

GeDiPNet Cluster 275 -- 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 21:39:35

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
vesicle localization	GO:0051648	1	MYO1A	2	10	934.35	1.070e-3	1.569e-2
intracellular pH elevation	GO:0051454	1	SLC26A3	3	10	622.90	1.605e-3	1.983e-2
epithelial cell morphogenesis involved in placental branching	GO:0060672	1	SPINT2	3	10	622.90	1.605e-3	1.983e-2
positive regulation of cellular extravasation	GO:0002693	1	PLVAP	5	10	373.74	2.673e-3	2.653e-2
long-chain fatty-acyl-CoA metabolic process	GO:0035336	1	DGAT1	7	10	266.96	3.741e-3	3.178e-2
microvillus assembly	GO:0030033	1	MYO1A	8	10	233.59	4.274e-3	3.381e-2
membrane hyperpolarization	GO:0060081	1	SLC26A3	8	10	233.59	4.274e-3	3.381e-2
monoacylglycerol biosynthetic process	GO:0006640	1	DGAT1	9	10	207.63	4.807e-3	3.579e-2
negative regulation of cell-cell adhesion mediated by cadherin	GO:2000048	1	EPCAM	11	10	169.88	5.872e-3	3.982e-2
receptor guanylyl cyclase signaling pathway	GO:0007168	1	GUCY2C	11	10	169.88	5.872e-3	3.982e-2
oxalate transport	GO:0019532	1	SLC26A3	11	10	169.88	5.872e-3	3.982e-2
very-low-density lipoprotein particle assembly	GO:0034379	1	DGAT1	12	10	155.73	6.405e-3	4.146e-2
negative regulation of neural precursor cell proliferation	GO:2000178	1	SPINT2	12	10	155.73	6.405e-3	4.146e-2
cGMP biosynthetic process	GO:0006182	1	GUCY2C	13	10	143.75	6.937e-3	4.329e-2
negative regulation of cell motility	GO:2000146	1	SPINT2	14	10	133.48	7.468e-3	4.462e-2