

GeDiPNet Cluster 594 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:51

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Yersinia infection	KEGG	3	IRAK1, MAP2K2, PTK2	138	14	18.65	4.925e-4	6.606e-3
Gastric cancer	KEGG	3	FGFR2, MAP2K2, SHH	150	14	17.16	6.283e-4	7.976e-3
Signaling by FGFR2 amplification mutants	Reactome	1	FGFR2	1	14	857.86	1.166e-3	1.272e-2
Signaling by FGFR2 fusions	Reactome	1	FGFR2	1	14	857.86	1.166e-3	1.272e-2
Proteoglycans in cancer	KEGG	3	MAP2K2, PTK2, SHH	204	14	12.62	1.531e-3	1.563e-2
Human immunodeficiency virus 1 infection	KEGG	3	IRAK1, MAP2K2, PTK2	213	14	12.08	1.733e-3	1.716e-2
VEGF signaling pathway	KEGG	2	MAP2K2, PTK2	60	14	28.60	2.149e-3	2.009e-2
Regulation of actin cytoskeleton	KEGG	3	FGFR2, MAP2K2, PTK2	232	14	11.09	2.213e-3	2.051e-2
Pathways in cancer	KEGG	4	FGFR2, MAP2K2, PTK2, SHH	533	14	6.44	2.690e-3	2.360e-2
Central carbon metabolism in cancer	KEGG	2	FGFR2, MAP2K2	71	14	24.16	2.995e-3	2.538e-2
Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	Reactome	1	TFAP2A	3	14	285.95	3.493e-3	2.829e-2
EGFR tyrosine kinase inhibitor resistance	KEGG	2	FGFR2, MAP2K2	80	14	21.45	3.786e-3	3.005e-2
ErbB signaling pathway	KEGG	2	MAP2K2, PTK2	86	14	19.95	4.361e-3	3.329e-2
MAPK signaling pathway	KEGG	3	FGFR2, IRAK1, MAP2K2	299	14	8.61	4.535e-3	3.421e-2
TFAP2 (AP-2) family regulates transcription of other transcription factors	Reactome	1	TFAP2A	4	14	214.46	4.655e-3	3.479e-2