

GeDiPNet Cluster 500 -- 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 00:03:13

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Colorectal cancer	KEGG	3	CTNNB1, TP53, RHOA	87	7	59.16	1.258e-5	3.526e-4
Interleukin-4 and Interleukin-13 signaling	Reactome	3	STAT6, BCL6, TP53	108	7	47.66	2.411e-5	6.086e-4
TP53 regulates transcription of several additional cell death genes whose specific roles in p53-dependent apoptosis remain uncertain	Reactome	2	BCL6, TP53	14	7	245.10	2.641e-5	6.544e-4
Fluid shear stress and atherosclerosis	KEGG	3	CTNNB1, TP53, RHOA	141	7	36.50	5.357e-5	1.151e-3
Wnt signaling pathway	KEGG	3	CTNNB1, TP53, RHOA	174	7	29.58	1.002e-4	1.900e-3
Pathways in cancer	KEGG	4	STAT6, CTNNB1, TP53, RHOA	533	7	12.88	1.206e-4	2.195e-3
Proteoglycans in cancer	KEGG	3	CTNNB1, TP53, RHOA	204	7	25.23	1.607e-4	2.766e-3
Thyroid cancer	KEGG	2	CTNNB1, TP53	37	7	92.74	1.921e-4	3.175e-3
Transcriptional Regulation by VENTX	Reactome	2	CTNNB1, TP53	38	7	90.30	2.027e-4	3.317e-3
Ovarian tumor domain proteases	Reactome	2	TP53, RHOA	38	7	90.30	2.027e-4	3.317e-3
Human cytomegalovirus infection	KEGG	3	CTNNB1, TP53, RHOA	226	7	22.77	2.176e-4	3.509e-3
Endometrial cancer	KEGG	2	CTNNB1, TP53	59	7	58.16	4.904e-4	6.586e-3
Basal cell carcinoma	KEGG	2	CTNNB1, TP53	63	7	54.47	5.592e-4	7.285e-3
Bacterial invasion of epithelial cells	KEGG	2	CTNNB1, RHOA	78	7	43.99	8.562e-4	1.007e-2
Regulation of TP53 Expression	Reactome	1	TP53	2	7	857.86	1.165e-3	1.272e-2