

GeDiPNet Cluster 503 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:18:21

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
action potential	GO:0001508	2	KCNA1, KCNQ2	53	4	176.29	4.718e-5	1.771e-3
negative regulation of short-term synaptic potentiation	GO:1905513	1	PRRT2	1	4	4671.75	2.141e-4	5.314e-3
potassium ion transmembrane transport	GO:0071805	2	KCNA1, KCNQ2	150	4	62.29	3.800e-4	7.887e-3
potassium ion transport	GO:0006813	2	KCNA1, KCNQ2	152	4	61.47	3.902e-4	8.042e-3
regulation of calcium-dependent activation of synaptic vesicle fusion	GO:0150037	1	PRRT2	2	4	2335.88	4.281e-4	8.531e-3
negative regulation of SNARE complex assembly	GO:0035544	1	PRRT2	2	4	2335.88	4.281e-4	8.531e-3
detection of mechanical stimulus involved in sensory perception of touch	GO:0050976	1	KCNA1	4	4	1167.94	8.560e-4	1.331e-2
cellular response to magnesium ion	GO:0071286	1	KCNA1	7	4	667.39	1.498e-3	1.821e-2
neuronal signal transduction	GO:0023041	1	KCNA1	7	4	667.39	1.498e-3	1.821e-2
cell communication by electrical coupling	GO:0010644	1	KCNA1	7	4	667.39	1.498e-3	1.821e-2
magnesium ion homeostasis	GO:0010960	1	KCNA1	8	4	583.97	1.711e-3	1.958e-2
membrane repolarization during action potential	GO:0086011	1	KCNA1	10	4	467.18	2.139e-3	2.189e-2
synaptic vesicle fusion to presynaptic active zone membrane	GO:0031629	1	PRRT2	10	4	467.18	2.139e-3	2.189e-2
monoatomic ion transmembrane transport	GO:0034220	2	KCNA1, KCNQ2	404	4	23.13	2.718e-3	2.484e-2
detection of mechanical stimulus involved in sensory perception of pain	GO:0050966	1	KCNA1	14	4	333.70	2.994e-3	2.594e-2