
GO:004852	Positive reg	153	5758	0.17	1.05E-05	133	5758	0.17	9.11E-05	
GO:00002E	Nuclear div	23	324	0.6	1.07E-05	NA	NA	NA	NA	
GO:004852	Negative re	132	4752	0.19	1.16E-05	113	4752	0.18	0.00024	
GO:00106C	Positive reg	107	3592	0.22	1.19E-05	84	3592	0.18	0.0072	
GO:004802	Regulation	14	116	0.83	1.19E-05	NA	NA	NA	NA	
GO:004851	Positive reg	165	6368	0.16	1.19E-05	146	6368	0.17	3.15E-05	
GO:00106C	Post-transc	33	623	0.47	1.20E-05	33	623	0.53	1.04E-06	
GO:001922	Regulation	170	6627	0.16	1.23E-05	145	6627	0.15	0.00041	
GO:005172	Regulation	46	1071	0.38	1.33E-05	NA	NA	NA	NA	

GO:001714	Negative re	16	160	0.75	1.46E-05	NA	NA	NA	NA	
GO:003472	Nucleosom	16	161	0.74	1.56E-05	NA	NA	NA	NA	
GO:000007	Mitotic sist	15	140	0.78	1.57E-05	NA	NA	NA	NA	
GO:000705	Chromosor	22	307	0.6	1.57E-05	NA	NA	NA	NA	
GO:000081	Sister chro	16	162	0.74	1.64E-05	NA	NA	NA	NA	
GO:001813	Heterocycl	39	836	0.42	1.72E-05	26	836	0.3	0.0437	
GO:000701	Cytoskelet	52	1308	0.35	1.77E-05	47	1308	0.36	3.80E-05	
GO:000625	DNA metab	37	770	0.43	1.79E-05	NA	NA	NA	NA	
GO:000705	Mitotic spir	12	86	0.89	2.13E-05	NA	NA	NA	NA	
GO:000633	Nucleosom	7	18	1.34	2.44E-05	NA	NA	NA	NA	
GO:000905	Biosyntheti	84	2636	0.25	2.56E-05	69	2636	0.22	0.0017	
GO:003304	Regulation	49	1214	0.35	2.60E-05	39	1214	0.31	0.0024	
GO:004851	Negative re	142	5319	0.17	2.60E-05	126	5319	0.18	6.61E-05	
GO:000697	Cellular res	35	720	0.43	2.88E-05	NA	NA	NA	NA	
GO:000988	Regulation	116	4090	0.2	2.90E-05	NA	NA	NA	NA	
GO:003132	Regulation	114	4002	0.2	3.07E-05	NA	NA	NA	NA	
GO:004424	Cellular bio	80	2480	0.26	3.12E-05	65	2480	0.22	0.0027	
GO:000046	Maturation	8	30	1.17	3.25E-05	8	30	1.23	2.36E-05	
GO:002240	Cell cycle p	38	831	0.41	3.52E-05	NA	NA	NA	NA	
GO:000633	Chromatin	21	300	0.59	3.65E-05	NA	NA	NA	NA	
GO:190157	Organic sul	82	2581	0.25	3.76E-05	67	2581	0.22	0.0027	
GO:000705	Spindle org	15	155	0.73	4.31E-05	NA	NA	NA	NA	
GO:190136	Organic cyc	41	957	0.38	5.74E-05	NA	NA	NA	NA	
GO:005122	Spindle ass	12	98	0.83	6.40E-05	NA	NA	NA	NA	
GO:000985	Positive reg	111	3939	0.2	7.19E-05	96	3939	0.19	6.00E-04	
GO:003450	Protein loca	17	213	0.65	8.46E-05	NA	NA	NA	NA	
GO:006500	Protein-cor	50	1312	0.33	8.46E-05	36	1312	0.24	0.0441	
GO:009881	Nuclear chr	18	238	0.63	8.46E-05	NA	NA	NA	NA	

GO:00062E	DNA repair	26	470	0.49	9.70E-05	NA	NA	NA	NA	
GO:00062E	DNA replica	16	192	0.67	1.00E-04	NA	NA	NA	NA	
GO:00434E	Regulation	15	168	0.7	1.00E-04	NA	NA	NA	NA	
GO:00513C	Establishm	11	85	0.86	0.00011	NA	NA	NA	NA	
GO:00063S	tRNA metal	16	195	0.66	0.00012	NA	NA	NA	NA	
GO:00090E	Macromole	57	1615	0.29	0.00013	NA	NA	NA	NA	
GO:00304S	Maturation	10	69	0.91	0.00013	NA	NA	NA	NA	
GO:00069S	Nucleus org	14	151	0.71	0.00014	9	151	0.58	0.0414	
GO:00340E	Stress gran	7	26	1.18	0.00014	NA	NA	NA	NA	
GO:190331	Positive reg	13	128	0.75	0.00014	NA	NA	NA	NA	
GO:000221	Activation c	8	39	1.06	0.00015	NA	NA	NA	NA	
GO:00070S	Nuclear mig	8	40	1.05	0.00017	7	40	1.05	0.00084	
GO:007182	protein-DN	17	228	0.62	0.00018	NA	NA	NA	NA	
GO:00434E	Regulation	14	155	0.7	0.00019	NA	NA	NA	NA	
GO:000022	Microtubule	30	624	0.43	2.00E-04	NA	NA	NA	NA	
GO:00062E	DNA-templ	13	135	0.73	0.00022	NA	NA	NA	NA	
GO:00346S	Nucleobase	34	765	0.39	0.00022	NA	NA	NA	NA	
GO:005164	Establishm	58	1689	0.28	0.00022	56	1689	0.33	3.07E-05	
GO:00105S	Positive reg	64	1945	0.26	0.00025	NA	NA	NA	NA	
GO:004227	Ribosomal	12	115	0.76	0.00025	NA	NA	NA	NA	
GO:005131	Metaphase	10	77	0.86	0.00028	NA	NA	NA	NA	
GO:200114	Regulation	92	3195	0.21	0.00031	NA	NA	NA	NA	
GO:000001	Regulation	13	144	0.7	4.00E-04	NA	NA	NA	NA	
GO:005112	Regulation	76	2504	0.23	0.00044	78	2504	0.3	1.32E-06	
GO:00063S	Regulation	91	3184	0.2	0.00046	NA	NA	NA	NA	
GO:001943	Aromatic co	35	838	0.37	0.00052	NA	NA	NA	NA	
GO:000641	tRNA amino	8	49	0.96	0.00058	6	49	0.89	0.0127	
GO:00070E	Mitotic met	9	66	0.88	0.00058	NA	NA	NA	NA	

GO:00510E	Negative re	13	150	0.68	0.00058	NA	NA	NA	NA	
GO:000641	Regulation	26	531	0.44	0.00062	32	531	0.59	1.13E-07	
GO:00333E	Protein loca	32	739	0.38	0.00064	32	739	0.44	8.43E-05	
GO:000691	Nucleocyto	17	260	0.56	0.00079	NA	NA	NA	NA	
GO:00094E	RNA modifi	13	156	0.67	0.00082	NA	NA	NA	NA	
GO:00314E	Chromatin	14	181	0.63	0.00082	13	181	0.66	0.0012	
GO:000701	Microtubule	36	902	0.35	0.00092	NA	NA	NA	NA	
GO:200011	Regulation	28	613	0.41	0.00092	34	613	0.55	2.30E-07	
GO:00004E	Maturation	8	54	0.92	0.001	NA	NA	NA	NA	
GO:003132	Positive reg	64	2046	0.24	0.001	NA	NA	NA	NA	
GO:00711C	DNA confor	11	115	0.73	0.0011	NA	NA	NA	NA	
GO:004324	Negative re	10	94	0.77	0.0012	NA	NA	NA	NA	
GO:00458E	Negative re	44	1227	0.3	0.0012	NA	NA	NA	NA	
GO:19026E	Positive reg	55	1686	0.26	0.0014	NA	NA	NA	NA	
GO:00602E	Regulation	7	41	0.98	0.0015	NA	NA	NA	NA	
GO:003277	RNA biosyn	22	432	0.45	0.0016	NA	NA	NA	NA	
GO:00705C	Regulation	13	170	0.63	0.0017	NA	NA	NA	NA	
GO:00468E	Regulation	5	16	1.24	0.002	NA	NA	NA	NA	
GO:00510E	Regulation	25	543	0.41	0.0022	NA	NA	NA	NA	
GO:19016C	Alpha-amin	14	201	0.59	0.0022	13	201	0.62	0.0027	
GO:00064C	RNA localiz	13	176	0.61	0.0023	10	176	0.56	0.0333	
GO:00458E	Positive reg	54	1678	0.25	0.0023	NA	NA	NA	NA	
GO:007092	Organelle a	34	872	0.34	0.0023	NA	NA	NA	NA	
GO:00063E	Transcriptic	21	418	0.45	0.0027	NA	NA	NA	NA	
GO:00442E	Small mole	54	1690	0.25	0.0027	75	1690	0.45	7.70E-13	
GO:19018E	Negative re	9	84	0.78	0.0027	NA	NA	NA	NA	
GO:00004E	Maturation	7	47	0.92	0.0029	NA	NA	NA	NA	
GO:000151	RNA methy	9	85	0.77	0.0029	NA	NA	NA	NA	

GO:00903C	Mitotic spir	7	48	0.91	0.0032	NA	NA	NA	NA
GO:00514S	Regulation	25	564	0.39	0.0035	NA	NA	NA	NA
GO:00106S	Negative re	19	367	0.46	0.0041	15	367	0.42	0.0437
GO:00512A	Regulation	76	2708	0.19	0.0044	82	2708	0.29	1.59E-06
GO:00516A	Cellular loc	75	2661	0.2	0.0044	85	2661	0.31	8.36E-08
GO:00310E	Regulation	10	114	0.69	0.0046	NA	NA	NA	NA
GO:00610A	Positive reg	9	92	0.74	0.0048	NA	NA	NA	NA
GO:00330A	Regulation	15	249	0.53	0.0049	12	249	0.49	0.0385
GO:00708A	Response t	7	52	0.88	0.0049	NA	NA	NA	NA
GO:00066C	Protein imp	10	116	0.68	0.0051	NA	NA	NA	NA
GO:00328E	Regulation	16	280	0.5	0.0051	NA	NA	NA	NA
GO:00725S	Establishm	18	344	0.47	0.0053	19	344	0.55	0.00055
GO:00440E	Regulation	37	1038	0.3	0.0054	34	1038	0.32	0.0048
GO:19015E	Organonitro	50	1579	0.25	0.0058	48	1579	0.29	0.0012
GO:00018Z	Blastocyst f	8	74	0.78	0.0061	NA	NA	NA	NA
GO:00432A	Regulation	11	144	0.63	0.0061	NA	NA	NA	NA
GO:00064T	Translation	28	700	0.35	0.0065	26	700	0.38	0.0053
GO:00432S	Regulation	20	416	0.43	0.0065	21	416	0.51	0.00061
GO:00469C	Intracellula	43	1297	0.27	0.0069	48	1297	0.37	1.47E-05
GO:19033T	Negative re	9	99	0.71	0.0076	NA	NA	NA	NA
GO:00335S	Cellular res	50	1609	0.24	0.0087	NA	NA	NA	NA
GO:00339E	P-body ass	4	12	1.27	0.0087	NA	NA	NA	NA
GO:00436C	Amide bios	31	830	0.32	0.0088	33	830	0.41	0.00027
GO:00510S	Regulation	19	394	0.43	0.0088	NA	NA	NA	NA
GO:00224T	Cellular co	16	300	0.47	0.0099	NA	NA	NA	NA
GO:00512A	Negative re	36	1035	0.29	0.01	32	1035	0.3	0.0161
GO:00093C	rRNA transc	4	13	1.23	0.0108	NA	NA	NA	NA
GO:00000C	Mitochondr	5	26	1.03	0.011	NA	NA	NA	NA

GO:00218(	Cerebral cc	5	26	1.03	0.011	NA	NA	NA	NA	
GO:004581	Negative re	8	83	0.73	0.0116	8	83	0.79	0.0063	
GO:00327E	Positive reg	6	43	0.89	0.0119	NA	NA	NA	NA	
GO:00511(	Positive reg	40	1212	0.27	0.0122	41	1212	0.34	6.00E-04	
GO:000651	Peptide me	31	850	0.31	0.0124	34	850	0.41	0.00017	
GO:004341	Macromole	15	276	0.48	0.0124	NA	NA	NA	NA	
GO:000644	Regulation	7	63	0.79	0.0127	NA	NA	NA	NA	
GO:00511E	Nuclear exp	10	133	0.62	0.0127	NA	NA	NA	NA	
GO:199083	Cellular res	10	133	0.62	0.0127	NA	NA	NA	NA	
GO:003312	Positive reg	6	45	0.87	0.0144	NA	NA	NA	NA	
GO:00436(	Cellular am	37	1102	0.27	0.0147	49	1102	0.45	5.71E-08	
GO:00650(	Biological r	262	12586	0.06	0.0147	234	12586	0.08	0.0054	
GO:002261	Ribonucleo	16	314	0.45	0.0148	NA	NA	NA	NA	
GO:002181	Nucleokine	3	5	1.52	0.0152	NA	NA	NA	NA	
GO:00507E	Regulation	249	11860	0.07	0.0153	225	11860	0.08	0.0025	
GO:00322E	Methylatior	16	316	0.45	0.0157	NA	NA	NA	NA	
GO:00090(	Glutamine	7	66	0.77	0.0158	NA	NA	NA	NA	
GO:00327E	Regulation	7	66	0.77	0.0158	NA	NA	NA	NA	
GO:001657	Histone mo	20	454	0.39	0.0166	NA	NA	NA	NA	
GO:000263	Regulation	7	67	0.77	0.017	NA	NA	NA	NA	
GO:00063E	Regulation	65	2341	0.19	0.017	NA	NA	NA	NA	
GO:00091(	Ribonucleo	7	67	0.77	0.017	NA	NA	NA	NA	
GO:00315(	Heterochro	7	67	0.77	0.017	6	67	0.76	0.0435	
GO:004591	Negative re	6	47	0.85	0.017	NA	NA	NA	NA	
GO:00713(	Cellular res	6	47	0.85	0.017	NA	NA	NA	NA	
GO:00063(	Transcriptic	5	30	0.97	0.0174	NA	NA	NA	NA	
GO:00105(	Regulation	8	90	0.7	0.0174	NA	NA	NA	NA	
GO:00310E	Regulation	13	226	0.51	0.0174	NA	NA	NA	NA	

