

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0021527	spinal cord association neuron different...	2	2	0.04	0.00039	0.0198
GO:0071280	cellular response to copper ion	3	2	0.06	0.00116	0.0198
GO:0046854	phosphatidylinositol phosphorylation	25	4	0.50	0.00137	0.0198
GO:0061512	protein localization to cilium	25	4	0.50	0.00137	0.0198
GO:0030258	lipid modification	140	9	2.77	0.00187	0.0198
GO:0021516	dorsal spinal cord development	4	2	0.08	0.00228	0.0198
GO:0060830	ciliary receptor clustering involved in ...	4	2	0.08	0.00228	0.0198
GO:0060971	embryonic heart tube left/right pattern ...	4	2	0.08	0.00228	0.0198
GO:0046834	lipid phosphorylation	29	4	0.57	0.00242	0.0198
GO:0015936	coenzyme A metabolic process	16	3	0.32	0.00355	0.0198
GO:0021522	spinal cord motor neuron differentiation	16	3	0.32	0.00355	0.0198
GO:0019087	transformation of host cell by virus	5	2	0.10	0.00376	0.0198
GO:0032484	Ral protein signal transduction	5	2	0.10	0.00376	0.0198
GO:0048842	positive regulation of axon extension in...	5	2	0.10	0.00376	0.0198
GO:1902669	positive regulation of axon guidance	5	2	0.10	0.00376	0.0198
GO:0046486	glycerolipid metabolic process	218	11	4.32	0.00413	0.0198
GO:0007033	vacuole organization	130	8	2.58	0.00431	0.0198
GO:0051188	cofactor biosynthetic process	104	7	2.06	0.00457	0.0198
GO:0042073	intraciliary transport	35	4	0.69	0.00486	0.0198
GO:0044088	regulation of vacuole organization	35	4	0.69	0.00486	0.0198
GO:0098840	protein transport along microtubule	35	4	0.69	0.00486	0.0198
GO:0021514	ventral spinal cord interneuron differen...	6	2	0.12	0.00556	0.0198
GO:0021515	cell differentiation in spinal cord	19	3	0.38	0.00588	0.0198
GO:0021517	ventral spinal cord development	19	3	0.38	0.00588	0.0198
GO:0009410	response to xenobiotic stimulus	37	4	0.73	0.00594	0.0198
GO:0033865	nucleoside bisphosphate metabolic proces...	20	3	0.40	0.00682	0.0198
GO:0033875	ribonucleoside bisphosphate metabolic pr...	20	3	0.40	0.00682	0.0198
GO:0034032	purine nucleoside bisphosphate metabolic...	20	3	0.40	0.00682	0.0198
GO:0051186	cofactor metabolic process	269	12	5.33	0.00738	0.0198
GO:0044255	cellular lipid metabolic process	633	22	12.54	0.00738	0.0198
GO:0006729	tetrahydrobiopterin biosynthetic process	7	2	0.14	0.00769	0.0198
GO:0014049	positive regulation of glutamate secreti...	7	2	0.14	0.00769	0.0198
GO:0046146	tetrahydrobiopterin metabolic process	7	2	0.14	0.00769	0.0198
GO:0070050	neuron cellular homeostasis	7	2	0.14	0.00769	0.0198
GO:0072488	ammonium transmembrane transport	7	2	0.14	0.00769	0.0198
GO:0097094	craniofacial suture morphogenesis	7	2	0.14	0.00769	0.0198
GO:0032892	positive regulation of organic acid tran...	21	3	0.42	0.00784	0.0198
GO:0021510	spinal cord development	40	4	0.79	0.00785	0.0198
GO:1903793	positive regulation of anion transport	40	4	0.79	0.00785	0.0198
GO:0031503	protein complex localization	91	6	1.80	0.00933	0.0198