

GeDiPNet Cluster 480 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 9 · Generated: 2026-10-19 23:21:20

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cholesterol biosynthesis	Reactome	4	FDPS, MVD, MVK, PMVK	21	8	285.95	4.813e-10	4.823e-8
Terpenoid backbone biosynthesis	KEGG	4	FDPS, MVD, MVK, PMVK	23	8	261.09	7.118e-10	6.822e-8
Activation of gene expression by SREBF (SREBP)	Reactome	4	FDPS, MVD, MVK, PMVK	42	8	142.98	8.952e-9	6.686e-7
Transport of connexons to the plasma membrane	Reactome	1	GJB2	1	8	1501.25	6.661e-4	8.310e-3
Peroxisome	KEGG	2	MVK, PMVK	83	8	36.17	1.286e-3	1.374e-2
Synthesis of Dolichyl-phosphate	Reactome	1	MVD	6	8	250.21	3.991e-3	3.122e-2
Metabolic pathways	KEGG	4	FDPS, MVD, MVK, PMVK	1563	8	3.84	1.295e-2	6.631e-2
Influenza A	KEGG	1	FDPS	173	8	8.68	1.096e-1	2.282e-1
Human T-cell leukemia virus 1 infection	KEGG	1	FDPS	224	8	6.70	1.399e-1	2.642e-1