

GeDiPNet Cluster 396 -- 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 21:18:03

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
TP53 Regulates Transcription of Caspase Activators and Caspases	Reactome	2	APAF1, TP63	12	23	87.03	2.289e-4	4.353e-3
POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation	Reactome	2	SALL1, SALL4	13	23	80.33	2.702e-4	4.947e-3
Signaling by FGFR2 amplification mutants	Reactome	1	FGFR2	1	23	522.17	1.915e-3	2.205e-2
Signaling by FGFR2 fusions	Reactome	1	FGFR2	1	23	522.17	1.915e-3	2.205e-2
FoxO signaling pathway	KEGG	3	CHUK, SOD2, TGFB2	133	23	11.78	1.999e-3	2.279e-2
MAPK signaling pathway	KEGG	4	CHUK, FGFR2, CACNA1C, TGFB2	299	23	6.99	2.294e-3	2.525e-2
Hepatitis B	KEGG	3	APAF1, CHUK, TGFB2	163	23	9.61	3.560e-3	3.472e-2
IKBKB deficiency causes SCID	Reactome	1	CHUK	3	23	174.06	5.735e-3	4.800e-2
IKBKG deficiency causes anhidrotic ectodermal dysplasia with immunodeficiency (EDA-ID) (via TLR)	Reactome	1	CHUK	3	23	174.06	5.735e-3	4.800e-2
Lipid and atherosclerosis	KEGG	3	APAF1, CHUK, SOD2	216	23	7.25	7.791e-3	5.867e-2
p53 signaling pathway	KEGG	2	APAF1, GORAB	75	23	13.92	8.943e-3	6.417e-2
Pancreatic cancer	KEGG	2	CHUK, TGFB2	77	23	13.56	9.408e-3	6.616e-2
Chronic myeloid leukemia	KEGG	2	CHUK, TGFB2	77	23	13.56	9.408e-3	6.616e-2
Formation of apoptosome	Reactome	1	APAF1	6	23	87.03	1.144e-2	7.438e-2
Activation of caspases through apoptosome-mediated cleavage	Reactome	1	APAF1	6	23	87.03	1.144e-2	7.438e-2