

GeDiPNet Cluster 621 -- 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: 7 · Generated: 2026-10-19 23:22:11

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
TP53 Regulates Transcription of DNA Repair Genes	Reactome	2	CDK13, CCNK	65	4	92.38	1.719e-4	2.917e-3
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	Reactome	1	CCNK	32	4	93.83	1.062e-2	5.902e-2
RNA Polymerase II Transcription Elongation	Reactome	1	CCNK	59	4	50.89	1.951e-2	8.457e-2
Formation of RNA Pol II elongation complex	Reactome	1	CCNK	61	4	49.22	2.016e-2	8.608e-2
RNA polymerase II transcribes snRNA genes	Reactome	1	CCNK	74	4	40.57	2.442e-2	9.625e-2
RNA Polymerase II Pre-transcription Events	Reactome	1	CCNK	84	4	35.74	2.769e-2	1.032e-1
Neutrophil degranulation	Reactome	1	CDK13	480	4	6.26	1.506e-1	2.763e-1