

GeDiPNet Cluster 217 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 19:04:30

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Loss of Nlp from mitotic centrosomes	Reactome	2	PAFAH1B1, YWHAE	70	13	26.40	2.506e-3	2.749e-2
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	2	PAFAH1B1, YWHAE	70	13	26.40	2.506e-3	2.749e-2
AURKA Activation by TPX2	Reactome	2	PAFAH1B1, YWHAE	73	13	25.31	2.722e-3	2.925e-2
Pyrimidine biosynthesis	Reactome	1	DHODH	3	13	307.95	3.244e-3	3.296e-2
Recruitment of mitotic centrosome proteins and complexes	Reactome	2	PAFAH1B1, YWHAE	82	13	22.53	3.421e-3	3.426e-2
Polycomb repressive complex	KEGG	2	BCOR, SUZ12	83	13	22.26	3.503e-3	3.481e-2
Regulation of PLK1 Activity at G2/M Transition	Reactome	2	PAFAH1B1, YWHAE	88	13	21.00	3.929e-3	3.781e-2
Recruitment of NuMA to mitotic centrosomes	Reactome	2	PAFAH1B1, YWHAE	94	13	19.66	4.470e-3	4.134e-2
Anchoring of the basal body to the plasma membrane	Reactome	2	PAFAH1B1, YWHAE	98	13	18.85	4.848e-3	4.364e-2
NADE modulates death signalling	Reactome	1	YWHAE	6	13	153.97	6.478e-3	5.312e-2
HSF1 activation	Reactome	1	YWHAE	12	13	76.99	1.292e-2	8.184e-2
Activation of BAD and translocation to mitochondria	Reactome	1	YWHAE	12	13	76.99	1.292e-2	8.184e-2
Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	Reactome	1	YWHAE	12	13	76.99	1.292e-2	8.184e-2
Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	Reactome	1	YWHAE	16	13	57.74	1.719e-2	9.741e-2
Telomere Extension By Telomerase	Reactome	1	TERT	16	13	57.74	1.719e-2	9.741e-2