

GeDiPNet Cluster 446 -- 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 23:18:44

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
involuntary skeletal muscle contraction	GO:0003011	1	ATP8A2	1	8	2335.88	4.281e-4	8.531e-3
cerebral cortex development	GO:0021987	2	TUBB2B, NDE1	88	8	53.09	6.027e-4	1.079e-2
positive regulation of axon guidance	GO:1902669	1	TUBB2B	2	8	1167.94	8.560e-4	1.331e-2
positive regulation of neuron projection development	GO:0010976	2	ATP8A2, KATNB1	121	8	38.61	1.135e-3	1.561e-2
chromosome localization	GO:0050000	1	NDE1	3	8	778.63	1.284e-3	1.669e-2
glycoprotein transport	GO:0034436	1	VLDLR	3	8	778.63	1.284e-3	1.669e-2
neuron migration	GO:0001764	2	TUBB2B, NDE1	132	8	35.39	1.348e-3	1.721e-2
mitotic chromosome movement towards spindle pole	GO:0007079	1	KATNB1	4	8	583.97	1.711e-3	1.958e-2
positive regulation of phospholipid translocation	GO:0061092	1	ATP8A2	4	8	583.97	1.711e-3	1.958e-2
nervous system development	GO:0007399	3	VLDLR, TUBB2B, NDE1	631	8	11.11	1.890e-3	2.066e-2
very-low-density lipoprotein particle clearance	GO:0034447	1	VLDLR	5	8	467.18	2.139e-3	2.189e-2
positive regulation of microtubule depolymerization	GO:0031117	1	KATNB1	5	8	467.18	2.139e-3	2.189e-2
somite specification	GO:0001757	1	RIPPLY1	5	8	467.18	2.139e-3	2.189e-2
mitotic centrosome separation	GO:0007100	1	NDE1	6	8	389.31	2.566e-3	2.402e-2
lipid transport	GO:0006869	2	VLDLR, ATP8A2	189	8	24.72	2.737e-3	2.488e-2