

GeDiPNet Cluster 606 -- 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 00:02:59

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Loss of Nlp from mitotic centrosomes	Reactome	1	TUBB	70	2	85.79	1.162e-2	6.224e-2
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	1	TUBB	70	2	85.79	1.162e-2	6.224e-2
AURKA Activation by TPX2	Reactome	1	TUBB	73	2	82.26	1.212e-2	6.395e-2
Recruitment of mitotic centrosome proteins and complexes	Reactome	1	TUBB	82	2	73.23	1.361e-2	6.862e-2
Regulation of PLK1 Activity at G2/M Transition	Reactome	1	TUBB	88	2	68.24	1.460e-2	7.143e-2
Gap junction	KEGG	1	TUBB	89	2	67.47	1.477e-2	7.207e-2
Recruitment of NuMA to mitotic centrosomes	Reactome	1	TUBB	94	2	63.88	1.559e-2	7.436e-2
Anchoring of the basal body to the plasma membrane	Reactome	1	TUBB	98	2	61.28	1.625e-2	7.605e-2
Phagosome	KEGG	1	TUBB	155	2	38.74	2.565e-2	9.896e-2
Motor proteins	KEGG	1	TUBB	194	2	30.95	3.205e-2	1.124e-1
Pathogenic Escherichia coli infection	KEGG	1	TUBB	200	2	30.03	3.303e-2	1.144e-1
Salmonella infection	KEGG	1	TUBB	248	2	24.21	4.087e-2	1.289e-1
Parkinson disease	KEGG	1	TUBB	268	2	22.41	4.413e-2	1.347e-1
Prion disease	KEGG	1	TUBB	275	2	21.84	4.527e-2	1.368e-1
Huntington disease	KEGG	1	TUBB	308	2	19.50	5.063e-2	1.459e-1