GO:004591	Positive reg	8	90	0.7	0.0174	NA	NA	NA	NA	
GO:190227	Regulation	6	48	0.84	0.0182	NA	NA	NA	NA	
GO:00314E	Positive reg	4	16	1.14	0.0183	NA	NA	NA	NA	
GO:00197E	Carboxylic	32	917	0.29	0.0186	47	917	0.52	1.86E-09	
GO:004682	Regulation	10	142	0.59	0.0186	NA	NA	NA	NA	
GO:00026E	Positive reg	6	49	0.83	0.0198	NA	NA	NA	NA	
GO:00069E	Nuclear en	6	49	0.83	0.0198	7	49	0.96	0.0023	
GO:00064C	tRNA modif	8	93	0.68	0.0204	NA	NA	NA	NA	
GO:00308E	Negative re	6	50	0.83	0.0214	6	50	0.89	0.0137	
GO:004594	Negative re	4	17	1.12	0.0215	NA	NA	NA	NA	
GO:003144	Regulation	5	32	0.94	0.0216	NA	NA	NA	NA	
GO:00329E	Positive reg	5	32	0.94	0.0216	NA	NA	NA	NA	
GO:00905C	RNA phosp	10	146	0.58	0.0218	NA	NA	NA	NA	
GO:00611E	mRNA dest	7	72	0.73	0.0229	NA	NA	NA	NA	
GO:00004E	Cleavage in	5	33	0.93	0.0241	NA	NA	NA	NA	
GO:001657	Histone ph	5	33	0.93	0.0241	NA	NA	NA	NA	
GO:00451E	Regulation	5	33	0.93	0.0241	NA	NA	NA	NA	
GO:00506E	Negative re	5	33	0.93	0.0241	NA	NA	NA	NA	
GO:00323E	Regulation	16	334	0.43	0.0243	NA	NA	NA	NA	
GO:00514E	Negative re	11	177	0.54	0.0243	NA	NA	NA	NA	
GO:005112	Negative re	27	740	0.31	0.0256	26	740	0.35	0.0106	
GO:00001E	rRNA modif	5	34	0.91	0.0264	NA	NA	NA	NA	
GO:00004E	Maturation	5	34	0.91	0.0264	NA	NA	NA	NA	
GO:00433E	Positive reg	6	53	0.8	0.0266	NA	NA	NA	NA	
GO:005164	Mitochondr	6	53	0.8	0.0266	NA	NA	NA	NA	
GO:00310E	Positive reg	7	75	0.72	0.0272	NA	NA	NA	NA	
GO:19029C	Regulation	18	408	0.39	0.0272	NA	NA	NA	NA	
GO:003111	Regulation	8	99	0.65	0.0273	NA	NA	NA	NA	

GO:00506E	RNA transp	10	152	0.56	0.0273	NA	NA	NA	NA	
GO:00068E	Intracellula	25	669	0.32	0.0281	28	669	0.43	0.00056	
GO:007142	Hematopoi	4	19	1.07	0.0281	NA	NA	NA	NA	
GO:00106E	Positive reg	22	557	0.34	0.029	20	557	0.36	0.035	
GO:003227	Regulation	12	213	0.5	0.0296	13	213	0.59	0.0044	
GO:00510E	Positive reg	16	343	0.42	0.0297	NA	NA	NA	NA	
GO:003112	RNA 3-end	8	101	0.65	0.0299	NA	NA	NA	NA	
GO:00091E	Ribonucleo	5	36	0.89	0.0312	NA	NA	NA	NA	
GO:000002	Ribosomal	8	102	0.64	0.0313	NA	NA	NA	NA	
GO:00511C	Negative re	10	156	0.55	0.0314	NA	NA	NA	NA	
GO:00027C	Regulation	10	157	0.55	0.0328	NA	NA	NA	NA	
GO:00108E	Regulation	3	8	1.32	0.0335	NA	NA	NA	NA	
GO:00069E	Response t	81	3187	0.15	0.0349	78	3187	0.19	0.0037	
GO:00507E	Regulation	235	11253	0.07	0.0349	NA	NA	NA	NA	
GO:00723E	Organelle t	7	80	0.69	0.0359	NA	NA	NA	NA	
GO:000654	Glutamine	4	21	1.03	0.0366	NA	NA	NA	NA	
GO:00102E	Endomemb	20	498	0.35	0.0392	25	498	0.51	0.00012	
GO:00310E	Negative re	6	59	0.75	0.0403	NA	NA	NA	NA	
GO:00511C	Regulation	8	107	0.62	0.0403	NA	NA	NA	NA	
GO:003102	Microtubul	8	109	0.61	0.0449	NA	NA	NA	NA	
GO:000182	Blastocyst	10	167	0.52	0.0485	NA	NA	NA	NA	
GO:000627	DNA replica	4	23	0.99	0.0485	NA	NA	NA	NA	
GO:00063E	DNA-templ	7	85	0.66	0.0485	NA	NA	NA	NA	
GO:00069E	Nuclear po	4	23	0.99	0.0485	NA	NA	NA	NA	
GO:00310E	Positive reg	9	138	0.56	0.0485	NA	NA	NA	NA	
GO:00063E	Regulation	5	41	0.83	0.0495	NA	NA	NA	NA	
GO:00063C	Double-stra	11	198	0.49	0.0496	NA	NA	NA	NA	
GO:00090E	Catabolic p	NA	NA	NA	NA	72	1999	0.36	2.23E-08	

GO:190157	Organic sul	NA	NA	NA	NA	67	1714	0.4	4.21E-09
GO:004424	Cellular cat	NA	NA	NA	NA	58	1557	0.38	5.24E-07
GO:00327E	Monocarbo	NA	NA	NA	NA	24	615	0.4	0.0049
GO:00463S	Carboxylic	NA	NA	NA	NA	14	214	0.62	0.0014
GO:19015E	Organonitro	NA	NA	NA	NA	147	5394	0.24	4.27E-10
GO:00159E	Energy deri	NA	NA	NA	NA	14	235	0.58	0.0031
GO:004424	Cellular lipi	NA	NA	NA	NA	NA	NA	NA	NA
GO:001604	Lipid catab	NA	NA	NA	NA	NA	NA	NA	NA
GO:190113	Carbohydra	NA	NA	NA	NA	35	1002	0.35	0.0013
GO:00442E	Small mole	NA	NA	NA	NA	21	354	0.58	8.43E-05
GO:000662	Lipid metat	NA	NA	NA	NA	NA	NA	NA	NA
GO:00453E	Cellular res	NA	NA	NA	NA	11	166	0.63	0.0073
GO:00060S	Tricarboxyli	NA	NA	NA	NA	9	35	1.22	5.68E-06
GO:00090E	Fatty acid c	NA	NA	NA	NA	NA	NA	NA	NA
GO:00066E	Fatty acid n	NA	NA	NA	NA	NA	NA	NA	NA
GO:00066E	Fatty acid b	NA	NA	NA	NA	8	59	0.94	0.00096
GO:00060S	Generation	NA	NA	NA	NA	20	416	0.49	0.0016
GO:00070C	Mitochondı	NA	NA	NA	NA	19	439	0.44	0.0073
GO:00090E	Aerobic res	NA	NA	NA	NA	10	139	0.66	0.0079
GO:004364	Dicarboxyli	NA	NA	NA	NA	12	93	0.92	2.05E-05
GO:00442S	Cellular lipi	NA	NA	NA	NA	NA	NA	NA	NA
GO:19015E	Organonitro	NA	NA	NA	NA	37	1061	0.35	0.00085
GO:00650C	Regulation	NA	NA	NA	NA	96	3854	0.2	0.00029
GO:005117	Localizatio	NA	NA	NA	NA	117	4471	0.22	1.54E-06
GO:00067S	Sulfur com	NA	NA	NA	NA	23	333	0.65	2.69E-06
GO:00090E	Branched-c	NA	NA	NA	NA	5	20	1.2	0.0031
GO:000597	Carbohydra	NA	NA	NA	NA	NA	NA	NA	NA
GO:00330S	Macromole	NA	NA	NA	NA	79	2366	0.33	6.10E-08

GO:00512З	Establishm	NA	NA	NA	NA	101	3839	0.23	1.77E-05
GO:00302Ѕ	Lipid modif	NA	NA	NA	NA	NA	NA	NA	NA
GO:003387	Ribonucleo	NA	NA	NA	NA	11	114	0.79	0.00053
GO:00340З	Purine nucl	NA	NA	NA	NA	11	114	0.79	0.00053
GO:00349Ɛ	Mitochondı	NA	NA	NA	NA	NA	NA	NA	NA
GO:00451Ɛ	Establishm	NA	NA	NA	NA	48	1173	0.42	9.19E-07
GO:00065С	Proteolysis	NA	NA	NA	NA	36	1197	0.28	0.0121
GO:00066З	acyl-CoA m	NA	NA	NA	NA	10	90	0.85	0.00048
GO:000681	Transport	NA	NA	NA	NA	91	3660	0.2	0.00055
GO:00550Ɛ	Nucleobası	NA	NA	NA	NA	27	582	0.47	0.00017
GO:006102	Membrane	NA	NA	NA	NA	30	684	0.45	0.00014
GO:00090Ɛ	Cellular am	NA	NA	NA	NA	NA	NA	NA	NA
GO:00081С	Protein loc	NA	NA	NA	NA	67	1924	0.35	3.56E-07
GO:00091Ѕ	Purine ribo	NA	NA	NA	NA	21	421	0.5	7.00E-04
GO:000911	Nucleotide	NA	NA	NA	NA	26	516	0.51	7.82E-05
GO:00196Ɛ	Ribose pho	NA	NA	NA	NA	23	456	0.51	0.00028
GO:00717С	Nitrogen cc	NA	NA	NA	NA	49	1456	0.33	0.00011
GO:00150З	Protein trar	NA	NA	NA	NA	41	1062	0.39	4.11E-05
GO:00196З	Organopho	NA	NA	NA	NA	29	934	0.3	0.0267
GO:003287	Regulation	NA	NA	NA	NA	63	2276	0.25	9.00E-04
GO:00717С	Organic sul	NA	NA	NA	NA	52	1835	0.26	0.0027
GO:00100З	Response t	NA	NA	NA	NA	73	2827	0.22	0.0015
GO:00061С	succinyl-C	NA	NA	NA	NA	3	10	1.28	0.0437
GO:00090Ѕ	Macromole	NA	NA	NA	NA	32	967	0.33	0.0063
GO:00065Ѕ	Isoleucine	NA	NA	NA	NA	3	6	1.51	0.017
GO:00061С	Succinate r	NA	NA	NA	NA	4	7	1.56	0.0017
GO:00161Ɛ	Vesicle-me	NA	NA	NA	NA	38	1231	0.3	0.0057
GO:005164	Nucleus lo	NA	NA	NA	NA	NA	NA	NA	NA

GO:00065	Leucine ca	NA	NA	NA	NA	3	8	1.38	0.0293
GO:00070	Lysosome	NA	NA	NA	NA	NA	NA	NA	NA
GO:00463	Ribose pho	NA	NA	NA	NA	10	186	0.54	0.0441
GO:00091	Purine ribo	NA	NA	NA	NA	NA	NA	NA	NA
GO:00481	Golgi vesicl	NA	NA	NA	NA	NA	NA	NA	NA
GO:00510	Positive reg	NA	NA	NA	NA	37	1045	0.36	0.00065
GO:00708	Cellular res	NA	NA	NA	NA	62	2646	0.18	0.0435
GO:00097	Response t	NA	NA	NA	NA	NA	NA	NA	NA
GO:00097	Response t	NA	NA	NA	NA	NA	NA	NA	NA
GO:19905	Mitochondr	NA	NA	NA	NA	NA	NA	NA	NA
GO:00061	Oxidative p	NA	NA	NA	NA	NA	NA	NA	NA
GO:00328	Regulation	NA	NA	NA	NA	32	939	0.34	0.0041
GO:00100	Response t	NA	NA	NA	NA	18	384	0.48	0.0048
GO:19016	Response t	NA	NA	NA	NA	34	1149	0.28	0.0218
GO:00603	Regulation	NA	NA	NA	NA	36	1043	0.34	0.0013
GO:00072	Multicellul	NA	NA	NA	NA	93	4353	0.14	0.0413
GO:00102	Response t	NA	NA	NA	NA	32	1056	0.29	0.0218
GO:00195	Protein me	NA	NA	NA	NA	106	4367	0.19	0.00024
GO:00066	Protein pro	NA	NA	NA	NA	3	4	1.68	0.0086
GO:00109	Regulation	NA	NA	NA	NA	54	1740	0.3	0.00027
GO:00605	Negative re	NA	NA	NA	NA	37	1125	0.32	0.0024
GO:00606	Regulation	NA	NA	NA	NA	25	647	0.39	0.0042
GO:00100	Response t	NA	NA	NA	NA	22	577	0.39	0.0114
GO:00516	Localizatio	NA	NA	NA	NA	20	550	0.37	0.0308
GO:00442	Cellular ca	NA	NA	NA	NA	5	32	1	0.015
GO:00447	Modulation	NA	NA	NA	NA	6	33	1.07	0.0025
GO:00064	Protein fol	NA	NA	NA	NA	12	243	0.5	0.033
GO:00161	Glycoside	NA	NA	NA	NA	3	8	1.38	0.0293

GO:00060E	Organic aci	NA	NA	NA	NA	49	956	0.52	7.17E-10
GO:003424	Regulation	NA	NA	NA	NA	35	592	0.58	2.98E-08
GO:00300E	Actin cytos	NA	NA	NA	NA	28	566	0.5	4.11E-05
GO:003002	Actin filame	NA	NA	NA	NA	29	625	0.47	8.14E-05
GO:001062	Positive reg	NA	NA	NA	NA	44	1226	0.36	8.46E-05
GO:007252	Purine-con	NA	NA	NA	NA	23	465	0.5	0.00036
GO:00061E	Purine nucl	NA	NA	NA	NA	22	436	0.51	0.00043
GO:00083E	Regulation	NA	NA	NA	NA	13	161	0.71	0.00047
GO:00430E	Regulation	NA	NA	NA	NA	49	1557	0.3	0.00051
GO:00092E	Ribonucleo	NA	NA	NA	NA	22	443	0.5	0.00052
GO:00226C	Regulation	NA	NA	NA	NA	19	347	0.54	0.00059
GO:00429E	Regulation	NA	NA	NA	NA	48	1531	0.3	0.00063
GO:00458C	Positive reg	NA	NA	NA	NA	11	121	0.76	0.00077
GO:009951	Actin filame	NA	NA	NA	NA	6	25	1.19	8.00E-04
GO:00458E	Positive reg	NA	NA	NA	NA	19	361	0.53	9.00E-04
GO:003132	Regulation	NA	NA	NA	NA	29	745	0.4	0.0012
GO:009743	Supramole	NA	NA	NA	NA	24	549	0.45	0.0012
GO:19028E	Regulation	NA	NA	NA	NA	9	86	0.83	0.0016
GO:00098E	Regulation	NA	NA	NA	NA	34	973	0.35	0.0017
GO:004854	Positive reg	NA	NA	NA	NA	4	9	1.45	0.0031
GO:003133	Negative re	NA	NA	NA	NA	14	237	0.58	0.0033
GO:00507E	Regulation	NA	NA	NA	NA	66	2555	0.22	0.0034
GO:00300E	Vesicle trar	NA	NA	NA	NA	5	21	1.18	0.0037
GO:004304	Peptide bio	NA	NA	NA	NA	27	724	0.38	0.0038
GO:00301C	Regulation	NA	NA	NA	NA	14	248	0.56	0.0049
GO:007012	Regulation	NA	NA	NA	NA	5	24	1.12	0.0058
GO:000091	Cytokinesis	NA	NA	NA	NA	9	107	0.73	0.0061
GO:00512E	Establishm	NA	NA	NA	NA	7	61	0.87	0.0063

