

GeDiPNet Cluster 446 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:16

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	2	TUBB2B, NDE1	94	8	31.94	1.646e-3	1.652e-2
Mitotic Prometaphase	Reactome	2	TUBB2B, NDE1	113	8	26.57	2.368e-3	2.155e-2
EML4 and NUDC in mitotic spindle formation	Reactome	2	TUBB2B, NDE1	117	8	25.66	2.536e-3	2.258e-2
Resolution of Sister Chromatid Cohesion	Reactome	2	TUBB2B, NDE1	126	8	23.83	2.934e-3	2.505e-2
Reelin signalling pathway	Reactome	1	VLDLR	5	8	300.25	3.327e-3	2.738e-2
VLDL clearance	Reactome	1	VLDLR	5	8	300.25	3.327e-3	2.738e-2
RHO GTPases Activate Formins	Reactome	2	TUBB2B, NDE1	140	8	21.45	3.608e-3	2.903e-2
Separation of Sister Chromatids	Reactome	2	TUBB2B, NDE1	190	8	15.80	6.547e-3	4.354e-2
VLDLR internalisation and degradation	Reactome	1	VLDLR	12	8	125.10	7.968e-3	4.940e-2
Nitrogen metabolism	KEGG	1	CA8	17	8	88.31	1.127e-2	6.122e-2
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	Reactome	1	TUBB2B	18	8	83.40	1.193e-2	6.320e-2
Cilium Assembly	Reactome	1	TUBB2B	19	8	79.01	1.259e-2	6.547e-2
Carboxyterminal post-translational modifications of tubulin	Reactome	1	TUBB2B	27	8	55.60	1.785e-2	8.027e-2
Sealing of the nuclear envelope (NE) by ESCRT-III	Reactome	1	TUBB2B	31	8	48.43	2.047e-2	8.699e-2
RHO GTPases activate IQGAPs	Reactome	1	TUBB2B	32	8	46.91	2.112e-2	8.838e-2