Supplementary Material 2

Table 1: KEGG pathways enriched in differentially expressed proteins in CHO-K1, CHO-SK15-EPO and CHO-DP12 on day 4 and day 7.

Day 4

		CHO-K1			CHO-SK15-EPO			CHO-DP12		
Term ID	Pathway	Count	Strength	FDR	Count	Strength	FDR	Count	Strength	FDR
cge01100	Metabolic pathways	129	0.48	8.60E-25	115	0.45	1.27E-19	122	0.37	3.78E-15
cge01200	Carbon metabolism	37	0.98	1.23E-19	30	0.91	3.51E-14	26	0.74	2.23E-09
cge05014	Amyotrophic lateral sclerosis	54	0.72	1.33E-18	21	0.32	0.0131	70	0.74	1.01E-24
cge05012	Parkinson disease	42	0.79	1.12E-16	-	-	-	46	0.74	2.99E-16
cge05020	Prion disease	38	0.71	6.11E-13	-	-	-	45	0.7	9.07E-15
cge05010	Alzheimer disease	43	0.62	4.03E-12	20	0.31	0.0188	47	0.58	1.29E-11
cge03040	Spliceosome	28	0.82	8.58E-12	21	0.71	5.38E-07	40	0.89	4.27E-18
cge03013	R- transport	29	0.76	5.07E-11	22	0.66	1.42E-06	39	0.8	1.64E-15
cge05016	Huntington disease	37	0.63	8.61E-11	-	-	-	48	0.66	1.38E-14
cge03050	Proteasome	16	1.06	1.01E-09	-	-	-	17	1	2.23E-09
cge05132	Salmonella infection	29	0.65	6.30E-09	18	0.47	0.0015	19	0.38	0.0056
cge00020	Citrate cycle (TCA cycle)	13	1.11	2.15E-08	9	0.97	7.61E-05	13	1.02	2.02E-07
cge01230	Biosynthesis of amino acids	18	0.86	2.84E-08	15	0.8	5.10E-06	10	0.51	0.0112
cge04141	Protein processing in endoplasmic reticulum	24	0.7	2.84E-08	27	0.77	4.45E-10	27	0.66	2.12E-08
cge00280	Valine, leucine and isoleucine degradation	14	0.95	1.78E-07	11	0.86	5.31E-05	10	0.72	0.00091
cge00230	Purine metabolism	19	0.75	2.46E-07	10	0.49	0.0158	11	0.43	0.0215
cge05100	Bacterial invasion of epithelial cells	16	0.85	2.46E-07	7	0.51	0.0419	12	0.63	0.00091
cge00630	Glyoxylate and dicarboxylate metabolism	11	1.04	1.15E-06	9	0.97	7.61E-05	7	0.75	0.0044
cge00970	Aminoacyl-tR- biosynthesis	12	0.95	1.65E-06	15	1.07	8.85E-09	9	0.74	0.0013
cge04530	Tight junction	19	0.68	1.70E-06	13	0.54	0.0023	15	0.5	0.0021
cge05203	Viral carcinogenesis	22	0.61	2.09E-06	19	0.57	7.86E-05	19	0.46	0.001
cge03010	Ribosome	25	0.56	2.45E-06	-	-	-	38	0.66	1.81E-11
cge05017	Spinocerebellar ataxia	18	0.66	6.44E-06	-	-	-	20	0.62	1.10E-05
cge00030	Pentose phosphate pathway	10	0.98	9.22E-06	7	0.84	0.002	5	0.59	0.0478
cge00010	Glycolysis / Gluconeogenesis	13	0.8	1.06E-05	10	0.71	0.0011	9	0.55	0.0112
cge04810	Regulation of actin cytoskeleton	21	0.56	1.72E-05	17	0.49	0.0012	20	0.46	0.00091
cge05205	Proteoglycans in cancer	20	0.58	1.72E-05	15	0.48	0.0031	15	0.37	0.0163
cge00520	Amino sugar and nucleotide sugar metabolism	11	0.86	2.33E-05	7	0.68	0.0093	8	0.63	0.008
cge03018	R- degradation	13	0.75	2.92E-05	8	0.56	0.017	8	0.45	0.043
cge04210	Apoptosis	15	0.64	7.63E-05	11	0.52	0.0073	14	0.52	0.002

cge00240	Pyrimidine metabolism	10	0.81	0.00013	-	-	-	7	0.57	0.0215
cge03015	mR- surveillance pathway	13	0.68	0.00013	-	-	-	14	0.62	0.00034
cge04612	Antigen processing and presentation	10	0.77	0.00024	-	-	-	8	0.59	0.0113
cge00620	Pyruvate metabolism	8	0.9	0.00027	8	0.92	0.00037	9	0.86	0.00027
cge00640	Propanoate metabolism	8	0.88	0.00032	11	1.04	2.59E-06	6	0.67	0.0162
cge04114	Oocyte meiosis	13	0.63	0.00033	-	-	-	16	0.63	9.01E-05
cge04670	Leukocyte transendothelial migration	13	0.62	0.00036	-	-	-	10	0.42	0.0319
cge05135	Yersinia infection	14	0.59	0.00041	-	-	-	-	-	-
cge00190	Oxidative phosphorylation	15	0.55	0.00047	10	0.4	0.0448	21	0.61	7.71E-06
cge04066	HIF-1 sig-ling pathway	13	0.61	0.00047	10	0.51	0.0131	-	-	-
cge05160	Hepatitis C	17	0.51	0.00047	12	0.38	0.033	16	0.4	0.0089
cge05418	Fluid shear stress and atherosclerosis	14	0.57	0.00049	16	0.65	7.53E-05	17	0.57	0.00022
cge00480	Glutathione metabolism	10	0.71	0.00054	11	0.77	0.00018	14	0.77	1.63E-05
cge05170	Human immunodeficiency virus 1 infection	19	0.47	0.00057	16	0.41	0.0079	22	0.44	0.00067
cge00072	Synthesis and degradation of ketone bodies	5	1.17	0.00068	-	-	-	4	0.99	0.0112
cge01523	Antifolate resistance	7	0.89	0.00069	-	-	-	-	-	-
cge00071	Fatty acid degradation	8	0.77	0.0011	-	-	-	9	0.74	0.0013
cge00983	Drug metabolism - other enzymes	10	0.66	0.0011	8	0.59	0.0133	9	0.53	0.0132
cge00650	Butanoate metabolism	6	0.93	0.0014	-	-	-	-	-	-
cge04110	Cell cycle	13	0.55	0.0014	-	-	-	12	0.42	0.0163
cge04962	Vasopressin-regulated water reabsorption	8	0.75	0.0014	-	-	-	7	0.61	0.0162
cge00051	Fructose and mannose metabolism	7	0.81	0.0017	7	0.83	0.0021	8	0.78	0.0016
cge04151	PI3K-Akt sig-ling pathway	23	0.37	0.0017	23	0.39	0.0019	21	0.25	0.0467
cge00900	Terpenoid backbone biosynthesis	6	0.88	0.0021	-	-	-	5	0.72	0.022
cge04144	Endocytosis	18	0.42	0.0022	20	0.48	0.00045	26	0.49	3.02E-05
cge04152	AMPK sig-ling pathway	12	0.54	0.0022	15	0.66	8.64E-05	-	-	-
cge04722	Neurotrophin sig-ling pathway	11	0.55	0.003	-	-	-	-	-	-
cge01212	Fatty acid metabolism	8	0.67	0.0038	-	-	-	-	-	-
cge04260	Cardiac muscle contraction	8	0.67	0.0038	-	-	-	-	-	-
cge00100	Steroid biosynthesis	5	0.92	0.0042	-	-	-	-	-	-
cge00670	One carbon pool by folate	5	0.92	0.0042	-	-	-	-	-	-
cge01210	2-Oxocarboxylic acid metabolism	5	0.92	0.0042	4	0.84	0.0249	5	0.83	0.0112
cge00052	Galactose metabolism	6	0.79	0.0045	7	0.88	0.0015	5	0.62	0.0422
cge05206	MicroR-s in cancer	13	0.47	0.0045	11	0.42	0.0268	-	-	-
cge04932	Non-alcoholic fatty liver disease	13	0.47	0.0047	-	-	-	18	0.52	0.00038
cge04520	Adherens junction	8	0.64	0.0048	-	-	-	7	0.5	0.0423

cge03030	D- replication	6	0.77	0.0051	-	-	-	8	0.81	0.0012
cge03320	PPAR sig-ling pathway	9	0.58	0.0053	9	0.6	0.007	-	-	-
cge04510	Focal adhesion	14	0.44	0.0053	13	0.43	0.0136	16	0.41	0.0076
cge05142	Chagas disease	10	0.54	0.0055	-	-	-	-	-	-
cge04071	Sphingolipid sig-ling pathway	11	0.5	0.0057	-	-	-	12	0.46	0.0112
cge05034	Alcoholism	12	0.48	0.0057	-	-	-	15	0.49	0.0024
cge00270	Cysteine and methionine metabolism	7	0.67	0.0063	-	-	-	8	0.64	0.0076
cge04015	Rap1 sig-ling pathway	14	0.41	0.008	-	-	-	14	0.33	0.0398
cge00380	Tryptophan metabolism	6	0.71	0.0085	-	-	-	-	-	-
cge04714	Thermogenesis	16	0.38	0.0085	18	0.45	0.002	26	0.5	2.21E-05
cge05169	Epstein-Barr virus infection	15	0.39	0.0089	-	-	-	15	0.3	0.0439
cge04261	Adrenergic sig-ling in cardiomyocytes	10	0.5	0.0096	-	-	-	11	0.45	0.0162
cge00510	N-Glycan biosynthesis	7	0.62	0.0106	6	0.57	0.0387	-	-	-
cge05134	Legionellosis	7	0.62	0.0106	-	-	-	-	-	-
cge05133	Pertussis	7	0.61	0.0115	-	-	-	-	-	-
cge04146	Peroxisome	8	0.55	0.0122	7	0.51	0.0393	-	-	-
cge04062	Chemokine sig-ling pathway	13	0.4	0.0132	-	-	-	-	-	-
cge04145	Phagosome	11	0.44	0.0134	13	0.53	0.0024	15	0.49	0.0023
cge04730	Long-term depression	7	0.59	0.0136	-	-	-	8	0.56	0.0151
cge05165	Human papillomavirus infection	19	0.31	0.0172	28	0.49	1.87E-05	-	-	-
cge04360	Axon guidance	12	0.4	0.0195	-	-	-	-	-	-
cge05211	Re-l cell carcinoma	7	0.56	0.0195	-	-	-	9	0.58	0.0084
cge04915	Estrogen sig-ling pathway	10	0.44	0.0198	-	-	-	13	0.47	0.0076
cge05161	Hepatitis B	12	0.39	0.0199	-	-	-	-	-	-
cge05164	Influenza A	12	0.39	0.0199	-	-	-	15	0.4	0.0111
cge05230	Central carbon metabolism in cancer	7	0.55	0.0205	10	0.72	0.00085	-	-	-
cge05215	Prostate cancer	8	0.5	0.0214	-	-	-	-	-	-
cge04918	Thyroid hormone synthesis	7	0.54	0.0219	-	-	-	8	0.51	0.0236
cge04390	Hippo sig-ling pathway	11	0.4	0.022	-	-	-	-	-	-
cge05145	Toxoplasmosis	9	0.46	0.0221	-	-	-	-	-	-
cge04660	T cell receptor sig-ling pathway	8	0.49	0.0222	-	-	-	-	-	-
cge04666	Fc gamma R-mediated phagocytosis	8	0.49	0.0238	-	-	-	-	-	-
cge04922	Glucagon sig-ling pathway	8	0.47	0.0273	10	0.59	0.0048	-	-	-
cge03008	Ribosome biogenesis in eukaryotes	7	0.51	0.0291	11	0.72	4.00E-04	8	0.48	0.0336
cge04919	Thyroid hormone sig-ling pathway	9	0.43	0.0293	12	0.58	0.0021	-	-	-
cge05200	Pathways in cancer	25	0.23	0.0302	28	0.3	0.0066	33	0.27	0.0076
cge05163	Human cytomegalovirus infection	14	0.33	0.031	16	0.4	0.0091	16	0.3	0.0424