GO:200037	Regulation	NA	NA	NA	NA	11	167	0.62	0.0076
GO:00301(	Regulation	NA	NA	NA	NA	26	724	0.36	0.0081
GO:00447(	Positive reg	NA	NA	NA	NA	4	13	1.29	0.0081
GO:00516(	Nuclear po	NA	NA	NA	NA	3	4	1.68	0.0086
GO:00325(	Developme	NA	NA	NA	NA	119	5590	0.13	0.0091
GO:00226(	Regulation	NA	NA	NA	NA	32	993	0.31	0.0092
GO:190437	Positive reg	NA	NA	NA	NA	7	66	0.83	0.0092
GO:005082	Protein stal	NA	NA	NA	NA	14	271	0.52	0.0101
GO:00070(	Plasma me	NA	NA	NA	NA	10	147	0.64	0.0113
GO:190382	Positive reg	NA	NA	NA	NA	20	498	0.41	0.0116
GO:00308(	Regulation	NA	NA	NA	NA	10	148	0.64	0.0117
GO:005124	Positive reg	NA	NA	NA	NA	43	1529	0.26	0.0121
GO:007012	Mitochondı	NA	NA	NA	NA	3	5	1.58	0.0125
GO:003004	Actin filam	NA	NA	NA	NA	8	96	0.73	0.0133
GO:000641	Translation	NA	NA	NA	NA	7	72	0.79	0.0137
GO:009951	Vesicle cyt	NA	NA	NA	NA	7	72	0.79	0.0137
GO:005124	Positive reg	NA	NA	NA	NA	44	1593	0.25	0.014
GO:003164	Regulation	NA	NA	NA	NA	17	393	0.44	0.0143
GO:00488(	Anatomical	NA	NA	NA	NA	110	5157	0.14	0.015
GO:190288	Negative re	NA	NA	NA	NA	5	32	1	0.015
GO:00430(	Negative re	NA	NA	NA	NA	31	988	0.3	0.0158
GO:00098(	Negative re	NA	NA	NA	NA	15	328	0.47	0.0182
GO:00516(	Establishm	NA	NA	NA	NA	10	164	0.59	0.022
GO:00342(	Positive reg	NA	NA	NA	NA	11	196	0.56	0.0222
GO:00353(	Peroxisom	NA	NA	NA	NA	3	7	1.44	0.0228
GO:00516(	Actin filam	NA	NA	NA	NA	5	36	0.95	0.0228
GO:00343(	Cell junctio	NA	NA	NA	NA	21	578	0.37	0.0247
GO:005101	Actin filam	NA	NA	NA	NA	6	58	0.82	0.0254

GO:00995€	Modificatio	NA	NA	NA	NA	4	20	1.11	0.0258
GO:190217	Regulation	NA	NA	NA	NA	4	20	1.11	0.0258
GO:190307	Regulation	NA	NA	NA	NA	8	109	0.67	0.0258
GO:004572	Positive reg	NA	NA	NA	NA	10	169	0.58	0.0264
GO:190437	Regulation	NA	NA	NA	NA	9	140	0.61	0.0284
GO:190307	Positive reg	NA	NA	NA	NA	6	60	0.81	0.029
GO:004218	Ketone cata	NA	NA	NA	NA	4	21	1.09	0.0292
GO:200064	Positive reg	NA	NA	NA	NA	3	8	1.38	0.0293
GO:004327	Apoptotic c	NA	NA	NA	NA	5	39	0.91	0.0296
GO:004002	Regulation	NA	NA	NA	NA	9	142	0.61	0.03
GO:000701	Actin filam	NA	NA	NA	NA	13	281	0.47	0.035
GO:00508(	Synapse or	NA	NA	NA	NA	15	357	0.43	0.036
GO:000652	Regulation	NA	NA	NA	NA	3	9	1.33	0.0363
GO:004408	Positive reg	NA	NA	NA	NA	20	560	0.36	0.0365
GO:007252	Purine-con	NA	NA	NA	NA	10	179	0.55	0.0365
GO:014037	Antiviral inr	NA	NA	NA	NA	4	23	1.05	0.0365
GO:005123	Regulation	NA	NA	NA	NA	66	2847	0.17	0.0393
GO:014005	Mitochondı	NA	NA	NA	NA	7	91	0.69	0.0394
GO:004306	Negative re	NA	NA	NA	NA	29	967	0.28	0.0401
GO:004858	Regulation	NA	NA	NA	NA	84	3843	0.15	0.0407
GO:00517(	Biological p	NA	NA	NA	NA	7	92	0.69	0.0413
GO:003001	Establishm	NA	NA	NA	NA	9	153	0.58	0.0437
GO:005079	Regulation	NA	NA	NA	NA	54	2223	0.19	0.0437
GO:008013	Regulation	NA	NA	NA	NA	35	1261	0.25	0.0437
GO:009023	Regulation	NA	NA	NA	NA	3	10	1.28	0.0437
GO:009888	Modificatio	NA	NA	NA	NA	3	10	1.28	0.0437
GO:001095	Positive reg	NA	NA	NA	NA	10	188	0.53	0.0473
GO:00307(	Cytoskelet	NA	NA	NA	NA	10	188	0.53	0.0473

PROCESS_D7_30mM_UP

#term ID	term description.NIST	observed gc	backgrounc	strength.NI	false disco	observed gene cou	backgrounc	strength.DF	false discovery rate.DP12
GO:00099E	Cellular process	524	15994	0.14	8.31E-41	289	15994	0.14	1.32E-20
GO:00090E	Catabolic process	149	1999	0.49	2.74E-31	63	1999	0.38	8.90E-08
GO:005164	Cellular localization	170	2661	0.43	4.84E-29	77	2661	0.34	2.72E-08
GO:00330E	Macromolecule localization	158	2366	0.45	1.19E-28	79	2366	0.4	2.75E-11
GO:00081C	Protein localization	140	1924	0.48	2.37E-28	67	1924	0.42	5.72E-10
GO:00081E	Metabolic process	342	8581	0.22	1.74E-27	191	8581	0.23	8.87E-15
GO:00469C	Intracellular transport	110	1297	0.55	1.38E-26	56	1297	0.51	2.45E-11
GO:005117	Localization	223	4471	0.32	7.27E-26	100	4471	0.23	1.16E-05
GO:190157	Organic substance catabolic process	126	1714	0.49	1.18E-25	59	1714	0.42	1.59E-08
GO:000681	Transport	196	3660	0.35	1.78E-25	89	3660	0.26	2.34E-06
GO:00512E	Establishment of localization	201	3839	0.34	3.87E-25	92	3839	0.26	2.34E-06
GO:00150E	Protein transport	96	1062	0.58	7.61E-25	47	1062	0.52	8.91E-10
GO:00451E	Establishment of protein localization	101	1173	0.56	8.40E-25	49	1173	0.5	1.94E-09
GO:00717C	Organic substance metabolic process	323	8137	0.22	1.03E-24	184	8137	0.23	1.18E-14
GO:004424	Cellular catabolic process	114	1557	0.49	7.51E-23	47	1557	0.36	4.00E-05
GO:005164	Establishment of localization in cell	119	1689	0.47	1.09E-22	62	1689	0.44	5.72E-10
GO:00717C	Nitrogen compound transport	109	1456	0.5	1.84E-22	59	1456	0.49	4.73E-11
GO:003287	Regulation of localization	140	2276	0.41	5.29E-22	50	2276	0.22	0.0234
GO:00161E	Vesicle-mediated transport	98	1231	0.52	9.95E-22	40	1231	0.39	5.48E-05
GO:00442E	Cellular metabolic process	285	7040	0.23	2.07E-21	167	7040	0.25	2.07E-14
GO:00717C	Organic substance transport	122	1835	0.44	2.14E-21	65	1835	0.43	5.72E-10
GO:00068E	Intracellular protein transport	69	669	0.64	3.22E-20	37	669	0.62	6.89E-10
GO:00442E	Primary metabolic process	298	7736	0.21	1.76E-19	175	7736	0.23	1.54E-13
GO:00442E	Small molecule metabolic process	112	1690	0.44	2.74E-19	68	1690	0.48	6.99E-13
GO:19015E	Organonitrogen compound metabolic process	233	5394	0.26	2.82E-19	122	5394	0.23	8.90E-08
GO:00100E	Response to organic substance	153	2827	0.36	2.95E-19	67	2827	0.25	0.00029
GO:00301E	Protein catabolic process	70	741	0.6	1.19E-18	27	741	0.44	0.00048
GO:00090E	Macromolecule catabolic process	79	967	0.53	9.17E-18	35	967	0.44	3.44E-05
GO:19015E	Organonitrogen compound catabolic process	82	1061	0.51	3.70E-17	32	1061	0.36	0.002
GO:005112	Regulation of cellular component organization	136	2504	0.36	8.10E-17	53	2504	0.2	0.0329
GO:005104	Regulation of transport	114	1906	0.4	1.66E-16	44	1906	0.24	0.0209
GO:00708E	Cellular response to chemical stimulus	138	2646	0.34	1.09E-15	60	2646	0.23	0.0029
GO:00516C	Proteolysis involved in protein catabolic process	58	635	0.58	1.36E-14	NA	NA	NA	NA
GO:00065C	Proteolysis	82	1197	0.46	2.59E-14	NA	NA	NA	NA
GO:004851	Positive regulation of biological process	244	6368	0.21	6.36E-14	124	6368	0.17	0.00016
GO:00650C	Biological regulation	397	12586	0.12	1.01E-13	209	12586	0.1	0.00018
GO:00650C	Regulation of biological quality	171	3854	0.27	1.07E-13	NA	NA	NA	NA
GO:00064E	Protein folding	35	243	0.78	1.61E-13	17	243	0.72	1.88E-05

GO:004222	Response to chemical	189	4477	0.25	1.69E-13	NA	NA	NA	NA	NA	
GO:00161	Endosomal transport	33	215	0.81	2.06E-13		12	215	0.62	0.0046	
GO:00068	Nitrogen compound metabolic process	262	7145	0.19	4.00E-13		153	7145	0.21	4.48E-09	
GO:000651	Ubiquitin-dependent protein catabolic process	51	552	0.59	6.36E-13		23	552	0.5	0.00034	
GO:00442	Cellular macromolecule catabolic process	60	755	0.52	1.06E-12		31	755	0.49	1.71E-05	
GO:006034	Regulation of cellular localization	72	1043	0.46	1.33E-12	NA	NA	NA	NA	NA	
GO:004852	Positive regulation of cellular process	222	5758	0.21	1.86E-12		110	5758	0.16	0.0016	
GO:00507	Regulation of biological process	375	11860	0.12	3.20E-12		189	11860	0.08	0.0166	
GO:00650	Regulation of molecular function	137	2956	0.29	9.73E-12		61	2956	0.19	0.0243	
GO:005124	Regulation of protein metabolic process	129	2708	0.3	9.98E-12		65	2708	0.26	0.00029	
GO:001604	Cellular component organization	215	5621	0.2	1.46E-11		114	5621	0.19	9.01E-05	
GO:00328	Regulation of protein localization	65	939	0.46	2.51E-11	NA	NA	NA	NA	NA	
GO:006062	Regulation of vesicle-mediated transport	52	647	0.53	4.53E-11	NA	NA	NA	NA	NA	
GO:00104	Proteasomal protein catabolic process	39	379	0.63	5.17E-11	NA	NA	NA	NA	NA	
GO:00440	Regulation of cellular component biogenesis	68	1038	0.44	6.94E-11	NA	NA	NA	NA	NA	
GO:00481	Golgi vesicle transport	33	276	0.7	8.84E-11		15	276	0.61	0.00087	
GO:00510	Positive regulation of transport	68	1045	0.44	8.99E-11	NA	NA	NA	NA	NA	
GO:001953	Protein metabolic process	176	4367	0.23	1.26E-10		84	4367	0.16	0.0159	
GO:003304	Regulation of organelle organization	74	1214	0.41	1.51E-10		33	1214	0.31	0.0087	
GO:00461	Alcohol biosynthetic process	21	101	0.94	1.74E-10		11	101	0.92	5.48E-05	
GO:007184	Cellular component organization or biogenesis	218	5887	0.19	2.02E-10		119	5887	0.18	5.47E-05	
GO:007131	Cellular response to organic substance	104	2069	0.32	2.06E-10		51	2069	0.27	0.0017	
GO:19016	Response to nitrogen compound	71	1149	0.41	2.40E-10	NA	NA	NA	NA	NA	
GO:001024	Response to organonitrogen compound	67	1056	0.42	3.58E-10	NA	NA	NA	NA	NA	
GO:001094	Regulation of cell death	92	1740	0.35	3.71E-10	NA	NA	NA	NA	NA	
GO:00442	Small molecule biosynthetic process	39	428	0.58	1.35E-09		28	428	0.69	1.01E-08	
GO:00514	Regulation of cytoskeleton organization	45	564	0.52	2.06E-09	NA	NA	NA	NA	NA	
GO:00507	Regulation of cellular process	349	11253	0.11	3.14E-09		179	11253	0.08	0.0327	
GO:00060	Alcohol metabolic process	33	325	0.63	4.08E-09		19	325	0.65	3.92E-05	
GO:000674	Glutathione metabolic process	17	72	1	4.08E-09		7	72	0.87	0.0071	
GO:00507	Regulation of catalytic activity	105	2223	0.3	4.94E-09	NA	NA	NA	NA	NA	
GO:190161	Organic hydroxy compound metabolic process	40	473	0.55	5.52E-09		25	473	0.6	4.09E-06	
GO:00067	Sulfur compound metabolic process	33	333	0.62	7.01E-09		13	333	0.47	0.0432	
GO:00164	Cytosolic transport	22	142	0.81	7.01E-09	NA	NA	NA	NA	NA	
GO:00508	Response to stimulus	268	8055	0.14	1.12E-08	NA	NA	NA	NA	NA	
GO:00197	Carboxylic acid metabolic process	58	917	0.42	1.19E-08		39	917	0.51	1.61E-07	
GO:004851	Negative regulation of biological process	195	5319	0.19	1.46E-08	NA	NA	NA	NA	NA	
GO:00060	Organic acid metabolic process	59	956	0.41	1.94E-08	NA	NA	NA	NA	NA	
GO:001407	Response to organic cyclic compound	59	964	0.41	2.57E-08	NA	NA	NA	NA	NA	
GO:00432	Regulation of protein-containing complex assembly	36	416	0.56	2.72E-08	NA	NA	NA	NA	NA	

GO:190113 Carbohydrate derivative metabolic process	60	1002	0.4	3.88E-08		34	1002	0.41	0.00016
GO:00069 Response to stress	132	3187	0.24	3.96E-08		65	3187	0.19	0.0209
GO:00550 Nucleobase-containing small molecule metabolic process	43	582	0.49	4.57E-08		27	582	0.54	1.28E-05
GO:00196 Organophosphate metabolic process	57	934	0.41	5.60E-08		35	934	0.45	1.83E-05
GO:00421 Retrograde transport, endosome to Golgi	16	77	0.94	6.55E-08		6	77	0.77	0.0475
GO:00436 Cellular amide metabolic process	63	1102	0.38	7.33E-08	NA	NA	NA	NA	
GO:19054 Regulation of protein localization to membrane	24	198	0.71	7.33E-08	NA	NA	NA	NA	
GO:00485 Negative regulation of cellular process	176	4752	0.19	8.41E-08	NA	NA	NA	NA	
GO:19016 Organic hydroxy compound biosynthetic process	22	167	0.74	9.22E-08		13	167	0.77	0.00015
GO:00226 Cellular component assembly	110	2516	0.26	9.53E-08		57	2516	0.23	0.0046
GO:00431 Proteasome-mediated ubiquitin-dependent protein catabolic process	31	334	0.59	9.61E-08		16	334	0.56	0.0018
GO:00097 Response to endogenous stimulus	74	1425	0.34	1.11E-07		35	1425	0.27	0.0289
GO:00192 Regulation of metabolic process	226	6627	0.15	1.30E-07		119	6627	0.13	0.0084
GO:00511 Positive regulation of cellular component organization	66	1212	0.36	1.65E-07	NA	NA	NA	NA	
GO:19029 Regulation of supramolecular fiber organization	34	408	0.54	1.84E-07	NA	NA	NA	NA	
GO:00327 Monocarboxylic acid metabolic process	43	615	0.47	1.91E-07		27	615	0.52	2.98E-05
GO:00333 Protein localization to organelle	48	739	0.43	1.98E-07		30	739	0.49	2.98E-05
GO:00702 Regulation of establishment of protein localization	41	570	0.48	2.12E-07	NA	NA	NA	NA	
GO:00059 Carbohydrate metabolic process	39	527	0.49	2.54E-07		22	527	0.5	0.00051
GO:00066 Lipid metabolic process	65	1202	0.36	2.73E-07		35	1202	0.34	0.0017
GO:00098 Regulation of catabolic process	56	973	0.38	4.91E-07		27	973	0.32	0.024
GO:00610 Chaperone-mediated protein folding	15	78	0.91	4.91E-07	NA	NA	NA	NA	
GO:00300 Actin cytoskeleton organization	40	566	0.47	5.13E-07	NA	NA	NA	NA	
GO:00421 Regulation of protein catabolic process	31	363	0.55	5.31E-07	NA	NA	NA	NA	
GO:19038 Positive regulation of protein localization	37	498	0.49	5.68E-07	NA	NA	NA	NA	
GO:00322 Regulation of protein polymerization	23	213	0.66	1.03E-06	NA	NA	NA	NA	
GO:00067 Phosphorus metabolic process	88	1940	0.28	1.14E-06		51	1940	0.3	0.00038
GO:00082 Cholesterol metabolic process	17	113	0.8	1.15E-06		13	113	0.94	4.09E-06
GO:00800 Regulation of primary metabolic process	199	5780	0.16	1.15E-06		107	5780	0.15	0.0071
GO:00068 Endocytosis	33	422	0.52	1.19E-06		16	422	0.46	0.0185
GO:19026 Secondary alcohol metabolic process	18	129	0.77	1.19E-06		14	129	0.91	2.34E-06
GO:00335 Cellular response to stress	77	1609	0.3	1.24E-06	NA	NA	NA	NA	
GO:00069 Organelle organization	139	3632	0.2	1.31E-06		83	3632	0.24	6.92E-05
GO:00431 Macromolecule metabolic process	213	6322	0.15	1.38E-06		117	6322	0.15	0.0029
GO:00430 Regulation of programmed cell death	75	1557	0.3	1.48E-06	NA	NA	NA	NA	
GO:19017 Response to oxygen-containing compound	78	1648	0.3	1.50E-06	NA	NA	NA	NA	
GO:00510 Regulation of secretion	46	746	0.41	1.65E-06	NA	NA	NA	NA	
GO:00488 Anatomical structure development	181	5157	0.17	1.92E-06	NA	NA	NA	NA	
GO:00516 Localization within membrane	38	550	0.46	1.93E-06	NA	NA	NA	NA	
GO:00196 Ribose phosphate metabolic process	34	456	0.49	1.96E-06	NA	NA	NA	NA	

