

GeDiPNet Cluster 376 -- 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 12:59:46

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Zinc efflux and compartmentalization by the SLC30 family	Reactome	1	SLC30A8	4	11	272.95	3.659e-3	3.541e-2
Telomere C-strand (Lagging Strand) Synthesis	Reactome	1	POLD3	5	11	218.36	4.572e-3	4.128e-2
Thyroid hormone signaling pathway	KEGG	2	MED30, PIK3R1	122	11	17.90	5.302e-3	4.551e-2
MET activates PI3K/AKT signaling	Reactome	1	PIK3R1	6	11	181.97	5.484e-3	4.649e-2
IRS-mediated signalling	Reactome	1	PIK3R1	6	11	181.97	5.484e-3	4.649e-2
Processive synthesis on the C-strand of the telomere	Reactome	1	POLD3	8	11	136.48	7.306e-3	5.623e-2
PI3K/AKT activation	Reactome	1	PIK3R1	9	11	121.31	8.216e-3	6.072e-2
Mismatch repair (MMR) directed by MSH2:MSH3 (MutSbeta)	Reactome	1	POLD3	10	11	109.18	9.125e-3	6.495e-2
Processive synthesis on the lagging strand	Reactome	1	POLD3	10	11	109.18	9.125e-3	6.495e-2
PI3K events in ERBB4 signaling	Reactome	1	PIK3R1	10	11	109.18	9.125e-3	6.495e-2
Signaling by FGFR3 fusions in cancer	Reactome	1	PIK3R1	10	11	109.18	9.125e-3	6.495e-2
JAK-STAT signaling pathway	KEGG	2	IL11, PIK3R1	168	11	13.00	9.847e-3	6.803e-2
Removal of the Flap Intermediate from the C-strand	Reactome	1	POLD3	11	11	99.26	1.003e-2	6.856e-2
Signaling by FGFR4 in disease	Reactome	1	PIK3R1	11	11	99.26	1.003e-2	6.856e-2
Costimulation by the CD28 family	Reactome	1	PIK3R1	11	11	99.26	1.003e-2	6.856e-2