cge04217	Necroptosis	11	0.37	0.033	-	-	-	14	0.39	0.0162
cge05220	Chronic myeloid leukemia	7	0.49	0.0352	8	0.56	0.0161	-	-	-
cge05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	7	0.48	0.0376	7	0.5	0.0447	-	-	-
cge05221	Acute myeloid leukemia	6	0.52	0.0397	7	0.61	0.017	-	-	-
cge04540	Gap junction	7	0.47	0.0398	-	-	-	11	0.58	0.0029
cge00500	Starch and sucrose metabolism	4	0.69	0.0405	-	-	-	-	-	-
cge04621	NOD-like receptor sig-ling pathway	11	0.35	0.0405	-	-	-	-	-	-
cge00513	Various types of N-glycan biosynthesis	5	0.57	0.0461	-	-	-	-	-	-
cge04014	Ras sig-ling pathway	13	0.31	0.0463	-	-	-	-	-	-
cge04137	Mitophagy - animal	6	0.5	0.0483	-	-	-	-	-	-
cge04971	Gastric acid secretion	6	0.5	0.0483	-	-	-	7	0.48	0.047
cge04142	Lysosome	-	-	-	16	0.65	7.61E-05	17	0.57	0.00023
cge04910	Insulin sig-ling pathway	-	-	-	14	0.59	0.00069	-	-	-
cge05225	Hepatocellular carcinoma	-	-	-	15	0.5	0.002	-	-	-
cge04012	ErbB sig-ling pathway	-	-	-	9	0.61	0.0066	-	-	-
cge01524	Platinum drug resistance	-	-	-	8	0.62	0.0091	10	0.62	0.0031
cge05412	Arrhythmogenic right ventricular cardiomyopathy	-	-	-	7	0.65	0.0131	-	-	-
cge00980	Metabolism of xenobiotics by cytochrome P450	-	-	-	7	0.64	0.0135	10	0.69	0.0013
cge00860	Porphyrin and chlorophyll metabolism	-	-	-	5	0.78	0.0158	-	-	-
cge04218	Cellular senescence	-	-	-	11	0.44	0.0197	-	-	-
cge05214	Glioma	-	-	-	7	0.59	0.0197	-	-	-
cge05410	Hypertrophic cardiomyopathy	-	-	-	7	0.57	0.025	-	-	-
cge04213	Longevity regulating pathway - multiple species	-	-	-	7	0.56	0.0268	-	-	-
cge05222	Small cell lung cancer	-	-	-	8	0.51	0.0268	-	-	-
cge04150	mTOR sig-ling pathway	-	-	-	11	0.41	0.0303	-	-	-
cge04512	ECM-receptor interaction	-	-	-	7	0.54	0.033	-	-	-
cge05414	Dilated cardiomyopathy	-	-	-	7	0.54	0.033	-	-	-
cge04912	GnRH sig-ling pathway	-	-	-	7	0.53	0.0344	8	0.48	0.0336
cge04120	Ubiquitin mediated proteolysis	-	-	-	-	-	-	15	0.5	0.002
cge03430	Mismatch repair	-	-	-	-	-	-	6	0.86	0.0037
cge04216	Ferroptosis	-	-	-	-	-	-	7	0.65	0.0112
cge04961	Endocrine and other factor-regulated calcium reabsorption	-	-	-	-	-	-	7	0.64	0.0117
cge00330	Arginine and proline metabolism	-	-	-	-	-	-	7	0.63	0.0132

cge04723	Retrograde endocan-binoid sig-ling	-	-	-	-	-	-	13	0.39	0.0204
cge05204	Chemical carcinogenesis	-	-	-	-	-	-	8	0.52	0.022
cge04728	Dopaminergic sy-pse	-	-	-	-	-	-	11	0.42	0.0221
cge00770	Pantothe-te and CoA biosynthesis	-	-	-	-	-	-	4	0.74	0.0411
cge00982	Drug metabolism - cytochrome P450	-	-	-	-	-	-	6	0.55	0.0422
cge04914	Progesterone-mediated oocyte maturation	-	-	-	-	-	-	8	0.45	0.043
cge04720	Long-term potentiation	-	-	-	-	-	-	6	0.54	0.0439
cge04713	Circadian entrainment	-	-	-	-	-	-	8	0.44	0.0471
cge04923	Regulation of lipolysis in adipocytes	-	-	-	-	-	-	6	0.53	0.0471

Day 7

		CHO-K1			CHO-SK15-EPO			CHO-DP12		
Term ID	Pathway	Count	Strength	FDR	Count	Strength	FDR	Count	Strength	FDR
cge01100	Metabolic pathways	198	0.52	1.17E-42	106	0.43	9.92E-17	164	0.56	9.71E-41
cge05012	Parkinson disease	59	0.79	1.77E-22	15	0.38	0.0322	39	0.73	1.63E-13
cge01200	Carbon metabolism	46	0.92	5.04E-22	18	0.7	1.03E-05	30	0.86	2.18E-13
cge05014	Amyotrophic lateral sclerosis	67	0.66	5.50E-20	22	0.36	0.0104	51	0.66	2.58E-15
cge05020	Prion disease	52	0.7	8.11E-17	-	-	-	34	0.63	8.02E-10
cge05010	Alzheimer disease	58	0.61	3.28E-15	19	0.31	0.0434	38	0.54	1.15E-08
cge03013	R- transport	38	0.73	4.04E-13	18	0.59	0.00018	26	0.68	1.76E-08
cge05016	Huntington disease	49	0.61	5.94E-13	-	-	-	38	0.62	1.69E-10
cge03050	Proteasome	21	1.03	8.78E-12	10	0.89	0.00018	15	1.01	1.81E-08
cge04141	Protein processing in endoplasmic reticulum	33	0.69	1.25E-10	22	0.7	7.06E-07	33	0.81	1.79E-13
cge01230	Biosynthesis of amino acids	24	0.83	3.59E-10	11	0.68	0.0016	14	0.72	3.08E-05
cge04142	Lysosome	28	0.72	1.06E-09	12	0.54	0.0093	28	0.84	3.48E-12
cge00280	Valine, leucine and isoleucine degradation	19	0.93	1.76E-09	7	0.68	0.0208	13	0.89	2.94E-06
cge00020	Citrate cycle (TCA cycle)	16	1.05	2.50E-09	7	0.88	0.003	12	1.05	3.88E-07
cge03040	Spliceosome	28	0.67	9.08E-09	21	0.73	7.06E-07	20	0.64	4.08E-06
cge00190	Oxidative phosphorylation	27	0.66	2.47E-08	-	-	-	14	0.5	0.0025
cge05017	Spinocerebellar ataxia	26	0.67	2.89E-08	-	-	-	19	0.66	5.07E-06
cge04714	Thermogenesis	33	0.54	1.26E-07	-	-	-	21	0.47	0.00032
cge00230	Purine metabolism	23	0.69	1.36E-07	10	0.51	0.0257	18	0.7	3.45E-06
cge00640	Propanoate metabolism	14	0.98	1.37E-07	5	0.71	0.0434	9	0.91	9.59E-05
cge00071	Fatty acid degradation	15	0.9	2.65E-07	-	-	-	11	0.88	1.75E-05
cge00983	Drug metabolism - other enzymes	18	0.77	4.16E-07	7	0.54	0.0434	14	0.78	8.34E-06
cge00010	Glycolysis / Gluconeogenesis	17	0.77	1.01E-06	9	0.68	0.0066	14	0.81	5.13E-06

cge00520	Amino sugar and nucleotide sugar metabolism	14	0.81	5.09E-06	10	0.85	0.00022	12	0.87	9.22E-06
cge05132	Salmonella infection	28	0.49	1.16E-05	16	0.43	0.0114	19	0.44	0.0012
cge01212	Fatty acid metabolism	14	0.76	1.48E-05	-	-	-	13	0.85	5.13E-06
cge00052	Galactose metabolism	11	0.9	1.50E-05	-	-	-	9	0.94	6.28E-05
cge00620	Pyruvate metabolism	11	0.89	1.95E-05	5	0.73	0.0415	8	0.87	0.00044
cge04932	Non-alcoholic fatty liver disease	22	0.55	2.10E-05	-	-	-	12	0.41	0.0192
cge00970	Aminoacyl-tR-biosynthesis	12	0.8	3.41E-05	9	0.86	0.00049	7	0.69	0.0067
cge05170	Human immunodeficiency virus 1 infection	26	0.45	9.01E-05	14	0.37	0.0434	16	0.36	0.0134
cge00240	Pyrimidine metabolism	12	0.74	9.71E-05	6	0.63	0.0434	12	0.87	9.22E-06
cge00630	Glyoxylate and dicarboxylate metabolism	10	0.85	9.73E-05	-	-	-	5	0.67	0.0282
cge03030	D- replication	10	0.85	9.73E-05	-	-	-	7	0.81	0.0019
cge01210	2-Oxocarboxylic acid metabolism	8	0.98	0.00013	-	-	-	5	0.89	0.006
cge00330	Arginine and proline metabolism	11	0.76	0.00014	-	-	-	-	-	-
cge00480	Glutathione metabolism	13	0.68	0.00015	7	0.59	0.0385	14	0.83	3.57E-06
cge00270	Cysteine and methionine metabolism	11	0.72	3.00E-04	-	-	-	10	0.8	0.00018
cge00531	Glycosaminoglycan degradation	7	1.01	3.00E-04	-	-	-	6	1.06	0.00055
cge00650	Butanoate metabolism	8	0.9	3.00E-04	-	-	-	8	1.02	6.42E-05
cge05205	Proteoglycans in cancer	21	0.45	0.00046	-	-	-	20	0.55	4.57E-05
cge04146	Peroxisome	13	0.61	0.00048	9	0.64	0.0102	9	0.58	0.0069
cge00051	Fructose and mannose metabolism	9	0.77	0.00065	9	0.95	0.00018	8	0.84	0.00061
cge04210	Apoptosis	16	0.52	0.00071	10	0.5	0.028	13	0.55	0.0015
cge00380	Tryptophan metabolism	9	0.74	0.00095	-	-	-	7	0.75	0.0034
cge00410	beta-Alanine metabolism	8	0.8	0.001	-	-	-	7	0.86	0.0012
cge05100	Bacterial invasion of epithelial cells	12	0.57	0.0018	7	0.52	0.0482	8	0.52	0.0211
cge04114	Oocyte meiosis	14	0.51	0.002	-	-	-	-	-	-
cge04510	Focal adhesion	19	0.42	0.002	-	-	-	12	0.35	0.0436
cge00030	Pentose phosphate pathway	8	0.73	0.0022	5	0.71	0.0434	-	-	-
cge04723	Retrograde endocan-binoid sig-ling	17	0.44	0.0023	-	-	-	-	-	-
cge00250	Alanine, aspartate and glutamate metabolism	8	0.72	0.0026	5	0.7	0.0434	6	0.72	0.01
cge00072	Synthesis and degradation of ketone bodies	5	1.02	0.0027	-	-	-	5	1.14	0.0011
cge04810	Regulation of actin cytoskeleton	20	0.39	0.0027	14	0.42	0.0242	20	0.52	0.00013
cge05203	Viral carcinogenesis	19	0.4	0.003	13	0.42	0.028	16	0.45	0.0029
cge00511	Other glycan degradation	6	0.85	0.0034	-	-	-	4	0.8	0.0267
cge00670	One carbon pool by folate	6	0.85	0.0034	-	-	-	4	0.8	0.0267

cge00860	Porphyrin and chlorophyll metabolism	7	0.76	0.0034	5	0.8	0.028	6	0.82	0.0044
cge00310	Lysine degradation	9	0.62	0.0042	-	-	-	-	-	-
cge04922	Glucagon sig-ling pathway	12	0.5	0.0053	8	0.51	0.0434	-	-	-
cge04670	Leukocyte transendothelial migration	13	0.47	0.0054	-	-	-	10	0.48	0.0141
cge00513	Various types of N-glycan biosynthesis	8	0.62	0.0072	-	-	-	7	0.69	0.0067
cge00980	Metabolism of xenobiotics by cytochrome P450	9	0.58	0.0072	-	-	-	8	0.65	0.0054
cge04612	Antigen processing and presentation	9	0.58	0.0072	6	0.59	0.0458	9	0.7	0.0015
cge05418	Fluid shear stress and atherosclerosis	14	0.42	0.0086	-	-	-	13	0.51	0.0028
cge00900	Terpenoid backbone biosynthesis	6	0.73	0.0093	-	-	-	6	0.86	0.0031
cge04962	Vasopressin-regulated water reabsorption	8	0.6	0.0093	-	-	-	7	0.67	0.0081
cge05169	Epstein-Barr virus infection	19	0.34	0.0099	-	-	-	18	0.44	0.0016
cge04145	Phagosome	14	0.4	0.0132	-	-	-	15	0.55	6.00E-04
cge03420	Nucleotide excision repair	7	0.62	0.0139	-	-	-	-	-	-
cge03018	R- degradation	10	0.49	0.0142	-	-	-	-	-	-
cge05211	Re-l cell carcinoma	9	0.52	0.0147	-	-	-	-	-	-
cge00100	Steroid biosynthesis	5	0.77	0.0148	-	-	-	-	-	-
cge01040	Biosynthesis of unsaturated fatty acids	6	0.68	0.0148	-	-	-	7	0.86	0.0012
cge03320	PPAR sig-ling pathway	10	0.48	0.0149	-	-	-	9	0.55	0.0088
cge04066	HIF-1 sig-ling pathway	12	0.42	0.0157	9	0.48	0.0434	10	0.47	0.017
cge04979	Cholesterol metabolism	7	0.58	0.0194	-	-	-	-	-	-
cge00510	N-Glycan biosynthesis	8	0.53	0.0196	6	0.59	0.0458	9	0.7	0.0015
cge04910	Insulin sig-ling pathway	13	0.39	0.0196	-	-	-	12	0.47	0.0072
cge03430	Mismatch repair	5	0.72	0.0205	-	-	-	-	-	-
cge00061	Fatty acid biosynthesis	4	0.84	0.0225	-	-	-	-	-	-
cge04144	Endocytosis	19	0.29	0.0258	21	0.52	0.00021	-	-	-
cge04666	Fc gamma R-mediated phagocytosis	10	0.43	0.0261	-	-	-	8	0.46	0.0383
cge04015	Rap1 sig-ling pathway	16	0.32	0.0263	-	-	-	-	-	-
cge04520	Adherens junction	8	0.49	0.0282	-	-	-	-	-	-
cge04611	Platelet activation	11	0.4	0.0305	-	-	-	9	0.43	0.0364
cge03015	mR- surveillance pathway	10	0.41	0.0319	-	-	-	8	0.44	0.0455
cge04130	S-RE interactions in vesicular transport	6	0.58	0.0319	5	0.68	0.0434	-	-	-
cge04971	Gastric acid secretion	8	0.47	0.0331	-	-	-	-	-	-
cge04110	Cell cycle	12	0.36	0.0358	-	-	-	10	0.4	0.0363
cge00500	Starch and sucrose metabolism	5	0.63	0.0367	-	-	-	5	0.76	0.0153
cge00604	Glycosphingolipid biosynthesis - ganglio series	4	0.73	0.039	-	-	-	-	-	-

