

GeDiPNet Cluster 96 -- 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: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-10 16:19:47

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Hedgehog signaling pathway	KEGG	16	BOC, CDON, DISP1, GLI1, GLI2, GLI3, HHAT, HHIP, IHH, KIF3A, PTCH1, PTCH2	56	76	45.15	4.211e-23	5.320e-20
Hedgehog 'off' state	Reactome	11	GLI1, GLI2, GLI3, IFT172, IFT52, IFT88, KIF3A, PTCH1, SMO, SUFU, TULP3	56	76	31.04	3.644e-14	1.010e-11
Activation of SMO	Reactome	8	BOC, CDON, IHH, KIF3A, PTCH1, SMO, GAS1, SHH	18	76	70.23	7.324e-14	1.885e-11
Ligand-receptor interactions	Reactome	6	CDON, HHIP, IHH, PTCH1, GAS1, SHH	7	76	135.45	3.658e-13	8.455e-11
Basal cell carcinoma	KEGG	9	GLI1, GLI2, GLI3, HHIP, PTCH1, PTCH2, SMO, SUFU, SHH	63	76	22.58	1.798e-10	2.493e-8
Pathways in cancer	KEGG	18	FGF8, KIT, PDGFRA, CTNNA1, GLI1, GLI2, GLI3, HHIP, PTCH1, PTCH2, RB1, SMO	533	76	5.34	3.819e-9	3.935e-7
GLI proteins bind promoters of Hh responsive genes to promote transcription	Reactome	3	GLI1, GLI2, GLI3	3	76	158.03	2.435e-7	1.522e-5
HHAT G278V abrogates palmitoylation of Hh-Np	Reactome	3	HHAT, IHH, SHH	4	76	118.52	9.698e-7	5.095e-5
Hedgehog 'on' state	Reactome	6	GLI1, GLI2, GLI3, PTCH1, SMO, SUFU	70	76	13.55	4.998e-6	2.025e-4
Citric acid cycle (TCA cycle)	Reactome	3	SDHA, SDHB, SDHC	22	76	21.55	3.439e-4	6.166e-3
Intraflagellar transport	Reactome	4	IFT172, IFT52, IFT88, KIF3A	54	76	11.71	3.685e-4	6.523e-3
Myogenesis	Reactome	3	BOC, CDON, CTNNA1	27	76	17.56	6.386e-4	9.984e-3
Release of Hh-Np from the secreting cell	Reactome	2	IHH, SHH	7	76	45.15	8.130e-4	1.200e-2
Citrate cycle (TCA cycle)	KEGG	3	SDHA, SDHB, SDHC	30	76	15.80	8.744e-4	1.263e-2
Melanoma	KEGG	4	FGF8, PDGFRA, RB1, FGFR1	73	76	8.66	1.158e-3	1.573e-2