

GeDiPNet Cluster 487 -- 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 23:18:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
locomotory behavior	GO:0007626	3	GNAO1, NKX2-1, CHRN2	99	11	51.48	2.308e-5	1.029e-3
cardiac muscle cell action potential involved in contraction	GO:0086002	2	SCN8A, SCN1A	24	11	141.57	8.633e-5	2.773e-3
endoderm development	GO:0007492	2	NKX2-1, NCKAP1	34	11	99.93	1.749e-4	4.614e-3
action potential	GO:0001508	2	SCN8A, SCN1A	53	11	64.11	4.270e-4	8.531e-3
lateral geniculate nucleus development	GO:0021771	1	CHRN2	1	11	1698.82	5.886e-4	1.058e-2
regulation of circadian sleep/wake cycle, REM sleep	GO:0042320	1	CHRN2	1	11	1698.82	5.886e-4	1.058e-2
developmental induction	GO:0031128	1	NKX2-1	1	11	1698.82	5.886e-4	1.058e-2
histidyl-tRNA aminoacylation	GO:0006427	1	HARS1	2	11	849.41	1.177e-3	1.592e-2
response to Thyroglobulin triiodothyronine	GO:1904016	1	SLC2A1	2	11	849.41	1.177e-3	1.592e-2
basal protein localization	GO:0045175	1	NCKAP1	2	11	849.41	1.177e-3	1.592e-2
zygotic determination of anterior/posterior axis, embryo	GO:0007354	1	NCKAP1	2	11	849.41	1.177e-3	1.592e-2
forebrain neuron fate commitment	GO:0021877	1	NKX2-1	2	11	849.41	1.177e-3	1.592e-2
monoatomic ion transmembrane transport	GO:0034220	3	SCN8A, CHRN2, SCN1A	404	11	12.61	1.454e-3	1.800e-2
regulation of synaptic transmission, dopaminergic	GO:0032225	1	CHRN2	3	11	566.27	1.765e-3	1.990e-2
paraxial mesoderm morphogenesis	GO:0048340	1	NCKAP1	3	11	566.27	1.765e-3	1.990e-2