Appendix 1.

Blue Cluster

Category:	Term:	Gene Count:	% of Total Cluster:	PValue:
KEGG_PATHWAY	ssc05310:Asthma	9	1.55	2.05E-04
GOTERM_CC_FAT	GO:0042613~MHC class II protein complex	6	1.03	1.84E-03
SP_PIR_KEYWORDS	MHC II	6	1.03	2.21E-03
SMART	SM00407:IGc1	9	1.55	3.19E-03
KEGG_PATHWAY	ssc05416:Viral myocarditis	11	1.89	3.35E-03
INTERPRO	IPR003597:Immunoglobulin C1-set	9	1.55	3.53E-03
PIR_SUPERFAMILY	PIRSF001991:class II histocompatibility antigen	6	1.03	3.75E-03
GOTERM_BP_FAT	GO:0019882~antigen processing and presentation	9	1.55	4.80E-03
GOTERM_BP_FAT	GO:0006955~immune response	23	3.96	5.75E-03
INTERPRO	IPR003006:Immunoglobulin/major histocompatibility complex, conserved site	8	1.38	6.55E-03
GOTERM_CC_FAT	GO:0042611~MHC protein complex	8	1.38	6.55E-03
GOTERM_BP_FAT	GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	5	0.86	6.80E-03
INTERPRO	IPR007110:Immunoglobulin-like	15	2.58	6.89E-03
KEGG_PATHWAY	ssc04514:Cell adhesion molecules (CAMs)	13	2.24	7.23E-03
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	21	3.61	0.0166
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	21	3.61	0.0166
SP_PIR_KEYWORDS	tyrosine-protein kinase	6	1.03	0.0168
INTERPRO	IPR008266:Tyrosine protein kinase, active site	6	1.03	0.0173
KEGG_PATHWAY	ssc05322:Systemic lupus erythematosus	14	2.41	0.0193
INTERPRO	IPR014745:MHC class II, alpha/beta chain, N-terminal	4	0.69	0.0196
KEGG_PATHWAY	ssc05330:Allograft rejection	8	1.38	0.0233
INTERPRO	IPR013783:Immunoglobulin-like fold	15	2.58	0.0244
GOTERM_BP_FAT	GO:0007268~synaptic transmission	5	0.86	0.0246
KEGG_PATHWAY	ssc04672:Intestinal immune network for IgA production	8	1.38	0.0270
GOTERM_BP_FAT	GO:0001505~regulation of neurotransmitter levels	4	0.69	0.0323
GOTERM_BP_FAT	GO:0045087~innate immune response	7	1.20	0.0324
INTERPRO	IPR002129:Pyridoxal phosphate-dependent decarboxylase	3	0.52	0.0326
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	5	0.86	0.0339
GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	6	1.03	0.0341
KEGG_PATHWAY	ssc04940:Type I diabetes mellitus	8	1.38	0.0357
SMART	SM00219:TyrKc	6	1.03	0.0360
INTERPRO	IPR001245:Tyrosine protein kinase	6	1.03	0.0376
KEGG_PATHWAY	ssc04612:Antigen processing and presentation	10	1.72	0.0389
SP_PIR_KEYWORDS	signal	53	9.12	0.0442
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	5	0.86	0.0449
GOTERM_BP_FAT	GO:0016485~protein processing	5	0.86	0.0449
GOTERM_BP_FAT	GO:0051604~protein maturation	5	0.86	0.0449
GOTERM_BP_FAT	GO:0051605~protein maturation by peptide bond cleavage	5	0.86	0.0449
GOTERM_MF_FAT	GO:0048037~cofactor binding	11	1.89	0.0462
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	6	1.03	0.0481
SP_PIR_KEYWORDS	activator	8	1.38	0.0491
UP_SEQ_FEATURE	active site: Proton donor	7	1.20	0.0491

