

GeDiPNet Cluster 124 -- 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 20:13:11

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	12	TUBA1A, TUBB2A, PAFAH1B1, TUBB3, NDE1, DYNC1H1, MZT2B, TUBA3E, TUBB, TUBB2B, TUBG1, TUBGCP2	94	87	17.62	2.816e-12	5.624e-10
Recycling pathway of L1	Reactome	8	KIF4A, L1CAM, TUBA1A, TUBB2A, TUBB3, ACTG1, TUBA3E, TUBB2B	40	87	27.61	3.477e-10	4.430e-8
COPI-independent Golgi-to-ER retrograde traffic	Reactome	8	PLA2G6, TUBA1A, TUBB2A, PAFAH1B1, TUBB3, DYNC1H1, TUBA3E, TUBB2B	51	87	21.65	2.699e-9	2.705e-7
Motor proteins	KEGG	12	KIF4A, TUBA1A, TUBB2A, TUBB3, ACTG1, DYNC1H1, MYH11, TUBA3E, TUBB, TUBB2B, TUBG1, KIF21B	194	87	8.54	1.382e-8	1.155e-6
RHO GTPases Activate Formins	Reactome	10	TUBA1A, TUBB2A, PAFAH1B1, B9D2, TUBB3, NDE1, ACTG1, DYNC1H1, TUBA3E, TUBB2B	140	87	9.86	6.250e-8	4.355e-6
RHO GTPases activate IQGAPs	Reactome	6	TUBA1A, TUBB2A, TUBB3, ACTG1, TUBA3E, TUBB2B	32	87	25.88	9.455e-8	6.233e-6
Mitotic Prometaphase	Reactome	9	TUBA1A, TUBB2A, PAFAH1B1, B9D2, TUBB3, NDE1, DYNC1H1, TUBA3E, TUBB2B	113	87	10.99	1.164e-7	7.493e-6
Recruitment of mitotic centrosome proteins and complexes	Reactome	8	TUBA1A, PAFAH1B1, NDE1, DYNC1H1, MZT2B, TUBB, TUBG1, TUBGCP2	82	87	13.47	1.260e-7	7.995e-6
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	Reactome	5	TUBA1A, TUBB2A, TUBB3, TUBA3E, TUBB2B	18	87	38.35	1.413e-7	8.821e-6
EML4 and NUDC in mitotic spindle formation	Reactome	9	TUBA1A, TUBB2A, PAFAH1B1, B9D2, TUBB3, NDE1, DYNC1H1, TUBA3E, TUBB2B	117	87	10.62	1.573e-7	9.701e-6
Cilium Assembly	Reactome	5	TUBA1A, TUBB2A, TUBB3, TUBA3E, TUBB2B	19	87	36.33	1.907e-7	1.148e-5
Kinesins	Reactome	7	KIF4A, TUBA1A, TUBB2A, TUBB3, TUBA3E, TUBB2B, KIF21B	59	87	16.38	2.061e-7	1.226e-5
Resolution of Sister Chromatid Cohesion	Reactome	9	TUBA1A, TUBB2A, PAFAH1B1, B9D2, TUBB3, NDE1, DYNC1H1, TUBA3E, TUBB2B	126	87	9.86	2.975e-7	1.700e-5
Aggrephagy	Reactome	6	TUBA1A, TUBB2A, TUBB3, DYNC1H1, TUBA3E, TUBB2B	40	87	20.71	3.823e-7	2.128e-5
Anchoring of the basal body to the plasma membrane	Reactome	8	TUBA1A, PAFAH1B1, B9D2, TMEM216, NDE1, DYNC1H1, TUBB, TUBG1	98	87	11.27	5.063e-7	2.711e-5