Supplemental table S3. GO terms significantly enriched in significantly downregulated 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:0019752] carboxylic acid metabolism	7	4.44E-16	24	521
[GO:0006091] generation of precursor metabolites and energy	6	6.66E-16	27	698
[GO:0006732] coenzyme metabolism	7	1.55E-15	18	179
[GO:0006082] organic acid metabolism	6	2.78E-15	24	522
[GO:0015980] energy derivation by oxidation of organic compounds	7	4.44E-15	15	175
[GO:0051186] cofactor metabolism	6	6.44E-15	18	208
[GO:0006092] main pathways of carbohydrate metabolism	12	2.22E-13	12	123
[GO:0009060] aerobic respiration	9	6.97E-13	8	31
[GO:0006084] acetyl-CoA metabolism	8	3.35E-12	8	37
[GO:0045333] cellular respiration	8	3.35E-12	8	37
[GO:0006631] fatty acid metabolism	11	1.04E-11	12	170
[GO:0006099] tricarboxylic acid cycle	23	1.08E-11	7	25
[GO:0046356] acetyl-CoA catabolism	13	1.47E-11	7	26
[GO:0050875] cellular physiological process	3	2.15E-11	76	10888
[GO:0009109] coenzyme catabolism	11	5.78E-11	7	31
[GO:0007582] physiological process	1	1.33E-10	82	13342
[GO:0008152] metabolism	2	1.44E-10	65	8216
[GO:0051187] cofactor catabolism	9	1.46E-10	7	35
[GO:0006100] tricarboxylic acid cycle intermediate metabolism	13	1.53E-10	6	19
[GO:0044248] cellular catabolism	7	1.63E-10	17	542
[GO:0044262] cellular carbohydrate metabolism	6	4.57E-10	14	357
[GO:0044237] cellular metabolism	5	1.82E-09	61	7694
[GO:0009056] catabolism	3	1.87E-09	17	636
[GO:0043648] dicarboxylic acid metabolism	8	5.10E-09	4	6
[GO:0006637] acyl-CoA metabolism	14	6.00E-09	5	16
[GO:0005975] carbohydrate metabolism	5	1.96E-08	14	479

[GO:0006108] malate metabolism	17	8.05E-07	3	5
[GO:0044255] cellular lipid metabolism	8	5.11E-06	12	554
[GO:0051188] cofactor biosynthesis	9	9.23E-06	6	111
[GO:0006733] oxidoreduction coenzyme metabolism	8	1.12E-05	4	32
[GO:0006519] amino acid and derivative metabolism	7	1.55E-05	9	334
[GO:0008150] biological_process	0	1.65E-05	83	16056
[GO:0006603] phosphocreatine metabolism	10	1.89E-05	2	2
[GO:0019439] aromatic compound catabolism	9	2.85E-05	3	14
[GO:0006629] lipid metabolism	4	3.02E-05	12	662
[GO:0006118] electron transport	7	3.11E-05	10	458
[GO:0009987] cellular process	1	5.70E-05	76	13877
[GO:0009108] coenzyme biosynthesis	11	6.38E-05	5	96
[GO:0044238] primary metabolism	3	9.55E-05	50	7431
[GO:0006599] phosphagen metabolism	9	0.000113	2	4
[GO:0009063] amino acid catabolism	17	0.000121	4	58
[GO:0006810] transport	6	0.000182	24	2558
[GO:0006572] tyrosine catabolism	23	0.000188	2	5
[GO:0006006] glucose metabolism	13	0.000222	5	125
[GO:0051234] establishment of localization	3	0.000229	26	2935
[GO:0009310] amine catabolism	11	0.000238	4	69
[GO:0044270] nitrogen compound catabolism	9	0.000252	4	70
[GO:0051179] localization	2	0.000285	26	2975
[GO:0006066] alcohol metabolism	6	0.000346	7	300
[GO:0006559] L-phenylalanine catabolism	23	0.000392	2	7
[GO:0019395] fatty acid oxidation	12	0.000402	3	33
[GO:0006575] amino acid derivative metabolism	8	0.00044	4	81
[GO:0006743] ubiquinone metabolism	10	0.000521	2	8
[GO:0006558] L-phenylalanine metabolism	15	0.000521	2	8
[GO:0006744] ubiquinone biosynthesis	16	0.000521	2	8
[GO:0045426] quinone cofactor biosynthesis	13	0.000668	2	9
[GO:0046395] carboxylic acid catabolism	11	0.000833	2	10
[GO:0016054] organic acid catabolism	9	0.000833	2	10

