

GeDiPNet Cluster 201 -- 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 17:27:25

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	11	23.23	3.184e-3	3.251e-2
Mitotic Prometaphase	Reactome	2	TUBB2B, NDE1	113	11	19.32	4.566e-3	4.188e-2
Reelin signalling pathway	Reactome	1	VLDLR	5	11	218.36	4.572e-3	4.188e-2
VLDL clearance	Reactome	1	VLDLR	5	11	218.36	4.572e-3	4.188e-2
EML4 and NUDC in mitotic spindle formation	Reactome	2	TUBB2B, NDE1	117	11	18.66	4.886e-3	4.387e-2
Resolution of Sister Chromatid Cohesion	Reactome	2	TUBB2B, NDE1	126	11	17.33	5.645e-3	4.850e-2
RHO GTPases Activate Formins	Reactome	2	TUBB2B, NDE1	140	11	15.60	6.926e-3	5.546e-2
VLDLR internalisation and degradation	Reactome	1	VLDLR	12	11	90.98	1.094e-2	7.412e-2
Separation of Sister Chromatids	Reactome	2	TUBB2B, NDE1	190	11	11.49	1.247e-2	8.014e-2
Nitrogen metabolism	KEGG	1	CA8	17	11	64.22	1.547e-2	9.134e-2
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	Reactome	1	TUBB2B	18	11	60.66	1.637e-2	9.456e-2
Cilium Assembly	Reactome	1	TUBB2B	19	11	57.46	1.727e-2	9.767e-2
Carboxyterminal post-translational modifications of tubulin	Reactome	1	TUBB2B	27	11	40.44	2.446e-2	1.192e-1
Laminin interactions	Reactome	1	LAMA1	28	11	38.99	2.536e-2	1.213e-1
MET activates PTK2 signaling	Reactome	1	LAMA1	30	11	36.39	2.715e-2	1.257e-1