Supplemental table S4. GO terms significantly enriched in significantly upregulated proteins of the proteome. K: number of genes from the input cluster in the given category. F: number of total genes in the given category.

Biological Process GO Terms: Over Representation		Sorting Results by: the p-Value in an ascending order.		
Category	GO Level	p-value	k	f
[GO:0007010] cytoskeleton organization and biogenesis	6	4.88E-15	27	528
[GO:0006996] organelle organization and biogenesis	5	7.33E-14	35	1236
[GO:0050875] cellular physiological process	3	2.42E-13	111	10888
[GO:0030029] actin filament-based process	7	5.64E-13	16	210
[GO:0030036] actin cytoskeleton organization and biogenesis	8	1.72E-12	15	189
[GO:0016043] cell organization and biogenesis	4	1.07E-11	43	2181
[GO:0008150] biological_process	0	3.07E-11	127	16056
[GO:0007582] physiological process	1	3.23E-11	118	13342
[GO:0009987] cellular process	1	7.41E-09	117	13877
[GO:0019538] protein metabolism	5	2.34E-08	50	3565
[GO:0006457] protein folding	11	6.21E-08	12	241
[GO:0051261] protein depolymerization	11	1.37E-07	6	37
[GO:0007517] muscle development	4	1.41E-07	10	166
[GO:0051128] regulation of cell organization and biogenesis	9	4.08E-07	7	71
[GO:0051649] establishment of cellular localization	8	6.74E-07	19	774
[GO:0051641] cellular localization	6	8.98E-07	19	789
[GO:0043118] negative regulation of physiological process	5	9.41E-07	20	871
[GO:0007017] microtubule-based process	7	9.89E-07	10	205
[GO:0051248] negative regulation of protein metabolism	13	1.10E-06	7	82
[GO:0044260] cellular macromolecule metabolism	7	1.26E-06	44	3316
[GO:0046907] intracellular transport	10	2.27E-06	18	760
[GO:0044267] cellular protein metabolism	10	2.30E-06	43	3272
[GO:0051179] localization	2	3.48E-06	40	2975
[GO:0006950] response to stress	2	3.65E-06	19	868
[GO:0051129] negative regulation of cell organization and biogenesis	14	4.67E-06	5	38
[GO:0006809] nitric oxide biosynthesis	6	4.98E-06	4	18

[GO:0046209] nitric oxide metabolism	4	4.98E-06	4	18
[GO:0006986] response to unfolded protein	6	5.01E-06	6	67
[GO:0051789] response to protein stimulus	3	5.01E-06	6	67
[GO:0051234] establishment of localization	3	6.49E-06	39	2935
[GO:0008152] metabolism	2	1.06E-05	78	8216
[GO:0008064] regulation of actin polymerization and/or depolymerization	24	1.10E-05	5	45
[GO:0030832] regulation of actin filament length	9	1.22E-05	5	46
[GO:0048519] negative regulation of biological process	2	1.41E-05	20	1043
[GO:0048513] organ development	3	1.55E-05	22	1234
[GO:0044238] primary metabolism	3	1.86E-05	72	7431
[GO:0007015] actin filament organization	9	2.25E-05	5	52
[GO:0030834] regulation of actin filament depolymerization	28	2.33E-05	4	26
[GO:0030042] actin filament depolymerization	18	2.33E-05	4	26
[GO:0006936] muscle contraction	3	2.73E-05	7	133
[GO:0030705] cytoskeleton-dependent intracellular transport	11	3.15E-05	7	136
[GO:0051243] negative regulation of cellular physiological process	11	3.15E-05	17	835
[GO:0051258] protein polymerization	11	3.24E-05	5	56
[GO:0044237] cellular metabolism	5	3.41E-05	73	7694
[GO:0008154] actin polymerization and/or depolymerization	13	3.84E-05	5	58
[GO:0009892] negative regulation of metabolism	8	4.29E-05	11	382
[GO:0000910] cytokinesis	5	5.45E-05	4	32
[GO:0043170] macromolecule metabolism	3	5.62E-05	64	6493
[GO:0048856] anatomical structure development	2	7.70E-05	28	1998
[GO:0006915] apoptosis	7	0.000126	14	670
[GO:0019471] 4-hydroxyproline metabolism	12	0.000127	2	3
[GO:0019511] peptidyl-proline hydroxylation	16	0.000127	2	3
[GO:0018401] peptidyl-proline hydroxylation to 4-hydroxy-L-proline	23	0.000127	2	3
[GO:0007018] microtubule-based movement	15	0.000138	6	120
[GO:0051246] regulation of protein metabolism	9	0.000145	9	296
[GO:0012501] programmed cell death	6	0.000149	14	681
[GO:0048523] negative regulation of cellular process	5	0.000163	17	955
[GO:0008219] cell death	5	0.000226	14	709