cge01524	Platinum drug resistance	8	0.46	0.039	-	-	-	10	0.68	0.0012
cge05204	Chemical carcinogenesis	8	0.46	0.039	-	-	-	8	0.58	0.011
cge05230	Central carbon metabolism in cancer	8	0.46	0.039	7	0.58	0.041	-	-	-
cge00603	Glycosphingolipid biosynthesis - globo and isoglobo series	4	0.7	0.0459	-	-	-	4	0.83	0.0229
cge04120	Ubiquitin mediated proteolysis	12	0.34	0.0462	-	-	-	-	-	-
cge04216	Ferroptosis	6	0.52	0.0472	-	-	-	-	-	-
cge04530	Tight junction	12	0.34	0.0482	-	-	-	12	0.46	0.0093
cge05134	Legionellosis	7	0.47	0.0482	-	-	-	-	-	-
cge05206	MicroR-s in cancer	-	-	-	12	0.47	0.0224	-	-	-
cge03008	Ribosome biogenesis in eukaryotes	-	-	-	8	0.6	0.0242	8	0.54	0.0167
cge04912	GnRH sig-ling pathway	-	-	-	8	0.6	0.0242	-	-	-
cge04919	Thyroid hormone sig-ling pathway	-	-	-	10	0.51	0.0248	-	-	-
cge04918	Thyroid hormone synthesis	-	-	-	7	0.58	0.0422	8	0.57	0.0121
cge00562	Inositol phosphate metabolism	-	-	-	7	0.57	0.0434	-	-	-
cge00600	Sphingolipid metabolism	-	-	-	6	0.61	0.0434	-	-	-
cge05034	Alcoholism	-	-	-	10	0.43	0.0434	-	-	-
cge05216	Thyroid cancer	-	-	-	5	0.7	0.0434	-	-	-
cge05412	Arrhythmogenic right ventricular cardiomyopathy	-	-	-	6	0.6	0.0434	-	-	-
cge04152	AMPK sig-ling pathway	-	-	-	9	0.45	0.0457	-	-	-
cge04540	Gap junction	-	-	-	-	-	-	10	0.6	0.0031
cge04217	Necroptosis	-	-	-	-	-	-	14	0.45	0.0057
cge00770	Pantothe-te and CoA biosynthesis	-	-	-	-	-	-	5	0.89	0.006
cge04614	Renin-angiotensin system	-	-	-	-	-	-	5	0.87	0.0069
cge00062	Fatty acid elongation	-	-	-	-	-	-	5	0.78	0.0134
cge00982	Drug metabolism - cytochrome P450	-	-	-	-	-	-	6	0.61	0.0244
cge05200	Pathways in cancer	-	-	-	-	-	-	27	0.24	0.0258
cge05416	Viral myocarditis	-	-	-	-	-	-	7	0.54	0.0267
cge05322	Systemic lupus erythematosus	-	-	-	-	-	-	8	0.46	0.0364
cge00040	Pentose and glucuro-te interconversions	-	-	-	-	-	-	4	0.72	0.0404
cge04512	ECM-receptor interaction	-	-	-	-	-	-	7	0.49	0.0416

Table 2: The KEGG pathways, molecular functions and processes enriched in **ubiquitinated differentially expressed proteins** in CHO-K1, CHO-SK15-EPO and CHO-DP12 on day 4 and day 7.

Day 4

		CHO-SK15-EPO			CHO-DP12		
KEGG	Description	Count	Strength	FDR	Count	Strength	FDR
cge05012	Parkinson disease	7	0.87	0.02	9	1.01	4.51E-05

cge04120	Ubiquitin mediated proteolysis	5	0.97	0.0271	-	-	-
cge04130	S-RE interactions in vesicular transport	3	1.28	0.0271	-	-	-
cge04145	Phagosome	5	0.96	0.0271	-	-	-
cge04510	Focal adhesion	5	0.85	0.0271	-	-	-
cge04520	Adherens junction	4	1.2	0.0271	3	1.1	0.0432
cge04810	Regulation of actin cytoskeleton	6	0.88	0.0271	5	0.83	0.0246
cge05014	Amyotrophic lateral sclerosis	7	0.69	0.0271	9	0.82	0.00046
cge05100	Bacterial invasion of epithelial cells	4	1.1	0.0271	-	-	-
cge05132	Salmonella infection	6	0.83	0.0271	-	-	-
cge05135	Yersinia infection	5	1	0.0271	-	-	-
cge05170	Human immunodeficiency virus 1 infection	6	0.82	0.0271	-	-	-
cge03050	Proteasome	3	1.19	0.0295	8	1.65	1.44E-08
cge05017	Spinocerebellar ataxia	-	-	-	8	1.2	1.30E-05
cge03010	Ribosome	-	-	-	9	1	4.51E-05
cge05203	Viral carcinogenesis	-	-	-	8	1.06	4.86E-05
cge05016	Huntington disease	-	-	-	9	0.91	0.00014
cge05020	Prion disease	-	-	-	8	0.92	0.00035
cge05034	Alcoholism	-	-	-	6	1.06	0.00069
cge05010	Alzheimer disease	-	-	-	8	0.78	0.0023
cge05169	Epstein-Barr virus infection	-	-	-	6	0.88	0.0053
cge05322	Systemic lupus erythematosus	-	-	-	4	1.08	0.0121
cge05205	Proteoglycans in cancer	-	-	-	5	0.87	0.018
cge04530	Tight junction	-	-	-	4	0.89	0.0432

		CHO-K1			CHO-SK15-EPO			CHO-DP12		
Term ID	Function	Count	Strength	FDR	Count	Strength	FDR	Count	Strength	FDR
GO:0005488	Binding	293	0.13	1.20E-11	111	0.19	2.28E-11	98	0.17	1.76E-06
GO:0005515	Protein binding	183	0.17	2.64E-07	79	0.3	1.32E-09	67	0.25	2.50E-05
GO:0000166	Nucleotide binding	75	0.28	7.37E-05	28	0.34	0.0303	-	-	-
GO:0036094	Small molecule binding	81	0.26	7.37E-05	-	-	-	-	-	-
GO:0043168	Anion binding	76	0.25	0.00033	-	-	-	-	-	-
GO:0008092	Cytoskeletal protein binding	43	0.36	0.00037	-	-	-	-	-	-
GO:0017076	Purine nucleotide binding	64	0.27	0.00052	-	-	-	-	-	-
GO:0032553	Ribonucleotide binding	64	0.27	0.00052	-	-	-	-	-	-
GO:0032555	Purine ribonucleotide binding	63	0.27	0.00057	-	-	-	-	-	-
GO:0097159	Organic cyclic compound binding	140	0.15	0.00057	55	0.24	0.0051	52	0.24	0.0041
GO:1901363	Heterocyclic compound binding	139	0.16	0.00057	54	0.23	0.0067	52	0.24	0.0035
GO:0035639	Purine ribonucleoside triphosphate binding	61	0.27	0.00066	24	0.35	0.0478	-	-	-
GO:0097367	Carbohydrate derivative binding	69	0.25	0.00066	-	-	-	-	-	-
GO:0017111	Nucleoside-triphosphatase activity	28	0.42	0.0014	-	-	-	12	0.57	0.0333
GO:0043167	Ion binding	129	0.15	0.0014	-	-	-	-	-	-
GO:0019899	Enzyme binding	67	0.24	0.0018	34	0.43	6.93E-05	27	0.36	0.0167

GO:0044877	Protein-containing complex binding	50	0.29	0.0018	-	-	-	23	0.46	0.0029
GO:0003824	Catalytic activity	131	0.13	0.0086	-	-	-	-	-	-
GO:0016787	Hydrolase activity	63	0.2	0.023	-	-	-	-	-	-
GO:0016887	ATP hydrolysis activity	16	0.47	0.0269	-	-	-	-	-	-
GO:0140657	ATP-dependent activity	24	0.36	0.0269	-	-	-	-	-	-
GO:0008574	Plus-end-directed microtubule motor activity	4	1.14	0.0444	-	-	-	-	-	-
GO:0030554	Adenyl nucleotide binding	47	0.23	0.0456	-	-	-	-	-	-
GO:0003723	R- binding	-	-	-	21	0.42	0.0268	19	0.4	0.0433
GO:0031625	Ubiquitin protein ligase binding	-	-	-	9	0.69	0.0432	-	-	-
GO:0005198	Structural molecule activity	-	-	-	-	-	-	20	0.59	0.00025
GO:0030527	Structural constituent of chromatin	-	-	-	-	-	-	5	1.11	0.0227
GO:0016818	Hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	-	-	-	-	-	-	13	0.56	0.0233
GO:0019904	Protein domain specific binding	-	-	-	-	-	-	14	0.51	0.0333

		CHO-K1			CHO-SK15-EPO			CHO-DP12		
Term ID	Process	Count	Strength	FDR	Count	Strength	FDR	Count	Strength	FDR
GO:0009987	Cellular process	322	0.1	110	15994	0.12	0.00026	106	0.13	7.61E-06
GO:0016043	Cellular component organization	132	0.17	49	5621	0.22	0.0279	48	0.24	0.007
GO:0071840	Cellular component organization or biogenesis	137	0.16	52	5887	0.23	0.0146	51	0.25	0.0031
GO:0006996	Organelle organization	92	0.2	39	3632	0.32	0.0098	41	0.37	0.00017
GO:0007010	Cytoskeleton organization	44	0.32	-	-	-	-	-	-	-
GO:0048522	Positive regulation of cellular process	131	0.15	-	-	-	-	-	-	-
GO:0046907	Intracellular transport	43	0.32	-	-	-	-	-	-	-
GO:0030162	Regulation of proteolysis	29	0.4	-	-	-	-	-	-	-
GO:0048518	Positive regulation of biological process	140	0.14	56	6368	0.23	0.0113	-	-	-
GO:0051179	Localization	106	0.17	44	4471	0.28	0.0113	-	-	-
GO:0051649	Establishment of localization in cell	51	0.28	-	-	-	-	-	-	-
GO:0051641	Cellular localization	70	0.22	33	2661	0.38	0.004	-	-	-
GO:0006810	Transport	89	0.18	37	3660	0.29	0.0201	-	-	-
GO:0051234	Establishment of localization	92	0.18	-	-	-	-	-	-	-
GO:0031323	Regulation of cellular metabolic process	123	0.14	-	-	-	-	-	-	-
GO:0008104	Protein localization	-	-	28	1924	0.45	0.0036	-	-	-
GO:0033036	Macromolecule localization	-	-	31	2366	0.4	0.0037	-	-	-
GO:0009607	Response to biotic stimulus	-	-	20	1261	0.48	0.0113	-	-	-
GO:0016192	Vesicle-mediated transport	-	-	20	1231	0.5	0.0113	-	-	-
GO:0023051	Regulation of sig-ling	-	-	36	3347	0.32	0.0113	-	-	-
GO:0031349	Positive regulation of defense response	-	-	9	241	0.86	0.0113	-	-	-

GO:0044419	Biological process involved in interspecies interaction between organisms	-	-	21	1351	0.48	0.0113	-	-	-
GO:0048583	Regulation of response to stimulus	-	-	40	3843	0.3	0.0113	-	-	-
GO:0010033	Response to organic substance	-	-	32	2827	0.34	0.0134	29	0.32	0.0211
GO:0051707	Response to other organism	-	-	19	1213	0.48	0.0146	-	-	-
GO:0071705	Nitrogen compound transport	-	-	21	1456	0.44	0.0146	20	0.45	0.009
GO:0010646	Regulation of cell communication	-	-	35	3331	0.31	0.0171	-	-	-
GO:0019538	Protein metabolic process	-	-	42	4367	0.27	0.0171	44	0.32	0.00056
GO:0015031	Protein transport	-	-	17	1062	0.49	0.0225	-	-	-
GO:1901564	Organonitrogen compound metabolic process	-	-	48	5394	0.23	0.0225	51	0.29	0.00034
GO:0051246	Regulation of protein metabolic process	-	-	30	2708	0.33	0.024	-	-	-
GO:0065007	Biological regulation	-	-	87	12586	0.12	0.0279	-	-	-
GO:0050794	Regulation of cellular process	-	-	80	11253	0.14	0.0342	-	-	-
GO:0006897	Endocytosis	-	-	10	422	0.66	0.0369	-	-	-
GO:0006909	Phagocytosis	-	-	6	135	0.93	0.0382	-	-	-
GO:0044085	Cellular component biogenesis	-	-	30	2815	0.31	0.0382	32	0.37	0.0023
GO:0048523	Negative regulation of cellular process	-	-	43	4752	0.24	0.0382	-	-	-
GO:0060255	Regulation of macromolecule metabolic process	-	-	51	6089	0.21	0.0402	-	-	-
GO:0051050	Positive regulation of transport	-	-	16	1045	0.47	0.0422	-	-	-
GO:0009605	Response to exter-l stimulus	-	-	26	2319	0.33	0.0484	-	-	-
GO:0043170	Macromolecule metabolic process	-	-	52	6322	0.2	0.0484	53	0.24	0.004
GO:0044260	Cellular macromolecule metabolic process	-	-	-	-	-	-	38	0.44	1.81E-05
GO:0019941	Modification-dependent protein catabolic process	-	-	-	-	-	-	16	0.77	7.92E-05
GO:0044237	Cellular metabolic process	-	-	-	-	-	-	62	0.26	0.00017
GO:0006511	Ubiquitin-dependent protein catabolic process	-	-	-	-	-	-	15	0.75	0.00018
GO:0030163	Protein catabolic process	-	-	-	-	-	-	17	0.67	2.00E-04
GO:0044238	Primary metabolic process	-	-	-	-	-	-	65	0.24	2.00E-04
GO:0071704	Organic substance metabolic process	-	-	-	-	-	-	66	0.22	0.00047
GO:0008152	Metabolic process	-	-	-	-	-	-	68	0.21	0.00056
GO:0006807	Nitrogen compound metabolic process	-	-	-	-	-	-	60	0.24	0.00069
GO:0044249	Cellular biosynthetic process	-	-	-	-	-	-	30	0.4	0.0016
GO:1901576	Organic substance biosynthetic process	-	-	-	-	-	-	30	0.38	0.0031
GO:1903829	Positive regulation of protein localization	-	-	-	-	-	-	12	0.7	0.004
GO:0022607	Cellular component assembly	-	-	-	-	-	-	29	0.38	0.0042
GO:0032880	Regulation of protein localization	-	-	-	-	-	-	16	0.54	0.0064
GO:0042176	Regulation of protein catabolic process	-	-	-	-	-	-	10	0.75	0.0064
GO:0045862	Positive regulation of proteolysis	-	-	-	-	-	-	10	0.76	0.0064
GO:0060341	Regulation of cellular localization	-	-	-	-	-	-	17	0.53	0.0064
GO:0006508	Proteolysis	-	-	-	-	-	-	18	0.49	0.0079

