

GeDiPNet Cluster 592 -- 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 00:02:45

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	2	GJA1, TUBA3C	18	33	40.44	1.090e-3	1.209e-2
Defective MAN1B1 causes MRT15	Reactome	1	MAN1B1	1	33	363.94	2.748e-3	2.394e-2
Regulation of gap junction activity	Reactome	1	GJA1	3	33	121.31	8.221e-3	5.037e-2
Assembly and cell surface presentation of NMDA receptors	Reactome	1	GRIN3A	6	33	60.66	1.638e-2	7.625e-2
Nef and signal transduction	Reactome	1	DOCK2	8	33	45.49	2.178e-2	9.002e-2
Ca2+ activated K+ channels	Reactome	1	KCNN2	9	33	40.44	2.447e-2	9.626e-2
Gap junction	KEGG	2	GJA1, TUBA3C	89	33	8.18	2.471e-2	9.672e-2
Formation of annular gap junctions	Reactome	1	GJA1	11	33	33.09	2.983e-2	1.079e-1
Calcium signaling pathway	KEGG	3	CAMK1D, GRIN3A, ITPKC	254	33	4.30	3.198e-2	1.124e-1
Gap junction degradation	Reactome	1	GJA1	12	33	30.33	3.249e-2	1.133e-1
Gap junction assembly	Reactome	1	GJA1	18	33	20.22	4.835e-2	1.421e-1
Cilium Assembly	Reactome	1	TUBA3C	19	33	19.15	5.097e-2	1.464e-1
ER Quality Control Compartment (ERQC)	Reactome	1	MAN1B1	21	33	17.33	5.619e-2	1.548e-1
Carboxyterminal post-translational modifications of tubulin	Reactome	1	TUBA3C	27	33	13.48	7.167e-2	1.780e-1
Synthesis of IP3 and IP4 in the cytosol	Reactome	1	ITPKC	28	33	13.00	7.423e-2	1.818e-1