

GeDiPNet Cluster 343 -- 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: 9 · Generated: 2026-10-07 23:59:04

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	KEGG	9	PGAP2, PGAP3, PIGL, PIGO, PIGV, PIGW, PIGY, PIGB, PIGG	30	13	277.15	7.117e-22	6.808e-19
Synthesis of glycosylphosphatidylinositol (GPI)	Reactome	6	PIGL, PIGV, PIGW, PIGY, PIGB, PIGG	17	13	326.06	5.074e-15	1.555e-12
Metabolic pathways	KEGG	9	PGAP2, PGAP3, PIGL, PIGO, PIGV, PIGW, PIGY, PIGB, PIGG	1563	13	5.32	4.576e-6	1.801e-4
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	Reactome	1	CCNK	32	13	28.87	3.411e-2	1.421e-1
RNA Polymerase II Transcription Elongation	Reactome	1	CCNK	59	13	15.66	6.204e-2	1.952e-1
Formation of RNA Pol II elongation complex	Reactome	1	CCNK	61	13	15.15	6.408e-2	1.985e-1
TP53 Regulates Transcription of DNA Repair Genes	Reactome	1	CCNK	65	13	14.21	6.815e-2	2.051e-1
RNA polymerase II transcribes snRNA genes	Reactome	1	CCNK	74	13	12.48	7.724e-2	2.190e-1
RNA Polymerase II Pre-transcription Events	Reactome	1	CCNK	84	13	11.00	8.725e-2	2.333e-1