GO:0010498	Proteasomal protein catabolic process	-	-	-	-	-	-	10	0.73	0.0079
GO:0051276	Chromosome organization	-	-	-	-	-	-	16	0.53	0.0079
GO:0006334	Nucleosome assembly	-	-	-	-	-	-	6	1.04	0.009
GO:0043434	Response to peptide hormone	-	-	-	-	-	-	10	0.72	0.0092
GO:0045116	Protein neddylation	-	-	-	-	-	-	3	1.79	0.0101
GO:0007049	Cell cycle	-	-	-	-	-	-	17	0.5	0.0105
GO:1901698	Response to nitrogen compound	-	-	-	-	-	-	17	0.48	0.0143
GO:0044248	Cellular catabolic process	-	-	-	-	-	-	20	0.42	0.02
GO:0048285	Organelle fission	-	-	-	-	-	-	9	0.72	0.02
GO:0051052	Regulation of D- metabolic process	-	-	-	-	-	-	11	0.62	0.0229
GO:0009894	Regulation of catabolic process	-	-	-	-	-	-	15	0.5	0.0238
GO:0009059	Macromolecule biosynthetic process	-	-	-	-	-	-	20	0.41	0.0292
GO:0006338	Chromatin remodeling	-	-	-	-	-	-	8	0.74	0.034
GO:0044271	Cellular nitrogen compound biosynthetic process	-	-	-	-	-	-	20	0.39	0.0402

Day 7

		CHO-K1			CHO-SK15-EPO			CHO-DP12		
KEGG	Description	Count	Strength	FDR	Count	Strength	FDR	Count	Strength	FDR
cge03010	Ribosome	34	0.96	2.81E-18	-	-	-	-	-	-
cge04530	Tight junction	16	0.88	3.36E-07	5	0.99	0.0328	6	1.44	3.44E-05
cge05014	Amyotrophic lateral sclerosis	25	0.65	3.36E-07	6	0.64	0.0498	-	-	-
cge05017	Spinocerebellar ataxia	16	0.88	3.36E-07	-	-	-	-	-	-
cge03050	Proteasome	10	1.13	1.44E-06	3	1.22	0.0328	-	-	-
cge05203	Viral carcinogenesis	16	0.75	6.18E-06	-	-	-	-	-	-
cge05016	Huntington disease	19	0.61	2.80E-05	-	-	-	-	-	-
cge05012	Parkinson disease	16	0.64	9.61E-05	8	0.95	0.0015	4	1.03	0.0193
cge05132	Salmonella infection	15	0.64	0.00018	-	-	-	-	-	-
cge04151	PI3K-Akt sig-ling pathway	18	0.54	0.00037	-	-	-	-	-	-
cge05160	Hepatitis C	13	0.66	0.00037	-	-	-	-	-	-
cge04670	Leukocyte transendothelial migration	10	0.78	0.00042	4	0.99	0.0328	4	1.37	0.0034
cge04261	Adrenergic sig-ling in cardiomyocytes	10	0.77	0.00047	4	0.98	0.0328	-	-	-
cge04141	Protein processing in endoplasmic reticulum	12	0.67	0.00053	-	-	-	-	-	-
cge05020	Prion disease	15	0.58	0.00053	-	-	-	-	-	-
cge05165	Human papillomavirus infection	17	0.53	0.00055	-	-	-	-	-	-
cge03013	R- transport	12	0.65	0.00071	-	-	-	-	-	-

cge04144	Endocytosis	14	0.58	0.00073	6	0.83	0.0328	-	-	-
cge05212	Pancreatic cancer	8	0.84	0.00073	-	-	-	-	-	-
cge05142	Chagas disease	9	0.76	0.00083	-	-	-	-	-	-
cge04146	Peroxisome	8	0.82	0.00089	4	1.13	0.0328	-	-	-
cge05010	Alzheimer disease	17	0.49	0.0011	6	0.65	0.0498	-	-	-
cge04120	Ubiquitin mediated proteolysis	10	0.68	0.0013	5	0.99	0.0328	-	-	-
cge04520	Adherens junction	7	0.85	0.0015	3	1.1	0.0498	-	-	-
cge04728	Dopaminergic sy-pse	9	0.69	0.0022	4	0.95	0.0328	-	-	-
cge05230	Central carbon metabolism in cancer	7	0.82	0.0022	-	-	-	-	-	-
cge05200	Pathways in cancer	20	0.41	0.0026	-	-	-	-	-	-
cge05205	Proteoglycans in cancer	11	0.59	0.0026	-	-	-	4	1.14	0.0124
cge01523	Antifolate resistance	5	1.02	0.0027	-	-	-	-	-	-
cge05135	Yersinia infection	9	0.66	0.0028	-	-	-	3	1.18	0.0314
cge01100	Metabolic pathways	41	0.26	0.0031	-	-	-	-	-	-
cge04110	Cell cycle	9	0.66	0.0031	-	-	-	-	-	-
cge05163	Human cytomegalovirus infection	12	0.53	0.0039	-	-	-	-	-	-
cge03320	PPAR sig-ling pathway	7	0.74	0.0044	4	1.11	0.0328	-	-	-
cge04145	Phagosome	9	0.63	0.0044	-	-	-	6	1.44	3.44E-05
cge04540	Gap junction	7	0.74	0.0044	-	-	-	3	1.37	0.0143
cge05145	Toxoplasmosis	8	0.68	0.0044	-	-	-	-	-	-
cge04730	Long-term depression	6	0.79	0.0058	-	-	-	-	-	-
cge05169	Epstein-Barr virus infection	11	0.53	0.006	-	-	-	-	-	-
cge04071	Sphingolipid sig-ling pathway	8	0.64	0.0068	-	-	-	3	1.2	0.0296
cge04971	Gastric acid secretion	6	0.77	0.0071	3	1.08	0.0498	3	1.46	0.0124
cge04961	Endocrine and other factor-regulated calcium reabsorption	5	0.85	0.0086	-	-	-	-	-	-
cge04915	Estrogen sig-ling pathway	8	0.61	0.0087	-	-	-	-	-	-
cge05170	Human immunodeficiency virus 1 infection	11	0.5	0.0088	-	-	-	-	-	-
cge05418	Fluid shear stress and atherosclerosis	8	0.6	0.01	-	-	-	3	1.16	0.0316
cge04910	Insulin sig-ling pathway	8	0.6	0.0104	-	-	-	-	-	-
cge05414	Dilated cardiomyopathy	6	0.72	0.0106	-	-	-	-	-	-
cge00983	Drug metabolism - other enzymes	6	0.71	0.0112	-	-	-	-	-	-
cge04140	Autophagy - animal	8	0.59	0.0112	-	-	-	-	-	-
cge05161	Hepatitis B	9	0.54	0.0118	-	-	-	-	-	-
cge04114	Oocyte meiosis	7	0.63	0.0124	-	-	-	-	-	-
cge00240	Pyrimidine metabolism	5	0.78	0.0131	-	-	-	-	-	-

cge05100	Bacterial invasion of epithelial cells	6	0.69	0.0131	-	-	-	-	-	-
cge04611	Platelet activation	7	0.62	0.0133	-	-	-	-	-	-
cge00061	Fatty acid biosynthesis	3	1.13	0.0142	-	-	-	-	-	-
cge02010	ABC transporters	4	0.9	0.0142	-	-	-	-	-	-
cge04062	Chemokine sig-ling pathway	9	0.51	0.0152	-	-	-	-	-	-
cge00052	Galactose metabolism	4	0.88	0.0156	-	-	-	-	-	-
cge05412	Arrhythmogenic right ventricular cardiomyopathy	5	0.75	0.0156	-	-	-	-	-	-
cge04612	Antigen processing and presentation	5	0.74	0.0165	-	-	-	-	-	-
cge00230	Purine metabolism	7	0.59	0.0168	-	-	-	-	-	-
cge01212	Fatty acid metabolism	5	0.73	0.017	-	-	-	-	-	-
cge01230	Biosynthesis of amino acids	6	0.65	0.017	4	1.09	0.0328	-	-	-
cge04390	Hippo sig-ling pathway	8	0.54	0.017	-	-	-	-	-	-
cge05146	Amoebiasis	6	0.65	0.017	-	-	-	-	-	-
cge04015	Rap1 sig-ling pathway	9	0.49	0.0171	-	-	-	-	-	-
cge04152	AMPK sig-ling pathway	7	0.58	0.0171	-	-	-	-	-	-
cge05215	Prostate cancer	6	0.64	0.0171	-	-	-	-	-	-
cge04973	Carbohydrate digestion and absorption	4	0.84	0.0187	-	-	-	-	-	-
cge04371	Apelin sig-ling pathway	7	0.56	0.0205	-	-	-	-	-	-
cge04922	Glucagon sig-ling pathway	6	0.62	0.0206	-	-	-	-	-	-
cge03015	mR- surveillance pathway	6	0.61	0.0217	-	-	-	-	-	-
cge04810	Regulation of actin cytoskeleton	9	0.47	0.0226	5	0.82	0.0328	4	1.11	0.0143
cge03420	Nucleotide excision repair	4	0.79	0.0239	-	-	-	-	-	-
cge00100	Steroid biosynthesis	3	0.97	0.0251	-	-	-	-	-	-
cge01524	Platinum drug resistance	5	0.67	0.0251	-	-	-	-	-	-
cge05167	Kaposi sarcoma-associated herpesvirus infection	9	0.46	0.0251	-	-	-	-	-	-
cge05410	Hypertrophic cardiomyopathy	5	0.67	0.0251	-	-	-	-	-	-
cge04022	cGMP-PKG sig-ling pathway	7	0.53	0.0256	-	-	-	-	-	-
cge04920	Adipocytokine sig-ling pathway	5	0.66	0.0256	-	-	-	-	-	-
cge01200	Carbon metabolism	7	0.52	0.0265	-	-	-	-	-	-
cge04216	Ferroptosis	4	0.77	0.0265	3	1.26	0.0328	-	-	-
cge05034	Alcoholism	7	0.51	0.0299	4	0.88	0.0498	4	1.26	0.0066
cge04510	Focal adhesion	8	0.47	0.0311	-	-	-	-	-	-
cge00040	Pentose and glucuro-te interconversions	3	0.9	0.0346	-	-	-	-	-	-
cge05162	Measles	7	0.5	0.0346	-	-	-	-	-	-
cge04721	Sy-ptic vesicle cycle	5	0.62	0.0348	-	-	-	-	-	-

cge04962	Vasopressin-regulated water reabsorption	4	0.72	0.0348	-	-	-	-	-	-
cge04066	HIF-1 sig-ling pathway	6	0.54	0.0364	-	-	-	-	-	-
cge04923	Regulation of lipolysis in adipocytes	4	0.71	0.037	-	-	-	-	-	-
cge03040	Spliceosome	7	0.48	0.0372	-	-	-	-	-	-
cge03018	R- degradation	5	0.6	0.0373	-	-	-	-	-	-
cge00520	Amino sugar and nucleotide sugar metabolism	4	0.69	0.0416	-	-	-	-	-	-
cge04713	Circadian entrainment	5	0.59	0.0416	-	-	-	-	-	-
cge04924	Renin secretion	4	0.69	0.0416	-	-	-	-	-	-
cge04150	mTOR sig-ling pathway	7	0.46	0.0452	-	-	-	-	-	-
cge04935	Growth hormone synthesis, secretion and action	6	0.51	0.0468	-	-	-	-	-	-
cge04970	Salivary secretion	-	-	-	3	1.08	0.0498	-	-	-
cge05322	Systemic lupus erythematosus	-	-	-	-	-	-	3	1.33	0.0161
cge05206	MicroR-s in cancer	-	-	-	-	-	-	3	1.1	0.0455

