

Module		Enriched Subset					
ID	Gene Count		Top Ontology	Gene Count	%	PValue	Bonferroni
24	51		BP immune response	18	34.62	8.50E-12	7.91E-09
			CC lysosome	8	15.38	3.50E-06	4.55E-04
			MF IgG binding	3	5.77	2.08E-04	4.08E-02
37	48		BP immune response	14	29.79	5.57E-08	3.63E-05
			CC receptor complex	5	10.64	3.18E-04	3.98E-02
			MF signal transducer activity	16	34.04	4.02E-04	6.87E-02
34	46		BP response to external stimulus	14	31.11	1.04E-06	7.68E-04
			CC lytic vacuole	12	26.67	6.83E-12	1.09E-09
			MF cysteine-type endopeptidase activity	5	11.11	4.16E-05	6.97E-03
1	34		BP cell cycle	21	63.64	3.07E-19	1.58E-16
			CC nucleus	27	81.82	7.73E-10	8.11E-08
			MF ATP binding	12	36.36	1.36E-04	1.90E-02
22	34		BP extracellular matrix organization	12	36.36	3.87E-17	1.79E-14
			CC proteinaceous extracellular matrix	19	57.58	2.90E-23	4.20E-21
			MF extracellular matrix structural constituent	13	39.39	6.50E-20	7.48E-18
23	31		BP immune response	12	40.00	1.39E-08	7.17E-06
			CC plasma membrane	18	60.00	3.18E-05	3.55E-03
			MF molecular transducer activity	10	33.33	5.81E-03	5.39E-01
46	26		BP collagen fibril organization	5	20.83	6.80E-08	3.51E-05
			CC extracellular matrix	11	45.83	1.80E-11	2.39E-09
			MF platelet-derived growth factor binding	5	20.83	1.09E-09	1.29E-07
26	24		BP response to external stimulus	12	52.17	1.53E-08	9.49E-06
			CC extracellular region	11	47.83	5.61E-05	5.60E-03
			MF kininogen binding	2	8.70	4.35E-03	4.45E-01
4	21		BP translational elongation	16	80.00	3.54E-32	8.46E-30
			CC ribosome	16	80.00	7.43E-27	3.56E-25
			MF structural constituent of ribosome	16	80.00	3.35E-28	1.51E-26
39	17		BP anatomical structure morphogenesis	9	56.25	2.28E-06	1.14E-03
			CC basal lamina	3	18.75	1.12E-04	1.12E-02
			MF protein binding	14	87.50	8.42E-03	5.56E-01
43	16		BP cell adhesion	7	46.67	1.85E-05	5.13E-03
			CC proteinaceous extracellular matrix	4	26.67	2.49E-03	2.38E-01
			MF extracellular matrix structural constituent	3	20.00	2.78E-03	1.99E-01
10	15		BP NONE	-	-	-	-
			CC NONE	-	-	-	-
			MF NONE	-	-	-	-
21	15		BP establishment of localization in cell	6	42.86	1.55E-04	2.91E-02
			CC endoplasmic reticulum	9	64.29	1.68E-07	1.36E-05
			MF isomerase activity	3	21.43	3.29E-03	2.59E-01
18	13		BP response to external stimulus	6	50.00	1.14E-04	5.31E-02
			CC plasma membrane	6	50.00	3.97E-02	9.28E-01
			MF anion transmembrane transporter activity	2	16.67	9.30E-02	1.00E+00
38	13		BP antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	9	75.00	1.60E-20	4.37E-18
			CC MHC class II protein complex	8	66.67	3.65E-18	1.94E-16
			MF MHC class II receptor activity	7	58.33	7.46E-16	4.66E-14
11	12		BP NONE	-	-	-	-
			CC membrane part	7	63.64	5.87E-02	9.11E-01
			MF NONE	-	-	-	-
13	12		BP synaptic transmission	3	27.27	8.70E-03	8.59E-01
			CC compact myelin	2	18.18	2.26E-03	1.35E-01
			MF structural constituent of myelin sheath	2	18.18	2.97E-03	1.81E-01
17	12		BP nitrogen compound metabolic process	9	81.82	1.80E-04	4.60E-02
			CC macromolecular complex	8	72.73	7.94E-05	5.62E-03
			MF transcription activator activity	5	45.45	5.99E-05	5.67E-03
25	12		BP immune system process	6	54.55	3.26E-05	1.30E-02
			CC membrane raft	3	27.27	3.44E-03	1.98E-01
			MF enzyme binding	3	27.27	2.90E-02	9.27E-01
2	11		BP RNA splicing	6	60.00	3.75E-07	4.84E-05
			CC ribonucleoprotein complex	7	70.00	8.65E-08	4.06E-06
			MF RNA binding	7	70.00	8.27E-07	4.38E-05
3	11		BP RNA metabolic process	5	50.00	5.76E-04	1.11E-01
			CC intracellular membrane-bounded organelle	10	100.00	2.01E-03	9.94E-02
			MF RNA binding	3	30.00	6.48E-02	9.78E-01
29	11		BP cell fate commitment	3	30.00	1.96E-03	3.41E-01
			CC NONE	-	-	-	-
			MF transcription regulator activity	4	40.00	2.56E-02	8.24E-01
40	11		BP response to biotic stimulus	3	30.00	1.85E-02	9.96E-01
