

GeDiPNet Cluster 301 -- 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 11:31:30

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cohesin Loading onto Chromatin	Reactome	4	SMC1A, NIPBL, RAD21, SMC3	10	13	369.54	1.727e-10	2.378e-8
Establishment of Sister Chromatid Cohesion	Reactome	3	SMC1A, RAD21, SMC3	11	13	251.96	1.627e-7	9.976e-6
Cell cycle	KEGG	5	SMC1A, HDAC8, NIPBL, RAD21, SMC3	158	13	29.24	4.372e-7	2.383e-5
Resolution of Sister Chromatid Cohesion	Reactome	4	SMC1A, HDAC8, RAD21, SMC3	126	13	29.33	7.675e-6	2.684e-4
Separation of Sister Chromatids	Reactome	4	SMC1A, HDAC8, RAD21, SMC3	190	13	19.45	3.881e-5	1.036e-3
SUMOylation of DNA damage response and repair proteins	Reactome	3	SMC1A, RAD21, SMC3	77	13	35.99	6.920e-5	1.658e-3
Estrogen-dependent gene expression	Reactome	3	SMC1A, RAD21, SMC3	150	13	18.48	4.982e-4	7.948e-3
RNA Polymerase II Pre-transcription Events	Reactome	2	TAF6, AFF4	84	13	22.00	3.586e-3	3.489e-2
Oocyte meiosis	KEGG	2	SMC1A, SMC3	138	13	13.39	9.410e-3	6.616e-2
tRNA modification in the nucleus and cytosol	Reactome	1	TRMT61A	19	13	48.62	2.038e-2	1.039e-1
Notch-HLH transcription pathway	Reactome	1	HDAC8	28	13	32.99	2.990e-2	1.285e-1
RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known	Reactome	1	ARID1B	38	13	24.31	4.038e-2	1.526e-1
Basal transcription factors	KEGG	1	TAF6	44	13	21.00	4.662e-2	1.648e-1
RNA Polymerase II Promoter Escape	Reactome	1	TAF6	47	13	19.66	4.972e-2	1.710e-1
RNA Polymerase II Transcription Pre-Initiation And Promoter Opening	Reactome	1	TAF6	47	13	19.66	4.972e-2	1.710e-1