		CHO-K1			CHO-SK15-EPO			CHO-DP12		
Term ID	Function	Count	Strength	FDR	Count	Strength	FDR	Count	Strength	FDR
GO:0005488	Binding	400	0.16	1.62E-29	96	0.15	2.95E-05	44	0.19	0.003
GO:0097159	Organic cyclic compound binding	225	0.26	1.22E-19	-	-	-	-	-	-
GO:1901363	Heterocyclic compound binding	223	0.26	1.22E-19	-	-	-	-	-	-
GO:0005515	Protein binding	254	0.22	1.56E-17	69	0.26	9.24E-06	30	0.28	0.0194
GO:0036094	Small molecule binding	128	0.36	4.68E-16	29	0.33	0.0375	-	-	-
GO:0043168	Anion binding	122	0.36	4.49E-15	-	-	-	-	-	-
GO:0000166	Nucleotide binding	116	0.37	5.62E-15	-	-	-	-	-	-
GO:0017076	Purine nucleotide binding	105	0.39	1.42E-14	-	-	-	-	-	-
GO:0032555	Purine ribonucleotide binding	104	0.39	2.03E-14	-	-	-	-	-	-
GO:0035639	Purine ribonucleoside triphosphate binding	100	0.38	9.42E-14	-	-	-	-	-	-
GO:0097367	Carbohydrate derivative binding	109	0.35	8.81E-13	-	-	-	-	-	-
GO:0044877	Protein-containing complex binding	83	0.4	3.72E-12	-	-	-	12	0.56	0.0357
GO:0030554	Adenyl nucleotide binding	86	0.39	6.89E-12	-	-	-	-	-	-
GO:0032559	Adenyl ribonucleotide binding	85	0.39	1.21E-11	-	-	-	-	-	-
GO:0005198	Structural molecule activity	63	0.47	1.40E-11	-	-	-	-	-	-
GO:0019899	Enzyme binding	104	0.33	4.66E-11	30	0.4	0.0011	16	0.51	0.014
GO:0005524	ATP binding	81	0.38	6.73E-11	-	-	-	-	-	-
GO:0003824	Catalytic activity	194	0.2	9.35E-11	-	-	-	-	-	-
GO:0003723	R- binding	75	0.38	5.46E-10	-	-	-	-	-	-
GO:0043167	Ion binding	182	0.2	8.01E-10	-	-	-	-	-	-

GO:0016462	Pyrophosphatase activity	47	0.51	1.04E-09	-	-	-	-	-	-
GO:0140657	ATP-dependent activity	43	0.52	5.36E-09	-	-	-	-	-	-
GO:0003735	Structural constituent of ribosome	37	0.56	1.15E-08	-	-	-	-	-	-
GO:0016787	Hydrolase activity	98	0.3	1.15E-08	-	-	-	-	-	-
GO:0017111	Nucleoside-triphosphatase activity	43	0.5	1.15E-08	-	-	-	-	-	-
GO:0140662	ATP-dependent protein folding chaperone	12	1.09	2.39E-07	-	-	-	-	-	-
GO:0003676	Nucleic acid binding	126	0.23	2.52E-07	-	-	-	-	-	-
GO:0016887	ATP hydrolysis activity	27	0.59	6.74E-07	-	-	-	-	-	-
GO:0044183	Protein folding chaperone	14	0.92	6.94E-07	-	-	-	-	-	-
GO:0042802	Identical protein binding	84	0.28	8.90E-07	-	-	-	-	-	-
GO:0044389	Ubiquitin-like protein ligase binding	28	0.57	9.94E-07	-	-	-	-	-	-
GO:0031625	Ubiquitin protein ligase binding	27	0.58	1.18E-06	-	-	-	-	-	-
GO:0101005	Deubiquitinase activity	13	0.75	0.00014	-	-	-	-	-	-
GO:0051082	Unfolded protein binding	13	0.71	0.00034	-	-	-	-	-	-
GO:0019904	Protein domain specific binding	39	0.34	0.00061	-	-	-	-	-	-
GO:0016874	Ligase activity	15	0.62	0.00062	-	-	-	-	-	-
GO:0008289	Lipid binding	36	0.35	0.00075	-	-	-	-	-	-
GO:0019843	rR- binding	13	0.66	0.00086	-	-	-	-	-	-
GO:0032561	Guanyl ribonucleotide binding	25	0.43	0.001	-	-	-	-	-	-
GO:0005525	GTP binding	24	0.44	0.0013	-	-	-	-	-	-
GO:0042626	ATPase-coupled transmembrane transporter activity	11	0.7	0.0017	-	-	-	-	-	-
GO:0005543	Phospholipid binding	26	0.4	0.002	-	-	-	-	-	-
GO:0035615	Clathrin adaptor activity	5	1.22	0.0024	-	-	-	-	-	-
GO:0140492	Metal-dependent deubiquiti-se activity	5	1.19	0.003	-	-	-	-	-	-
GO:0008097	5S rR- binding	7	0.9	0.0039	-	-	-	-	-	-
GO:0003729	mR- binding	21	0.43	0.0041	-	-	-	-	-	-
GO:0043130	Ubiquitin binding	10	0.69	0.0044	8	1.21	6.96E-05	-	-	-
GO:0008022	Protein C-terminus binding	16	0.5	0.0054	-	-	-	-	-	-
GO:0097157	pre-mR- intronic binding	5	1.12	0.0054	-	-	-	-	-	-
GO:0032182	Ubiquitin-like protein binding	11	0.63	0.0062	-	-	-	-	-	-
GO:0036002	pre-mR- binding	7	0.84	0.0071	-	-	-	-	-	-
GO:0097718	Disordered domain specific binding	7	0.84	0.0071	-	-	-	-	-	-
GO:0030620	U2 snR- binding	4	1.26	0.0094	-	-	-	-	-	-
GO:0031072	Heat shock protein binding	11	0.58	0.0142	-	-	-	-	-	-
GO:0019901	Protein ki-se binding	33	0.29	0.0177	-	-	-	-	-	-
GO:0004843	Cysteine-type deubiquiti-se activity	9	0.64	0.0186	-	-	-	-	-	-
GO:0140096	Catalytic activity, acting on a protein	73	0.18	0.0198	-	-	-	-	-	-
GO:0034634	Glutathione transmembrane transporter activity	3	1.47	0.0201	-	-	-	-	-	-

GO:0019900	Ki-se binding	35	0.27	0.0206	-	-	-	-	-	-
GO:0017056	Structural constituent of nuclear pore	5	0.95	0.0212	-	-	-	-	-	-
GO:0044548	S100 protein binding	4	1.09	0.0268	-	-	-	-	-	-
GO:0036402	Proteasome-activating activity	3	1.4	0.0275	-	-	-	-	-	-
GO:0030623	U5 snR- binding	3	1.33	0.0377	-	-	-	-	-	-
GO:0035091	Phosphatidylinositol binding	16	0.4	0.0434	-	-	-	-	-	-
GO:0016740	Transferase activity	71	0.16	0.0479	-	-	-	-	-	-
GO:0140640	Catalytic activity, acting on a nucleic acid	25	0.3	0.0479	-	-	-	-	-	-
GO:0004749	Ribose phosphate diphosphoki-se activity	3	1.27	0.0484	-	-	-	-	-	-
GO:0019829	ATPase-coupled cation transmembrane transporter activity	6	0.74	0.0495	-	-	-	-	-	-
GO:0033218	Amide binding	19	0.36	0.0495	-	-	-	-	-	-
GO:0051117	ATPase binding	-	-	-	-	-	-	5	1.38	0.0044
GO:0008525	Phosphatidylcholine transporter activity	-	-	-	-	-	-	3	1.96	0.0084
GO:0005200	Structural constituent of cytoskeleton	-	-	-	-	-	-	4	1.29	0.0337
GO:0031267	Small GTPase binding	-	-	-	-	-	-	6	0.95	0.0337

		CHO-K1			CHO-SK15-EPO			CHO-DP12		
Term ID	Process	Count	Strength	FDR	Count	Strength	FDR	Count	Strength	FDR
GO:0009987	Cellular process	437	0.13	4.84E-31	108	0.14	1.03E-06	-	-	-
GO:0008152	Metabolic process	303	0.24	3.57E-29	65	0.19	0.011	-	-	-
GO:0044238	Primary metabolic process	282	0.26	3.40E-28	-	-	-	-	-	-
GO:0071704	Organic substance metabolic process	291	0.25	3.40E-28	-	-	-	-	-	-
GO:0044237	Cellular metabolic process	262	0.27	2.30E-26	58	0.23	0.005	-	-	-
GO:0006807	Nitrogen compound metabolic process	264	0.26	2.91E-26	-	-	-	-	-	-
GO:1901564	Organonitrogen compound metabolic process	213	0.29	2.84E-22	-	-	-	-	-	-
GO:0043170	Macromolecule metabolic process	234	0.27	1.05E-21	-	-	-	-	-	-
GO:0044260	Cellular macromolecule metabolic process	140	0.39	9.72E-21	-	-	-	-	-	-
GO:0019538	Protein metabolic process	179	0.31	4.02E-19	-	-	-	-	-	-
GO:0034641	Cellular nitrogen compound metabolic process	164	0.33	5.76E-19	-	-	-	-	-	-

GO:0071840	Cellular component organization or biogenesis	213	0.26	1.20E-17	-	-	-	-	-	-
GO:0009058	Biosynthetic process	123	0.37	1.09E-15	-	-	-	-	-	-
GO:0016043	Cellular component organization	200	0.25	2.90E-15	-	-	-	-	-	-
GO:0044271	Cellular nitrogen compound biosynthetic process	92	0.44	2.90E-15	-	-	-	-	-	-
GO:1901576	Organic substance biosynthetic process	120	0.36	3.55E-15	-	-	-	-	-	-
GO:0060341	Regulation of cellular localization	70	0.52	5.05E-15	-	-	-	13	0.78	0.0017
GO:0044249	Cellular biosynthetic process	115	0.36	2.39E-14	-	-	-	-	-	-
GO:0032879	Regulation of localization	108	0.37	5.99E-14	29	0.41	0.0021	16	0.53	0.0067
GO:0032880	Regulation of protein localization	64	0.53	6.59E-14	-	-	-	12	0.79	0.0022
GO:0006996	Organelle organization	145	0.3	1.23E-13	-	-	-	-	-	-
GO:0051179	Localization	165	0.26	4.58E-13	45	0.31	0.0017	22	0.38	0.0144
GO:0051246	Regulation of protein metabolic process	118	0.34	5.42E-13	-	-	-	-	-	-
GO:0030163	Protein catabolic process	54	0.56	1.30E-12	-	-	-	-	-	-
GO:0043043	Peptide biosynthetic process	53	0.56	1.94E-12	-	-	-	-	-	-
GO:0006412	Translation	52	0.57	2.00E-12	-	-	-	-	-	-
GO:0051603	Proteolysis involved in protein catabolic process	49	0.58	3.26E-12	16	0.71	0.00072	-	-	-
GO:0010033	Response to organic substance	119	0.32	3.63E-12	-	-	-	-	-	-
GO:0051234	Establishment of localization	146	0.28	3.63E-12	42	0.35	0.00072	21	0.43	0.0071
GO:0009056	Catabolic process	95	0.37	3.98E-12	25	0.41	0.011	-	-	-
GO:0006518	Peptide metabolic process	57	0.52	4.58E-12	-	-	-	-	-	-
GO:0043603	Cellular amide metabolic process	66	0.47	4.80E-12	-	-	-	-	-	-
GO:0043604	Amide biosynthetic process	56	0.53	5.92E-12	-	-	-	-	-	-

GO:0019941	Modification-dependent protein catabolic process	45	0.6	9.20E-12	14	0.71	0.0021	-	-	-
GO:0033036	Macromolecule localization	104	0.34	1.77E-11	-	-	-	17	0.54	0.0037
GO:0008104	Protein localization	91	0.37	1.81E-11	24	0.41	0.0147	16	0.61	0.0025
GO:0009057	Macromolecule catabolic process	60	0.49	1.81E-11	-	-	-	-	-	-
GO:1901360	Organic cyclic compound metabolic process	126	0.29	4.77E-11	-	-	-	-	-	-
GO:1901566	Organonitrogen compound biosynthetic process	79	0.4	6.60E-11	-	-	-	-	-	-
GO:0044265	Cellular macromolecule catabolic process	51	0.53	7.34E-11	-	-	-	-	-	-
GO:0071705	Nitrogen compound transport	75	0.41	7.34E-11	-	-	-	13	0.64	0.0063
GO:0006810	Transport	137	0.27	7.83E-11	39	0.34	0.0021	20	0.43	0.0106
GO:1901575	Organic substance catabolic process	82	0.38	1.87E-10	-	-	-	-	-	-
GO:0044248	Cellular catabolic process	77	0.39	2.19E-10	22	0.46	0.0074	-	-	-
GO:0006511	Ubiquitin-dependent protein catabolic process	42	0.58	2.73E-10	13	0.68	0.005	-	-	-
GO:0006139	Nucleobase-containing compound metabolic process	112	0.3	3.57E-10	-	-	-	-	-	-
GO:0051128	Regulation of cellular component organization	104	0.32	3.84E-10	-	-	-	17	0.52	0.0063
GO:0046907	Intracellular transport	68	0.42	4.44E-10	-	-	-	-	-	-
GO:0006725	Cellular aromatic compound metabolic process	117	0.29	4.71E-10	-	-	-	-	-	-
GO:0009894	Regulation of catabolic process	57	0.46	5.36E-10	-	-	-	10	0.7	0.0144
GO:1901565	Organonitrogen compound catabolic process	60	0.45	5.36E-10	-	-	-	-	-	-
GO:0048519	Negative regulation of biological process	175	0.21	5.44E-10	-	-	-	-	-	-
GO:0010467	Gene expression	100	0.32	8.50E-10	-	-	-	-	-	-
GO:0009059	Macromolecule biosynthetic process	77	0.38	1.01E-09	-	-	-	-	-	-

