

GeDiPNet Cluster 400 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-07 22:17:20

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
neuronal action potential propagation	GO:0019227	2	ATP1A2, SCN1A	11	5	679.53	3.147e-6	2.113e-4
neuromuscular process controlling posture	GO:0050884	2	PRRT2, SCN1A	15	5	498.32	6.006e-6	3.547e-4
olfactory cortex development	GO:0021989	1	ATP1A2	1	5	3737.40	2.676e-4	6.316e-3
negative regulation of short-term synaptic potentiation	GO:1905513	1	PRRT2	1	5	3737.40	2.676e-4	6.316e-3
monoatomic ion transport	GO:0006811	3	ATP1A2, CACNA1A, SCN1A	667	5	16.81	4.290e-4	8.779e-3
sodium ion transmembrane transport	GO:0035725	2	ATP1A2, SCN1A	134	5	55.78	5.032e-4	9.800e-3
regulation of glutamate uptake involved in transmission of nerve impulse	GO:0051946	1	ATP1A2	2	5	1868.70	5.351e-4	1.019e-2
regulation of calcium-dependent activation of synaptic vesicle fusion	GO:0150037	1	PRRT2	2	5	1868.70	5.351e-4	1.019e-2
negative regulation of SNARE complex assembly	GO:0035544	1	PRRT2	2	5	1868.70	5.351e-4	1.019e-2
sodium ion transport	GO:0006814	2	ATP1A2, SCN1A	144	5	51.91	5.808e-4	1.082e-2
negative regulation of striated muscle contraction	GO:0045988	1	ATP1A2	3	5	1245.80	8.025e-4	1.336e-2
negative regulation of calcium ion transmembrane transport	GO:1903170	1	ATP1A2	3	5	1245.80	8.025e-4	1.336e-2
amygdala development	GO:0021764	1	ATP1A2	4	5	934.35	1.070e-3	1.602e-2
nucleophagy	GO:0044804	1	WDR45	5	5	747.48	1.337e-3	1.833e-2
negative regulation of heart contraction	GO:0045822	1	ATP1A2	6	5	622.90	1.605e-3	2.035e-2