[GO:0009074] aromatic amino acid family catabolism	21	0.000833	2	10
[GO:0042375] quinone cofactor metabolism	7	0.000833	2	10
[GO:0019318] hexose metabolism	12	0.000881	5	169
[GO:0005996] monosaccharide metabolism	11	0.001004	5	174
[GO:0009065] glutamine family amino acid catabolism	19	0.001215	2	12
[GO:0019363] pyridine nucleotide biosynthesis	22	0.001215	2	12
[GO:0044275] cellular carbohydrate catabolism	15	0.001388	4	110
[GO:0016052] carbohydrate catabolism	8	0.001388	4	110
[GO:0006570] tyrosine metabolism	15	0.001432	2	13
[GO:0000051] urea cycle intermediate metabolism	4	0.001432	2	13
[GO:0006725] aromatic compound metabolism	6	0.001797	4	118
[GO:0009058] biosynthesis	3	0.002046	15	1501
[GO:0042364] water-soluble vitamin biosynthesis	11	0.002769	2	18
[GO:0006807] nitrogen compound metabolism	3	0.003046	7	437
[GO:0006096] glycolysis	27	0.003588	3	70
[GO:0009110] vitamin biosynthesis	9	0.003768	2	21
[GO:0006635] fatty acid beta-oxidation	13	0.003768	2	21
[GO:0006769] nicotinamide metabolism	15	0.003768	2	21
[GO:0046502] uroporphyrinogen III metabolism	9	0.004378	1	1
[GO:0006780] uroporphyrinogen III biosynthesis	14	0.004378	1	1
[GO:0046314] phosphocreatine biosynthesis	15	0.004378	1	1
[GO:0006781] succinyl-CoA pathway	15	0.004378	1	1
[GO:0001315] age-dependent response to reactive oxygen species	12	0.004378	1	1
[GO:0006106] fumarate metabolism	17	0.004378	1	1
[GO:0006741] NADP biosynthesis	25	0.004378	1	1
[GO:0019362] pyridine nucleotide metabolism	14	0.004911	2	24
[GO:0006007] glucose catabolism	23	0.005039	3	79
[GO:0006090] pyruvate metabolism	8	0.005322	2	25
[GO:0044249] cellular biosynthesis	7	0.005581	13	1347
[GO:0009072] aromatic amino acid family metabolism	14	0.00575	2	26
[GO:0019320] hexose catabolism	21	0.005978	3	84
[GO:0046365] monosaccharide catabolism	19	0.005978	3	84

[GO:0046164] alcohol catabolism	9	0.006381	3	86
[GO:0006520] amino acid metabolism	12	0.007073	5	274
[GO:0006879] iron ion homeostasis	12	0.007609	2	30
[GO:0006826] iron ion transport	12	0.008111	2	31
[GO:0006919] caspase activation	22	0.008111	2	31
[GO:0006591] ornithine metabolism	15	0.008737	1	2
[GO:0009448] gamma-aminobutyric acid metabolism	14	0.008737	1	2
[GO:0046359] butyrate catabolism	13	0.008737	1	2
[GO:0006101] citrate metabolism	16	0.008737	1	2
[GO:0009082] branched chain family amino acid biosynthesis	19	0.008737	1	2
[GO:0019794] nonprotein amino acid metabolism	13	0.008737	1	2
[GO:0000303] response to superoxide	13	0.008737	1	2
[GO:0009450] gamma-aminobutyric acid catabolism	23	0.008737	1	2
[GO:0015810] aspartate transport	12	0.008737	1	2
[GO:0016197] endosome transport	12	0.009158	2	33
[GO:0009308] amine metabolism	7	0.009527	6	413
[GO:0043280] positive regulation of caspase activity	20	0.009703	2	34