GO:0045184	Establishment of protein localization	63	0.43	1.07E-09	17	0.47	0.0358	12	0.7	0.0044
GO:0046483	Heterocycle metabolic process	114	0.29	1.40E-09	-	-	-	-	-	-
GO:0015031	Protein transport	59	0.44	1.47E-09	-	-	-	11	0.7	0.0071
GO:0006886	Intracellular protein transport	45	0.52	1.65E-09	-	-	-	-	-	-
GO:0060255	Regulation of macromolecule metabolic process	191	0.19	1.79E-09	-	-	-	-	-	-
GO:0051641	Cellular localization	106	0.3	2.06E-09	-	-	-	17	0.49	0.0092
GO:0006508	Proteolysis	63	0.42	2.20E-09	17	0.46	0.0389	-	-	-
GO:0044085	Cellular component biogenesis	110	0.29	2.26E-09	29	0.32	0.0382	-	-	-
GO:0080090	Regulation of primary metabolic process	183	0.2	2.96E-09	-	-	-	-	-	-
GO:0042176	Regulation of protein catabolic process	32	0.64	3.31E-09	-	-	-	8	1.03	0.0025
GO:0034645	Cellular macromolecule biosynthetic process	59	0.43	3.38E-09	-	-	-	-	-	-
GO:0019222	Regulation of metabolic process	202	0.18	3.54E-09	-	-	-	-	-	-
GO:0071702	Organic substance transport	82	0.35	3.54E-09	-	-	-	16	0.63	0.0022
GO:0071310	Cellular response to organic substance	88	0.33	6.62E-09	-	-	-	-	-	-
GO:1903829	Positive regulation of protein localization	37	0.57	8.10E-09	-	-	-	7	0.84	0.0323
GO:0048523	Negative regulation of cellular process	157	0.22	8.36E-09	-	-	-	-	-	-
GO:0048518	Positive regulation of biological process	194	0.18	1.27E-08	-	-	-	-	-	-
GO:0051726	Regulation of cell cycle	57	0.42	1.34E-08	-	-	-	-	-	-
GO:0051247	Positive regulation of protein metabolic process	71	0.36	1.83E-08	-	-	-	-	-	-
GO:0051171	Regulation of nitrogen compound metabolic process	175	0.19	2.70E-08	-	-	-	-	-	-
GO:0070887	Cellular response to chemical stimulus	102	0.28	2.79E-08	-	-	-	-	-	-
GO:0051649	Establishment of localization in cell	74	0.34	8.24E-08	-	-	-	-	-	-

GO:0010498	Proteasomal protein catabolic process	30	0.6	1.32E-07	10	0.73	0.0147	-	-	-
GO:0010638	Positive regulation of organelle organization	37	0.52	1.35E-07	-	-	-	-	-	-
GO:0007049	Cell cycle	56	0.4	1.53E-07	-	-	-	-	-	-
GO:0065007	Biological regulation	319	0.1	1.60E-07	-	-	-	-	-	-
GO:0022607	Cellular component assembly	96	0.28	1.74E-07	27	0.34	0.038	-	-	-
GO:0051049	Regulation of transport	79	0.31	2.12E-07	24	0.41	0.0134	13	0.52	0.0389
GO:0048522	Positive regulation of cellular process	175	0.18	2.36E-07	-	-	-	-	-	-
GO:0050789	Regulation of biological process	304	0.11	2.49E-07	-	-	-	-	-	-
GO:1901362	Organic cyclic compound biosynthetic process	50	0.41	3.28E-07	-	-	-	-	-	-
GO:0061077	Chaperone-mediated protein folding	14	0.95	4.92E-07	-	-	-	-	-	-
GO:1904951	Positive regulation of establishment of protein localization	27	0.6	5.50E-07	-	-	-	-	-	-
GO:0070201	Regulation of establishment of protein localization	36	0.5	7.13E-07	-	-	-	-	-	-
GO:0009893	Positive regulation of metabolic process	130	0.22	7.41E-07	-	-	-	-	-	-
GO:0051130	Positive regulation of cellular component organization	57	0.37	8.32E-07	-	-	-	-	-	-
GO:1901698	Response to nitrogen compound	55	0.38	8.74E-07	-	-	-	-	-	-
GO:0031647	Regulation of protein stability	29	0.56	9.34E-07	-	-	-	-	-	-
GO:0010604	Positive regulation of macromolecule metabolic process	121	0.22	9.49E-07	-	-	-	-	-	-
GO:0031323	Regulation of cellular metabolic process	167	0.17	2.32E-06	-	-	-	-	-	-
GO:1904814	Regulation of protein localization to chromosome, telomeric region	8	1.34	3.20E-06	-	-	-	-	-	-
GO:0016192	Vesicle-mediated transport	56	0.35	3.22E-06	-	-	-	11	0.64	0.0168
GO:0055086	Nucleobase-containing small	35	0.48	3.39E-06	-	-	-	-	-	-

	molecule metabolic process									
GO:0065008	Regulation of biological quality	125	0.21	4.10E-06	-	-	-	-	-	-
GO:0033043	Regulation of organelle organization	55	0.35	4.81E-06	-	-	-	-	-	-
GO:0032273	Positive regulation of protein polymerization	14	0.86	5.01E-06	-	-	-	-	-	-
GO:0050794	Regulation of cellular process	286	0.1	5.01E-06	-	-	-	-	-	-
GO:1903828	Negative regulation of protein localization	20	0.67	5.01E-06	-	-	-	-	-	-
GO:0006950	Response to stress	108	0.23	5.47E-06	-	-	-	-	-	-
GO:0009117	Nucleotide metabolic process	32	0.49	6.56E-06	-	-	-	-	-	-
GO:0070647	Protein modification by small protein conjugation or removal	43	0.4	9.50E-06	-	-	-	-	-	-
GO:0051173	Positive regulation of nitrogen compound metabolic process	107	0.22	1.00E-05	-	-	-	-	-	-
GO:0042221	Response to chemical	138	0.19	1.14E-05	-	-	-	-	-	-
GO:2001252	Positive regulation of chromosome organization	15	0.78	1.14E-05	-	-	-	-	-	-
GO:0036211	Protein modification process	97	0.24	1.18E-05	-	-	-	-	-	-
GO:1901998	Toxin transport	10	1.04	1.19E-05	-	-	-	-	-	-
GO:0033044	Regulation of chromosome organization	21	0.62	1.21E-05	-	-	-	-	-	-
GO:0022402	Cell cycle process	42	0.4	1.23E-05	-	-	-	-	-	-
GO:0010243	Response to organonitrogen compound	49	0.36	1.24E-05	-	-	-	-	-	-
GO:0043933	Protein-containing complex organization	62	0.31	1.42E-05	-	-	-	-	-	-
GO:0031329	Regulation of cellular catabolic process	39	0.42	1.45E-05	-	-	-	-	-	-
GO:0045732	Positive regulation of protein catabolic process	18	0.68	1.45E-05	-	-	-	5	1.12	0.0215

GO:0061024	Membrane organization	37	0.43	1.45E-05	14	0.62	0.0077	-	-	-
GO:0019693	Ribose phosphate metabolic process	29	0.5	1.49E-05	-	-	-	-	-	-
GO:0061136	Regulation of proteasomal protein catabolic process	18	0.68	1.51E-05	-	-	-	-	-	-
GO:1904851	Positive regulation of establishment of protein localization to telomere	7	1.37	1.51E-05	-	-	-	-	-	-
GO:0023051	Regulation of sig-ling	110	0.21	1.56E-05	-	-	-	-	-	-
GO:0043412	Macromolecule modification	101	0.22	1.74E-05	-	-	-	-	-	-
GO:1903050	Regulation of proteolysis involved in protein catabolic process	20	0.63	1.79E-05	-	-	-	-	-	-
GO:0051640	Organelle localization	32	0.46	1.89E-05	-	-	-	-	-	-
GO:0051050	Positive regulation of transport	48	0.36	2.02E-05	-	-	-	-	-	-
GO:0010646	Regulation of cell communication	109	0.21	2.12E-05	-	-	-	-	-	-
GO:0043161	Proteasome-mediated ubiquitin-dependent protein catabolic process	24	0.55	2.12E-05	-	-	-	-	-	-
GO:0031334	Positive regulation of protein-containing complex assembly	18	0.67	2.14E-05	-	-	-	5	1.1	0.0245
GO:0033554	Cellular response to stress	64	0.3	2.50E-05	-	-	-	-	-	-
GO:0010564	Regulation of cell cycle process	37	0.42	2.65E-05	-	-	-	-	-	-
GO:0006457	Protein folding	20	0.61	2.91E-05	-	-	-	-	-	-
GO:1905475	Regulation of protein localization to membrane	18	0.66	2.94E-05	-	-	-	-	-	-
GO:1902531	Regulation of intracellular sig-l transduction	66	0.29	2.97E-05	-	-	-	-	-	-
GO:0065009	Regulation of molecular function	99	0.22	3.03E-05	-	-	-	-	-	-
GO:0010605	Negative regulation of macromolecule metabolic process	92	0.23	3.18E-05	-	-	-	-	-	-
GO:0050821	Protein stabilization	21	0.59	3.60E-05	-	-	-	-	-	-
GO:0032388	Positive regulation of intracellular transport	18	0.65	3.73E-05	-	-	-	-	-	-

GO:1904375	Regulation of protein localization to cell periphery	15	0.73	4.06E-05	-	-	-	-	-	-
GO:0090304	Nucleic acid metabolic process	80	0.25	4.61E-05	-	-	-	-	-	-
GO:0009165	Nucleotide biosynthetic process	19	0.62	4.81E-05	-	-	-	-	-	-
GO:0009892	Negative regulation of metabolic process	97	0.22	4.91E-05	-	-	-	-	-	-
GO:0010629	Negative regulation of gene expression	42	0.37	5.39E-05	-	-	-	-	-	-
GO:0034654	Nucleobase-containing compound biosynthetic process	38	0.39	5.81E-05	-	-	-	-	-	-
GO:0033365	Protein localization to organelle	37	0.4	6.79E-05	-	-	-	-	-	-
GO:0045862	Positive regulation of proteolysis	24	0.52	6.84E-05	-	-	-	-	-	-
GO:0018130	Heterocycle biosynthetic process	40	0.38	7.08E-05	-	-	-	-	-	-
GO:1903076	Regulation of protein localization to plasma membrane	13	0.77	7.38E-05	-	-	-	-	-	-
GO:0065003	Protein-containing complex assembly	54	0.31	7.69E-05	-	-	-	-	-	-
GO:0009719	Response to endogenous stimulus	57	0.3	8.84E-05	-	-	-	-	-	-
GO:0072594	Establishment of protein localization to organelle	23	0.52	1.00E-04	-	-	-	-	-	-
GO:0044281	Small molecule metabolic process	64	0.27	0.00011	-	-	-	-	-	-
GO:0051052	Regulation of D-metabolic process	30	0.44	0.00011	-	-	-	7	0.8	0.0496
GO:0006163	Purine nucleotide metabolic process	26	0.47	0.00015	-	-	-	-	-	-
GO:0034341	Response to interferon-gamma	14	0.71	0.00015	-	-	-	-	-	-
GO:0019637	Organophosphate metabolic process	42	0.35	0.00016	-	-	-	-	-	-
GO:0072521	Purine-containing compound metabolic process	27	0.46	0.00016	-	-	-	-	-	-
GO:0044087	Regulation of cellular component biogenesis	45	0.33	0.00017	-	-	-	12	0.75	0.0025
GO:0010256	Endomembrane system organization	28	0.45	0.00018	-	-	-	-	-	-

GO:0009259	Ribonucleotide metabolic process	26	0.47	2.00E-04	-	-	-	-	-	-
GO:0009896	Positive regulation of catabolic process	28	0.44	2.00E-04	-	-	-	-	-	-
GO:0032386	Regulation of intracellular transport	22	0.52	2.00E-04	-	-	-	-	-	-
GO:0044089	Positive regulation of cellular component biogenesis	30	0.43	2.00E-04	-	-	-	-	-	-
GO:0046390	Ribose phosphate biosynthetic process	16	0.63	0.00021	-	-	-	-	-	-
GO:1902905	Positive regulation of supramolecular fiber organization	16	0.63	0.00022	-	-	-	-	-	-
GO:0080134	Regulation of response to stress	51	0.3	0.00023	-	-	-	-	-	-
GO:0030162	Regulation of proteolysis	35	0.38	0.00024	-	-	-	-	-	-
GO:0051223	Regulation of protein transport	29	0.43	0.00024	-	-	-	-	-	-
GO:0051495	Positive regulation of cytoskeleton organization	17	0.6	0.00024	-	-	-	-	-	-
GO:0090407	Organophosphate biosynthetic process	27	0.45	0.00024	-	-	-	-	-	-
GO:2000573	Positive regulation of D- biosynthetic process	12	0.76	0.00024	-	-	-	-	-	-
GO:0034504	Protein localization to nucleus	17	0.6	0.00025	-	-	-	-	-	-
GO:0002181	Cytoplasmic translation	15	0.64	3.00E-04	-	-	-	-	-	-
GO:0032204	Regulation of telomere mainte-nce	12	0.75	3.00E-04	-	-	-	-	-	-
GO:0008361	Regulation of cell size	18	0.57	0.00032	-	-	-	-	-	-
GO:0051276	Chromosome organization	42	0.33	0.00032	-	-	-	-	-	-
GO:1901700	Response to oxygen-containing compound	61	0.27	0.00034	-	-	-	-	-	-
GO:0009966	Regulation of sig-l transduction	93	0.2	0.00036	-	-	-	-	-	-
GO:0032535	Regulation of cellular component size	25	0.46	0.00036	-	-	-	-	-	-
GO:0032212	Positive regulation of telomere mainte-nce via telomerase	8	0.98	0.00038	-	-	-	-	-	-

