

GeDiPNet Cluster 439 -- 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: 2026-10-20 00:01:20

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of cell-matrix adhesion	GO:0001954	2	DISC1, SKAP1	27	21	65.92	4.151e-4	8.406e-3
regulation of postsynapse organization	GO:0099175	2	DISC1, EPHA7	34	21	52.34	6.603e-4	1.137e-2
positive regulation of BMP signaling pathway	GO:0030513	2	ELAPOR2, TBX20	40	21	44.49	9.143e-4	1.390e-2
positive regulation of ion transmembrane transporter activity	GO:0032414	1	TRPC6	1	21	889.86	1.124e-3	1.550e-2
diadenosine triphosphate catabolic process	GO:0015964	1	FHIT	1	21	889.86	1.124e-3	1.550e-2
positive regulation of serotonin secretion	GO:0014064	1	SLC6A4	1	21	889.86	1.124e-3	1.550e-2
regulation of thalamus size	GO:0090067	1	SLC6A4	1	21	889.86	1.124e-3	1.550e-2
tricuspid valve development	GO:0003175	1	TBX20	1	21	889.86	1.124e-3	1.550e-2
embryonic heart tube elongation	GO:0036306	1	TBX20	1	21	889.86	1.124e-3	1.550e-2
lateral mesoderm formation	GO:0048370	1	TBX20	1	21	889.86	1.124e-3	1.550e-2
epinephrine secretion	GO:0048242	1	VIP	1	21	889.86	1.124e-3	1.550e-2
negative regulation of nervous system development	GO:0051961	1	ELAPOR2	1	21	889.86	1.124e-3	1.550e-2
regulation of protein autophosphorylation	GO:0031952	1	EPHA7	2	21	444.93	2.246e-3	2.244e-2
pulmonary vein morphogenesis	GO:0060577	1	TBX20	2	21	444.93	2.246e-3	2.244e-2
negative regulation of cerebellar granule cell precursor proliferation	GO:0021941	1	SLC6A4	2	21	444.93	2.246e-3	2.244e-2