

GeDiPNet Cluster 614 -- 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: 2026-10-20 00:02:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Transport to the Golgi and subsequent modification	Reactome	2	LMAN1, MCFD2	2	4	3002.50	8.320e-8	4.748e-6
Cargo concentration in the ER	Reactome	2	LMAN1, MCFD2	33	4	181.97	4.378e-5	9.844e-4
COPII-mediated vesicle transport	Reactome	2	LMAN1, MCFD2	68	4	88.31	1.881e-4	3.129e-3
Synthesis of PIPs at the ER membrane	Reactome	1	PI4KA	5	4	600.50	1.664e-3	1.665e-2
Synthesis of PIPs at the Golgi membrane	Reactome	1	PI4KA	18	4	166.81	5.982e-3	4.097e-2
Inositol phosphate metabolism	KEGG	1	PI4KA	73	4	41.13	2.410e-2	9.548e-2
Phosphatidylinositol signaling system	KEGG	1	PI4KA	98	4	30.64	3.225e-2	1.128e-1
Protein processing in endoplasmic reticulum	KEGG	1	LMAN1	171	4	17.56	5.575e-2	1.542e-1
Metabolic pathways	KEGG	1	PI4KA	1563	4	1.92	4.275e-1	5.524e-1