

Cluster A

System	Category	LH	LT	PH	PT	EASE Score	Fisher Exact
biological_process	regulation of muscle contraction	4	67	15	7524	0.000272	0.00000728
cellular_component	sarcomere	5	67	38	7778	0.000281	0.0000164
cellular_component	myofibril	5	67	39	7778	0.000311	0.0000187
cellular_component	muscle fiber	5	67	40	7778	0.000344	0.0000212
cellular_component	extracellular	33	67	2250	7778	0.000586	0.000336
biological_process	muscle contraction	5	67	45	7524	0.000614	0.0000446
cellular_component	extracellular space	31	67	2116	7778	0.00107	0.000615
biological_process	muscle development	5	67	72	7524	0.00355	0.000425
cellular_component	actin cytoskeleton	6	67	123	7778	0.00377	0.000628
cellular_component	striated muscle thin filament	3	67	13	7778	0.00521	0.000164
molecular_function	isomerase activity	5	67	90	8294	0.0056	0.000765
molecular_function	cytokine binding	4	67	52	8294	0.00806	0.000787
biological_process	cell motility	6	67	151	7524	0.0102	0.00215
biological_process	defense response	10	67	434	7524	0.0129	0.00472
molecular_function	intramolecular isomerase activity	3	67	23	8294	0.0142	0.000795
cellular_component	endoplasmic reticulum	8	67	310	7778	0.0155	0.0049
biological_process	response to biotic stimulus	10	67	475	7524	0.022	0.00879
biological_process	response to stimulus	14	67	828	7524	0.0258	0.0129
cellular_component	myosin	3	67	31	7778	0.0282	0.00231
molecular_function	binding	47	67	4797	8294	0.0318	0.0256
molecular_function	calcium ion binding	8	67	389	8294	0.0341	0.0126
biological_process	response to external stimulus	12	67	699	7524	0.0393	0.0192
biological_process	development	16	67	1099	7524	0.0504	0.0291

molecular_function	sugar binding	4	67	117	8294	0.066	0.0146
molecular_function	carbohydrate binding	4	67	120	8294	0.0701	0.0159
biological_process	humoral immune response	3	67	51	7524	0.0734	0.0104
biological_process	immune response	7	67	345	7524	0.0809	0.0329
biological_process	response to pest/pathogen/parasite	5	67	187	7524	0.0812	0.0251
biological_process	response to chemical substance	4	67	116	7524	0.0813	0.0195
biological_process	response to stress	7	67	383	7524	0.118	0.0529
biological_process	protein folding	3	67	70	7524	0.125	0.0242
cellular_component	cytoskeleton	7	67	405	7778	0.128	0.0585
cellular_component	lytic vacuole	3	67	74	7778	0.13	0.0256
cellular_component	lysosome	3	67	74	7778	0.13	0.0256
molecular_function	metal ion binding	10	67	741	8294	0.131	0.0725
biological_process	chemotaxis	3	67	74	7524	0.137	0.0279
biological_process	taxis	3	67	74	7524	0.137	0.0279
biological_process	morphogenesis	10	67	680	7524	0.138	0.077
cellular_component	vacuole	3	67	81	7778	0.15	0.0324
molecular_function	transmembrane receptor activity	8	67	559	8294	0.155	0.0798
biological_process	heterophilic cell adhesion	3	67	83	7524	0.165	0.0374
biological_process	organogenesis	9	67	616	7524	0.169	0.0943
biological_process	inflammatory response	3	67	92	7524	0.193	0.0484
biological_process	innate immune response	3	67	95	7524	0.203	0.0523

Cluster B

System	Category	LH	LT	PH	PT	EASE Score	Fisher Exact
cellular_component	extracellular	44	69	2250	7778	3.89E-09	1.74E-09
cellular_component	extracellular space	39	69	2116	7778	0.000000528	0.000000249
cellular_component	extracellular matrix	10	69	226	7778	0.00014	0.0000266
biological_process	muscle development	6	67	72	7524	0.000396	0.0000391
molecular_function	copper ion binding	4	68	30	8294	0.00175	0.0000965
molecular_function	metal ion binding	15	68	741	8294	0.00203	0.000791
molecular_function	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor	3	68	12	8294	0.00403	0.00011
molecular_function	heparin binding	4	68	42	8294	0.00462	0.000366
molecular_function	oxidoreductase activity, acting on the CH-NH2 group of donors	3	68	14	8294	0.00549	0.00018
molecular_function	extracellular matrix structural constituent	4	68	53	8294	0.00885	0.000895
molecular_function	glycosaminoglycan binding	4	68	55	8294	0.0098	0.00103
cellular_component	actin cytoskeleton	5	69	123	7778	0.0223	0.00457
molecular_function	extracellular matrix structural constituent conferring tensile strength	3	68	29	8294	0.0227	0.00165
biological_process	cell adhesion	9	67	404	7524	0.0242	0.00911
biological_process	complement activation	3	67	29	7524	0.0264	0.00209
cellular_component	myosin	3	69	31	7778	0.0298	0.00251
cellular_component	collagen	3	69	31	7778	0.0298	0.00251
biological_process	immune response	8	67	345	7524	0.0307	0.0111
biological_process	catabolism	11	67	595	7524	0.0333	0.0151
molecular_function	calcium ion binding	8	68	389	8294	0.0366	0.0137
molecular_function	oxidoreductase activity	9	68	475	8294	0.0366	0.0149
biological_process	humoral defense mechanism (sensu Vertebrata)	3	67	37	7524	0.0415	0.00422
biological_process	organismal physiological process	12	67	707	7524	0.0422	0.0208
cellular_component	sarcomere	3	69	38	7778	0.0433	0.00451
cellular_component	myofibril	3	69	39	7778	0.0453	0.00486

