

GeDiPNet Cluster 171 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 17:20:51

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Phase 0 - rapid depolarisation	Reactome	3	SCN9A, SCN10A, SCN11A	44	9	90.98	3.795e-6	1.517e-4
Abnormal conversion of 2-oxoglutarate to 2-hydroxyglutarate	Reactome	1	IDH1	1	9	1334.44	7.494e-4	1.092e-2
NADPH regeneration	Reactome	1	IDH1	1	9	1334.44	7.494e-4	1.092e-2
TRKA activation by NGF	Reactome	1	NGF	2	9	667.22	1.498e-3	1.846e-2
NFG and proNGF binds to p75NTR	Reactome	1	NGF	2	9	667.22	1.498e-3	1.846e-2
Inflammatory mediator regulation of TRP channels	KEGG	2	NGF, TRPA1	99	9	26.96	2.332e-3	2.554e-2
Axonal growth stimulation	Reactome	1	NGF	4	9	333.61	2.995e-3	3.068e-2
NGF processing	Reactome	1	NGF	4	9	333.61	2.995e-3	3.068e-2
ARMS-mediated activation	Reactome	1	NGF	5	9	266.89	3.742e-3	3.593e-2
NADE modulates death signalling	Reactome	1	NGF	6	9	222.41	4.489e-3	4.079e-2
PI3K/AKT activation	Reactome	1	NGF	9	9	148.27	6.726e-3	5.319e-2
Retrograde neurotrophin signalling	Reactome	1	NGF	11	9	121.31	8.216e-3	6.072e-2
Formation of annular gap junctions	Reactome	1	CLTCL1	11	9	121.31	8.216e-3	6.072e-2
Frs2-mediated activation	Reactome	1	NGF	12	9	111.20	8.960e-3	6.417e-2
Gap junction degradation	Reactome	1	CLTCL1	12	9	111.20	8.960e-3	6.417e-2