

GeDiPNet Cluster 352 -- 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 08:04:38

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Nucleotide excision repair	KEGG	8	ERCC1, ERCC2, ERCC5, ERCC6, BIVM-ERCC5, ERCC4, ERCC8, UVSSA	63	10	152.51	1.614e-17	8.448e-15
Dual incision in TC-NER	Reactome	7	ERCC1, ERCC2, ERCC5, ERCC6, ERCC4, ERCC8, UVSSA	66	10	127.38	1.292e-14	3.932e-12
Dual Incision in GG-NER	Reactome	4	ERCC1, ERCC2, ERCC5, ERCC4	41	10	117.17	2.418e-8	1.908e-6
Formation of Incision Complex in GG-NER	Reactome	4	ERCC1, ERCC2, ERCC5, ERCC4	43	10	111.72	2.945e-8	2.262e-6
Transcription-Coupled Nucleotide Excision Repair (TC-NER)	Reactome	4	ERCC2, ERCC6, ERCC8, UVSSA	45	10	106.76	3.552e-8	2.646e-6
Formation of TC-NER Pre-Incision Complex	Reactome	4	ERCC2, ERCC6, ERCC8, UVSSA	54	10	88.96	7.513e-8	5.084e-6
Gap-filling DNA repair synthesis and ligation in TC-NER	Reactome	4	ERCC2, ERCC6, ERCC8, UVSSA	65	10	73.91	1.601e-7	9.842e-6
HDR through Single Strand Annealing (SSA)	Reactome	2	ERCC1, ERCC4	37	10	64.92	4.092e-4	6.826e-3
Fanconi Anemia Pathway	Reactome	2	ERCC1, ERCC4	40	10	60.05	4.786e-4	7.706e-3
RNA Polymerase I Transcription Initiation	Reactome	2	ERCC2, ERCC6	45	10	53.38	6.061e-4	9.263e-3
Fanconi anemia pathway	KEGG	2	ERCC1, ERCC4	54	10	44.48	8.726e-4	1.222e-2
RNA Pol II CTD phosphorylation and interaction with CE	Reactome	1	ERCC2	27	10	44.48	2.226e-2	1.093e-1
mRNA Capping	Reactome	1	ERCC2	29	10	41.41	2.389e-2	1.137e-1
RNA Polymerase I Transcription Termination	Reactome	1	ERCC2	32	10	37.53	2.634e-2	1.199e-1
Formation of the Early Elongation Complex	Reactome	1	ERCC2	33	10	36.39	2.715e-2	1.220e-1