

GeDiPNet Cluster 280 -- 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 11:32:03

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
FOXO-mediated transcription of cell cycle genes	Reactome	1	FOXG1	11	8	136.48	7.306e-3	5.623e-2
Virion - Lassa virus and SFTS virus	KEGG	1	MYH10	17	8	88.31	1.127e-2	7.364e-2
RHO GTPases activate PAKs	Reactome	1	MYH10	23	8	65.27	1.522e-2	8.776e-2
Deactivation of the beta-catenin transactivating complex	Reactome	1	CHD8	42	8	35.74	2.764e-2	1.234e-1
Collagen chain trimerization	Reactome	1	COL25A1	44	8	34.12	2.894e-2	1.264e-1
COPI-independent Golgi-to-ER retrograde traffic	Reactome	1	RAB3GAP1	51	8	29.44	3.348e-2	1.372e-1
Collagen degradation	Reactome	1	COL25A1	52	8	28.87	3.413e-2	1.388e-1
RNA Polymerase II Transcription Elongation	Reactome	1	SUPT16H	59	8	25.44	3.864e-2	1.488e-1
Formation of RNA Pol II elongation complex	Reactome	1	SUPT16H	61	8	24.61	3.993e-2	1.517e-1
TP53 Regulates Transcription of DNA Repair Genes	Reactome	1	SUPT16H	65	8	23.10	4.250e-2	1.569e-1
Collagen biosynthesis and modifying enzymes	Reactome	1	COL25A1	67	8	22.41	4.378e-2	1.593e-1
RNA Polymerase II Pre-transcription Events	Reactome	1	SUPT16H	84	8	17.87	5.462e-2	1.795e-1
RAB GEFs exchange GTP for GDP on RABs	Reactome	1	RAB3GAP1	90	8	16.68	5.842e-2	1.858e-1
Regulation of TP53 Activity through Phosphorylation	Reactome	1	SUPT16H	92	8	16.32	5.968e-2	1.877e-1
Protein digestion and absorption	KEGG	1	COL25A1	103	8	14.58	6.660e-2	1.990e-1