cellular_component	muscle fiber	3	69	40	7778	0.0475	0.00522
biological_process	integrin-mediated signaling pathway	3	67	42	7524	0.0521	0.00605
molecular_function	transition metal ion binding	6	68	264	8294	0.0616	0.0207
molecular_function	metallopeptidase activity	4	68	113	8294	0.063	0.0136
molecular_function	hematopoietin/interferon-class (D200-domain) cytokine receptor activity	3	68	51	8294	0.0636	0.00829
biological_process	cell growth	3	67	48	7524	0.0661	0.00877
molecular_function	peptidase activity	8	68	447	8294	0.0679	0.029
biological_process	humoral immune response	3	67	51	7524	0.0734	0.0104
biological_process	response to pest/pathogen/parasite	5	67	187	7524	0.0812	0.0251
biological_process	response to chemical substance	4	67	116	7524	0.0813	0.0195
biological_process	defense response	8	67	434	7524	0.0845	0.0379
molecular_function	hydrolase activity, acting on glycosyl bonds	3	68	64	8294	0.0942	0.0154
molecular_function	metalloendopeptidase activity	3	68	74	8294	0.12	0.0226
biological_process	response to biotic stimulus	8	67	475	7524	0.121	0.0589
cellular_component	lytic vacuole	3	69	74	7778	0.136	0.0277
cellular_component	lysosome	3	69	74	7778	0.136	0.0277
biological_process	taxis	3	67	74	7524	0.137	0.0279
biological_process	chemotaxis	3	67	74	7524	0.137	0.0279
molecular_function	endopeptidase activity	5	68	246	8294	0.137	0.0507
molecular_function	structural molecule activity	7	68	435	8294	0.138	0.0644
cellular_component	cytoskeleton	7	69	405	7778	0.142	0.0665
biological_process	embryonic development	3	67	76	7524	0.143	0.0299
cellular_component	vacuole	3	69	81	7778	0.158	0.0349

Cluster C

System	Category	LH	LT	PH	PT	EASE Score	Fisher Exact
cellular_component	extracellular	79	112	2250	7778	1.14E-19	4.58E-20
cellular_component	extracellular matrix	26	112	226	7778	4.83E-16	5.45E-17
cellular_component	extracellular space	70	112	2116	7778	9.14E-15	4.05E-15
molecular_function	extracellular matrix structural constituent	14	102	53	8294	3.3E-14	1.14E-15
cellular_component	collagen	12	112	31	7778	2.01E-13	4.8E-15
biological_process	cell adhesion	29	104	404	7524	3.46E-13	6.24E-14
molecular_function	extracellular matrix structural constituent conferring tensile strength	11	102	29	8294	7.53E-13	1.59E-14
molecular_function	structural molecule activity	19	102	435	8294	0.00000417	0.00000112
cellular_component	basement membrane	6	112	36	7778	0.000143	0.0000107
molecular_function	calcium ion binding	15	102	389	8294	0.000243	0.0000739
molecular_function	peptidyl-prolyl cis-trans isomerase activity	5	102	26	8294	0.000252	0.0000137
molecular_function	cis-trans isomerase activity	5	102	27	8294	0.000293	0.0000166
cellular_component	fibrillar collagen	3	112	3	7778	0.0006	0.00000291
cellular_component	collagen type V	3	112	3	7778	0.0006	0.00000291
molecular_function	isomerase activity	7	102	90	8294	0.000766	0.000112
cellular_component	endoplasmic reticulum	13	112	310	7778	0.00149	0.000483
molecular_function	serine-type endopeptidase inhibitor activity	6	102	72	8294	0.00178	0.000242
molecular_function	metal ion binding	19	102	741	8294	0.00333	0.00153
molecular_function	enzyme inhibitor activity	7	102	139	8294	0.00686	0.00157
molecular_function	endopeptidase inhibitor activity	6	102	103	8294	0.00828	0.00163
molecular_function	protease inhibitor activity	6	102	104	8294	0.00862	0.00171
biological_process	cell communication	36	104	1767	7524	0.00978	0.0064
biological_process	protein folding	5	104	70	7524	0.0152	0.00272
biological_process	cell growth	4	104	48	7524	0.0276	0.0042
biological_process	response to biotic stimulus	13	104	475	7524	0.0283	0.0134