GO:003002	Actin filament-based process	41	625	0.44	2.01E-06	NA	NA	NA	NA	NA	
GO:00440E	Cellular component biogenesis	114	2815	0.23	2.14E-06		62	2815	0.22	0.0046	
GO:00325C	Developmental process	192	5590	0.16	2.69E-06	NA	NA	NA	NA	NA	
GO:000911	Nucleotide metabolic process	36	516	0.47	3.49E-06		25	516	0.56	1.80E-05	
GO:00070E	Vacuole organization	20	176	0.68	3.75E-06	NA	NA	NA	NA	NA	
GO:00513E	Regulation of hydrolase activity	54	996	0.36	5.02E-06	NA	NA	NA	NA	NA	
GO:00324E	Endocytic recycling	13	69	0.9	5.21E-06	NA	NA	NA	NA	NA	
GO:000972	Response to hormone	47	809	0.39	5.65E-06	NA	NA	NA	NA	NA	
GO:009887	Vesicle-mediated transport to the plasma membrane	17	130	0.74	6.10E-06	NA	NA	NA	NA	NA	
GO:000941	Response to xenobiotic stimulus	34	483	0.47	6.54E-06	NA	NA	NA	NA	NA	
GO:00487E	System development	144	3916	0.19	6.54E-06	NA	NA	NA	NA	NA	
GO:00106E	Positive regulation of organelle organization	37	557	0.44	6.78E-06	NA	NA	NA	NA	NA	
GO:000727	Multicellular organism development	156	4353	0.18	7.40E-06	NA	NA	NA	NA	NA	
GO:00440E	Positive regulation of cellular component biogenesis	37	560	0.44	7.59E-06	NA	NA	NA	NA	NA	
GO:00440E	Positive regulation of molecular function	73	1571	0.29	7.91E-06	NA	NA	NA	NA	NA	
GO:005122	Regulation of protein transport	36	537	0.45	8.03E-06	NA	NA	NA	NA	NA	
GO:003497	Response to endoplasmic reticulum stress	21	206	0.63	8.56E-06		10	206	0.56	0.0382	
GO:00092E	Ribonucleotide metabolic process	32	443	0.48	8.72E-06		21	443	0.55	0.00016	
GO:00067E	Phosphate-containing compound metabolic process	84	1919	0.26	8.87E-06		50	1919	0.29	0.00057	
GO:00066E	Fatty acid metabolic process	29	375	0.51	9.08E-06		15	375	0.48	0.0168	
GO:005171	Cellular response to stimulus	214	6532	0.14	9.93E-06	NA	NA	NA	NA	NA	
GO:00323E	Regulation of intracellular transport	27	334	0.53	1.09E-05		13	334	0.47	0.0442	
GO:19049E	Positive regulation of establishment of protein localization	27	334	0.53	1.09E-05	NA	NA	NA	NA	NA	
GO:00429E	Regulation of apoptotic process	71	1531	0.29	1.23E-05	NA	NA	NA	NA	NA	
GO:003297	Regulation of actin filament-based process	31	428	0.48	1.25E-05	NA	NA	NA	NA	NA	
GO:00974E	Supramolecular fiber organization	36	549	0.44	1.25E-05	NA	NA	NA	NA	NA	
GO:00070E	Vacuolar transport	18	157	0.68	1.35E-05	NA	NA	NA	NA	NA	
GO:00066E	Cholesterol biosynthetic process	10	40	1.02	1.62E-05		8	40	1.18	4.36E-05	
GO:190307	Regulation of protein localization to plasma membrane	15	109	0.76	1.74E-05	NA	NA	NA	NA	NA	
GO:005112	Negative regulation of cellular component organization	43	740	0.39	1.80E-05	NA	NA	NA	NA	NA	
GO:00060E	Generation of precursor metabolites and energy	30	416	0.48	2.07E-05		19	416	0.54	0.00066	
GO:005104	Positive regulation of secretion	29	394	0.49	2.19E-05	NA	NA	NA	NA	NA	
GO:000861	Lipid biosynthetic process	34	515	0.44	2.28E-05		20	515	0.47	0.0029	
GO:00091E	Purine ribonucleotide metabolic process	30	421	0.47	2.57E-05		20	421	0.55	0.00027	
GO:00602E	Regulation of macromolecule metabolic process	200	6089	0.14	2.69E-05		107	6089	0.12	0.0406	
GO:00090E	Biosynthetic process	104	2636	0.22	2.73E-05		77	2636	0.34	1.84E-08	
GO:190353	Regulation of secretion by cell	40	676	0.39	2.97E-05	NA	NA	NA	NA	NA	
GO:00102E	Endomembrane system organization	33	498	0.44	3.06E-05		21	498	0.5	0.00066	
GO:00329E	Regulation of actin cytoskeleton organization	28	379	0.49	3.14E-05	NA	NA	NA	NA	NA	
GO:006054	Negative regulation of cell death	56	1125	0.32	3.18E-05	NA	NA	NA	NA	NA	

GO:190157 Organic substance biosynthetic process	102	2581	0.22	3.27E-05		74	2581	0.34	9.70E-08	
GO:001605 Vesicle organization	23	269	0.55	3.29E-05	NA	NA	NA	NA		
GO:011005 Regulation of actin filament organization	24	291	0.54	3.38E-05	NA	NA	NA	NA		
GO:001003 Response to inorganic substance	36	577	0.42	3.41E-05	NA	NA	NA	NA		
GO:001988 Antigen processing and presentation	13	85	0.81	3.44E-05	NA	NA	NA	NA		
GO:000691 Autophagy	24	292	0.54	3.51E-05	NA	NA	NA	NA		
GO:001003 Response to metal ion	28	384	0.48	3.81E-05	NA	NA	NA	NA		
GO:000651 Peptide metabolic process	46	850	0.36	4.03E-05	NA	NA	NA	NA		
GO:003253 Regulation of cellular component size	30	433	0.46	4.06E-05	NA	NA	NA	NA		
GO:002241 Cellular component disassembly	24	300	0.53	5.29E-05	NA	NA	NA	NA		
GO:004425 Cellular lipid metabolic process	49	944	0.34	5.29E-05		26	944	0.32	0.0319	
GO:003399 Response to lipid	46	861	0.35	5.49E-05	NA	NA	NA	NA		
GO:007252 Purine-containing compound metabolic process	31	465	0.45	5.54E-05	NA	NA	NA	NA		
GO:190437 Regulation of protein localization to cell periphery	16	140	0.68	5.67E-05	NA	NA	NA	NA		
GO:005117 Regulation of nitrogen compound metabolic process	185	5595	0.14	5.68E-05	NA	NA	NA	NA		
GO:190354 Positive regulation of exosomal secretion	7	17	1.24	6.12E-05	NA	NA	NA	NA		
GO:003083 Regulation of actin filament depolymerization	11	62	0.87	6.66E-05	NA	NA	NA	NA		
GO:001975 Polyol metabolic process	14	108	0.73	6.93E-05	NA	NA	NA	NA		
GO:001250 Programmed cell death	46	872	0.34	7.31E-05	NA	NA	NA	NA		
GO:000657 Cellular modified amino acid metabolic process	19	201	0.6	7.46E-05		13	201	0.69	0.00066	
GO:005124 Positive regulation of protein metabolic process	68	1529	0.27	7.60E-05		38	1529	0.27	0.0148	
GO:004617 Polyol biosynthetic process	10	50	0.92	7.74E-05	NA	NA	NA	NA		
GO:004440 Biological process involved in symbiotic interaction	19	203	0.59	8.33E-05	NA	NA	NA	NA		
GO:006102 Membrane organization	39	684	0.38	8.33E-05	NA	NA	NA	NA		
GO:009040 Organophosphate biosynthetic process	31	479	0.43	9.23E-05		24	479	0.58	1.80E-05	
GO:000821 Cell death	47	914	0.33	1.00E-04	NA	NA	NA	NA		
GO:000820 Steroid metabolic process	20	229	0.56	0.00012		16	229	0.72	3.97E-05	
GO:001603 Viral process	16	151	0.65	0.00013	NA	NA	NA	NA		
GO:003650 ERAD pathway	13	98	0.74	0.00013	NA	NA	NA	NA		
GO:000806 Regulation of actin polymerization or depolymerization	17	171	0.62	0.00014	NA	NA	NA	NA		
GO:000962 Response to abiotic stimulus	56	1190	0.29	0.00014	NA	NA	NA	NA		
GO:007259 Establishment of protein localization to organelle	25	344	0.48	0.00014		18	344	0.6	0.00025	
GO:000698 Response to unfolded protein	13	101	0.73	0.00016	NA	NA	NA	NA		
GO:000704 Lysosomal transport	14	118	0.7	0.00016	NA	NA	NA	NA		
GO:002305 Regulation of signaling	121	3347	0.18	0.00016	NA	NA	NA	NA		
GO:004426 Cellular macromolecule metabolic process	106	2825	0.2	0.00016		65	2825	0.24	0.00088	
GO:000701 Actin filament organization	22	281	0.52	0.00018	NA	NA	NA	NA		
GO:001905 Viral life cycle	14	119	0.69	0.00018		9	119	0.76	0.0046	
GO:004426 Cellular carbohydrate metabolic process	17	175	0.61	0.00018	NA	NA	NA	NA		
GO:005105 Negative regulation of transport	30	474	0.42	0.00019	NA	NA	NA	NA		

GO:001064	Regulation of cell communication	120	3331	0.18	2.00E-04	NA	NA	NA	NA	
GO:001967	NAD metabolic process	8	32	1.02	2.00E-04	NA	NA	NA	NA	
GO:001623	Macroautophagy	17	178	0.6	0.00021	NA	NA	NA	NA	
GO:000701	Cytoskeleton organization	59	1308	0.28	0.00024	NA	NA	NA	NA	
GO:001972	Cellular homeostasis	37	666	0.37	0.00024	NA	NA	NA	NA	
GO:003596	Response to topologically incorrect protein	14	123	0.68	0.00024	NA	NA	NA	NA	
GO:19017C	Cellular response to oxygen-containing compound	52	1095	0.3	0.00024	NA	NA	NA	NA	
GO:003000	Cellular monovalent inorganic cation homeostasis	13	106	0.71	0.00025	NA	NA	NA	NA	
GO:007149	Cellular response to endogenous stimulus	53	1127	0.29	0.00025	NA	NA	NA	NA	
GO:007265	Protein localization to membrane	30	482	0.42	0.00025	NA	NA	NA	NA	
GO:190353	Positive regulation of secretion by cell	25	359	0.46	0.00026	NA	NA	NA	NA	
GO:000604	UDP-N-acetylglucosamine biosynthetic process	5	7	1.48	0.00027	NA	NA	NA	NA	
GO:000697	Response to oxidative stress	25	360	0.46	0.00027		17	360	0.55	0.0012
GO:005122	Positive regulation of protein transport	23	313	0.49	0.00027	NA	NA	NA	NA	
GO:19029C	Negative regulation of supramolecular fiber organization	17	182	0.59	0.00027	NA	NA	NA	NA	
GO:001715	Regulation of exocytosis	22	291	0.5	0.00028	NA	NA	NA	NA	
GO:004393	Protein-containing complex organization	65	1505	0.26	0.00028		37	1505	0.27	0.0209
GO:000963	Response to toxic substance	18	204	0.57	0.00029	NA	NA	NA	NA	
GO:000989	Positive regulation of metabolic process	136	3939	0.16	3.00E-04	NA	NA	NA	NA	
GO:00714C	Cellular response to organic cyclic compound	32	541	0.39	0.00031	NA	NA	NA	NA	
GO:190547	Positive regulation of protein localization to membrane	13	110	0.69	0.00034	NA	NA	NA	NA	
GO:006113	Regulation of proteasomal protein catabolic process	17	187	0.58	0.00036	NA	NA	NA	NA	
GO:000599	Monosaccharide metabolic process	19	230	0.54	0.00037		11	230	0.56	0.0258
GO:003083	Regulation of actin filament polymerization	15	148	0.63	0.00037	NA	NA	NA	NA	
GO:003164	Regulation of protein stability	26	393	0.44	0.00037	NA	NA	NA	NA	
GO:005164	Organelle localization	32	547	0.39	0.00037	NA	NA	NA	NA	
GO:005169	Actin filament capping	8	36	0.97	0.00037	NA	NA	NA	NA	
GO:190211	Regulation of organelle assembly	19	230	0.54	0.00037	NA	NA	NA	NA	
GO:000691	Apoptotic process	42	826	0.33	4.00E-04	NA	NA	NA	NA	
GO:003464	Cellular nitrogen compound metabolic process	132	3820	0.16	4.00E-04		93	3820	0.26	9.37E-07
GO:19013E	Organic cyclic compound metabolic process	115	3212	0.18	4.00E-04		85	3212	0.3	1.40E-07
GO:190595	Regulation of lipid localization	16	170	0.6	0.00042	NA	NA	NA	NA	
GO:190595	Positive regulation of lipid localization	13	113	0.68	0.00042	NA	NA	NA	NA	
GO:000673	NADH metabolic process	8	37	0.96	0.00043	NA	NA	NA	NA	
GO:00463E	Monosaccharide catabolic process	8	37	0.96	0.00043	NA	NA	NA	NA	
GO:000660	Protein targeting	19	234	0.53	0.00044	NA	NA	NA	NA	
GO:003083	Negative regulation of actin filament depolymerization	9	50	0.88	0.00044	NA	NA	NA	NA	
GO:001605	Carbohydrate catabolic process	17	192	0.57	0.00045		10	192	0.59	0.0253
GO:003387	Ribonucleoside bisphosphate metabolic process	13	114	0.68	0.00045	NA	NA	NA	NA	
GO:003403	Purine nucleoside bisphosphate metabolic process	13	114	0.68	0.00045	NA	NA	NA	NA	