Green Cluster

Category:	Term:	Gene Count:	% of Total Cluster:	PValue:
GOTERM_BP_FAT	GO:0051301~cell division	10	2.13	2.05E-05
KEGG_PATHWAY	ssc04110:Cell cycle	15	3.19	4.59E-05
SP_PIR_KEYWORDS	cell division	9	1.91	6.19E-05
SP_PIR_KEYWORDS	mitosis	6	1.28	3.13E-04
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	6	1.28	3.26E-04
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	6	1.28	3.26E-04
GOTERM_BP_FAT	GO:0000280~nuclear division	6	1.28	3.26E-04
GOTERM_BP_FAT	GO:0007067~mitosis	6	1.28	3.26E-04
GOTERM_BP_FAT	GO:0048285~organelle fission	6	1.28	3.26E-04
GOTERM_BP_FAT	GO:0007155~cell adhesion	14	2.98	6.10E-04

GOTERM_BP_FAT	GO:0022610~biological adhesion	14	2.98	6.10E-04
KEGG_PATHWAY	ssc00900:Terpenoid backbone biosynthesis	5	1.06	1.21E-03
GOTERM_BP_FAT	GO:0000279~M phase	6	1.28	1.25E-03
GOTERM_BP_FAT	GO:0022403~cell cycle phase	6	1.28	1.25E-03
GOTERM_BP_FAT	GO:0022402~cell cycle process	6	1.28	2.12E-03
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	11	2.34	2.35E-03
GOTERM_CC_FAT	GO:0031012~extracellular matrix	11	2.34	2.88E-03
KEGG_PATHWAY	ssc04510:Focal adhesion	15	3.19	3.19E-03
SP_PIR_KEYWORDS	cell cycle	8	1.70	3.91E-03
SP_PIR_KEYWORDS	acetylation	37	7.87	4.89E-03
GOTERM_CC_FAT	GO:0005694~chromosome	8	1.70	5.05E-03
SP_PIR_KEYWORDS	lipid synthesis	6	1.28	6.97E-03
GOTERM_BP_FAT	GO:0007049~cell cycle	8	1.70	8.62E-03
KEGG_PATHWAY	ssc00100:Steroid biosynthesis	4	0.85	8.76E-03
KEGG_PATHWAY	ssc03030:DNA replication	4	0.85	8.76E-03
SP_PIR_KEYWORDS	phosphoprotein	53	11.28	9.94E-03
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	6	1.28	0.0101
COG_ONTOLOGY	Lipid metabolism	5	1.06	0.0105
SP_PIR_KEYWORDS	cyclin	4	0.85	0.0133
KEGG_PATHWAY	ssc04115:p53 signaling pathway	8	1.70	0.0144
KEGG_PATHWAY	ssc00620:Pyruvate metabolism	6	1.28	0.0189
SP_PIR_KEYWORDS	Steroid biosynthesis	4	0.85	0.0217
SP_PIR_KEYWORDS	sterol biosynthesis	4	0.85	0.0217
SP_PIR_KEYWORDS	chromosomal protein	6	1.28	0.0219
GOTERM_BP_FAT	GO:0016126~sterol biosynthetic process	4	0.85	0.0223
KEGG_PATHWAY	ssc04114:Oocyte meiosis	9	1.91	0.0225
GOTERM_MF_FAT	GO:0008092~cytoskeletal protein binding	10	2.13	0.0230
SP_PIR_KEYWORDS	cell adhesion	8	1.70	0.0260
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	7	1.49	0.0261
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	8	1.70	0.0271
GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	9	1.91	0.0273
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	11	2.34	0.0281
KEGG_PATHWAY	ssc04512:ECM-receptor interaction	7	1.49	0.0302
GOTERM_CC_FAT	GO:0030016~myofibril	4	0.85	0.0326
GOTERM_CC_FAT	GO:0043292~contractile fiber	4	0.85	0.0326
GOTERM_BP_FAT	GO:0001525~angiogenesis	4	0.85	0.0333
GOTERM_BP_FAT	GO:0001568~blood vessel development	4	0.85	0.0333
GOTERM_BP_FAT	GO:0001944~vasculature development	4	0.85	0.0333
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	4	0.85	0.0333
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	5	1.06	0.0372
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	10	2.13	0.0423
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	8	1.70	0.0431
KEGG_PATHWAY	ssc00640:Propanoate metabolism	5	1.06	0.0432
INTERPRO	IPR006670:Cyclin	3	0.64	0.0457
INTERPRO	IPR006671:Cyclin, N-terminal	3	0.64	0.0457
SMART	SM00385:CYCLIN	3	0.64	0.0465
KEGG_PATHWAY	ssc00010:Glycolysis / Gluconeogenesis	6	1.28	0.0466
SP_PIR_KEYWORDS	gluconeogenesis	3	0.64	0.0468
GOTERM_CC_FAT	GO:0044449~contractile fiber part	3	0.64	0.0470
GOTERM_CC_FAT	GO:0042470~melanosome	6	1.28	0.0496
GOTERM_CC_FAT	GO:0048770~pigment granule	6	1.28	0.0496

