

GeDiPNet Cluster 192 -- 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 14:38:41

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
GLI proteins bind promoters of Hh responsive genes to promote transcription	Reactome	2	GLI3, GLI2	3	9	889.63	1.497e-6	6.917e-5
Hedgehog signaling pathway	KEGG	3	GLI3, KIF7, GLI2	56	9	71.49	7.908e-6	2.759e-4
Hedgehog 'off' state	Reactome	3	GLI3, KIF7, GLI2	56	9	71.49	7.908e-6	2.759e-4
Basal cell carcinoma	KEGG	3	GLI3, KIF7, GLI2	63	9	63.54	1.130e-5	3.713e-4
Hedgehog 'on' state	Reactome	3	GLI3, KIF7, GLI2	70	9	57.19	1.553e-5	4.848e-4
Pathways in cancer	KEGG	4	GLI3, KIF7, SOS2, GLI2	533	9	10.01	4.043e-4	6.758e-3
Interleukin-15 signaling	Reactome	1	SOS2	13	9	102.65	9.703e-3	6.739e-2
tRNA modification in the nucleus and cytosol	Reactome	1	PUS3	19	9	70.23	1.415e-2	8.408e-2
Synthesis of IP3 and IP4 in the cytosol	Reactome	1	PLCD1	28	9	47.66	2.079e-2	1.050e-1
Transcriptional Regulation by E2F6	Reactome	1	CHEK1	35	9	38.13	2.593e-2	1.188e-1
Signaling by SCF-KIT	Reactome	1	CHEK1	37	9	36.07	2.740e-2	1.228e-1
Activation of ATR in response to replication stress	Reactome	1	CHEK1	37	9	36.07	2.740e-2	1.228e-1
Presynaptic phase of homologous DNA pairing and strand exchange	Reactome	1	CHEK1	39	9	34.22	2.886e-2	1.262e-1
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	Reactome	1	CHEK1	52	9	25.66	3.831e-2	1.480e-1
NRAGE signals death through JNK	Reactome	1	SOS2	55	9	24.26	4.048e-2	1.527e-1