GO:0021527 spinal cord association neuron different 2 2 0.04 0.00038 0.0198	GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
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: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:0060971 embryonic heart tube left/right pattern 4 2 0.08 0.00228 0.0198 GO:0016834 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:0015936 coenzyme A metabolic process 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: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:0048842 positive regulation of axon extension in 5 2 0.10 0.00376 0.0198 GO:0046486 glycerolipid metabolic process 218 11 4.32 0.00413 0.0198 GO:005188 cofactor biosynthetic process 104 7 2.06 0.00457 0.0198 GO:0044088 regulation of vacuole organization 35 4 0.69 0.00486 0.0198 GO:0044088 regulation of vacuole organization 35 4 0.69 0.00486 0.0198 GO:0021515 cell differentiation in spinal cord 19 3 0.38 0.00588 0.0198 GO:0021515 ventral spinal cord interneuron differen 6 2 0.12 0.00556 0.0198 GO:0021515 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GO:0021517 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GO:0021517 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GO:00033865 nucleoside bisphosphate metabolic process 7 2 0.14 0.00769 0.0198 GO:00014255 cellular lipid metabolic process 633 22 12.54 0.00738 0.0198 GO:00072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:00072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:000	GO:0021527	spinal cord association neuron different	2	2	0.04	0.00039	0.0198
GO:0061512 protein localization to cillium 25	GO:0071280	cellular response to copper ion	3	2	0.06	0.00116	0.0198
GC:0030258 lipid modification 140 9 2.77 0.00187 0.0198 GC:0021516 dorsal spinal cord development 4 2 0.08 0.00228 0.0198 GC:0060830 ciliary receptor clustering involved in 4 2 0.08 0.00228 0.0198 GC:0060831 embryonic heart tube left/right pattern 4 2 0.08 0.00228 0.0198 GC:0066834 lipid phosphorylation 29 4 0.57 0.00242 0.0198 GC:0015936 coenzyme A metabolic process 16 3 0.32 0.00355 0.0198 GC:0015936 coenzyme A metabolic process 16 3 0.32 0.00355 0.0198 GC:0015936 coenzyme A metabolic process 16 3 0.32 0.00355 0.0198 GC:0015936 coenzyme A metabolic process 16 3 0.32 0.00355 0.0198 GC:0015936 coenzyme A metabolic process 16 3 0.32 0.00355 0.0198 GC:0019087 transformation of host cell by virus 5 2 0.10 0.00376 0.0198 GC:0019087 transformation of host cell by virus 5 2 0.10 0.00376 0.0198 GC:00048842 positive regulation of axon extension in 5 2 0.10 0.00376 0.0198 GC:00048842 positive regulation of axon extension in 5 2 0.10 0.00376 0.0198 GC:00046486 glycerolipid metabolic process 218 11 4.32 0.00413 0.0198 GC:00046486 glycerolipid metabolic process 218 11 4.32 0.00413 0.0198 GC:0007033 vacuole organization 130 8 2.58 0.00431 0.0198 GC:00046488 colactor biosynthetic process 104 7 2.06 0.00457 0.0198 GC:00404088 regulation of axouloe organization 35 4 0.69 0.00486 0.0198 GC:00404088 regulation of vacuole organization 35 4 0.69 0.00486 0.0198 GC:0021514 ventral spinal cord interneuron differen 6 2 0.12 0.00556 0.0198 GC:0021517 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GC:0021517 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GC:0033865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0033865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisp	GO:0046854	phosphatidylinositol phosphorylation	25	4	0.50	0.00137	0.0198
GO:0021516 dorsal spinal cord development 4 2 0.08 0.00228 0.0198	GO:0061512	protein localization to cilium	25	4	0.50	0.00137	0.0198
GC:0060830 Ciliary receptor clustering involved in 4 2 0.08 0.00228 0.0198	GO:0030258	lipid modification	140	9	2.77	0.00187	0.0198
GO:0060971 embryonic heart tube left/right pattern	GO:0021516	dorsal spinal cord development	4	2	0.08	0.00228	0.0198