GO:0000278	Mitotic cell cycle	32	0.39	4.00E-04	-	-	-	-	-	-
GO:0006417	Regulation of translation	28	0.42	0.00049	-	-	-	-	-	-
GO:2000278	Regulation of D-biosynthetic process	14	0.65	5.00E-04	-	-	-	-	-	-
GO:0043254	Regulation of protein-containing complex assembly	24	0.46	0.00054	-	-	-	7	0.91	0.014
GO:0032210	Regulation of telomere mainte-nce via telomerase	9	0.87	0.00055	-	-	-	-	-	-
GO:1901701	Cellular response to oxygen-containing compound	45	0.31	0.00055	-	-	-	-	-	-
GO:0044419	Biological process involved in interspecies interaction between organisms	52	0.28	0.00061	-	-	-	-	-	-
GO:0050790	Regulation of catalytic activity	75	0.22	0.00061	-	-	-	-	-	-
GO:0009150	Purine ribonucleotide metabolic process	24	0.45	0.00064	-	-	-	-	-	-
GO:0080135	Regulation of cellular response to stress	32	0.38	0.00067	-	-	-	-	-	-
GO:0034097	Response to cytokine	37	0.34	0.00072	-	-	-	-	-	-
GO:0051222	Positive regulation of protein transport	20	0.5	0.00074	-	-	-	-	-	-
GO:0031325	Positive regulation of cellular metabolic process	98	0.19	0.00076	-	-	-	-	-	-
GO:0031399	Regulation of protein modification process	58	0.26	0.00079	-	-	-	-	-	-
GO:0007339	Binding of sperm to zo- pellucida	7	1.01	0.00086	-	-	-	-	-	-
GO:0032271	Regulation of protein polymerization	16	0.57	0.00086	-	-	-	-	-	-
GO:2000112	Regulation of cellular macromolecule biosynthetic process	30	0.39	0.00086	-	-	-	-	-	-
GO:0006998	Nuclear envelope organization	8	0.91	0.00093	-	-	-	-	-	-
GO:0071495	Cellular response to endogenous stimulus	45	0.3	0.001	-	-	-	-	-	-

GO:0044093	Positive regulation of molecular function	57	0.26	0.0011	-	-	-	-	-	-
GO:0032446	Protein modification by small protein conjugation	32	0.36	0.0012	-	-	-	-	-	-
GO:0048583	Regulation of response to stimulus	113	0.17	0.0012	-	-	-	-	-	-
GO:0051338	Regulation of transferase activity	37	0.33	0.0013	-	-	-	-	-	-
GO:0006997	Nucleus organization	13	0.63	0.0014	-	-	-	-	-	-
GO:0016032	Viral process	13	0.63	0.0014	-	-	-	-	-	-
GO:1901135	Carbohydrate derivative metabolic process	41	0.31	0.0014	-	-	-	-	-	-
GO:0009988	Cell-cell recognition	8	0.88	0.0015	-	-	-	-	-	-
GO:0031326	Regulation of cellular biosynthetic process	116	0.16	0.0015	-	-	-	-	-	-
GO:2000058	Regulation of ubiquitin-dependent protein catabolic process	14	0.6	0.0015	-	-	-	-	-	-
GO:0006793	Phosphorus metabolic process	66	0.23	0.0016	-	-	-	-	-	-
GO:0009889	Regulation of biosynthetic process	118	0.16	0.0016	-	-	-	-	-	-
GO:0023056	Positive regulation of sig-ling	61	0.24	0.0016	-	-	-	-	-	-
GO:0006897	Endocytosis	23	0.43	0.0017	-	-	-	7	0.91	0.0144
GO:0032434	Regulation of proteasomal ubiquitin-dependent protein catabolic process	12	0.66	0.0017	-	-	-	-	-	-
GO:0051129	Negative regulation of cellular component organization	33	0.35	0.0017	-	-	-	10	0.82	0.0037
GO:1901800	Positive regulation of proteasomal protein catabolic process	11	0.69	0.0017	-	-	-	-	-	-
GO:0006796	Phosphate-containing compound metabolic process	65	0.23	0.002	-	-	-	-	-	-
GO:0010556	Regulation of macromolecule	111	0.16	0.002	-	-	-	-	-	-

	biosynthetic process									
GO:0031116	Positive regulation of microtubule polymerization	7	0.94	0.002	-	-	-	-	-	-
GO:1905666	Regulation of protein localization to endosome	5	1.22	0.002	-	-	-	3	1.99	0.0063
GO:0007163	Establishment or mainte-nce of cell polarity	17	0.51	0.0021	-	-	-	6	1.05	0.0106
GO:0022613	Ribonucleoprotein complex biogenesis	29	0.37	0.0021	-	-	-	-	-	-
GO:0045785	Positive regulation of cell adhesion	24	0.41	0.0021	-	-	-	-	-	-
GO:0051054	Positive regulation of D- metabolic process	20	0.46	0.0022	-	-	-	-	-	-
GO:0006606	Protein import into nucleus	11	0.67	0.0024	-	-	-	-	-	-
GO:0010647	Positive regulation of cell communication	60	0.23	0.0024	-	-	-	-	-	-
GO:0032206	Positive regulation of telomere mainte-nce	9	0.77	0.0024	-	-	-	-	-	-
GO:1900180	Regulation of protein localization to nucleus	13	0.6	0.0024	-	-	-	-	-	-
GO:0071346	Cellular response to interferon-gamma	11	0.67	0.0025	-	-	-	-	-	-
GO:1903320	Regulation of protein modification by small protein conjugation or removal	17	0.51	0.0025	-	-	-	-	-	-
GO:0060284	Regulation of cell development	28	0.37	0.0028	-	-	-	-	-	-
GO:0031324	Negative regulation of cellular metabolic process	72	0.2	0.0031	-	-	-	-	-	-
GO:0031397	Negative regulation of protein ubiquiti-tion	10	0.7	0.0031	-	-	-	-	-	-
GO:0051051	Negative regulation of transport	24	0.4	0.0031	-	-	-	-	-	-
GO:0045653	Negative regulation of megakaryocyte differentiation	4	1.4	0.0033	-	-	-	-	-	-
GO:2000643	Positive regulation of early endosome to late endosome transport	4	1.4	0.0033	-	-	-	-	-	-
GO:0007010	Cytoskeleton organization	48	0.26	0.0034	-	-	-	-	-	-

GO:0009895	Negative regulation of catabolic process	19	0.46	0.0034	-	-	-	-	-	-
GO:0051984	Positive regulation of chromosome segregation	6	1	0.0034	-	-	-	-	-	-
GO:0006694	Steroid biosynthetic process	10	0.69	0.0035	-	-	-	-	-	-
GO:0030155	Regulation of cell adhesion	33	0.33	0.0036	-	-	-	-	-	-
GO:1903047	Mitotic cell cycle process	26	0.38	0.0037	-	-	-	-	-	-
GO:0009124	Nucleoside monophosphate biosynthetic process	7	0.88	0.0038	-	-	-	-	-	-
GO:0006164	Purine nucleotide biosynthetic process	13	0.58	0.0039	-	-	-	-	-	-
GO:0010941	Regulation of cell death	59	0.23	0.004	-	-	-	-	-	-
GO:0043434	Response to peptide hormone	21	0.42	0.0041	-	-	-	-	-	-
GO:0071345	Cellular response to cytokine stimulus	32	0.33	0.0041	-	-	-	-	-	-
GO:0072665	Protein localization to vacuole	8	0.79	0.0041	-	-	-	-	-	-
GO:0051172	Negative regulation of nitrogen compound metabolic process	74	0.2	0.0042	-	-	-	-	-	-
GO:2000641	Regulation of early endosome to late endosome transport	5	1.12	0.0044	-	-	-	-	-	-
GO:0009260	Ribonucleotide biosynthetic process	13	0.57	0.0046	-	-	-	-	-	-
GO:0050793	Regulation of developmental process	79	0.19	0.0046	-	-	-	-	-	-
GO:0006403	R- localization	13	0.57	0.0048	-	-	-	-	-	-
GO:0042177	Negative regulation of protein catabolic process	10	0.67	0.0048	-	-	-	-	-	-
GO:1904377	Positive regulation of protein localization to cell periphery	8	0.78	0.0049	-	-	-	-	-	-
GO:0010628	Positive regulation of gene expression	45	0.26	0.0052	-	-	-	-	-	-
GO:0016126	Sterol biosynthetic process	7	0.85	0.0052	-	-	-	-	-	-
GO:0072666	Establishment of protein localization to vacuole	7	0.85	0.0052	-	-	-	-	-	-

GO:0010468	Regulation of gene expression	129	0.13	0.0057	-	-	-	-	-	-
GO:0002376	Immune system process	62	0.21	0.0058	-	-	-	-	-	-
GO:0031396	Regulation of protein ubiquiti-tion	15	0.51	0.0058	-	-	-	-	-	-
GO:0031497	Chromatin assembly	13	0.55	0.0061	-	-	-	-	-	-
GO:1905477	Positive regulation of protein localization to membrane	10	0.66	0.0061	-	-	-	-	-	-
GO:0006281	D- repair	23	0.39	0.0062	-	-	-	-	-	-
GO:0006605	Protein targeting	15	0.5	0.0062	-	-	-	-	-	-
GO:0045185	Mainte-nce of protein location	9	0.7	0.0062	-	-	-	-	-	-
GO:2001242	Regulation of intrinsic apoptotic sig-ling pathway	12	0.58	0.0062	-	-	-	-	-	-
GO:0050896	Response to stimulus	201	0.09	0.0064	-	-	-	-	-	-
GO:0051983	Regulation of chromosome segregation	10	0.65	0.0064	-	-	-	-	-	-
GO:0009725	Response to hormone	33	0.31	0.0069	-	-	-	-	-	-
GO:0019220	Regulation of phosphate metabolic process	50	0.24	0.0069	-	-	-	-	-	-
GO:0031330	Negative regulation of cellular catabolic process	15	0.5	0.0069	-	-	-	-	-	-
GO:0051301	Cell division	21	0.4	0.0069	-	-	-	-	-	-
GO:0070849	Response to epidermal growth factor	7	0.83	0.0069	-	-	-	-	-	-
GO:2001233	Regulation of apoptotic sig-ling pathway	20	0.42	0.0069	-	-	-	-	-	-
GO:0009156	Ribonucleoside monophosphate biosynthetic process	6	0.92	0.007	-	-	-	-	-	-
GO:0051085	Chaperone cofactor-dependent protein refolding	6	0.92	0.007	-	-	-	-	-	-
GO:0071108	Protein K48-linked deubiquiti-tion	6	0.92	0.007	-	-	-	-	-	-
GO:0042325	Regulation of phosphorylation	45	0.25	0.0075	-	-	-	-	-	-

GO:0045595	Regulation of cell differentiation	55	0.22	0.0075	-	-	-	-	-	-
GO:0016050	Vesicle organization	16	0.47	0.0079	-	-	-	-	-	-
GO:0090218	Positive regulation of lipid ki-se activity	6	0.91	0.0079	-	-	-	-	-	-
GO:0051656	Establishment of organelle localization	20	0.41	0.008	-	-	-	-	-	-
GO:0030838	Positive regulation of actin filament polymerization	7	0.81	0.0081	-	-	-	-	-	-
GO:0042327	Positive regulation of phosphorylation	33	0.3	0.0081	-	-	-	-	-	-
GO:0009408	Response to heat	11	0.6	0.0082	-	-	-	-	-	-
GO:0051248	Negative regulation of protein metabolic process	39	0.27	0.0082	-	-	-	-	-	-
GO:0060627	Regulation of vesicle-mediated transport	28	0.33	0.0082	-	-	-	-	-	-
GO:0016567	Protein ubiquiti-tion	28	0.33	0.0087	-	-	-	-	-	-
GO:0008037	Cell recognition	10	0.63	0.0088	-	-	-	-	-	-
GO:0090066	Regulation of a-tomical structure size	26	0.35	0.0089	-	-	-	-	-	-
GO:0060712	Spongiotrophoblast layer development	4	1.22	0.0091	-	-	-	-	-	-
GO:0001558	Regulation of cell growth	21	0.39	0.0098	-	-	-	-	-	-
GO:0019058	Viral life cycle	10	0.62	0.0099	6	1.01	0.0199	-	-	-
GO:0030100	Regulation of endocytosis	15	0.48	0.01	-	-	-	-	-	-
GO:0051664	Nuclear pore localization	3	1.57	0.01	-	-	-	-	-	-
GO:2000026	Regulation of multicellular organismal development	50	0.23	0.0102	-	-	-	-	-	-
GO:0007059	Chromosome segregation	17	0.44	0.0105	-	-	-	-	-	-
GO:0019219	Regulation of nucleobase-containing compound metabolic process	107	0.14	0.0105	-	-	-	-	-	-
GO:0045807	Positive regulation of endocytosis	10	0.61	0.011	-	-	-	-	-	-

GO:0051347	Positive regulation of transferase activity	25	0.35	0.0112	-	-	-	-	-	-
GO:1902533	Positive regulation of intracellular sig-l transduction	38	0.27	0.0113	-	-	-	-	-	-
GO:0045834	Positive regulation of lipid metabolic process	12	0.54	0.0115	-	-	-	-	-	-
GO:0006259	D- metabolic process	31	0.3	0.012	-	-	-	-	-	-
GO:0006356	Regulation of transcription by R-polymerase I	6	0.86	0.012	-	-	-	-	-	-
GO:0032507	Mainte-nce of protein location in cell	7	0.77	0.0123	-	-	-	-	-	-
GO:0043067	Regulation of programmed cell death	52	0.22	0.0123	-	-	-	-	-	-
GO:0016070	R- metabolic process	52	0.22	0.0124	-	-	-	-	-	-
GO:1901652	Response to peptide	22	0.37	0.0132	-	-	-	-	-	-
GO:1903078	Positive regulation of protein localization to plasma membrane	7	0.76	0.0133	-	-	-	-	-	-
GO:0010720	Positive regulation of cell development	19	0.4	0.0135	-	-	-	-	-	-
GO:0031099	Regeneration	12	0.53	0.0136	-	-	-	-	-	-
GO:0031401	Positive regulation of protein modification process	38	0.26	0.0136	-	-	-	-	-	-
GO:1905668	Positive regulation of protein localization to endosome	4	1.15	0.0139	-	-	-	-	-	-
GO:1902115	Regulation of organelle assembly	14	0.48	0.0141	-	-	-	-	-	-
GO:1902532	Negative regulation of intracellular sig-l transduction	24	0.35	0.0142	-	-	-	-	-	-
GO:0042981	Regulation of apoptotic process	51	0.22	0.0144	-	-	-	-	-	-
GO:0009607	Response to biotic stimulus	44	0.24	0.0145	-	-	-	-	-	-
GO:0043403	Skeletal muscle tissue regeneration	6	0.84	0.0145	-	-	-	-	-	-
GO:0048585	Negative regulation of response to stimulus	52	0.22	0.0145	-	-	-	-	-	-

