

GeDiPNet Cluster 475 -- 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](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 00:02:45

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Telomere Extension By Telomerase	Reactome	4	RTEL1, TERT, WRAP53, DKC1	16	7	428.93	7.334e-11	8.963e-9
Telomere C-strand synthesis initiation	Reactome	1	POLA2	7	7	245.10	4.074e-3	3.169e-2
DNA replication initiation	Reactome	1	POLA2	8	7	214.46	4.655e-3	3.479e-2
Processive synthesis on the lagging strand	Reactome	1	POLA2	10	7	171.57	5.815e-3	4.033e-2
Inhibition of replication initiation of damaged DNA by RB1/E2F1	Reactome	1	POLA2	10	7	171.57	5.815e-3	4.033e-2
rRNA modification in the nucleus and cytosol	Reactome	1	DKC1	12	7	142.98	6.975e-3	4.528e-2
Polymerase switching	Reactome	1	POLA2	14	7	122.55	8.133e-3	5.006e-2
Removal of the Flap Intermediate	Reactome	1	POLA2	14	7	122.55	8.133e-3	5.006e-2
KSRP (KHSRP) binds and destabilizes mRNA	Reactome	1	PARN	15	7	114.38	8.712e-3	5.219e-2
Polymerase switching on the C-strand of the telomere	Reactome	1	POLA2	17	7	100.92	9.869e-3	5.651e-2
ATF4 activates genes in response to endoplasmic reticulum stress	Reactome	1	PARN	18	7	95.32	1.045e-2	5.837e-2
Deadenylation of mRNA	Reactome	1	PARN	24	7	71.49	1.391e-2	6.943e-2
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	Reactome	1	RTEL1	26	7	65.99	1.506e-2	7.270e-2
Cargo concentration in the ER	Reactome	1	CD59	33	7	51.99	1.908e-2	8.331e-2
Activation of the pre-replicative complex	Reactome	1	POLA2	33	7	51.99	1.908e-2	8.331e-2