

GeDiPNet Cluster 324 -- 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: 5 · Generated: 2026-10-07 13:02:26

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
SUMOylation of DNA methylation proteins	Reactome	1	DNMT3B	4	6	500.42	1.997e-3	2.278e-2
Cysteine and methionine metabolism	KEGG	1	DNMT3B	52	6	38.49	2.570e-2	1.182e-1
PRC2 methylates histones and DNA	Reactome	1	DNMT3B	73	6	27.42	3.593e-2	1.431e-1
MicroRNAs in cancer	KEGG	1	DNMT3B	311	6	6.44	1.457e-1	3.045e-1
Metabolic pathways	KEGG	1	DNMT3B	1563	6	1.28	5.669e-1	6.993e-1