

GeDiPNet Cluster 207 -- 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 00:40:11

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Hedgehog signaling pathway	KEGG	4	GLI2, PTCH1, SUFU, SHH	56	15	57.19	5.570e-7	2.929e-5
Basal cell carcinoma	KEGG	4	GLI2, PTCH1, SUFU, SHH	63	15	50.84	8.986e-7	4.428e-5
Ligand-receptor interactions	Reactome	2	PTCH1, SHH	7	15	228.76	3.047e-5	8.600e-4
Hedgehog 'off' state	Reactome	3	GLI2, PTCH1, SUFU	56	15	42.89	4.199e-5	1.127e-3
Hedgehog 'on' state	Reactome	3	GLI2, PTCH1, SUFU	70	15	34.31	8.206e-5	1.931e-3
Activation of SMO	Reactome	2	PTCH1, SHH	18	15	88.96	2.202e-4	4.252e-3
Pathways in cancer	KEGG	5	GLI2, PTCH1, SUFU, SHH, RAC3	533	15	7.51	3.502e-4	6.160e-3
Axon guidance	KEGG	3	PTCH1, SHH, RAC3	183	15	13.13	1.384e-3	1.778e-2
GLI proteins bind promoters of Hh responsive genes to promote transcription	Reactome	1	GLI2	3	15	266.89	3.743e-3	3.650e-2
TWIK related potassium channel (TREK)	Reactome	1	KCNK4	3	15	266.89	3.743e-3	3.650e-2
HHAT G278V abrogates palmitoylation of Hh-Np	Reactome	1	SHH	4	15	200.17	4.987e-3	4.437e-2
Release of Hh-Np from the secreting cell	Reactome	1	SHH	7	15	114.38	8.712e-3	6.435e-2
DNA replication initiation	Reactome	1	POLE	8	15	100.08	9.951e-3	6.966e-2
Insulin processing	Reactome	1	EXOC4	14	15	57.19	1.735e-2	9.779e-2
Class B/2 (Secretin family receptors)	Reactome	1	PTH	18	15	44.48	2.226e-2	1.126e-1