molecular_function	glycosaminoglycan binding	4	102	55	8294	0.0291	0.00455
biological_process	regulation of biological process	8	104	223	7524	0.0329	0.0118
biological_process	defense response	12	104	434	7524	0.0345	0.0162
biological_process	cellular process	65	104	3973	7524	0.0345	0.0284
biological_process	regulation of cellular process	7	104	180	7524	0.0366	0.0121
biological_process	immune response	10	104	345	7524	0.0461	0.0205
molecular_function	heparin binding	3	102	42	8294	0.0924	0.0147
biological_process	response to external stimulus	15	104	699	7524	0.0941	0.0564
biological_process	regulation of cell growth	3	104	39	7524	0.0992	0.0164
biological_process	blood coagulation	3	104	40	7524	0.104	0.0175
biological_process	coagulation	3	104	40	7524	0.104	0.0175
biological_process	heterophilic cell adhesion	4	104	83	7524	0.105	0.0275
biological_process	hemostasis	3	104	42	7524	0.112	0.0199
biological_process	response to pest/pathogen/parasite	6	104	187	7524	0.113	0.0445
molecular_function	lipid binding	4	102	98	8294	0.117	0.0323
molecular_function	nucleotide receptor activity, G-protein coupled	3	102	49	8294	0.12	0.0221
molecular_function	nucleotide receptor activity	3	102	49	8294	0.12	0.0221
molecular_function	purinergic nucleotide receptor activity	3	102	49	8294	0.12	0.0221
molecular_function	purinergic nucleotide receptor activity, G-protein coupled	3	102	49	8294	0.12	0.0221
biological_process	regulation of body fluids	3	104	44	7524	0.121	0.0226

Cluster D

System	Category	LH	LT	PH	PT	EASE Score	Fisher Exact
cellular_component	intermediate filament cytoskeleton	4	41	57	7778	0.00304	0.000215
cellular_component	intermediate filament	4	41	57	7778	0.00304	0.000215
cellular_component	intercellular junction	4	41	72	7778	0.00588	0.000528
molecular_function	structural molecule activity	8	45	435	8294	0.00739	0.00208
cellular_component	apicolateral plasma membrane	4	41	86	7778	0.0096	0.00103
cellular_component	cell junction	4	41	92	7778	0.0115	0.00133
cellular_component	cytoskeleton	7	41	405	7778	0.0164	0.00476
biological_process	cell communication	16	39	1767	7524	0.0201	0.0111
biological_process	neuropeptide signaling pathway	3	39	56	7524	0.0322	0.00295
biological_process	cellular process	27	39	3973	7524	0.0371	0.0275
biological_process	organelle organization and biogenesis	5	39	267	7524	0.0445	0.0116
molecular_function	receptor signaling protein activity	3	45	77	8294	0.0627	0.00825
biological_process	G-protein coupled receptor protein signaling pathway	6	39	430	7524	0.0633	0.0221
molecular_function	structural constituent of cytoskeleton	3	45	79	8294	0.0655	0.00886
biological_process	cytoplasm organization and biogenesis	5	39	333	7524	0.0855	0.0276
biological_process	intracellular signaling cascade	6	39	491	7524	0.0987	0.039
biological_process	cytoskeleton organization and biogenesis	4	39	224	7524	0.103	0.0279
biological_process	signal transduction	11	39	1327	7524	0.119	0.0693
biological_process	cell surface receptor linked signal transduction	7	39	739	7524	0.164	0.0825
biological_process	cell-cell signaling	3	39	145	7524	0.166	0.0387