GO:00098	Positive regulation of catabolic process	30	502	0.4	0.00046	NA	NA	NA	NA	NA	
GO:00313	Positive regulation of protein-containing complex assembly	17	193	0.57	0.00048	NA	NA	NA	NA	NA	
GO:00304	Ubiquitin-dependent ERAD pathway	11	81	0.75	0.00049	NA	NA	NA	NA	NA	
GO:00510	De novo post-translational protein folding	8	38	0.95	0.00049	NA	NA	NA	NA	NA	
GO:00485	Animal organ development	119	3378	0.17	0.00051	NA	NA	NA	NA	NA	
GO:00301	Regulation of proteolysis	38	724	0.34	0.00052	NA	NA	NA	NA	NA	
GO:00442	Small molecule catabolic process	24	354	0.45	0.00052	NA	NA	NA	NA	NA	
GO:20001	Regulation of cellular macromolecule biosynthetic process	34	613	0.37	0.00052	NA	NA	NA	NA	NA	
GO:00430	Positive regulation of catalytic activity	52	1139	0.28	0.00056	NA	NA	NA	NA	NA	
GO:00066	Steroid biosynthetic process	12	101	0.7	0.00064		11	101	0.92	5.48E-05	
GO:00517	Biological process involved in interaction with host	13	119	0.66	0.00064	NA	NA	NA	NA	NA	
GO:19018	Regulation of protein depolymerization	12	101	0.7	0.00064	NA	NA	NA	NA	NA	
GO:00459	Positive regulation of mitotic cell cycle	14	138	0.63	0.00065	NA	NA	NA	NA	NA	
GO:00510	Barbed-end actin filament capping	6	18	1.14	7.00E-04	NA	NA	NA	NA	NA	
GO:00070	Lysosome organization	11	87	0.72	0.00085	NA	NA	NA	NA	NA	
GO:20006	Regulation of early endosome to late endosome transport	6	19	1.12	0.00089	NA	NA	NA	NA	NA	
GO:00313	Regulation of cellular catabolic process	38	745	0.33	9.00E-04		22	745	0.35	0.0352	
GO:00444	Biological process involved in interspecies interaction between organisms	58	1351	0.25	0.00092	NA	NA	NA	NA	NA	
GO:00712	Cellular response to metal ion	17	205	0.54	0.00092	NA	NA	NA	NA	NA	
GO:00313	Regulation of cell projection organization	39	776	0.32	0.00095	NA	NA	NA	NA	NA	
GO:19019	Positive regulation of mitotic cell cycle phase transition	12	106	0.68	0.00096	NA	NA	NA	NA	NA	
GO:00432	Regulation of protein-containing complex disassembly	14	144	0.61	0.00097	NA	NA	NA	NA	NA	
GO:00226	Regulation of cell morphogenesis	23	347	0.44	0.001	NA	NA	NA	NA	NA	
GO:00425	Homeostatic process	61	1451	0.25	0.001	NA	NA	NA	NA	NA	
GO:00457	Positive regulation of protein catabolic process	16	186	0.56	0.001	NA	NA	NA	NA	NA	
GO:19013	Organic cyclic compound biosynthetic process	45	957	0.29	0.001		33	957	0.42	0.00016	
GO:00066	acyl-CoA metabolic process	11	90	0.71	0.0011	NA	NA	NA	NA	NA	
GO:00070	Vacuolar acidification	6	20	1.1	0.0011	NA	NA	NA	NA	NA	
GO:00092	Nucleotide-sugar metabolic process	7	31	0.98	0.0011	NA	NA	NA	NA	NA	
GO:00140	Glutamate secretion	5	11	1.28	0.0011	NA	NA	NA	NA	NA	
GO:00329	Protein-containing complex disassembly	14	147	0.6	0.0011	NA	NA	NA	NA	NA	
GO:00510	Actin filament bundle assembly	9	58	0.81	0.0011	NA	NA	NA	NA	NA	
GO:00514	Intracellular pH reduction	7	31	0.98	0.0011	NA	NA	NA	NA	NA	
GO:00900	Regulation of anatomical structure size	32	584	0.36	0.0011	NA	NA	NA	NA	NA	
GO:00514	Positive regulation of cytoskeleton organization	17	212	0.53	0.0013	NA	NA	NA	NA	NA	
GO:01200	Regulation of plasma membrane bounded cell projection organization	38	760	0.32	0.0013	NA	NA	NA	NA	NA	
GO:00322	Negative regulation of protein polymerization	10	76	0.74	0.0014	NA	NA	NA	NA	NA	
GO:00906	Ubiquitin-independent protein catabolic process via the multivesicular body	4	5	1.53	0.0014	NA	NA	NA	NA	NA	
GO:00193	Hexose catabolic process	7	33	0.95	0.0015	NA	NA	NA	NA	NA	
GO:00313	Regulation of cellular metabolic process	176	5592	0.12	0.0015	NA	NA	NA	NA	NA	

GO:004424 Cellular biosynthetic process	91	2480	0.19	0.0015		69	2480	0.32	1.30E-06	
GO:00726E Protein localization to plasma membrane	17	215	0.52	0.0015	NA	NA	NA	NA	NA	
GO:190211 Positive regulation of organelle assembly	11	94	0.69	0.0015	NA	NA	NA	NA	NA	
GO:000662 Protein targeting to lysosome	6	22	1.06	0.0016	NA	NA	NA	NA	NA	
GO:00068E Endoplasmic reticulum to Golgi vesicle-mediated transport	12	113	0.65	0.0016		12	113	0.9	2.60E-05	
GO:003064 Regulation of cellular pH	10	78	0.73	0.0016	NA	NA	NA	NA	NA	
GO:003462 Cellular response to unfolded protein	10	78	0.73	0.0016	NA	NA	NA	NA	NA	
GO:00440S Negative regulation of molecular function	48	1072	0.27	0.0017	NA	NA	NA	NA	NA	
GO:006102 Establishment of endothelial barrier	7	34	0.94	0.0017	NA	NA	NA	NA	NA	
GO:199074 Cellular detoxification	11	96	0.68	0.0017	NA	NA	NA	NA	NA	
GO:00230E Positive regulation of signaling	69	1749	0.22	0.0018	NA	NA	NA	NA	NA	
GO:00359€ Cellular response to topologically incorrect protein	11	97	0.68	0.0018	NA	NA	NA	NA	NA	
GO:00313S Regulation of protein modification process	64	1588	0.23	0.0019	NA	NA	NA	NA	NA	
GO:00514S Negative regulation of cytoskeleton organization	15	177	0.55	0.0019	NA	NA	NA	NA	NA	
GO:007124 Cellular response to inorganic substance	18	243	0.49	0.0019	NA	NA	NA	NA	NA	
GO:00080E Cell recognition	12	117	0.63	0.002	NA	NA	NA	NA	NA	
GO:00300E Cell projection organization	54	1269	0.25	0.002	NA	NA	NA	NA	NA	
GO:00484€ Cell development	71	1825	0.21	0.002	NA	NA	NA	NA	NA	
GO:00510E Chaperone cofactor-dependent protein refolding	7	36	0.91	0.0022	NA	NA	NA	NA	NA	
GO:00323E Positive regulation of intracellular transport	16	202	0.52	0.0023	NA	NA	NA	NA	NA	
GO:000247 Antigen processing and presentation of peptide antigen via MHC class I	5	14	1.17	0.0024	NA	NA	NA	NA	NA	
GO:00069C Vesicle budding from membrane	9	66	0.76	0.0024	NA	NA	NA	NA	NA	
GO:004001 Positive regulation of locomotion	32	615	0.34	0.0024	NA	NA	NA	NA	NA	
GO:00433S Regulation of protein binding	17	226	0.5	0.0024	NA	NA	NA	NA	NA	
GO:00714S Cellular response to external stimulus	23	372	0.41	0.0024	NA	NA	NA	NA	NA	
GO:001064 Positive regulation of cell communication	68	1738	0.21	0.0025	NA	NA	NA	NA	NA	
GO:003162 Receptor internalization	9	67	0.75	0.0026	NA	NA	NA	NA	NA	
GO:012003 Plasma membrane bounded cell projection organization	52	1222	0.25	0.0026	NA	NA	NA	NA	NA	
GO:00440C Movement in host	10	84	0.7	0.0027	NA	NA	NA	NA	NA	
GO:01403E Export from cell	25	427	0.39	0.0027	NA	NA	NA	NA	NA	
GO:19016S Cellular response to nitrogen compound	34	676	0.32	0.0027	NA	NA	NA	NA	NA	
GO:19018E Negative regulation of protein depolymerization	10	84	0.7	0.0027	NA	NA	NA	NA	NA	
GO:00068S post-Golgi vesicle-mediated transport	11	103	0.65	0.0028	NA	NA	NA	NA	NA	
GO:00068S Receptor-mediated endocytosis	14	163	0.56	0.0028	NA	NA	NA	NA	NA	
GO:001081 Positive regulation of cell-substrate adhesion	13	143	0.58	0.003	NA	NA	NA	NA	NA	
GO:00463S Ribose phosphate biosynthetic process	15	186	0.53	0.0031	NA	NA	NA	NA	NA	
GO:200014 Positive regulation of cell motility	31	597	0.34	0.0031	NA	NA	NA	NA	NA	
GO:00160E Carbohydrate biosynthetic process	12	124	0.61	0.0032		9	124	0.74	0.006	
GO:00328E Regulation of microtubule-based process	19	280	0.45	0.0032	NA	NA	NA	NA	NA	
GO:19025E Regulation of intracellular signal transduction	66	1691	0.21	0.0032	NA	NA	NA	NA	NA	

GO:19029C	Positive regulation of supramolecular fiber organization	15	187	0.53	0.0032	NA	NA	NA	NA	
GO:004327	Apoptotic cell clearance	7	39	0.88	0.0033	NA	NA	NA	NA	
GO:00303E	Positive regulation of cell migration	30	573	0.34	0.0034	NA	NA	NA	NA	
GO:004001	Regulation of locomotion	47	1080	0.26	0.0034	NA	NA	NA	NA	
GO:19050E	Autophagosome organization	10	88	0.68	0.0036	NA	NA	NA	NA	
GO:00457E	Positive regulation of cell cycle	22	359	0.41	0.0037	NA	NA	NA	NA	
GO:00018E	Endothelial cell development	8	55	0.78	0.0038	NA	NA	NA	NA	
GO:001081	Regulation of cell-substrate adhesion	17	237	0.48	0.0039	NA	NA	NA	NA	
GO:001094	Positive regulation of cell death	33	664	0.32	0.0039	NA	NA	NA	NA	
GO:001604	Lipid catabolic process	19	285	0.45	0.0039	NA	NA	NA	NA	
GO:00163E	Dendrite development	13	148	0.57	0.0039	NA	NA	NA	NA	
GO:00516E	Establishment of organelle localization	23	387	0.4	0.0039	NA	NA	NA	NA	
GO:00705C	Regulation of microtubule cytoskeleton organization	14	170	0.54	0.004	NA	NA	NA	NA	
GO:00614E	Protein localization to lysosome	7	41	0.85	0.0041	NA	NA	NA	NA	
GO:200064	Positive regulation of early endosome to late endosome transport	4	8	1.32	0.0044	NA	NA	NA	NA	
GO:004887	Chemical homeostasis	43	972	0.27	0.0046	NA	NA	NA	NA	
GO:007084	Response to growth factor	27	501	0.35	0.0047	NA	NA	NA	NA	
GO:00430E	Positive regulation of programmed cell death	30	587	0.33	0.0048	NA	NA	NA	NA	
GO:00507C	Regulation of protein secretion	19	291	0.44	0.0048	NA	NA	NA	NA	
GO:00510E	Regulation of binding	23	394	0.39	0.0048	NA	NA	NA	NA	
GO:00515E	Response to calcium ion	13	152	0.55	0.0048	NA	NA	NA	NA	
GO:00990C	Vesicle-mediated transport in synapse	13	152	0.55	0.0048	NA	NA	NA	NA	
GO:000641	Regulation of translation	28	531	0.34	0.0049		20	531	0.45	0.0042
GO:00340E	Protein localization to Golgi apparatus	6	29	0.94	0.0049	NA	NA	NA	NA	
GO:00512E	Maintenance of location	14	174	0.53	0.0049	NA	NA	NA	NA	
GO:00324E	Regulation of proteasomal ubiquitin-dependent protein catabolic process	12	132	0.58	0.005	NA	NA	NA	NA	
GO:003117	Neuron projection development	36	765	0.29	0.0051	NA	NA	NA	NA	
GO:00488E	Cellular developmental process	115	3449	0.15	0.0051	NA	NA	NA	NA	
GO:199077	Protein localization to cell periphery	18	269	0.45	0.0052	NA	NA	NA	NA	
GO:00301E	Cell differentiation	114	3418	0.15	0.0053	NA	NA	NA	NA	
GO:00507E	Regulation of developmental process	90	2555	0.17	0.0053	NA	NA	NA	NA	
GO:00987E	Cellular response to interleukin-7	5	18	1.07	0.0054	NA	NA	NA	NA	
GO:000167	Long-chain fatty acid metabolic process	11	114	0.61	0.0056	NA	NA	NA	NA	
GO:00190E	Virion assembly	6	30	0.92	0.0056	NA	NA	NA	NA	
GO:004592	Negative regulation of exocytosis	6	30	0.92	0.0056	NA	NA	NA	NA	
GO:00067E	NADP metabolic process	7	44	0.82	0.0057	NA	NA	NA	NA	
GO:001922	Regulation of phosphate metabolic process	57	1434	0.22	0.0057	NA	NA	NA	NA	
GO:00075E	Female pregnancy	14	178	0.52	0.0058	NA	NA	NA	NA	
GO:00070E	Endosome organization	8	60	0.75	0.0059	NA	NA	NA	NA	
GO:00108E	Regulation of lipid storage	8	60	0.75	0.0059	NA	NA	NA	NA	

