

GeDiPNet Cluster 612 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:15

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Dual Incision in GG-NER	Reactome	2	ERCC4, POLE	41	2	292.93	1.137e-5	3.238e-4
Nucleotide excision repair	KEGG	2	ERCC4, POLE	63	2	190.63	2.708e-5	6.686e-4
Dual incision in TC-NER	Reactome	2	ERCC4, POLE	66	2	181.97	2.974e-5	7.192e-4
DNA replication initiation	Reactome	1	POLE	8	2	750.63	1.332e-3	1.409e-2
PCNA-Dependent Long Patch Base Excision Repair	Reactome	1	POLE	21	2	285.95	3.494e-3	2.829e-2
Gap-filling DNA repair synthesis and ligation in GG-NER	Reactome	1	POLE	25	2	240.20	4.159e-3	3.210e-2
Recognition of DNA damage by PCNA-containing replication complex	Reactome	1	POLE	30	2	200.17	4.990e-3	3.635e-2
Termination of translesion DNA synthesis	Reactome	1	POLE	32	2	187.66	5.322e-3	3.802e-2
Activation of the pre-replicative complex	Reactome	1	POLE	33	2	181.97	5.488e-3	3.872e-2
DNA replication	KEGG	1	POLE	36	2	166.81	5.986e-3	4.098e-2
HDR through Single Strand Annealing (SSA)	Reactome	1	ERCC4	37	2	162.30	6.152e-3	4.182e-2
Fanconi Anemia Pathway	Reactome	1	ERCC4	40	2	150.13	6.650e-3	4.392e-2
Formation of Incision Complex in GG-NER	Reactome	1	ERCC4	43	2	139.65	7.148e-3	4.607e-2
Base excision repair	KEGG	1	POLE	44	2	136.48	7.314e-3	4.669e-2
HDR through Homologous Recombination (HRR)	Reactome	1	POLE	48	2	125.10	7.978e-3	4.942e-2