

GeDiPNet Cluster 304 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 04:04:33

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Peroxisomal protein import	Reactome	4	PEX7, AGPS, GNPAT, PEX5	63	18	42.36	1.991e-6	8.843e-5
Peroxisome	KEGG	4	PEX7, AGPS, GNPAT, PEX5	83	18	32.16	6.028e-6	2.249e-4
Plasmalogen biosynthesis	Reactome	2	AGPS, GNPAT	3	18	444.81	6.359e-6	2.351e-4
Aggrephagy	Reactome	2	HDAC6, DYNC1H1	40	18	33.36	1.600e-3	1.983e-2
Cholesterol biosynthesis via desmosterol	Reactome	1	EBP	4	18	166.81	5.982e-3	5.030e-2
Cholesterol biosynthesis via lathosterol	Reactome	1	EBP	4	18	166.81	5.982e-3	5.030e-2
TGF-beta signaling pathway	KEGG	2	GDF5, BMPR1B	108	18	12.36	1.116e-2	7.504e-2
Sulfur metabolism	KEGG	1	BPNT2	10	18	66.72	1.489e-2	8.912e-2
Pexophagy	Reactome	1	PEX5	10	18	66.72	1.489e-2	8.912e-2
HSF1 activation	Reactome	1	HDAC6	12	18	55.60	1.785e-2	9.951e-2
Transcriptional regulation by RUNX2	Reactome	1	HDAC6	12	18	55.60	1.785e-2	9.951e-2
The activation of arylsulfatases	Reactome	1	ARSL	13	18	51.32	1.932e-2	1.040e-1
Hippo signaling pathway	KEGG	2	GDF5, BMPR1B	157	18	8.50	2.265e-2	1.138e-1
Cytosolic sulfonation of small molecules	Reactome	1	BPNT2	18	18	37.07	2.666e-2	1.247e-1
Class B/2 (Secretin family receptors)	Reactome	1	PTH1R	18	18	37.07	2.666e-2	1.247e-1