GO:190307	Positive regulation of protein localization to plasma membrane	8	60	0.75	0.0059	NA	NA	NA	NA	
GO:003015	Regulation of cell adhesion	36	775	0.29	0.0062	NA	NA	NA	NA	
GO:000004	Autophagosome assembly	9	78	0.68	0.0063	NA	NA	NA	NA	
GO:190199	Toxin transport	7	45	0.81	0.0063	NA	NA	NA	NA	
GO:000293	Response to ischemia	8	61	0.74	0.0064	NA	NA	NA	NA	
GO:004217	Xenobiotic catabolic process	5	19	1.04	0.0064	NA	NA	NA	NA	
GO:004675	Viral budding	5	19	1.04	0.0064	NA	NA	NA	NA	
GO:009020	Positive regulation of cholesterol metabolic process	5	19	1.04	0.0064	NA	NA	NA	NA	
GO:002260	Regulation of anatomical structure morphogenesis	43	993	0.26	0.0065	NA	NA	NA	NA	
GO:003294	Secretion by cell	22	379	0.39	0.0066	NA	NA	NA	NA	
GO:000916	Nucleotide biosynthetic process	16	229	0.47	0.007		14	229	0.66	0.00057
GO:003111	Regulation of microtubule polymerization	8	62	0.73	0.007	NA	NA	NA	NA	
GO:003403	Ribonucleoside bisphosphate biosynthetic process	7	46	0.8	0.007	NA	NA	NA	NA	
GO:003403	Purine nucleoside bisphosphate biosynthetic process	7	46	0.8	0.007	NA	NA	NA	NA	
GO:000940	Response to heat	12	139	0.56	0.0072	NA	NA	NA	NA	
GO:003086	Cortical actin cytoskeleton organization	6	32	0.9	0.0072	NA	NA	NA	NA	
GO:004306	Positive regulation of apoptotic process	29	577	0.32	0.0073	NA	NA	NA	NA	
GO:001891	Nitrobenzene metabolic process	3	3	1.62	0.0074	NA	NA	NA	NA	
GO:000689	Retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	7	47	0.8	0.0075	NA	NA	NA	NA	
GO:003133	Negative regulation of protein-containing complex assembly	12	140	0.56	0.0075	NA	NA	NA	NA	
GO:003226	Regulation of cellular protein metabolic process	4	10	1.22	0.0075	NA	NA	NA	NA	
GO:003295	Inositol trisphosphate metabolic process	4	10	1.22	0.0075	NA	NA	NA	NA	
GO:190113	Carbohydrate derivative biosynthetic process	28	550	0.33	0.0075		21	550	0.46	0.0023
GO:190296	Positive regulation of protein localization to early endosome	4	10	1.22	0.0075	NA	NA	NA	NA	
GO:003287	Cellular response to hormone stimulus	26	494	0.34	0.0076	NA	NA	NA	NA	
GO:001931	Hexose metabolic process	15	208	0.48	0.0077		10	208	0.56	0.0406
GO:003236	Regulation of lipid transport	12	141	0.55	0.0078	NA	NA	NA	NA	
GO:007266	Protein localization to vacuole	8	64	0.72	0.0081	NA	NA	NA	NA	
GO:190260	Proton transmembrane transport	11	121	0.58	0.0082	NA	NA	NA	NA	
GO:005165	Establishment of vesicle localization	13	164	0.52	0.0083	NA	NA	NA	NA	
GO:190188	Regulation of cell junction assembly	16	235	0.46	0.0088	NA	NA	NA	NA	
GO:003460	Cellular response to heat	9	83	0.66	0.0089	NA	NA	NA	NA	
GO:190382	Negative regulation of protein localization	15	212	0.47	0.0091	NA	NA	NA	NA	
GO:007266	Establishment of protein localization to vacuole	7	49	0.78	0.0092	NA	NA	NA	NA	
GO:001591	Sterol transport	9	84	0.65	0.0096	NA	NA	NA	NA	
GO:003112	Cytoplasmic microtubule organization	8	66	0.71	0.0096	NA	NA	NA	NA	
GO:004308	Negative regulation of catalytic activity	33	707	0.29	0.0096	NA	NA	NA	NA	
GO:200014	Regulation of cell motility	43	1017	0.25	0.0097	NA	NA	NA	NA	
GO:000996	Regulation of signal transduction	98	2903	0.15	0.0098	NA	NA	NA	NA	
GO:001063	Negative regulation of organelle organization	21	367	0.38	0.0101	NA	NA	NA	NA	

GO:00430€ Negative regulation of programmed cell death	42	988	0.25	0.0102	NA	NA	NA	NA	NA	
GO:00704€ Response to oxygen levels	20	341	0.39	0.0102	NA	NA	NA	NA	NA	
GO:00901€ Establishment of protein localization to membrane	15	215	0.47	0.0102	NA	NA	NA	NA	NA	
GO:00511€ Glucose 6-phosphate metabolic process	5	22	0.98	0.0103	NA	NA	NA	NA	NA	
GO:00650€ Protein-containing complex assembly	52	1312	0.22	0.0103	NA	NA	NA	NA	NA	
GO:00303€ Regulation of cell migration	41	961	0.25	0.011	NA	NA	NA	NA	NA	
GO:00550€ Cellular chemical homeostasis	28	566	0.32	0.011	NA	NA	NA	NA	NA	
GO:001921 Regulation of steroid metabolic process	10	106	0.6	0.0112	NA	NA	NA	NA	NA	
GO:00015€ Regulation of cell growth	23	426	0.35	0.0114	NA	NA	NA	NA	NA	
GO:00025€ Peptide antigen assembly with MHC class I protein complex	3	4	1.5	0.0117	NA	NA	NA	NA	NA	
GO:005071 Positive regulation of protein secretion	12	149	0.53	0.0117	NA	NA	NA	NA	NA	
GO:19035€ Positive regulation of extracellular exosome assembly	3	4	1.5	0.0117	NA	NA	NA	NA	NA	
GO:00091€ Nucleoside diphosphate metabolic process	13	172	0.5	0.0119	NA	NA	NA	NA	NA	
GO:00430€ Regulation of GTPase activity	21	373	0.37	0.0119	NA	NA	NA	NA	NA	
GO:00468€ Regulation of lipid biosynthetic process	14	195	0.48	0.0119	NA	NA	NA	NA	NA	
GO:00108€ Positive regulation of lipid storage	5	23	0.96	0.012	NA	NA	NA	NA	NA	
GO:001907 Viral release from host cell	5	23	0.96	0.012	NA	NA	NA	NA	NA	
GO:00485€ Regulation of response to stimulus	123	3843	0.13	0.012	NA	NA	NA	NA	NA	
GO:005134 Positive regulation of hydrolase activity	28	571	0.31	0.0121	NA	NA	NA	NA	NA	
GO:006201 Positive regulation of small molecule metabolic process	12	150	0.53	0.0121	NA	NA	NA	NA	NA	
GO:00060€ acetyl-CoA metabolic process	6	37	0.83	0.0127	NA	NA	NA	NA	NA	
GO:00060€ Glucose metabolic process	13	174	0.5	0.0129	NA	NA	NA	NA	NA	
GO:00073€ Nervous system development	76	2147	0.17	0.0129	NA	NA	NA	NA	NA	
GO:001081 Regulation of hormone levels	27	545	0.32	0.0129	NA	NA	NA	NA	NA	
GO:005082 Protein stabilization	17	271	0.42	0.0129	NA	NA	NA	NA	NA	
GO:005124 Negative regulation of protein metabolic process	43	1035	0.24	0.0129	NA	NA	NA	NA	NA	
GO:00323€ Negative regulation of intracellular transport	7	53	0.74	0.0131	NA	NA	NA	NA	NA	
GO:00316€ Cellular response to extracellular stimulus	18	298	0.4	0.0134	NA	NA	NA	NA	NA	
GO:00092€ Ribonucleotide biosynthetic process	13	175	0.49	0.0135		10	175	0.64	0.0142	
GO:00320€ Positive regulation of protein binding	10	110	0.58	0.014	NA	NA	NA	NA	NA	
GO:19030€ Organelle disassembly	10	110	0.58	0.014	NA	NA	NA	NA	NA	
GO:007141 Cellular response to organonitrogen compound	29	608	0.3	0.0142	NA	NA	NA	NA	NA	
GO:00308€ Cortical cytoskeleton organization	7	54	0.73	0.0143	NA	NA	NA	NA	NA	
GO:00480€ Antigen processing and presentation of peptide antigen	7	54	0.73	0.0143	NA	NA	NA	NA	NA	
GO:00091€ Ribonucleoside diphosphate metabolic process	12	154	0.51	0.0145	NA	NA	NA	NA	NA	
GO:00060€ Pentose-phosphate shunt	4	13	1.11	0.0146	NA	NA	NA	NA	NA	
GO:00031€ Endothelium development	9	91	0.62	0.0147	NA	NA	NA	NA	NA	
GO:00331€ Regulation of intracellular protein transport	15	225	0.45	0.0147	NA	NA	NA	NA	NA	
GO:00060€ Glucose catabolic process	5	25	0.92	0.0158	NA	NA	NA	NA	NA	
GO:00082€ Isoprenoid biosynthetic process	5	25	0.92	0.0158		6	25	1.26	0.00038	

GO:007252	Purine-containing compound biosynthetic process	13	179	0.48	0.0159	NA	NA	NA	NA	
GO:004592	Positive regulation of exocytosis	11	134	0.54	0.0161	NA	NA	NA	NA	
GO:001087	Lipid localization	21	385	0.36	0.0163	NA	NA	NA	NA	
GO:19016E	Response to peptide	24	470	0.33	0.0168	NA	NA	NA	NA	
GO:00069C	Phagocytosis	11	135	0.53	0.0169	NA	NA	NA	NA	
GO:00346E	Cellular carbohydrate biosynthetic process	7	56	0.72	0.0169	NA	NA	NA	NA	
GO:00362E	Multivesicular body assembly	3	5	1.4	0.0169	NA	NA	NA	NA	
GO:003111	Positive regulation of microtubule polymerization	6	40	0.8	0.0172	NA	NA	NA	NA	
GO:00713E	Cellular response to growth factor stimulus	24	472	0.33	0.0175	NA	NA	NA	NA	
GO:00060C	Fructose 6-phosphate metabolic process	4	14	1.08	0.0178	NA	NA	NA	NA	
GO:006162	Canonical glycolysis	4	14	1.08	0.0178	NA	NA	NA	NA	
GO:005117	Positive regulation of nitrogen compound metabolic process	104	3188	0.14	0.0179	NA	NA	NA	NA	
GO:005081	Regulation of steroid biosynthetic process	8	75	0.65	0.0181	NA	NA	NA	NA	
GO:00018E	Maternal placenta development	6	41	0.79	0.019	NA	NA	NA	NA	
GO:00719E	Multivesicular body sorting pathway	6	41	0.79	0.019	NA	NA	NA	NA	
GO:00106C	Post-transcriptional regulation of gene expression	29	623	0.29	0.0192		22	623	0.43	0.0044
GO:00303C	Positive regulation of cell growth	13	184	0.47	0.0194	NA	NA	NA	NA	
GO:00091E	Purine ribonucleotide biosynthetic process	12	161	0.49	0.0197		9	161	0.63	0.0297
GO:00430E	Negative regulation of apoptotic process	40	967	0.24	0.02	NA	NA	NA	NA	
GO:004343	Response to peptide hormone	21	393	0.35	0.02	NA	NA	NA	NA	
GO:000691	Nucleocytoplasmic transport	16	260	0.41	0.0206		16	260	0.67	0.00015
GO:00080E	Axo-dendritic transport	8	77	0.64	0.0207	NA	NA	NA	NA	
GO:00159E	Energy derivation by oxidation of organic compounds	15	235	0.43	0.0208	NA	NA	NA	NA	
GO:003221	Positive regulation of telomere maintenance via telomerase	6	42	0.78	0.0208	NA	NA	NA	NA	
GO:003227	Positive regulation of protein polymerization	9	97	0.59	0.021	NA	NA	NA	NA	
GO:00068C	Xenobiotic metabolic process	10	118	0.55	0.0211	NA	NA	NA	NA	
GO:00397C	Viral budding via host ESCRT complex	4	15	1.05	0.0211	NA	NA	NA	NA	
GO:00420E	T cell proliferation	7	59	0.7	0.0211	NA	NA	NA	NA	
GO:00619E	Establishment of protein localization to plasma membrane	7	59	0.7	0.0211	NA	NA	NA	NA	
GO:19048E	Positive regulation of establishment of protein localization to telomere	4	15	1.05	0.0211	NA	NA	NA	NA	
GO:190121	Regulation of neuron death	21	397	0.35	0.0218	NA	NA	NA	NA	
GO:00068E	Lipid transport	19	342	0.37	0.0219	NA	NA	NA	NA	
GO:00512E	Regulation of multicellular organismal process	94	2847	0.14	0.022	NA	NA	NA	NA	
GO:000681	Ion transport	47	1203	0.21	0.0221	NA	NA	NA	NA	
GO:00307C	Cytoskeleton-dependent intracellular transport	13	188	0.46	0.0222	NA	NA	NA	NA	
GO:00316E	Cellular response to nutrient levels	16	263	0.41	0.0222	NA	NA	NA	NA	
GO:00359E	Endodermal cell differentiation	6	43	0.77	0.0224	NA	NA	NA	NA	
GO:004202	Protein refolding	5	28	0.87	0.0224	NA	NA	NA	NA	
GO:005197	Positive regulation of telomerase activity	6	43	0.77	0.0224	NA	NA	NA	NA	
GO:00901E	Regulation of cholesterol metabolic process	6	43	0.77	0.0224	NA	NA	NA	NA	

GO:000237 Immune system process	67	1887	0.17	0.0227	NA	NA	NA	NA	NA	
GO:00068 Mitochondrial transport	10	120	0.54	0.0227	NA	NA	NA	NA	NA	
GO:00198 Antigen processing and presentation of endogenous peptide antigen via MHC	3	6	1.32	0.0227	NA	NA	NA	NA	NA	
GO:002261 Membrane to membrane docking	3	6	1.32	0.0227	NA	NA	NA	NA	NA	
GO:00459 Positive regulation of growth	17	290	0.39	0.0227	NA	NA	NA	NA	NA	
GO:00300 Cellular cation homeostasis	22	428	0.33	0.023	NA	NA	NA	NA	NA	
GO:00106 Positive regulation of macromolecule metabolic process	114	3592	0.12	0.0231	NA	NA	NA	NA	NA	
GO:00081 Actin polymerization or depolymerization	7	61	0.68	0.024	NA	NA	NA	NA	NA	
GO:00091 Ribonucleoside triphosphate metabolic process	15	240	0.42	0.024		13	240	0.61	0.0031	
GO:00093 Protein secretion	9	100	0.58	0.0241	NA	NA	NA	NA	NA	
GO:005134 Negative regulation of hydrolase activity	18	319	0.37	0.0241	NA	NA	NA	NA	NA	
GO:00003 Response to reactive oxygen species	12	167	0.48	0.0244	NA	NA	NA	NA	NA	
GO:00070 Golgi organization	11	144	0.51	0.0245		9	144	0.67	0.0156	
GO:00431 Ubiquitin-dependent protein catabolic process via the multivesicular body sc	5	29	0.86	0.0248	NA	NA	NA	NA	NA	
GO:001921 Regulation of lipid metabolic process	20	376	0.35	0.0254	NA	NA	NA	NA	NA	
GO:19035 Negative regulation of secretion by cell	12	168	0.48	0.0254	NA	NA	NA	NA	NA	
GO:00060 Cellular aldehyde metabolic process	7	63	0.67	0.0277	NA	NA	NA	NA	NA	
GO:00068 intra-Golgi vesicle-mediated transport	5	30	0.84	0.0281	NA	NA	NA	NA	NA	
GO:00466 Decidualization	5	30	0.84	0.0281	NA	NA	NA	NA	NA	
GO:00109 Regulation of metal ion transport	22	437	0.32	0.0286	NA	NA	NA	NA	NA	
GO:003132 Positive regulation of cellular metabolic process	102	3172	0.13	0.0286	NA	NA	NA	NA	NA	
GO:00073 Gastrulation	12	171	0.47	0.0288	NA	NA	NA	NA	NA	
GO:00158 Acidic amino acid transport	6	46	0.74	0.0288		5	46	0.91	0.0358	
GO:003357 Response to testosterone	6	46	0.74	0.0288	NA	NA	NA	NA	NA	
GO:00458 Positive regulation of lipid metabolic process	12	171	0.47	0.0288	NA	NA	NA	NA	NA	
GO:00712 Cellular response to electrical stimulus	4	17	0.99	0.0288	NA	NA	NA	NA	NA	
GO:012017 Steroid hormone biosynthetic process	4	17	0.99	0.0288	NA	NA	NA	NA	NA	
GO:005104 Negative regulation of secretion	13	196	0.44	0.0294	NA	NA	NA	NA	NA	
GO:200057 Positive regulation of DNA biosynthetic process	9	104	0.56	0.0297	NA	NA	NA	NA	NA	
GO:00463 Carboxylic acid biosynthetic process	15	247	0.41	0.0298		11	247	0.53	0.0406	
GO:004822 Plasma membrane to endosome transport	3	7	1.25	0.0298	NA	NA	NA	NA	NA	
GO:00860 Regulation of cardiac muscle cell membrane potential	3	7	1.25	0.0298	NA	NA	NA	NA	NA	
GO:00486 Neuron development	38	932	0.23	0.0302	NA	NA	NA	NA	NA	
GO:00469 Nucleotide phosphorylation	11	149	0.49	0.0303	NA	NA	NA	NA	NA	
GO:00301 Regulation of endocytosis	15	248	0.4	0.0307	NA	NA	NA	NA	NA	
GO:003361 Membrane protein proteolysis	5	31	0.83	0.0309	NA	NA	NA	NA	NA	
GO:00516 Maintenance of location in cell	9	105	0.56	0.0312	NA	NA	NA	NA	NA	
GO:00508 Regulation of synapse organization	16	275	0.39	0.0314	NA	NA	NA	NA	NA	
GO:00601 Maternal process involved in female pregnancy	7	65	0.65	0.0315	NA	NA	NA	NA	NA	
GO:19011 Carbohydrate derivative catabolic process	11	150	0.49	0.0315	NA	NA	NA	NA	NA	

