

Module			Enriched Subset				
ID	Gene Count		Top Ontology	Gene Count	%	PValue	Bonferroni
20	76		BP transport	14	21.88	1.30E-02	1.00E+00
			CC NONE	-	-	-	-
			MF Ras GTPase activator activity	3	4.69	2.87E-02	9.96E-01
3	49		BP translational elongation	42	85.71	7.82E-90	3.09E-87
			CC ribosome	42	85.71	5.28E-75	2.74E-73
			MF structural constituent of ribosome	40	81.63	5.20E-73	3.22E-71
12	42		BP NONE	-	-	-	-
			CC NONE	-	-	-	-
			MF NONE	-	-	-	-
13	26		BP cellular component biogenesis	5	21.74	5.54E-03	9.05E-01
			CC NONE	-	-	-	-
			MF NONE	-	-	-	-
15	26		BP nuclear division	15	57.69	1.25E-19	4.99E-17
			CC spindle	11	42.31	1.07E-15	1.01E-13
			MF ATP binding	11	42.31	6.26E-05	6.43E-03
10	14		BP glycolysis	3	23.08	4.80E-04	2.08E-01
			CC extracellular region part	5	38.46	4.41E-03	3.04E-01
			MF protein binding	10	76.92	1.96E-02	8.62E-01
7	13		BP nervous system development	6	50.00	4.89E-04	2.64E-01
			CC cell fraction	4	33.33	3.44E-02	8.90E-01
			MF transporter activity	6	50.00	8.66E-04	1.14E-01
11	12		BP regulation of Ras protein signal transduction	2	20.00	5.82E-02	1.00E+00
			CC NONE	-	-	-	-
			MF ATPase activity, coupled to transmembrane movement of substances	2	20.00	2.85E-02	9.12E-01
1	11		BP oxidative phosphorylation	4	36.36	3.76E-05	7.56E-03
			CC mitochondrial inner membrane	6	54.55	5.94E-07	3.92E-05
			MF hydrogen ion transmembrane transporter activity	4	36.36	1.66E-05	8.80E-04
2	11		BP glycolysis	4	36.36	1.91E-06	4.36E-04
			CC NONE	-	-	-	-
			MF NONE	-	-	-	-

Legend

bonfferoni<0.01 bonfferoni<0.05 p<0.01 p<0.05

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ID	Gene Count		Top Ontology	Gene Count	%	PValue	Bonferroni
5	11		BP response to DNA damage stimulus	3	27.27	1.34E-02	9.65E-01
			CC nuclear lumen	5	45.45	5.95E-03	2.45E-01
			MF NONE	-	-	-	-
6	11		BP anti-apoptosis	3	27.27	7.13E-03	8.78E-01
			CC extracellular region	6	54.55	2.60E-03	1.77E-01
			MF protein binding	9	81.82	3.31E-02	7.73E-01
9	11		BP nervous system development	4	36.36	2.70E-02	9.99E-01
			CC microtubule	3	27.27	1.21E-02	5.31E-01
			MF protein binding	7	63.64	9.18E-02	9.96E-01
16	10		BP translational elongation	5	55.56	1.69E-07	4.56E-05
			CC cytosolic ribosome	5	55.56	4.30E-08	2.71E-06
			MF structural constituent of ribosome	5	55.56	9.88E-07	5.34E-05
4	9		BP protein folding	4	50.00	6.54E-05	1.53E-02
			CC endoplasmic reticulum lumen	6	75.00	5.90E-11	4.19E-09
			MF unfolded protein binding	4	50.00	1.46E-05	1.11E-03
8	8		BP response to organic substance	6	75.00	6.61E-06	1.63E-03
			CC synaptosome	2	25.00	2.64E-02	6.29E-01
			MF protein dimerization activity	3	37.50	2.38E-02	7.21E-01
19	8		BP DNA replication	4	50.00	8.07E-05	1.30E-02
			CC nucleoplasm	4	50.00	2.99E-03	1.44E-01
			MF ATP binding	4	50.00	2.40E-02	8.64E-01
21	8		BP response to inorganic substance	3	37.50	2.04E-03	2.06E-01
			CC cytoplasm	4	50.00	9.74E-02	9.83E-01
			MF copper ion binding	4	50.00	3.13E-06	1.34E-04
14	7		BP cellular amino acid metabolic process	2	33.33	3.18E-02	9.02E-01
			CC NONE	-	-	-	-
			MF NONE	-	-	-	-
17	7		BP anatomical structure development	4	57.14	7.48E-02	1.00E+00
			CC cell fraction	3	42.86	4.03E-02	8.82E-01
			MF NONE	-	-	-	-
18	7		BP antigen processing and presentation of peptide antigen	3	50.00	3.78E-05	9.07E-03
			CC MHC class I protein complex	2	33.33	8.77E-03	3.39E-01
			MF MHC class I receptor activity	2	33.33	5.60E-03	1.78E-01