

GeDiPNet Cluster 613 -- 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 00:00:30

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 cellular extravasation	GO:0002693	1	PLVAP	5	6	622.90	1.605e-3	1.885e-2
long-chain fatty-acyl-CoA metabolic process	GO:0035336	1	DGAT1	7	6	444.93	2.246e-3	2.244e-2
enteroendocrine cell differentiation	GO:0035883	1	PERCC1	7	6	444.93	2.246e-3	2.244e-2
monoacylglycerol biosynthetic process	GO:0006640	1	DGAT1	9	6	346.06	2.887e-3	2.555e-2
negative regulation of cell-cell adhesion mediated by cadherin	GO:2000048	1	EPCAM	11	6	283.14	3.527e-3	2.816e-2
receptor guanylyl cyclase signaling pathway	GO:0007168	1	GUCY2C	11	6	283.14	3.527e-3	2.816e-2
very-low-density lipoprotein particle assembly	GO:0034379	1	DGAT1	12	6	259.54	3.847e-3	2.937e-2
cGMP biosynthetic process	GO:0006182	1	GUCY2C	13	6	239.58	4.167e-3	3.062e-2
diacylglycerol metabolic process	GO:0046339	1	DGAT1	14	6	222.46	4.487e-3	3.173e-2
glycerolipid metabolic process	GO:0046486	1	DGAT1	15	6	207.63	4.807e-3	3.273e-2
regulation of vascular permeability	GO:0043114	1	PLVAP	16	6	194.66	5.127e-3	3.369e-2
fatty acid homeostasis	GO:0055089	1	DGAT1	18	6	173.03	5.766e-3	3.561e-2
cyclic nucleotide biosynthetic process	GO:0009190	1	GUCY2C	18	6	173.03	5.766e-3	3.561e-2
digestive tract morphogenesis	GO:0048546	1	PERCC1	19	6	163.92	6.086e-3	3.654e-2
nucleosome disassembly	GO:0006337	1	GRWD1	21	6	148.31	6.725e-3	3.838e-2