[GO:0016265] death	2	0.00023	14	710
[GO:0018208] peptidyl-proline modification	15	0.000253	2	4
[GO:0006930] substrate-bound cell migration, cell extension	11	0.000253	2	4
[GO:0001778] plasma membrane repair	14	0.000253	2	4
[GO:0042981] regulation of apoptosis	13	0.000266	11	470
[GO:0008360] regulation of cell shape	9	0.000272	4	48
[GO:0043067] regulation of programmed cell death	11	0.000296	11	476
[GO:0009266] response to temperature stimulus	3	0.000371	4	52
[GO:0051016] barbed-end actin filament capping	38	0.000384	3	22
[GO:0006810] transport	6	0.00042	31	2558
[GO:0051693] actin filament capping	37	0.00044	3	23
[GO:0042060] wound healing	8	0.000441	5	97
[GO:0007519] striated muscle development	5	0.000462	5	98
[GO:0030835] negative regulation of actin filament depolymerization	36	0.0005	3	24
[GO:0045428] regulation of nitric oxide biosynthesis	11	0.000872	2	7
[GO:0051674] localization of cell	3	0.000927	9	382
[GO:0006928] cell motility	8	0.000927	9	382
[GO:0040011] locomotion	2	0.001072	9	390
[GO:0009408] response to heat	5	0.001292	3	33
[GO:0043066] negative regulation of apoptosis	19	0.001376	6	185
[GO:0051130] positive regulation of cell organization and biogenesis	14	0.001483	2	9
[GO:0050819] negative regulation of coagulation	8	0.001483	2	9
[GO:0043069] negative regulation of programmed cell death	16	0.001493	6	188
[GO:0009653] morphogenesis	3	0.001557	17	1166
[GO:0007275] development	1	0.001563	29	2523
[GO:0045445] myoblast differentiation	12	0.001805	3	37
[GO:0001525] angiogenesis	9	0.001824	5	133
[GO:0031114] regulation of microtubule depolymerization	25	0.001846	2	10
[GO:0050818] regulation of coagulation	5	0.001846	2	10
[GO:0007026] negative regulation of microtubule depolymerization	36	0.001846	2	10
[GO:0006916] anti-apoptosis	20	0.001885	5	134
[GO:0006575] amino acid derivative metabolism	8	0.001969	4	81

[GO:0006605] protein targeting	15	0.002058	7	271
[GO:0007019] microtubule depolymerization	18	0.002246	2	11
[GO:0006929] substrate-bound cell migration	10	0.002246	2	11
[GO:0030866] cortical actin cytoskeleton organization and biogenesis	10	0.002246	2	11
[GO:0050791] regulation of physiological process	3	0.002274	38	3719
[GO:0006807] nitrogen compound metabolism	3	0.002334	9	437
[GO:0009887] organ morphogenesis	5	0.00259	11	622
[GO:0031111] negative regulation of microtubule polymerization or depolymerization	21	0.002684	2	12
[GO:0055002] striated muscle cell development	12	0.002684	2	12
[GO:0030239] myofibril assembly	27	0.002684	2	12
[GO:0007009] plasma membrane organization and biogenesis	6	0.002684	2	12
[GO:0055001] muscle cell development	6	0.002684	2	12
[GO:0051301] cell division	4	0.002861	6	214
[GO:0030199] collagen fibril organization	6	0.003158	2	13
[GO:0031109] microtubule polymerization or depolymerization	9	0.003158	2	13
[GO:0031110] regulation of microtubule polymerization or depolymerization	15	0.003158	2	13
[GO:0001654] eye development	5	0.003382	4	94
[GO:0030865] cortical cytoskeleton organization and biogenesis	7	0.003669	2	14
[GO:0050789] regulation of biological process	1	0.003788	41	4223
[GO:0000902] cell morphogenesis	8	0.003939	9	473
[GO:0048514] blood vessel morphogenesis	8	0.003944	5	159
[GO:0042692] muscle cell differentiation	4	0.004527	3	51
[GO:0051146] striated muscle cell differentiation	9	0.004797	2	16
[GO:0030516] regulation of axon extension	29	0.004797	2	16
[GO:0006461] protein complex assembly	6	0.004964	7	318
[GO:0048741] skeletal muscle fiber development	8	0.005045	3	53
[GO:0048747] muscle fiber development	5	0.005045	3	53
[GO:0048637] skeletal muscle development	6	0.005885	3	56
[GO:0051656] establishment of organelle localization	5	0.006064	2	18
[GO:0042219] amino acid derivative catabolism	11	0.006064	2	18
[GO:0001747] eye development (sensu Mammalia)	7	0.006489	3	58

[GO:0021592] fourth ventricle development	10	0.006541	1	1
[GO:0015886] heme transport	8	0.006541	1	1
[GO:0030328] prenylcysteine catabolism	26	0.006541	1	1
[GO:0030837] negative regulation of actin filament polymerization	33	0.006541	1	1
[GO:0021591] ventricular system development	8	0.006541	1	1
[GO:0030329] prenylcysteine metabolism	9	0.006541	1	1
[GO:0055013] cardiac muscle cell development	5	0.006541	1	1
[GO:0030240] muscle thin filament assembly	30	0.006541	1	1
[GO:0051295] establishment of meiotic spindle localization	19	0.006541	1	1
[GO:0055003] cardiac myofibril assembly	29	0.006541	1	1
[GO:0021678] third ventricle development	9	0.006541	1	1
[GO:0042989] sequestering of actin monomers	38	0.006541	1	1
[GO:0007132] meiotic metaphase I	11	0.006541	1	1
[GO:0021670] lateral ventricle development	11	0.006541	1	1
[GO:0048628] myoblast maturation	17	0.006749	2	19
[GO:0051169] nuclear transport	11	0.007116	4	116
[GO:0043010] eye development (sensu Vertebrata)	6	0.007129	3	60
[GO:0001568] blood vessel development	5	0.007425	5	185
[GO:0048627] myoblast development	14	0.007467	2	20
[GO:0001944] vasculature development	4	0.007931	5	188
[GO:0016192] vesicle-mediated transport	7	0.00819	8	438
[GO:0009206] purine ribonucleoside triphosphate biosynthesis	25	0.008518	3	64
[GO:0009145] purine nucleoside triphosphate biosynthesis	17	0.008518	3	64
[GO:0006334] nucleosome assembly	21	0.008713	4	123
[GO:0009201] ribonucleoside triphosphate biosynthesis	17	0.008888	3	65
[GO:0048675] axon extension	24	0.009001	2	22
[GO:0009611] response to wounding	4	0.009672	7	361