

GeDiPNet Cluster 101 -- 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 19:56:06

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Recruitment of NuMA to mitotic centrosomes	Reactome	16	CDK5RAP2, CEP135, CEP152, CEP63, MZT2B, TUBA3E, DYNC1H1, PLK4, TUBA1A, TUBG1, CENPJ, TUBGCP4	94	138	14.81	8.173e-15	2.406e-12
Recruitment of mitotic centrosome proteins and complexes	Reactome	15	CDK5RAP2, CEP135, CEP152, CEP63, MZT2B, DYNC1H1, PLK4, TUBA1A, TUBG1, CENPJ, TUBGCP4, TUBGCP6	82	138	15.92	1.920e-14	5.282e-12
Loss of Nlp from mitotic centrosomes	Reactome	12	CDK5RAP2, CEP135, CEP152, CEP63, DYNC1H1, PLK4, TUBA1A, TUBG1, CENPJ, NDE1, PPP2R1A, PCNT	70	138	14.92	1.968e-11	3.165e-9
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	12	CDK5RAP2, CEP135, CEP152, CEP63, DYNC1H1, PLK4, TUBA1A, TUBG1, CENPJ, NDE1, PPP2R1A, PCNT	70	138	14.92	1.968e-11	3.165e-9
AURKA Activation by TPX2	Reactome	12	CDK5RAP2, CEP135, CEP152, CEP63, DYNC1H1, PLK4, TUBA1A, TUBG1, CENPJ, NDE1, PPP2R1A, PCNT	73	138	14.31	3.303e-11	5.077e-9
Anchoring of the basal body to the plasma membrane	Reactome	13	CDK5RAP2, CEP135, CEP152, CEP63, RAB11A, DYNC1H1, PLK4, TUBA1A, TUBG1, CENPJ, NDE1, PPP2R1A	98	138	11.54	8.034e-11	1.124e-8
Regulation of PLK1 Activity at G2/M Transition	Reactome	12	CDK5RAP2, CEP135, CEP152, CEP63, DYNC1H1, PLK4, TUBA1A, TUBG1, CENPJ, NDE1, PPP2R1A, PCNT	88	138	11.87	3.188e-10	3.862e-8
Mitotic Prometaphase	Reactome	13	CENPE, KNL1, NUP37, TUBA3E, BUB1B, DYNC1H1, KIF2A, SPD11, TUBA1A, BUB1, NDE1, PPP2R1A	113	138	10.01	4.960e-10	5.738e-8
RHO GTPases Activate Formins	Reactome	14	CENPE, KNL1, NUP37, TUBA3E, BUB1B, DYNC1H1, KIF2A, SPD11, TUBA1A, BUB1, NDE1, PPP2R1A	140	138	8.70	6.820e-10	7.644e-8
EML4 and NUDC in mitotic spindle formation	Reactome	13	CENPE, KNL1, NUP37, TUBA3E, BUB1B, DYNC1H1, KIF2A, SPD11, TUBA1A, BUB1, NDE1, PPP2R1A	117	138	9.67	7.691e-10	8.482e-8
Resolution of Sister Chromatid Cohesion	Reactome	13	CENPE, KNL1, NUP37, TUBA3E, BUB1B, DYNC1H1, KIF2A, SPD11, TUBA1A, BUB1, NDE1, PPP2R1A	126	138	8.98	1.943e-9	1.948e-7
Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	Reactome	11	CENPE, KNL1, NUP37, BUB1B, DYNC1H1, KIF2A, SPD11, BUB1, NDE1, PPP2R1A, NUP85	96	138	9.97	1.184e-8	9.806e-7
Separation of Sister Chromatids	Reactome	13	CENPE, KNL1, NUP37, TUBA3E, BUB1B, DYNC1H1, KIF2A, SPD11, TUBA1A, BUB1, NDE1, PPP2R1A	190	138	5.95	2.706e-7	1.563e-5
HDR through Single Strand Annealing (SSA)	Reactome	6	RBBP8, TOP3A, NBN, ATR, ATRIP, DNA2	37	138	14.11	3.580e-6	1.465e-4
Presynaptic phase of homologous DNA pairing and strand exchange	Reactome	6	RBBP8, TOP3A, NBN, ATR, ATRIP, DNA2	39	138	13.39	4.930e-6	1.912e-4