GO:0048589	Developmental growth	23	0.35	0.0145	-	-	-	-	-	-
GO:1901699	Cellular response to nitrogen compound	28	0.31	0.0145	-	-	-	-	-	-
GO:0007338	Single fertilization	10	0.59	0.0154	-	-	-	-	-	-
GO:0031400	Negative regulation of protein modification process	24	0.34	0.0154	-	-	-	-	-	-
GO:0050708	Regulation of protein secretion	16	0.44	0.0157	-	-	-	-	-	-
GO:0010770	Positive regulation of cell morphogenesis involved in differentiation	9	0.63	0.0158	-	-	-	-	-	-
GO:0042908	Xenobiotic transport	6	0.83	0.0158	-	-	-	-	-	-
GO:0045814	Negative regulation of gene expression, epigenetic	8	0.68	0.0158	-	-	-	-	-	-
GO:0046931	Pore complex assembly	5	0.95	0.0158	-	-	-	-	-	-
GO:0009967	Positive regulation of sig-l transduction	51	0.22	0.0164	-	-	-	-	-	-
GO:0031331	Positive regulation of cellular catabolic process	20	0.38	0.0174	-	-	-	-	-	-
GO:0000910	Cytokinesis	9	0.62	0.0176	-	-	-	-	-	-
GO:0050767	Regulation of neurogenesis	21	0.36	0.0177	-	-	-	-	-	-
GO:0051668	Localization within membrane	24	0.34	0.0177	-	-	-	-	-	-
GO:0051716	Cellular response to stimulus	165	0.1	0.0177	-	-	-	-	-	-
GO:1901137	Carbohydrate derivative biosynthetic process	24	0.34	0.0177	-	-	-	-	-	-
GO:0045787	Positive regulation of cell cycle	18	0.4	0.0193	-	-	-	-	-	-
GO:0045087	In-te immune response	25	0.32	0.0197	-	-	-	-	-	-
GO:1903706	Regulation of hemopoiesis	18	0.39	0.0204	-	-	-	-	-	-
GO:0022411	Cellular component disassembly	16	0.42	0.0205	-	-	-	-	-	-
GO:0051647	Nucleus localization	6	0.8	0.0207	-	-	-	-	-	-
GO:0071364	Cellular response to epidermal growth factor stimulus	6	0.8	0.0207	-	-	-	-	-	-

GO:0051321	Meiotic cell cycle	13	0.48	0.0211	-	-	-	-	-	-
GO:0022414	Reproductive process	47	0.22	0.0212	-	-	-	-	-	-
GO:0045638	Negative regulation of myeloid cell differentiation	8	0.66	0.0215	-	-	-	-	-	-
GO:0009152	Purine ribonucleotide biosynthetic process	11	0.53	0.0217	-	-	-	-	-	-
GO:0031507	Heterochromatin assembly	7	0.72	0.0217	-	-	-	-	-	-
GO:0043085	Positive regulation of catalytic activity	40	0.24	0.0217	-	-	-	-	-	-
GO:0072659	Protein localization to plasma membrane	13	0.48	0.0217	-	-	-	-	-	-
GO:0032870	Cellular response to hormone stimulus	22	0.35	0.0221	-	-	-	-	-	-
GO:0072528	Pyrimidine-containing compound biosynthetic process	5	0.9	0.0224	-	-	-	-	-	-
GO:0046112	Nucleobase biosynthetic process	4	1.07	0.0231	-	-	-	-	-	-
GO:0015849	Organic acid transport	15	0.43	0.0234	-	-	-	-	-	-
GO:0006898	Receptor-mediated endocytosis	11	0.53	0.0235	-	-	-	-	-	-
GO:0008203	Cholesterol metabolic process	9	0.6	0.0237	-	-	-	-	-	-
GO:0060998	Regulation of dendritic spine development	9	0.6	0.0237	-	-	-	-	-	-
GO:0030036	Actin cytoskeleton organization	24	0.32	0.0242	-	-	-	-	-	-
GO:0070646	Protein modification by small protein removal	11	0.52	0.0244	-	-	-	-	-	-
GO:0032069	Regulation of nuclease activity	5	0.89	0.0249	-	-	-	-	-	-
GO:0045937	Positive regulation of phosphate metabolic process	34	0.26	0.0249	-	-	-	-	-	-
GO:0061003	Positive regulation of dendritic spine morphogenesis	5	0.89	0.0249	-	-	-	-	-	-
GO:0090169	Regulation of spindle assembly	5	0.89	0.0249	-	-	-	-	-	-
GO:0009628	Response to abiotic stimulus	41	0.23	0.0252	-	-	-	-	-	-

GO:0014070	Response to organic cyclic compound	35	0.26	0.0256	-	-	-	-	-	-
GO:0016579	Protein deubiquitination	10	0.55	0.0273	-	-	-	-	-	-
GO:1901617	Organic hydroxy compound biosynthetic process	11	0.52	0.0273	-	-	-	-	-	-
GO:0010592	Positive regulation of lamellipodium assembly	5	0.88	0.0274	-	-	-	-	-	-
GO:0071417	Cellular response to organonitrogen compound	25	0.31	0.0277	-	-	-	-	-	-
GO:1901799	Negative regulation of proteasomal protein catabolic process	6	0.77	0.0281	-	-	-	-	-	-
GO:0040029	Regulation of gene expression, epigenetic	10	0.54	0.0285	-	-	-	-	-	-
GO:0010811	Positive regulation of cell-substrate adhesion	10	0.54	0.0299	-	-	-	-	-	-
GO:0051653	Spindle localization	7	0.68	0.0299	-	-	-	-	-	-
GO:0099175	Regulation of postsy-pse organization	9	0.58	0.0299	-	-	-	-	-	-
GO:0040008	Regulation of growth	27	0.29	0.0302	-	-	-	-	-	-
GO:0007017	Microtubule-based process	33	0.26	0.0307	-	-	-	-	-	-
GO:0043393	Regulation of protein binding	13	0.46	0.0307	-	-	-	-	-	-
GO:0006974	Cellular response to D- damage stimulus	28	0.29	0.0308	-	-	-	-	-	-
GO:0051701	Biological process involved in interaction with host	9	0.58	0.0312	-	-	-	-	-	-
GO:0033047	Regulation of mitotic sister chromatid segregation	6	0.75	0.0329	-	-	-	-	-	-
GO:0120035	Regulation of plasma membrane bounded cell projection organization	29	0.28	0.033	-	-	-	-	-	-
GO:0006325	Chromatin organization	24	0.31	0.034	-	-	-	-	-	-
GO:0051707	Response to other organism	41	0.23	0.0341	-	-	-	-	-	-

GO:1905039	Carboxylic acid transmembrane transport	11	0.5	0.0342	-	-	-	-	-	-
GO:0019856	Pyrimidine nucleobase biosynthetic process	3	1.27	0.0343	-	-	-	-	-	-
GO:0035967	Cellular response to topologically incorrect protein	8	0.61	0.0346	-	-	-	-	-	-
GO:0007346	Regulation of mitotic cell cycle	21	0.33	0.0348	-	-	-	-	-	-
GO:0051235	Mainte-nce of location	11	0.5	0.0352	-	-	-	-	-	-
GO:0140694	Non-membrane-bounded organelle assembly	19	0.35	0.0359	-	-	-	-	-	-
GO:0032435	Negative regulation of proteasomal ubiquitin-dependent protein catabolic process	5	0.84	0.0366	-	-	-	-	-	-
GO:0044403	Biological process involved in symbiotic interaction	12	0.47	0.0366	-	-	-	-	-	-
GO:0089718	Amino acid import across plasma membrane	5	0.84	0.0366	-	-	-	-	-	-
GO:0006914	Autophagy	15	0.41	0.0368	-	-	-	-	-	-
GO:0035966	Response to topologically incorrect protein	9	0.56	0.0371	-	-	-	-	-	-
GO:0009605	Response to exter-l stimulus	68	0.16	0.0374	-	-	-	-	-	-
GO:0050714	Positive regulation of protein secretion	10	0.52	0.0374	-	-	-	-	-	-
GO:0016570	Histone modification	20	0.34	0.0377	-	-	-	-	-	-
GO:0043549	Regulation of ki-se activity	28	0.28	0.0388	-	-	-	-	-	-
GO:0045637	Regulation of myeloid cell differentiation	12	0.46	0.0388	-	-	-	-	-	-
GO:0009168	Purine ribonucleoside monophosphate biosynthetic process	4	0.98	0.0397	-	-	-	-	-	-
GO:0045216	Cell-cell junction organization	12	0.46	0.0401	-	-	-	-	-	-
GO:0050769	Positive regulation of neurogenesis	15	0.4	0.0406	-	-	-	-	-	-

GO:0051960	Regulation of nervous system development	23	0.31	0.0406	-	-	-	-	-	-
GO:0042254	Ribosome biogenesis	20	0.34	0.0418	-	-	-	-	-	-
GO:0032077	Positive regulation of deoxyribonuclease activity	3	1.22	0.0422	-	-	-	-	-	-
GO:0010810	Regulation of cell-substrate adhesion	13	0.44	0.0423	-	-	-	-	-	-
GO:0010506	Regulation of autophagy	15	0.4	0.0427	-	-	-	-	-	-
GO:0051098	Regulation of binding	18	0.36	0.0428	-	-	-	-	-	-
GO:2000113	Negative regulation of cellular macromolecule biosynthetic process	11	0.48	0.0428	-	-	-	-	-	-
GO:0006623	Protein targeting to vacuole	5	0.82	0.0429	-	-	-	-	-	-
GO:0030010	Establishment of cell polarity	10	0.51	0.0429	-	-	-	-	-	-
GO:0048584	Positive regulation of response to stimulus	63	0.17	0.0429	-	-	-	-	-	-
GO:0051239	Regulation of multicellular organismal process	80	0.15	0.0429	-	-	-	-	-	-
GO:0072595	Mainte-nce of protein localization in organelle	5	0.82	0.0429	-	-	-	-	-	-
GO:0098813	Nuclear chromosome segregation	13	0.43	0.0429	-	-	-	-	-	-
GO:1902229	Regulation of intrinsic apoptotic sig-ling pathway in response to D-damage	5	0.82	0.0429	-	-	-	-	-	-
GO:0007589	Body fluid secretion	7	0.64	0.0435	-	-	-	-	-	-
GO:0006206	Pyrimidine nucleobase metabolic process	4	0.96	0.0441	-	-	-	-	-	-
GO:0051156	Glucose 6-phosphate metabolic process	4	0.96	0.0441	-	-	-	-	-	-
GO:0071216	Cellular response to biotic stimulus	12	0.45	0.0445	-	-	-	-	-	-
GO:0002064	Epithelial cell development	12	0.45	0.0461	-	-	-	5	1.06	0.0345
GO:0010975	Regulation of neuron projection development	23	0.3	0.0461	-	-	-	-	-	-

GO:0051236	Establishment of R-localization	10	0.51	0.0461	-	-	-	-	-	-
GO:0032873	Negative regulation of stress-activated MAPK cascade	5	0.8	0.0462	-	-	-	-	-	-
GO:0061640	Cytoskeleton-dependent cytokinesis	8	0.58	0.0467	-	-	-	-	-	-
GO:0070848	Response to growth factor	21	0.32	0.0478	-	-	-	-	-	-
GO:0009314	Response to radiation	19	0.34	0.0487	-	-	-	-	-	-
GO:0015931	Nucleobase-containing compound transport	12	0.45	0.0487	-	-	-	-	-	-
GO:0071214	Cellular response to abiotic stimulus	15	0.39	0.0487	-	-	-	-	-	-
GO:0090068	Positive regulation of cell cycle process	14	0.41	0.0487	-	-	-	-	-	-
GO:0007034	Vacuolar transport	10	0.5	0.049	-	-	-	-	-	-
GO:0046887	Positive regulation of hormone secretion	10	0.5	0.049	-	-	-	-	-	-
GO:0006015	5-phosphoribose 1-diphosphate biosynthetic process	3	1.17	0.0497	-	-	-	-	-	-
GO:0006695	Cholesterol biosynthetic process	5	0.79	0.0497	-	-	-	-	-	-
GO:0007032	Endosome organization	6	0.7	0.0497	-	-	-	-	-	-
GO:0007097	Nuclear migration	5	0.79	0.0497	-	-	-	-	-	-
GO:0032570	Response to progesterone	5	0.79	0.0497	-	-	-	-	-	-
GO:0043534	Blood vessel endothelial cell migration	5	0.79	0.0497	-	-	-	-	-	-
GO:0045116	Protein neddylation	3	1.17	0.0497	-	-	-	-	-	-
GO:0060996	Dendritic spine development	5	0.79	0.0497	-	-	-	-	-	-
GO:0090235	Regulation of metaphase plate congression	3	1.17	0.0497	-	-	-	-	-	-
GO:1903051	Negative regulation of proteolysis involved in protein catabolic process	7	0.63	0.0497	-	-	-	-	-	-
GO:0031623	Receptor inter-lization	-	-	-	-	-	-	4	1.46	0.0096