

GeDiPNet Cluster 356 -- 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 15:30:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
PCNA-Dependent Long Patch Base Excision Repair	Reactome	3	POLD1, POLE, POLD2	21	7	245.10	1.605e-7	9.862e-6
Gap-filling DNA repair synthesis and ligation in GG-NER	Reactome	3	POLD1, POLE, POLD2	25	7	205.89	2.774e-7	1.595e-5
Recognition of DNA damage by PCNA-containing replication complex	Reactome	3	POLD1, POLE, POLD2	30	7	171.57	4.890e-7	2.631e-5
Termination of translesion DNA synthesis	Reactome	3	POLD1, POLE, POLD2	32	7	160.85	5.971e-7	3.118e-5
DNA replication	KEGG	3	POLD1, POLE, POLD2	36	7	142.98	8.586e-7	4.277e-5
Dual Incision in GG-NER	Reactome	3	POLD1, POLE, POLD2	41	7	125.54	1.280e-6	6.056e-5
Base excision repair	KEGG	3	POLD1, POLE, POLD2	44	7	116.98	1.590e-6	7.251e-5
HDR through Homologous Recombination (HRR)	Reactome	3	POLD1, POLE, POLD2	48	7	107.23	2.074e-6	9.067e-5
Telomere C-strand (Lagging Strand) Synthesis	Reactome	2	POLD1, POLD2	5	7	686.29	2.910e-6	1.210e-4
Nucleotide excision repair	KEGG	3	POLD1, POLE, POLD2	63	7	81.70	4.743e-6	1.821e-4
Gap-filling DNA repair synthesis and ligation in TC-NER	Reactome	3	POLD1, POLE, POLD2	65	7	79.19	5.215e-6	1.964e-4
Dual incision in TC-NER	Reactome	3	POLD1, POLE, POLD2	66	7	77.99	5.462e-6	2.039e-4
Processive synthesis on the C-strand of the telomere	Reactome	2	POLD1, POLD2	8	7	428.93	8.140e-6	2.819e-4
Mismatch repair (MMR) directed by MSH2:MSH3 (MutSbeta)	Reactome	2	POLD1, POLD2	10	7	343.14	1.308e-5	4.193e-4
Processive synthesis on the lagging strand	Reactome	2	POLD1, POLD2	10	7	343.14	1.308e-5	4.193e-4