

GeDiPNet Cluster 358 -- 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 09:12:10

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Caspase activation via Dependence Receptors in the absence of ligand	Reactome	1	DCC	4	4	750.63	1.332e-3	1.729e-2
HHAT G278V abrogates palmitoylation of Hh-Np	Reactome	1	SHH	4	4	750.63	1.332e-3	1.729e-2
Axon guidance	KEGG	2	SHH, DCC	183	4	32.81	1.358e-3	1.754e-2
Release of Hh-Np from the secreting cell	Reactome	1	SHH	7	4	428.93	2.330e-3	2.607e-2
Ligand-receptor interactions	Reactome	1	SHH	7	4	428.93	2.330e-3	2.607e-2
Netrin-1 signaling	Reactome	1	DCC	8	4	375.31	2.662e-3	2.882e-2
DCC mediated attractive signaling	Reactome	1	DCC	11	4	272.95	3.659e-3	3.598e-2
Activation of SMO	Reactome	1	SHH	18	4	166.81	5.982e-3	5.030e-2
Pathways in cancer	KEGG	2	SHH, DCC	533	4	11.27	1.111e-2	7.485e-2
Basal transcription factors	KEGG	1	TAF8	44	4	68.24	1.458e-2	8.793e-2
Hedgehog signaling pathway	KEGG	1	SHH	56	4	53.62	1.852e-2	1.016e-1
Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	Reactome	1	SHH	56	4	53.62	1.852e-2	1.016e-1
Hedgehog ligand biogenesis	Reactome	1	SHH	60	4	50.04	1.984e-2	1.052e-1
Basal cell carcinoma	KEGG	1	SHH	63	4	47.66	2.082e-2	1.084e-1
RNA polymerase II transcribes snRNA genes	Reactome	1	TAF8	74	4	40.57	2.442e-2	1.192e-1