

GeDiPNet Cluster 214 -- 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: 4 · Generated: 2026-10-08 10:39:08

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
O-linked glycosylation	Reactome	1	B3GALNT2	10	5	240.20	4.157e-3	3.931e-2
Mannose type O-glycan biosynthesis	KEGG	1	B3GALNT2	23	5	104.43	9.540e-3	6.798e-2
Generic Transcription Pathway	Reactome	1	ZNF750	346	5	6.94	1.360e-1	2.954e-1
Metabolic pathways	KEGG	1	B3GALNT2	1563	5	1.54	5.020e-1	6.452e-1