

GeDiPNet Cluster 359 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 01:43:45

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
magnesium ion transmembrane transport	GO:1903830	3	CLDN16, CNNM2, TRPM6	17	6	549.62	1.249e-8	2.075e-6
monoatomic ion transport	GO:0006811	5	CLDN16, CNNM2, FXYD2, TRPM6, TRPV6	667	6	23.35	3.325e-7	3.321e-5
metal ion transport	GO:0030001	2	CLDN16, TRPM6	30	6	207.63	3.722e-5	1.439e-3
intercellular transport	GO:0010496	1	CLDN16	1	6	3114.50	3.211e-4	7.027e-3
transmembrane transport	GO:0055085	3	FXYD2, TRPM6, TRPV6	557	6	16.77	4.925e-4	9.457e-3
parathyroid hormone secretion	GO:0035898	1	TRPV6	2	6	1557.25	6.421e-4	1.127e-2
calcium ion transmembrane transport	GO:0070588	2	TRPM6, TRPV6	149	6	41.81	9.276e-4	1.441e-2
calcium ion transport	GO:0006816	2	TRPM6, TRPV6	157	6	39.68	1.029e-3	1.535e-2
negative regulation of secretion	GO:0051048	1	EGF	4	6	778.63	1.284e-3	1.747e-2
positive regulation of hyaluronan biosynthetic process	GO:1900127	1	EGF	4	6	778.63	1.284e-3	1.747e-2
cellular hyperosmotic salinity response	GO:0071475	1	FXYD2	5	6	622.90	1.605e-3	1.983e-2
positive regulation of epithelial tube formation	GO:1905278	1	EGF	5	6	622.90	1.605e-3	1.983e-2
positive regulation of cerebellar granule cell precursor proliferation	GO:0021940	1	EGF	5	6	622.90	1.605e-3	1.983e-2
paracellular transport	GO:0160184	1	CLDN16	7	6	444.93	2.246e-3	2.412e-2
magnesium ion homeostasis	GO:0010960	1	CNNM2	8	6	389.31	2.566e-3	2.584e-2