GO:00158€ ATP transport	4	18	0.97	0.0333	NA	NA	NA	NA		
GO:005074 Regulation of lipoprotein metabolic process	4	18	0.97	0.0333	NA	NA	NA	NA		
GO:009963 Endosome to plasma membrane protein transport	4	18	0.97	0.0333	NA	NA	NA	NA		
GO:00070€ Mitotic metaphase plate congression	7	66	0.65	0.0336	NA	NA	NA	NA		
GO:005172 Regulation of cell cycle	42	1071	0.22	0.0341	NA	NA	NA	NA		
GO:004427 Cellular carbohydrate catabolic process	5	32	0.82	0.0342	NA	NA	NA	NA		
GO:007161 acyl-CoA biosynthetic process	5	32	0.82	0.0342	NA	NA	NA	NA		
GO:00300€ Myeloid cell differentiation	16	279	0.38	0.0351	NA	NA	NA	NA		
GO:00362€ Response to decreased oxygen levels	17	306	0.37	0.0351	NA	NA	NA	NA		
GO:00434C Regulation of MAPK cascade	30	688	0.26	0.0351	NA	NA	NA	NA		
GO:003001 Establishment of cell polarity	11	153	0.48	0.0354	NA	NA	NA	NA		
GO:00323E Response to estradiol	10	130	0.51	0.0356	NA	NA	NA	NA		
GO:001097 Regulation of neuron projection development	26	568	0.28	0.0369	NA	NA	NA	NA		
GO:007233 Monocarboxylic acid biosynthetic process	11	154	0.48	0.037	NA	NA	NA	NA		
GO:00065C Membrane protein ectodomain proteolysis	4	19	0.95	0.038	NA	NA	NA	NA		
GO:00108€ Positive regulation of sequestering of triglyceride	3	8	1.2	0.038	NA	NA	NA	NA		
GO:00303C Cholesterol transport	7	68	0.63	0.038	NA	NA	NA	NA		
GO:003134 Negative regulation of cell projection organization	14	229	0.41	0.038	NA	NA	NA	NA		
GO:00315E Activation of phospholipase D activity	3	8	1.2	0.038	NA	NA	NA	NA		
GO:004554 Regulation of cholesterol biosynthetic process	4	19	0.95	0.038	NA	NA	NA	NA		
GO:00988E Postsynaptic neurotransmitter receptor internalization	3	8	1.2	0.038	NA	NA	NA	NA		
GO:19900C Amyloid fibril formation	3	8	1.2	0.038	NA	NA	NA	NA		
GO:006042 Epithelium development	45	1180	0.2	0.0382	NA	NA	NA	NA		
GO:00098E Tissue development	64	1835	0.16	0.039	NA	NA	NA	NA		
GO:00466E Response to cadmium ion	6	50	0.7	0.039	NA	NA	NA	NA		
GO:19900€ Cellular response to nerve growth factor stimulus	6	50	0.7	0.039	NA	NA	NA	NA		
GO:004603 ATP metabolic process	13	205	0.42	0.0393		11	205	0.61	0.0117	
GO:00060€ Pyruvate metabolic process	11	156	0.47	0.0395		9	156	0.64	0.0248	
GO:00621€ Cellular response to chemical stress	15	257	0.39	0.0395	NA	NA	NA	NA		
GO:00451E Maintenance of protein location	8	89	0.58	0.0399	NA	NA	NA	NA		
GO:00073E Binding of sperm to zona pellucida	5	34	0.79	0.0412	NA	NA	NA	NA		
GO:00092C Purine ribonucleoside triphosphate metabolic process	14	232	0.4	0.0412		12	232	0.59	0.0084	
GO:00071E Establishment or maintenance of cell polarity	15	259	0.38	0.042	NA	NA	NA	NA		
GO:00516C Response to electrical stimulus	6	51	0.69	0.042	NA	NA	NA	NA		
GO:19017€ Negative regulation of proteasomal protein catabolic process	6	51	0.69	0.042	NA	NA	NA	NA		
GO:00353E Long-chain fatty-acyl-CoA metabolic process	4	20	0.92	0.0432	NA	NA	NA	NA		
GO:00427E Long-chain fatty acid biosynthetic process	4	20	0.92	0.0432	NA	NA	NA	NA		
GO:00619E Midbody abscission	4	20	0.92	0.0432	NA	NA	NA	NA		
GO:200081 Regulation of bicellular tight junction assembly	4	20	0.92	0.0432	NA	NA	NA	NA		
GO:00469C Secretion	24	517	0.29	0.0435	NA	NA	NA	NA		

GO:003433 Cell junction organization						26	578	0.28	0.0439	NA	NA	NA	NA
GO:002240 Membrane docking						8	91	0.57	0.0444	NA	NA	NA	NA
GO:003237 Positive regulation of lipid transport						8	91	0.57	0.0444	NA	NA	NA	NA
GO:003250 Endosome transport via multivesicular body sorting pathway						5	35	0.78	0.0451	NA	NA	NA	NA
GO:007084 Response to epidermal growth factor						6	52	0.68	0.0451	NA	NA	NA	NA
GO:004362 Response to estrogen						8	92	0.56	0.0469	NA	NA	NA	NA
GO:004554 Positive regulation of cholesterol biosynthetic process						3	9	1.14	0.0469	NA	NA	NA	NA
GO:190199 Regulation of mitotic cell cycle phase transition						17	318	0.35	0.0475	NA	NA	NA	NA
GO:000206 Epithelial cell development						13	211	0.41	0.0478	NA	NA	NA	NA
GO:000836 Regulation of cell shape						11	161	0.46	0.0478	NA	NA	NA	NA
GO:000090 Cell morphogenesis						33	803	0.24	0.048	NA	NA	NA	NA
GO:000597 Glycogen metabolic process						6	53	0.68	0.0484	NA	NA	NA	NA
GO:000998 Cell-cell recognition						6	53	0.68	0.0484	NA	NA	NA	NA
GO:004408 Regulation of vacuole organization						6	53	0.68	0.0484	NA	NA	NA	NA
GO:007140 Cellular response to low-density lipoprotein particle stimulus						4	21	0.9	0.0485	NA	NA	NA	NA
GO:000202 Regulation of sodium ion transport						8	93	0.56	0.0487	NA	NA	NA	NA
GO:000996 Positive regulation of signal transduction						55	1543	0.17	0.0488	NA	NA	NA	NA
GO:003243 Negative regulation of proteasomal ubiquitin-dependent protein catabolic pr						5	36	0.76	0.0489	NA	NA	NA	NA
GO:003250 Multicellular organismal process						192	6725	0.08	0.049	NA	NA	NA	NA
GO:000613 Nucleobase-containing compound metabolic process	NA	NA	NA	NA						69	2791	0.27	5.95E-05
GO:004648 Heterocycle metabolic process	NA	NA	NA	NA						72	2937	0.27	4.62E-05
GO:000672 Cellular aromatic compound metabolic process	NA	NA	NA	NA						73	2992	0.27	4.52E-05
GO:000639 RNA processing	NA	NA	NA	NA						26	941	0.32	0.0308
GO:001607 RNA metabolic process	NA	NA	NA	NA						37	1558	0.25	0.0347
GO:000838 RNA splicing	NA	NA	NA	NA						21	372	0.63	1.83E-05
GO:000639 mRNA processing	NA	NA	NA	NA						23	462	0.58	3.20E-05
GO:001607 mRNA metabolic process	NA	NA	NA	NA						24	625	0.46	0.00066
GO:000039 mRNA splicing, via spliceosome	NA	NA	NA	NA						15	267	0.63	0.00066
GO:000640 RNA localization	NA	NA	NA	NA						13	176	0.75	0.00023
GO:190331 Regulation of mRNA metabolic process	NA	NA	NA	NA						14	313	0.53	0.0098
GO:005117 Import into nucleus	NA	NA	NA	NA						11	124	0.83	0.00027
GO:190156 Organonitrogen compound biosynthetic process	NA	NA	NA	NA						45	1579	0.33	0.00024
GO:000660 Protein import into nucleus	NA	NA	NA	NA						10	116	0.81	0.00076
GO:005065 RNA transport	NA	NA	NA	NA						12	152	0.78	0.00028
GO:005102 mRNA transport	NA	NA	NA	NA						10	122	0.79	0.0011
GO:001593 Nucleobase-containing compound transport	NA	NA	NA	NA						13	213	0.66	0.0011
GO:003450 Protein localization to nucleus	NA	NA	NA	NA						14	213	0.7	0.00029
GO:000028 Nuclear division	NA	NA	NA	NA						13	324	0.48	0.0358
GO:004506 Regulation of viral genome replication	NA	NA	NA	NA						8	83	0.86	0.0026
GO:004802 Regulation of mRNA splicing, via spliceosome	NA	NA	NA	NA						10	116	0.81	0.00076

GO:19039C	Regulation of viral life cycle	NA	NA	NA	NA	10	132	0.76	0.0019
GO:00066C	NLS-bearing protein import into nucleus	NA	NA	NA	NA	3	10	1.36	0.0382
GO:00507S	Regulation of viral process	NA	NA	NA	NA	11	159	0.72	0.0017
GO:00485Z	Positive regulation of viral process	NA	NA	NA	NA	8	48	1.1	0.00012
GO:00450Z	Positive regulation of viral genome replication	NA	NA	NA	NA	6	24	1.28	0.00032
GO:00182C	Peptidyl-proline modification	NA	NA	NA	NA	7	72	0.87	0.0071
GO:00003E	Regulation of alternative mRNA splicing, via spliceosome	NA	NA	NA	NA	6	65	0.84	0.0248
GO:19908З	Cellular response to leukemia inhibitory factor	NA	NA	NA	NA	8	133	0.66	0.0366
GO:00434E	Regulation of ATP-dependent activity	NA	NA	NA	NA	6	59	0.89	0.0166
GO:00161Z	Sterol metabolic process	NA	NA	NA	NA	14	123	0.93	1.44E-06
GO:00091Ч	Nucleoside triphosphate metabolic process	NA	NA	NA	NA	14	256	0.62	0.0016
GO:00066S	Prostaglandin metabolic process	NA	NA	NA	NA	6	45	1	0.0049
GO:20006Z	Regulation of nuclear-transcribed mRNA catabolic process, nonsense-media	NA	NA	NA	NA	4	17	1.25	0.0122
GO:00423S	Cellular modified amino acid biosynthetic process	NA	NA	NA	NA	5	39	0.99	0.0208
GO:00060S	Glycolytic process	NA	NA	NA	NA	8	125	0.68	0.0269
GO:00340S	Response to cytokine	NA	NA	NA	NA	24	834	0.34	0.0297
GO:00075E	Aging	NA	NA	NA	NA	10	198	0.58	0.0306
GO:00067S	Glutathione biosynthetic process	NA	NA	NA	NA	3	9	1.4	0.0311
GO:00094З	Methylglyoxal metabolic process	NA	NA	NA	NA	3	10	1.36	0.0382
GO:00161Ι	Terpenoid biosynthetic process	NA	NA	NA	NA	3	11	1.31	0.0455
GO:00345S	Cellular response to oxidative stress	NA	NA	NA	NA	10	213	0.55	0.0463

FUNCTION_D7_30mM_Down

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DF	false discovery rate.DP12
GO:000372	RNA bindin	136	1541	0.69	6.45E-51	74	1541	0.49	6.43E-15
GO:000367	Nucleic aci	205	3725	0.49	1.12E-50	108	3725	0.27	1.27E-08
GO:00971	Organic cyc	259	6155	0.37	1.34E-47	187	6155	0.29	2.52E-20
GO:19013	Heterocycli	257	6088	0.37	2.17E-47	186	6088	0.29	2.52E-20
GO:00054	Binding	373	13754	0.18	5.26E-37	327	13754	0.18	8.17E-33
GO:014064	Catalytic ac	56	618	0.7	2.03E-19	24	618	0.4	0.0038
GO:01400	Catalytic ac	41	377	0.78	2.42E-16	17	377	0.46	0.0077
GO:000372	mRNA bind	39	385	0.75	1.46E-14	21	385	0.54	0.00015
GO:00043	Helicase ac	25	174	0.9	6.08E-12	NA	NA	NA	NA
GO:000372	RNA helica	17	79	1.08	3.16E-10	NA	NA	NA	NA
GO:004487	Protein-cor	73	1625	0.4	3.16E-10	73	1625	0.46	2.39E-13
GO:00001	Nucleotide	94	2478	0.33	1.04E-09	102	2478	0.42	6.61E-17
GO:00036	Chromatin	43	686	0.54	1.10E-09	NA	NA	NA	NA
GO:01406	ATP-depen	40	652	0.53	1.10E-08	30	652	0.47	3.36E-05
GO:00360	Small mole	98	2793	0.29	1.81E-08	113	2793	0.41	1.42E-18
GO:000551	Protein bin	202	7697	0.17	2.45E-08	195	7697	0.21	4.98E-13
GO:00431	Anion bindi	93	2671	0.29	8.39E-08	100	2671	0.38	5.07E-14
GO:000552	ATP binding	66	1663	0.35	3.57E-07	58	1663	0.35	1.80E-06
GO:00081	Transcriptic	36	638	0.5	6.60E-07	NA	NA	NA	NA
GO:00305	Adenyl nucl	67	1743	0.33	8.28E-07	65	1743	0.38	1.64E-08
GO:006162	RNA polym	26	381	0.58	2.63E-06	NA	NA	NA	NA
GO:000367	DNA bindin	76	2178	0.29	3.21E-06	NA	NA	NA	NA
GO:00356	Purine ribo	73	2054	0.3	3.21E-06	71	2054	0.34	4.57E-08
GO:000382	Catalytic ac	160	6043	0.17	3.82E-06	175	6043	0.27	1.86E-16
GO:00325	Ribonucleo	75	2149	0.29	3.82E-06	79	2149	0.37	3.01E-10
GO:01402	DNA-bindir	30	517	0.51	5.49E-06	NA	NA	NA	NA

