

GeDiPNet Cluster 631 -- 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 23:18:52

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
monoatomic ion transport	GO:0006811	5	CACNA1A, CACNB4, KCNA1, SCN2A, SLC1A3	667	9	15.56	6.383e-6	3.849e-4
monoatomic ion transmembrane transport	GO:0034220	4	CACNA1A, CACNB4, KCNA1, SCN2A	404	9	20.56	2.489e-5	1.087e-3
neuronal action potential	GO:0019228	2	KCNA1, SCN2A	34	9	122.14	1.148e-4	3.416e-3
chemical synaptic transmission	GO:0007268	3	CACNA1A, CACNB4, SLC1A3	236	9	26.39	1.579e-4	4.300e-3
action potential	GO:0001508	2	KCNA1, SCN2A	53	9	78.35	2.805e-4	6.465e-3
regulation of membrane potential	GO:0042391	2	CACNB4, KCNA1	85	9	48.85	7.210e-4	1.210e-2
intrinsic apoptotic signaling pathway in response to osmotic stress	GO:0008627	1	SCN2A	2	9	1038.17	9.630e-4	1.423e-2
negative regulation of HRI-mediated signaling	GO:0141191	1	UBR4	2	9	1038.17	9.630e-4	1.423e-2
cytoplasm protein quality control	GO:0140455	1	UBR4	3	9	692.11	1.444e-3	1.794e-2
cytoplasm protein quality control by the ubiquitin-proteasome system	GO:0071629	1	UBR4	3	9	692.11	1.444e-3	1.794e-2
gamma-aminobutyric acid secretion	GO:0014051	1	CACNB4	4	9	519.08	1.925e-3	2.069e-2
cranial nerve development	GO:0021545	1	SLC1A3	4	9	519.08	1.925e-3	2.069e-2
cAMP metabolic process	GO:0046058	1	CACNB4	4	9	519.08	1.925e-3	2.069e-2
detection of mechanical stimulus involved in sensory perception of touch	GO:0050976	1	KCNA1	4	9	519.08	1.925e-3	2.069e-2
transmembrane transport	GO:0055085	3	CACNA1A, KCNA1, SCN2A	557	9	11.18	1.935e-3	2.076e-2