Cluster E

System	Category	LH	LT	PH	PT	EASE Score	Fisher Exact
biological_process	organogenesis	12	51	616	7524	0.00197	0.000661
biological_process	development	16	51	1099	7524	0.00398	0.00179
biological_process	morphogenesis	12	51	680	7524	0.00428	0.00158
molecular_function	transcription factor activity	11	56	641	8294	0.00863	0.00324
molecular_function	transcription regulator activity	12	56	779	8294	0.012	0.00502
cellular_component	membrane	29	50	3161	7778	0.0141	0.00963
biological_process	transcription	14	51	1147	7524	0.0333	0.0176
molecular_function	calcium ion binding	7	56	389	8294	0.0428	0.0151
biological_process	regulation of transcription, DNA-dependent	13	51	1085	7524	0.0483	0.0258
cellular_component	transcription factor complex	6	50	319	7778	0.0492	0.0158
biological_process	regulation of transcription	13	51	1103	7524	0.0537	0.0292
biological_process	transcription, DNA-dependent	13	51	1105	7524	0.0544	0.0296
biological_process	skeletal development	3	51	63	7524	0.0654	0.00876
cellular_component	intercellular junction	3	50	72	7778	0.0752	0.0109
cellular_component	nucleoplasm	6	50	375	7778	0.0856	0.032
cellular_component	integral to membrane	22	50	2566	7778	0.0949	0.0677
cellular_component	cell	45	50	6360	7778	0.0956	0.0857
cellular_component	apicolateral plasma membrane	3	50	86	7778	0.102	0.0176
molecular_function	DNA binding	13	56	1225	8294	0.103	0.061
cellular_component	cell junction	3	50	92	7778	0.114	0.021
molecular_function	metal ion binding	9	56	741	8294	0.114	0.0586
biological_process	neurogenesis	4	51	199	7524	0.145	0.0452
biological_process	lipid biosynthesis	3	51	110	7524	0.166	0.0381

Cluster F

System	Category	LH	LT	PH	PT	EASE Score	Fisher Exact
biological_process	immune response	17	48	345	7524	1.11E-10	1.37E-11
biological_process	defense response	18	48	434	7524	3.5E-10	5.18E-11
biological_process	response to biotic stimulus	18	48	475	7524	1.42E-09	2.3E-10
biological_process	response to external stimulus	19	48	699	7524	7.38E-08	1.68E-08
biological_process	organismal physiological process	18	48	707	7524	0.000000528	0.000000129
biological_process	response to stimulus	19	48	828	7524	0.000000961	0.00000026
biological_process	response to wounding	5	48	125	7524	0.00746	0.00113
biological_process	regulation of biological process	6	48	223	7524	0.0122	0.00275
biological_process	regulation of cell proliferation	4	48	81	7524	0.0139	0.00169
molecular_function	cytokine activity	5	50	170	8294	0.0176	0.00343
biological_process	inflammatory response	4	48	92	7524	0.0195	0.0027
biological_process	innate immune response	4	48	95	7524	0.0212	0.00303
biological_process	regulation of cellular process	5	48	180	7524	0.0254	0.00552
biological_process	response to pest/pathogen/parasite	5	48	187	7524	0.0287	0.00648
biological_process	cell proliferation	8	48	556	7524	0.0554	0.023
biological_process	taxis	3	48	74	7524	0.0777	0.0115
biological_process	chemotaxis	3	48	74	7524	0.0777	0.0115
cellular_component	nucleus	16	44	1941	7778	0.0943	0.0611
molecular_function	electron transporter activity	3	50	89	8294	0.0969	0.0163
biological_process	cell differentiation	4	48	189	7524	0.114	0.0318
biological_process	response to chemical substance	3	48	116	7524	0.163	0.0374
biological_process	regulation of cell cycle	4	48	228	7524	0.17	0.0566

Cluster G

System	Category	LH	LT	PH	PT	EASE Score	Fisher Exact
molecular_function	oxidoreductase activity	3	7	475	8294	0.0421	0.00549

Cluster H

System	Category	LH	LT	PH	PT	EASE Score	Fisher Exact
biological_process	transport	6	14	1253	7524	0.0508	0.0189
biological_process	cell growth and/or maintenance	8	14	2290	7524	0.0668	0.0341
biological_process	physiological process	14	14	6119	7524	0.0679	0.0552
biological_process	intracellular protein transport	3	14	293	7524	0.0889	0.0155
biological_process	protein metabolism	6	14	1471	7524	0.0914	0.0395
biological_process	protein modification	4	14	652	7524	0.0963	0.0277
biological_process	protein transport	3	14	311	7524	0.0984	0.0181
biological_process	cellular physiological process	8	14	2613	7524	0.125	0.072
molecular_function	transferase activity	5	18	965	8294	0.127	0.0497
biological_process	intracellular transport	3	14	369	7524	0.131	0.0285
molecular_function	catalytic activity	10	18	3123	8294	0.147	0.0941
molecular_function	receptor binding	3	18	367	8294	0.172	0.0428
biological_process	phosphorus metabolism	3	14	479	7524	0.199	0.0552
biological_process	phosphate metabolism	3	14	479	7524	0.199	0.0552

Legend

LH - Number of genes in data set (cluster) belonging to this category

LT - Total number of genes in data set (cluster) with ontology annotation

PH - Number of genes belonging to this category in the entire annotated genome

PT - Total number of genes in the mouse genome with annotation.

EASE Score/Fisher Exact - the statistical probability that the overrepresentation of a specific GO term will arise