

GeDiPNet Cluster 466 -- 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: 2026-10-19 23:21:21

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	Reactome	1	TUBB4A	18	3	222.41	4.490e-3	3.394e-2
Cilium Assembly	Reactome	1	TUBB4A	19	3	210.70	4.739e-3	3.521e-2
Carboxyterminal post-translational modifications of tubulin	Reactome	1	TUBB4A	27	3	148.27	6.730e-3	4.425e-2
Sealing of the nuclear envelope (NE) by ESCRT-III	Reactome	1	TUBB4A	31	3	129.14	7.724e-3	4.840e-2
RHO GTPases activate IQGAPs	Reactome	1	TUBB4A	32	3	125.10	7.973e-3	4.940e-2
Aggrephagy	Reactome	1	TUBB4A	40	3	100.08	9.959e-3	5.666e-2
Recycling pathway of L1	Reactome	1	TUBB4A	40	3	100.08	9.959e-3	5.666e-2
COPI-independent Golgi-to-ER retrograde traffic	Reactome	1	TUBB4A	51	3	78.50	1.269e-2	6.571e-2
Intraflagellar transport	Reactome	1	TUBB4A	54	3	74.14	1.343e-2	6.795e-2
HSP90 chaperone cycle for steroid hormone receptors (SHR)	Reactome	1	TUBB4A	55	3	72.79	1.368e-2	6.873e-2
Hedgehog 'off' state	Reactome	1	TUBB4A	56	3	71.49	1.392e-2	6.947e-2
Kinesins	Reactome	1	TUBB4A	59	3	67.85	1.467e-2	7.167e-2
Loss of Nlp from mitotic centrosomes	Reactome	1	TUBB4A	70	3	57.19	1.739e-2	7.887e-2
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	1	TUBB4A	70	3	57.19	1.739e-2	7.887e-2
AURKA Activation by TPX2	Reactome	1	TUBB4A	73	3	54.84	1.813e-2	8.115e-2