GC:0046834 lipid phosphorylation 29 4 0.57 0.00242 0.0198 GC:0015936 coenzyme A metabolic process 16 3 0.32 0.00355 0.0198 GC:0021522 spinal cord motor neuron differentiation 16 3 0.32 0.00355 0.0198 GC:0019087 transformation of host cell by virus 5 2 0.10 0.00376 0.0198 GC:0032484 Ral protein signal transduction 5 2 0.10 0.00376 0.0198 GC:0032484 Ral protein signal transduction 5 2 0.10 0.00376 0.0198 GC:0034842 positive regulation of axon extension in 5 2 0.10 0.00376 0.0198 GC:0046886 glycerolipid metabolic process 218 11 4.32 0.00413 0.0198 GC:0007033 vacuole organization 130 8 2.58 0.00431 0.0198 GC:0007033 vacuole organization 130 8 2.58 0.00431 0.0198 GC:000273 intraciliary transport 35 4 0.69 0.00457 0.0198 GC:00044088 regulation of vacuole organization 35 4 0.69 0.00486 0.0198 GC:00044088 regulation of vacuole organization 35 4 0.69 0.00486 0.0198 GC:0021514 ventral spinal cord interneuron differen 6 2 0.12 0.00556 0.0198 GC:0021517 ventral spinal cord development 19 3 0.33 0.00588 0.0198 GC:0033865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:00046466 tetrahydrobiopterin biosynthetic process 7 2 0.14 0.00769 0.0198 GC:00046466 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GC:00070050 neuron cellular homeostasis 7 2 0.14 0.00769 0.0198 GC:00072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GC:00032892 positive regulation of organic acid tran 21 3 0.42 0.00784 0.0198 GC:00032892 positive regulation of organic acid tran 21 3 0.42 0.00785	GO:0060830	ciliary receptor clustering involved in	4	2	0.08	0.00228	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:0032484 positive regulation of axon extension in 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:004686 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:0033865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GO:0033875 ribonucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GO:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GO:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GO:0044255 cellular lipid metabolic process 633 22 12.54 0.00738 0.0198 GO:0044255 cellular lipid metabolic process 7 2 0.14 0.00769 0.0198 GO:004446 tetrahydrobiopterin biosynthetic process 7 2 0.14 0.00769 0.0198 GO:004446 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GO:004448 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:00032892 positive regulation of organic acid tran 21 3 0.42 0.00785 0.0198	GO:0060971	embryonic heart tube left/right pattern	4	2	0.08	0.00228	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:0042073 intraciliary transport 35 4 0.69 0.00457 0.0198 GO:0044088 regulation of vacuole organization 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:0033865 nucleoside bisphosphate metabolic process 20 3 0.40 0.00682 0.0198 GO:0034038 purine nucleoside bisphosphate metabolic process 269 12 5.33 0.00738 0.0198 GO:0034055 cellular lipid metabolic process 633 22 12.54 0.00738 0.0198 GO:0034056 cellular lipid metabolic process 7 2 0.14 0.00769 0.0198 GO:004266 tetrahydrobiopterin biosynthetic process 7 2 0.14 0.00769 0.0198 GO:004268 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:007248 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:007248 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0032892 positive regulation of organic acid tran 21 3 0.42 0.00785 0.0198	GO:0046834	lipid phosphorylation	29	4	0.57	0.00242	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 glycerollpid 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:0044088 regulation of vacuole organization 35 4 0.69 0.00486 0.0198 GO:0044088 regulation of vacuole organization 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:0021515 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GO:0021517 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GO:003865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GO:0034032 purine nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GO:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GO:0044255 cellular lipid metabolic process 269 12 5.33 0.00738 0.0198 GO:0044255 cellular lipid metabolic process 7 2 0.14 0.00769 0.0198 GO:0044046 tetrahydrobiopterin biosynthetic process 7 2 0.14 0.00769 0.0198 GO:0044046 tetrahydrobiopterin biosynthetic process 7 2 0.14 0.00769 0.0198 GO:0046146 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GO:0046146 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GO:007048 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:007048 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:007048 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:007048 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:007048 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:007048 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:007048 positive regulation of glutare transpo	GO:0015936	coenzyme A metabolic process	16	3	0.32	0.00355	0.0198
