

Panther Category (Biological Processes)	Number	%	P-Value	Bonferroni	Benjamini	FDR (X100)
BP00060:Protein metabolism and modification	133	17.7	2.50E-07	5.50E-05	5.50E-05	0
BP00125:Intracellular protein traffic	52	6.9	3.80E-07	8.30E-05	4.10E-05	0
BP00063:Protein modification	126	16.8	6.70E-07	1.50E-04	4.90E-05	0
BP00031:Nucleoside, nucleotide and nucleic acid metabolism	138	18.4	9.40E-06	2.00E-03	5.10E-04	0
BP00071:Proteolysis	200	26.7	2.10E-05	4.60E-03	9.30E-04	0
BP00286:Cell structure	138	18.4	2.60E-05	5.80E-03	9.70E-04	0
BP00179:Apoptosis	43	5.7	3.60E-05	7.80E-03	1.10E-03	0
BP00289:Other metabolism	123	16.4	4.50E-05	9.80E-03	1.20E-03	0.1
BP00064:Protein phosphorylation	101	13.5	4.60E-05	1.00E-02	1.10E-03	0.1
BP00133:Nuclear transport	19	2.5	2.40E-04	5.20E-02	5.30E-03	0.3
BP00224:Cell proliferation and differentiation	52	6.9	5.30E-04	1.10E-01	1.10E-02	0.7
BP00290:Lipid metabolism	20	2.7	7.10E-04	1.40E-01	1.30E-02	0.9
BP00044:mRNA transcription regulation	332	44.3	1.30E-03	2.50E-01	2.10E-02	1.6
BP00124:Cell adhesion	34	4.5	2.20E-03	3.80E-01	3.40E-02	2.7
BP00040:mRNA transcription	215	28.7	2.70E-03	4.40E-01	3.80E-02	3.3
BP00137:Protein targeting and localization	20	2.7	3.60E-03	5.50E-01	4.90E-02	4.5
BP00136:Other intracellular protein traffic	20	2.7	5.30E-03	6.90E-01	6.60E-02	6.6
BP00001:Carbohydrate metabolism	28	3.7	5.60E-03	7.10E-01	6.60E-02	6.9
BP00285:Cell structure and motility	60	8	6.80E-03	7.80E-01	7.60E-02	8.4
BP00110:Other receptor mediated signaling pathway	14	1.9	7.40E-03	8.00E-01	7.80E-02	9
BP00008:Tricarboxylic acid pathway	13	1.7	7.70E-03	8.20E-01	7.70E-02	9.4

Legend:

The nearest gene data set from S 4 was analyzed by the DAVID gene ontology program (5) and the most significant categories that are enriched are shown. The complete set of genes used is provided in S4. The number of genes in each category (count), p value. Bonferroni and Benjamini corrected values along with associated false discovery rate (FDR) are provided from the DAVID software.