GO:00167E	Hydrolase a	82	2470	0.27	5.73E-06	86	2470	0.35	3.62E-10
GO:001707	Purine nucl	74	2148	0.28	6.95E-06	79	2148	0.37	3.01E-10
GO:004302	Ribonucleo	18	203	0.69	8.84E-06	12	203	0.58	0.0072
GO:00325E	Purine ribo	73	2130	0.28	9.96E-06	78	2130	0.37	4.40E-10
GO:001692	Nuclear rec	16	171	0.72	2.22E-05	10	171	0.57	0.0246
GO:00080E	ATP-depen	14	132	0.77	3.07E-05	NA	NA	NA	NA
GO:00431E	Ion binding	148	5669	0.16	3.38E-05	161	5669	0.26	7.96E-14
GO:001687	Ligase activ	16	179	0.7	3.62E-05	16	179	0.76	7.96E-06
GO:01400E	Catalytic ac	19	259	0.61	5.03E-05	NA	NA	NA	NA
GO:00973E	Carbohydra	77	2440	0.25	8.61E-05	87	2440	0.36	8.92E-11
GO:00198E	Enzyme bin	76	2431	0.24	0.00014	84	2431	0.34	9.29E-10
GO:000371	Transcriptic	18	260	0.59	0.00019	NA	NA	NA	NA
GO:00168E	ATP hydroly	21	343	0.53	0.00019	17	343	0.5	0.0029
GO:000004	tRNA bindir	10	77	0.86	0.00024	9	77	0.87	0.00054
GO:003051	snoRNA bir	8	44	1.01	0.00025	NA	NA	NA	NA
GO:00423E	Histone bin	19	297	0.55	0.00028	NA	NA	NA	NA
GO:000367	DNA helica	10	80	0.84	3.00E-04	NA	NA	NA	NA
GO:00051E	Structural r	41	1060	0.33	4.00E-04	36	1060	0.34	0.0012
GO:000481	aminoacyl-	8	51	0.94	6.00E-04	6	51	0.88	0.0123
GO:01401C	Catalytic ac	12	132	0.71	0.00064	NA	NA	NA	NA
GO:000371	Transcriptic	24	486	0.44	0.00094	NA	NA	NA	NA
GO:00080E	Cytoskeleta	43	1184	0.31	0.00095	44	1184	0.38	2.09E-05
GO:00156E	Tubulin bin	23	459	0.45	0.0011	NA	NA	NA	NA
GO:014044	Cytoskelet	4	9	1.39	0.0036	NA	NA	NA	NA
GO:00303E	Nuclear est	7	51	0.88	0.0042	NA	NA	NA	NA
GO:000801	Microtubul	18	340	0.47	0.0044	NA	NA	NA	NA
GO:00428C	Identical pr	64	2174	0.22	0.0044	77	2174	0.36	2.74E-09
GO:199084	Promoter-s	8	79	0.75	0.0085	NA	NA	NA	NA

GO:00164€	Pyrophospł	28	721	0.34	0.0095	31	721	0.44	8.26E-05
GO:003451	U3 snoRNA	4	13	1.23	0.0103	NA	NA	NA	NA
GO:000817	RNA methy	7	64	0.79	0.0132	NA	NA	NA	NA
GO:00434ᵹ	Protein-me	5	28	1	0.0135	NA	NA	NA	NA
GO:00515ᵹ	4 iron, 4 sul	6	45	0.87	0.0135	NA	NA	NA	NA
GO:00020ᵹ	p53 binding	8	87	0.71	0.0138	NA	NA	NA	NA
GO:001711	Nucleoside	26	670	0.34	0.0143	29	670	0.44	0.00015
GO:00507ᵹ	RS domain	3	6	1.45	0.0204	NA	NA	NA	NA
GO:003067	Protein-ma	18	396	0.4	0.021	NA	NA	NA	NA
GO:00515ᵹ	Iron-sulfur	7	72	0.73	0.0229	NA	NA	NA	NA
GO:00010ᵹ	Basal RNA	7	73	0.73	0.0241	NA	NA	NA	NA
GO:005101	Actin filame	13	245	0.47	0.0316	23	245	0.78	5.62E-09
GO:014014	Nucleocyto	5	36	0.89	0.0323	NA	NA	NA	NA
GO:000802	Protein C-te	13	252	0.46	0.0394	NA	NA	NA	NA
GO:01401C	Molecular c	7	82	0.68	0.0427	NA	NA	NA	NA
GO:00314ᵹ	Nucleosom	6	60	0.75	0.0453	NA	NA	NA	NA
GO:00164ᵹ	Oxidoreduc	NA	NA	NA	NA	32	858	0.38	0.00065
GO:00325ᵹ	Adenyl ribo	NA	NA	NA	NA	64	1731	0.37	3.16E-08
GO:003321	Amide bind	NA	NA	NA	NA	19	417	0.46	0.0031
GO:00055C	Calcium ior	NA	NA	NA	NA	23	686	0.33	0.0303
GO:001662	Oxidoreduc	NA	NA	NA	NA	7	53	0.93	0.0023
GO:00039ᵹ	acyl-CoA d	NA	NA	NA	NA	4	11	1.37	0.0038
GO:00506€	Flavin aden	NA	NA	NA	NA	9	95	0.78	0.0022
GO:00512€	NAD bindin	NA	NA	NA	NA	12	138	0.75	0.00035
GO:00431€	Cation binc	NA	NA	NA	NA	91	3679	0.2	0.00042
GO:19016€	Sulfur com	NA	NA	NA	NA	13	230	0.56	0.006
GO:00168€	Ligase activ	NA	NA	NA	NA	5	8	1.6	1.00E-04
GO:00082ᵹ	Peptidase a	NA	NA	NA	NA	25	613	0.42	0.0014

GO:00435	ADP bindin	NA	NA	NA	NA	7	47	0.98	0.0012
GO:00468	Metal ion b	NA	NA	NA	NA	85	3580	0.18	0.0031
GO:00164	CoA carbox	NA	NA	NA	NA	4	7	1.56	0.0012
GO:00082	Metallopep	NA	NA	NA	NA	14	196	0.66	0.00042
GO:00000	fatty-acyl-C	NA	NA	NA	NA	4	25	1.01	0.0403
GO:00042	Metalloend	NA	NA	NA	NA	8	116	0.64	0.0303
GO:00325	Guanyl ribo	NA	NA	NA	NA	17	459	0.37	0.0494
GO:00314	Carboxylic	NA	NA	NA	NA	9	159	0.56	0.0494
GO:00039	acetyl-CoA	NA	NA	NA	NA	3	8	1.38	0.0249
GO:00483	Calcium-de	NA	NA	NA	NA	7	84	0.73	0.0246
GO:00509	Quaternary	NA	NA	NA	NA	5	43	0.87	0.0357
GO:00082	Lipid bindir	NA	NA	NA	NA	31	794	0.4	0.00042
GO:00037	Actin bindir	NA	NA	NA	NA	27	481	0.56	3.52E-06
GO:00480	mRNA 5-UT	NA	NA	NA	NA	7	36	1.1	0.00035
GO:00469	Protein dim	NA	NA	NA	NA	37	1036	0.36	0.00038
GO:00428	Protein hon	NA	NA	NA	NA	29	712	0.42	4.00E-04
GO:00055	Phospholip	NA	NA	NA	NA	23	512	0.46	0.00078
GO:00451	Translation	NA	NA	NA	NA	12	158	0.69	0.00098
GO:00900	Translation	NA	NA	NA	NA	10	122	0.72	0.0024
GO:00166	Oxidoreduc	NA	NA	NA	NA	3	3	1.81	0.0039
GO:00199	Protein kin	NA	NA	NA	NA	28	845	0.33	0.0117
GO:00052	Structural c	NA	NA	NA	NA	8	100	0.71	0.0134
GO:01403	Cargo adap	NA	NA	NA	NA	4	18	1.15	0.0159
GO:00081	Translation	NA	NA	NA	NA	8	107	0.68	0.02
GO:00037	mRNA 3-UT	NA	NA	NA	NA	8	111	0.66	0.0246
GO:00001	Microfilam	NA	NA	NA	NA	5	40	0.9	0.0279
GO:00166	Oxidoreduc	NA	NA	NA	NA	3	9	1.33	0.0311

FUNCTION_D7_30mM_UP

#term ID	term descri	observed g	backgrounc	strength.NI	false disco	observed g	backgrounc	strength.DI	false discovery rate.DP12
GO:000551	Protein binc	121	7697	0.32	9.04E-19	172	7697	0.23	4.81E-13
GO:000548	Binding	153	13754	0.17	5.74E-13	269	13754	0.17	3.01E-22
GO:00428(	Identical pr	53	2174	0.51	7.19E-12	60	2174	0.32	8.02E-06
GO:00431(	Ion binding	82	5669	0.29	6.38E-08	124	5669	0.22	1.74E-07
GO:000382	Catalytic ac	81	6043	0.25	3.35E-06	153	6043	0.28	2.65E-15
GO:001985	Enzyme bin	44	2431	0.39	1.42E-05	67	2431	0.32	1.26E-06
GO:000828	Lipid bindir	23	794	0.59	1.98E-05	NA	NA	NA	NA
GO:004487	Protein-cor	34	1625	0.45	2.14E-05	44	1625	0.31	0.00076
GO:004335	Proteoglyca	7	43	1.34	3.02E-05	NA	NA	NA	NA
GO:00051(	Signaling re	31	1451	0.46	4.70E-05	NA	NA	NA	NA
GO:003321	Amide bind	16	417	0.71	4.70E-05	16	417	0.46	0.0135
GO:190168	Sulfur comp	12	230	0.84	7.46E-05	NA	NA	NA	NA
GO:007234	Modified ar	8	84	1.11	0.00011	NA	NA	NA	NA
GO:001645	Oxidoreduc	22	858	0.54	0.00015	33	858	0.46	1.15E-05
GO:00431(	Cation binc	53	3679	0.29	0.00024	NA	NA	NA	NA
GO:003605	Small mole	44	2793	0.32	0.00025	91	2793	0.39	3.92E-13
GO:000517	Integrin bin	9	145	0.92	0.00044	NA	NA	NA	NA
GO:00431(	Anion bindi	42	2671	0.32	0.00045	78	2671	0.34	6.61E-09
GO:003024	Carbohydra	11	241	0.79	0.00052	13	241	0.61	0.0031
GO:001990	Protein dor	21	883	0.5	0.00061	NA	NA	NA	NA
GO:004698	Protein dim	23	1036	0.47	0.00061	NA	NA	NA	NA
GO:001982	ATPase-cou	6	54	1.17	0.00081	NA	NA	NA	NA
GO:00043(	Glutathione	5	30	1.35	0.00082	NA	NA	NA	NA
GO:004687	Metal ion bi	50	3580	0.27	0.00083	NA	NA	NA	NA
GO:005108	Chaperone	8	124	0.94	0.00085	NA	NA	NA	NA
GO:00428(	Protein hon	18	712	0.53	0.0011	21	712	0.35	0.0392

GO:00973€	Carbohydra	37	2440	0.31	0.003	73	2440	0.35	1.04E-08
GO:00314(	Carboxylic	8	159	0.83	0.0042	9	159	0.63	0.0232
GO:000554	Phospholip	14	512	0.56	0.0045	NA	NA	NA	NA
GO:00508(	Cell adhesi	11	335	0.64	0.0063	NA	NA	NA	NA
GO:004227	Peptide bin	11	337	0.64	0.0064	13	337	0.46	0.0402
GO:00055(	Calcium ior	16	686	0.5	0.0073	NA	NA	NA	NA
GO:00017€	Phosphatid	5	55	1.09	0.0082	NA	NA	NA	NA
GO:001984	Vitamin bin	7	136	0.84	0.0094	NA	NA	NA	NA
GO:000842	Phosphatid	3	10	1.6	0.0102	NA	NA	NA	NA
GO:001661	Oxidoreduc	7	144	0.81	0.0125	10	144	0.72	0.0033
GO:00055(	Fatty acid b	4	36	1.17	0.0176	NA	NA	NA	NA
GO:00332€	Monocarbo	5	68	0.99	0.0176	NA	NA	NA	NA
GO:00199(	Kinase binc	18	929	0.41	0.0191	NA	NA	NA	NA
GO:00046(	Peroxidase	4	39	1.14	0.0219	NA	NA	NA	NA
GO:000377	Actin bindir	12	481	0.52	0.0242	NA	NA	NA	NA
GO:000397	UDP-N-ace	2	2	2.13	0.0242	NA	NA	NA	NA
GO:00171€	Vinculin bir	3	16	1.4	0.0254	NA	NA	NA	NA
GO:00309€	Potassium	3	16	1.4	0.0254	NA	NA	NA	NA
GO:00509€	Quaternary	4	43	1.1	0.0271	NA	NA	NA	NA
GO:00046(	Glutathione	3	18	1.35	0.0317	NA	NA	NA	NA
GO:004802	Monosacch	5	83	0.91	0.0323	9	83	0.91	4.00E-04
GO:00341€	Apolipopro	3	21	1.28	0.0456	NA	NA	NA	NA
GO:00001€	Nucleotide	33	2478	0.25	0.0482	80	2478	0.39	4.34E-11
GO:00156€	P-type ion t	3	22	1.26	0.0482	NA	NA	NA	NA
GO:00168€	Isomerase	7	198	0.68	0.0482	22	198	0.92	6.29E-11
GO:00309€	Kininogen b	2	4	1.83	0.0482	NA	NA	NA	NA
GO:00425€	Hormone b	5	93	0.86	0.0482	NA	NA	NA	NA
GO:004317	Organic aci	6	143	0.75	0.0482	10	143	0.72	0.0032

GO:00433	Heparan su	3	22	1.26	0.0482	NA	NA	NA	NA		
GO:00611	Peptidase r	7	199	0.67	0.0482	NA	NA	NA	NA		
GO:01200	Phosphatid	2	4	1.83	0.0482	NA	NA	NA	NA		
GO:00037	RNA bindin	NA	NA	NA	NA		48	1541	0.37	7.27E-06	
GO:19013	Heterocycli	NA	NA	NA	NA		142	6088	0.25	4.42E-11	
GO:00971	Organic cyc	NA	NA	NA	NA		143	6155	0.24	4.42E-11	
GO:00356	Purine ribo	NA	NA	NA	NA		65	2054	0.38	1.37E-08	
GO:00055	ATP binding	NA	NA	NA	NA		54	1663	0.39	2.45E-07	
GO:00325	Purine ribo	NA	NA	NA	NA		67	2130	0.38	1.04E-08	
GO:00325	Adenyl ribo	NA	NA	NA	NA		56	1731	0.39	1.64E-07	
GO:00037	mRNA bind	NA	NA	NA	NA		24	385	0.67	1.87E-07	
GO:01406	ATP-depen	NA	NA	NA	NA		22	652	0.41	0.0063	
GO:00451	Translation	NA	NA	NA	NA		10	158	0.68	0.0057	
GO:00171	Nucleoside	NA	NA	NA	NA		21	670	0.37	0.0203	
GO:00164	Pyrophospl	NA	NA	NA	NA		24	721	0.4	0.0043	
GO:00900	Translation	NA	NA	NA	NA		8	122	0.69	0.0201	
GO:00310	Heat shock	NA	NA	NA	NA		13	144	0.83	2.10E-05	
GO:00430	Ribonucleo	NA	NA	NA	NA		10	203	0.57	0.0312	
GO:00510	GTPase bin	NA	NA	NA	NA		18	364	0.57	4.00E-04	
GO:00305	Hsp70 prot	NA	NA	NA	NA		6	52	0.94	0.0076	
GO:00312	Small GTPa	NA	NA	NA	NA		16	330	0.56	0.0015	
GO:00518	Hsp90 prot	NA	NA	NA	NA		5	52	0.86	0.0463	
GO:00168	Ligase activ	NA	NA	NA	NA		13	179	0.74	2.00E-04	
GO:00037	Peptidyl-pr	NA	NA	NA	NA		7	61	0.94	0.0029	
GO:00081	Nuclear loc	NA	NA	NA	NA		6	27	1.23	0.00044	
GO:00616	Nuclear im	NA	NA	NA	NA		4	21	1.16	0.0188	
GO:00325	Ribonucleo	NA	NA	NA	NA		68	2149	0.38	6.61E-09	
GO:00168	Intramolec	NA	NA	NA	NA		7	50	1.02	0.00098	

GO:00616(	Ubiquitin c	NA	NA	NA	NA	5	31	1.09	0.0071
GO:00168	Ligase acti	NA	NA	NA	NA	6	58	0.89	0.0126
GO:00325(	Guanyl ribo	NA	NA	NA	NA	16	459	0.42	0.0332
GO:00352	UDP-gluco	NA	NA	NA	NA	3	10	1.36	0.0332
GO:00002	Magnesium	NA	NA	NA	NA	11	252	0.52	0.0397
GO:00228	Alanine tra	NA	NA	NA	NA	3	11	1.31	0.0397
GO:00055	GTP bindin	NA	NA	NA	NA	15	437	0.41	0.0498
GO:00190(	GDP bindin	NA	NA	NA	NA	6	81	0.75	0.05