			CC endoplasmic reticulum lumen	3	30.00	8.79E-04	7.12E-02
			MF enzyme inhibitor activity	3	30.00	1.05E-02	6.77E-01
5	10		BP NONE	-	-	-	-
			CC NONE	-	-	-	-
			MF NONE	-	-	-	-

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ID	Gene Count		Top Ontology	Gene Count	%	PValue	Bonferroni
7	10		BP antigen processing and presentation	5	62.50	3.84E-08	6.33E-06
			CC MHC class I protein complex	3	37.50	6.24E-05	3.55E-03
			MF MHC class I receptor activity	2	25.00	7.83E-03	3.61E-01
30	10		BP NONE	-	-	-	-
			CC synaptic vesicle membrane	2	2.27	1.15E-02	6.17E-01
			MF ATPase activity, coupled to transmembrane	3	3.41	1.05E-03	6.52E-02
41	10		BP regulation of microtubule depolymerization	2	22.22	6.78E-03	7.42E-01
			CC protein complex	5	55.56	1.62E-02	6.64E-01
			MF microtubule binding	2	22.22	2.82E-02	7.98E-01
47	10		BP cellular component organization	6	66.67	2.64E-03	3.71E-01
			CC basal lamina	2	22.22	8.52E-03	4.60E-01
			MF carbohydrate binding	3	33.33	1.39E-02	6.30E-01
6	9		BP generation of precursor metabolites and	5	62.50	7.87E-06	2.20E-03
			CC respiratory chain	4	50.00	3.48E-06	2.22E-04
			MF NADH dehydrogenase (quinone) activity	3	37.50	1.17E-04	8.88E-03
16	9		BP regulation of cell differentiation	3	37.50	1.66E-02	9.98E-01
			CC membrane raft	2	25.00	5.27E-02	9.79E-01
			MF NONE	-	-	-	-
19	9		BP NONE	-	-	-	-
			CC cytoplasmic membrane-bounded vesicle	3	37.50	2.23E-02	7.48E-01
			MF NONE	-	-	-	-
20	9		BP cellular carbohydrate metabolic process	3	37.50	1.44E-02	9.81E-01
			CC cytoplasmic part	6	75.00	3.21E-02	8.28E-01
			MF NONE	-	-	-	-
27	9		BP macromolecule metabolic process	4	50.00	6.62E-02	1.00E+00
			CC NONE	-	-	-	-
			MF ATP binding	4	50.00	1.48E-02	6.47E-01
44	9		BP vesicle-mediated transport	4	50.00	1.23E-03	2.68E-01
			CC cytoplasmic part	7	87.50	4.37E-03	3.02E-01
			MF small GTPase binding	2	25.00	4.58E-02	9.84E-01
8	8		BP cellular amino acid metabolic process	2	28.57	7.75E-02	1.00E+00
			CC NONE	-	-	-	-
			MF catalytic activity	5	71.43	5.03E-02	9.77E-01
9	8		BP cellular amino acid metabolic process	3	42.86	2.47E-03	2.55E-01
			CC NONE	-	-	-	-
			MF catalytic activity	5	71.43	5.03E-02	9.52E-01
12	8		BP cellular amino acid metabolic process	2	28.57	7.75E-02	9.99E-01
			CC mitochondrion	3	42.86	5.82E-02	9.65E-01
			MF NONE	-	-	-	-
14	8		BP cellular component organization	4	57.14	7.26E-02	1.00E+00
			CC NONE	-	-	-	-
			MF NONE	-	-	-	-
15	8		BP cellular amino acid metabolic process	2	33.33	7.75E-02	1.00E+00
			CC perinuclear region of cytoplasm	2	33.33	8.73E-02	9.94E-01
			MF NONE	-	-	-	-
28	8		BP RNA metabolic process	5	71.43	2.61E-04	3.56E-02
			CC nuclear lumen	4	57.14	1.22E-02	3.42E-01
			MF catalytic activity	6	85.71	2.04E-02	7.95E-01
31	8		BP regulation of developmental process	4	57.14	1.01E-03	1.70E-01
			CC basement membrane	3	42.86	3.52E-04	1.53E-02
			MF extracellular matrix structural constituent	3	42.86	4.71E-04	2.60E-02
32	8		BP regulation of multicellular organismal	3	42.86	5.52E-02	1.00E+00
			CC plasma membrane	5	71.43	3.13E-02	8.56E-01
			MF protein complex binding	3	42.86	2.42E-03	1.52E-01
33	8		BP NONE	-	-	-	-
			CC lysosome	4	57.14	4.47E-05	1.87E-03
			MF hydrolase activity, hydrolyzing O-glycosyl	2	28.57	3.07E-02	7.83E-01
35	8		BP antigen processing and presentation of	5	71.43	3.70E-10	1.07E-07
			CC MHC class II protein complex	4	57.14	1.09E-07	5.75E-06
			MF MHC class II receptor activity	4	57.14	3.34E-08	2.00E-06
36	8		BP carboxylic acid metabolic process	3	42.86	1.43E-02	8.94E-01
			CC cytoplasm	6	85.71	7.62E-02	9.33E-01
			MF NONE	-	-	-	-
42	8		BP G-protein coupled receptor protein signaling	3	42.86	5.38E-02	1.00E+00
			CC plasma membrane	6	85.71	3.62E-03	1.66E-01
			MF receptor activity	5	71.43	9.77E-04	7.52E-02
45	8		BP NONE	-	-	-	-
			CC cytoplasm	6	85.71	7.62E-02	9.79E-01