Red Cluster

Category:	Term:	Gene Count:	% of Total Cluster:	PValue:
KEGG_PATHWAY	ssc04612:Antigen processing and presentation	11	5.64	4.31E-06
GOTERM_BP_FAT	GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	5	2.56	4.29E-05
GOTERM_BP_FAT	GO:0048002~antigen processing and presentation of peptide antigen	5	2.56	4.29E-05
SP_PIR_KEYWORDS	mhc i	5	2.56	5.45E-05
GOTERM_CC_FAT	GO:0042612~MHC class I protein complex	6	3.08	1.12E-04
KEGG_PATHWAY	ssc04514:Cell adhesion molecules (CAMs)	9	4.62	7.47E-04

INTERPRO	IPR010579:MHC class I, alpha chain, C-terminal	4	2.05	7.74E-04
INTERPRO	IPR001039:MHC class I, alpha chain, alpha1 and alpha2	5	2.56	1.33E-03
GOTERM_CC_FAT	GO:0042611~MHC protein complex	6	3.08	2.12E-03
INTERPRO	IPR003006:Immunoglobulin/major histocompatibility complex, conserved site	6	3.08	2.15E-03
KEGG_PATHWAY	ssc04512:ECM-receptor interaction	6	3.08	2.18E-03
INTERPRO	IPR011161:MHC class I-like antigen recognition	5	2.56	2.51E-03
INTERPRO	IPR003597:Immunoglobulin C1-set	6	3.08	3.91E-03
GOTERM_BP_FAT	GO:0019882~antigen processing and presentation	6	3.08	4.00E-03
INTERPRO	IPR007110:Immunoglobulin-like	9	4.62	6.02E-03
SP_PIR_KEYWORDS	immune response	6	3.08	6.15E-03
SMART	SM00407:IGc1	6	3.08	7.07E-03
GOTERM_CC_FAT	GO:0000502~proteasome complex	4	2.05	9.32E-03
SP_PIR_KEYWORDS	proteasome	4	2.05	0.0113
KEGG_PATHWAY	ssc05416:Viral myocarditis	6	3.08	0.0118
KEGG_PATHWAY	ssc05332:Graft-versus-host disease	5	2.56	0.0139
INTERPRO	IPR013783:Immunoglobulin-like fold	9	4.62	0.0143
SP_PIR_KEYWORDS	acetylation	20	10.26	0.0144
SP_PIR_KEYWORDS	cytoplasm	18	9.23	0.0189
KEGG_PATHWAY	ssc05330:Allograft rejection	5	2.56	0.0213
GOTERM_BP_FAT	GO:0006955~immune response	11	5.64	0.0234
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	4	2.05	0.0281
KEGG_PATHWAY	ssc04940:Type I diabetes mellitus	5	2.56	0.0283
KEGG_PATHWAY	ssc05414:Dilated cardiomyopathy	5	2.56	0.0336
KEGG_PATHWAY	ssc04510:Focal adhesion	7	3.59	0.0355
GOTERM_BP_FAT	GO:0030029~actin filament-based process	4	2.05	0.0385
KEGG_PATHWAY	ssc05320:Autoimmune thyroid disease	5	2.56	0.0395
KEGG_PATHWAY	ssc03050:Proteasome	4	2.05	0.0432
GOTERM_CC_FAT	GO:0005829~cytosol	5	2.56	0.0472

Orange Cluster

Category:	Term:	Gene Count:	% of Total Cluster:	PValue:
SP_PIR_KEYWORDS	transport	7	7.61	0.0339
SP_PIR_KEYWORDS	nad	3	3.26	0.0493