GC: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:0040703 vacuole organization 130 8 2.58 0.00431 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:0044088 regulation of vacuole organization 35 4 0.69 0.00486 0.0198 GO:0021514 ventral spinal cord interneuron differen 6 2 0.12 0.00556 0.0198 GO:0021517 ventral spinal cord development 19 3 0.38 0.00588	GO:0021522	spinal cord motor neuron differentiation	16	3	0.32	0.00355	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:0021517 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GO:0033865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GO:0033875 ribonucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GO:0034032 purine nucleoside bisphosphate 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:0044255 cellular lipid metabolic process 7 2 0.14 0.00769 0.0198 GO:004146 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:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.	GO:0019087	transformation of host cell by virus	5	2	0.10	0.00376	0.0198
GC:1902669 positive regulation of axon guidance 5 2 0.10 0.00376 0.0198 GC:0046486 glycerolipid metabolic process 218 11 4.32 0.00413 0.0198 GC:0007033 vacuole organization 130 8 2.58 0.00431 0.0198 GC:0051188 cofactor biosynthetic process 104 7 2.06 0.00457 0.0198 GC:0042073 intraciliary transport 35 4 0.69 0.00486 0.0198 GC:0044088 regulation of vacuole organization 35 4 0.69 0.00486 0.0198 GC:0098840 protein transport along microtubule 35 4 0.69 0.00486 0.0198 GC:0021514 ventral spinal cord interneuron differen 6 2 0.12 0.00556 0.0198 GC:0021515 cell differentiation in spinal cord 19 3 0.38 0.00588 0.0198 GC:0021517 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GC:0033865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0033875 ribonucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GC:0034032 purine nucleoside bisphosphate metabolic 20 3 0.40 0.00682 0.0198 GC:0044255 cellular lipid metabolic process 633 22 12.54 0.00738 0.0198 GC:0046146 tetrahydrobiopterin biosynthetic process 7 2 0.14 0.00769 0.0198 GC:0046146 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GC:0046146 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GC:0070488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GC:0070488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GC:0070488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GC:0070488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GC:00032892 positive regulation of organic acid tran 21 3 0.42 0.00784 0.0198	GO:0032484	Ral protein signal transduction	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:0033865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GO:0033865 nucleoside bisphosphate metabolic pr 20 3 0.40 0.00682 0.0198 GO:0034032 purine nucleoside bisphosphate metabolic pr 20 3 0.40 0.00682 0.0198 GO:0034032 purine nucleoside bisphosphate metabolic pr 20 3 0.40 0.00682 0.0198 GO:0051186 cofactor metabolic process 269 12 5.33 0.00738 0.0198 GO:0051186 cofactor metabolic process 633 22 12.54 0.00738 0.0198 GO:0044255 cellular lipid metabolic process 7 2 0.14 0.00769 0.0198 GO:0044256 tetrahydrobiopterin biosynthetic process 7 2 0.14 0.00769 0.0198 GO:0044264 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GO:0046146 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 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:0032892 positive regulation of organic acid tran 21 3 0.42 0.00785 0.0198	GO:0048842	positive regulation of axon extension in	5	2	0.10	0.00376	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:0034032 purine nucleoside bisphosphate metabolic pr 20 3 0.40 0.00682 0.0198 GO:0051186 cofactor metabolic process 269 12 5.33 0.00738 0.0198 GO:0004255 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: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:0032892 positive regulation of organic acid tran 21 3 0.42 0.00784 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:1902669	positive regulation of axon guidance	5	2	0.10	0.00376	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:0021517 ventral spinal cord development 19 3 0.38 0.00588 0.0198 GO:0003865 nucleoside bisphosphate metabolic proces 20 3 0.40 0.00682 0.0198 GO:0033865 nucleoside bisphosphate metabolic proces 