

GeDiPNet Cluster 533 -- 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: 2026-10-19 23:21:21

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	NIPBL, RAD21, SMC1A, SMC3	10	14	343.14	2.416e-10	2.585e-8
Establishment of Sister Chromatid Cohesion	Reactome	3	RAD21, SMC1A, SMC3	11	14	233.96	2.069e-7	1.056e-5
Cell cycle	KEGG	5	HDAC8, NIPBL, RAD21, SMC1A, SMC3	158	14	27.15	6.729e-7	2.956e-5
Resolution of Sister Chromatid Cohesion	Reactome	4	HDAC8, RAD21, SMC1A, SMC3	126	14	27.23	1.066e-5	3.067e-4
Separation of Sister Chromatids	Reactome	4	HDAC8, RAD21, SMC1A, SMC3	190	14	18.06	5.366e-5	1.152e-3
SUMOylation of DNA damage response and repair proteins	Reactome	3	RAD21, SMC1A, SMC3	77	14	33.42	8.767e-5	1.710e-3
Estrogen-dependent gene expression	Reactome	3	RAD21, SMC1A, SMC3	150	14	17.16	6.283e-4	7.976e-3
RNA Polymerase II Pre-transcription Events	Reactome	2	TAF6, AFF4	84	14	20.43	4.165e-3	3.213e-2
Oocyte meiosis	KEGG	2	SMC1A, SMC3	138	14	12.43	1.090e-2	6.008e-2
tRNA modification in the nucleus and cytosol	Reactome	1	TRMT61A	19	14	45.15	2.193e-2	9.030e-2
Notch-HLH transcription pathway	Reactome	1	HDAC8	28	14	30.64	3.217e-2	1.126e-1
RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known	Reactome	1	ARID1B	38	14	22.58	4.342e-2	1.335e-1
Basal transcription factors	KEGG	1	TAF6	44	14	19.50	5.011e-2	1.450e-1
RNA Polymerase II Promoter Escape	Reactome	1	TAF6	47	14	18.25	5.344e-2	1.502e-1
RNA Polymerase II Transcription Pre-Initiation And Promoter Opening	Reactome	1	TAF6	47	14	18.25	5.344e-2	1.502e-1