

GeDiPNet Cluster 332 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 14:41:45

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective PMM2 causes PMM2-CDG (CDG-1a)	Reactome	1	PMM2	1	9	1334.44	7.494e-4	1.092e-2
Synthesis of GDP-mannose	Reactome	1	PMM2	3	9	444.81	2.247e-3	2.484e-2
SUMOylation of DNA methylation proteins	Reactome	1	DNMT1	4	9	333.61	2.995e-3	3.068e-2
Type I hemidesmosome assembly	Reactome	1	DST	11	9	121.31	8.216e-3	6.072e-2
Purine salvage	Reactome	1	DGUOK	13	9	102.65	9.703e-3	6.739e-2
KSRP (KHSRP) binds and destabilizes mRNA	Reactome	1	EXOSC9	15	9	88.96	1.119e-2	7.338e-2
mRNA decay by 3' to 5' exoribonuclease	Reactome	1	EXOSC9	16	9	83.40	1.193e-2	7.605e-2
Butyrate Response Factor 1 (BRF1) binds and destabilizes mRNA	Reactome	1	EXOSC9	17	9	78.50	1.267e-2	7.872e-2
Tristetraprolin (TTP, ZFP36) binds and destabilizes mRNA	Reactome	1	EXOSC9	17	9	78.50	1.267e-2	7.872e-2
ATF4 activates genes in response to endoplasmic reticulum stress	Reactome	1	EXOSC9	18	9	74.14	1.341e-2	8.136e-2
Fructose and mannose metabolism	KEGG	1	PMM2	34	9	39.25	2.520e-2	1.169e-1
Biosynthesis of nucleotide sugars	KEGG	1	PMM2	37	9	36.07	2.740e-2	1.228e-1
Amino sugar and nucleotide sugar metabolism	KEGG	1	PMM2	38	9	35.12	2.813e-2	1.244e-1
Phase 0 - rapid depolarisation	Reactome	1	SCN11A	44	9	30.33	3.250e-2	1.348e-1
Assembly of collagen fibrils and other multimeric structures	Reactome	1	DST	51	9	26.17	3.759e-2	1.464e-1