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:00702488 ammonium transmembrane transport 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:0007094 craniofacial suture morphogenesis 7 2 0.14 0.00769 0.0198 GO:0007094 craniofacial suture morphogenesis 7 2 0.14 0.00769 0.0198 GO:0007094 craniofacial suture morphogenesis 7 2 0.14 0.00769 0.0198 GO:00072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0007094 craniofacial suture morphogenesis 7 2 0.14 0.00769 0.0198 GO:00072480 positive regulation of organic acid tran 21 3 0.42 0.00784 0.0198 GO:00072510 spinal cord development 40 4 0.79 0.00785 0.0198	GO:0046486	glycerolipid metabolic process	218	11	4.32	0.00413	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: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:0007033	vacuole organization	130	8	2.58	0.00431	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: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: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:004255 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:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 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:0032892 positive regulation of organic acid tran 21 3 0.42 0.00784 0.0198	GO:0051188	cofactor biosynthetic process	104	7	2.06	0.00457	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:0070488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 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:0042073	intraciliary transport	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:00702488 ammonium transmembrane transport 7 2 0.14 0.00769 0.0198 GO:0072488 ammonium transmembrane transport 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:0032892 positive regulation of organic acid tran 21 3 0.42 0.00785 0.0198 GO:0021510 spinal cord development 40 4 0.79 0.00785 0.0198	GO:0044088	regulation of vacuole organization	35	4	0.69	0.00486	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: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:0098840	protein transport along microtubule	35	4	0.69	0.00486	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:0046729 tetrahydrobiopterin biosynthetic process 7 2 0.14 0.00769 0.0198 GO:0046146 tetrahydrobiopterin metabolic process 7 2 0.14 0.00769 0.0198 GO:0070488 ammonium transmembrane transport 7 2 0.1	GO:0021514	ventral spinal cord interneuron differen	6	2	0.12	0.00556	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:0021515	cell differentiation in spinal cord	19	3	0.38	0.00588	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:0021517	ventral spinal cord development	19	3	0.38	0.00588	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:0009410	response to xenobiotic stimulus	37	4	0.73	0.00594	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 <td>GO:0033865 I</td> <td>nucleoside bisphosphate metabolic proces</td> <td>20</td> <td>3</td> <td>0.40</td> <td>0.00682</td> <td>0.0198</td>	GO:0033865 I	nucleoside bisphosphate metabolic proces	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 0.0078	GO:0033875	ribonucleoside bisphosphate metabolic pr	20	3	0.40	0.00682	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:0034032	purine nucleoside bisphosphate metabolic	20	3	0.40	0.00682	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:0051186	cofactor metabolic process	269	12	5.33	0.00738	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:0044255	cellular lipid metabolic process	633	22	12.54	0.00738	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:0006729	tetrahydrobiopterin biosynthetic 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:0014049	positive regulation of glutamate secreti	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:0046146	tetrahydrobiopterin metabolic process	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:0070050	neuron cellular homeostasis	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:0072488	ammonium transmembrane transport	7	2	0.14	0.00769	0.0198
GO:0021510 spinal cord development 40 4 0.79 0.00785 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:1903793 positive regulation of anion transport 40 4 0.70 0.00795 0.0109	GO:0021510	spinal cord development	40	4	0.79	0.00785	0.0198
40 4 0.18 0.00163 0.0186	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	GO:0031503	protein complex localization	91	6	1.80	0.00933	0.0198