

GeDiPNet Cluster 88 -- 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 15:32:41

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Bladder cancer	KEGG	6	TP53, CCND1, RB1, MDM2, CDKN2A, VEGFA	41	32	54.92	9.171e-10	1.038e-7
Cellular senescence	KEGG	8	TP53, ATM, CCND1, MTOR, RB1, ATR, MDM2, CDKN2A	157	32	19.12	5.748e-9	5.403e-7
Human papillomavirus infection	KEGG	10	TP53, ATM, CCND1, MTOR, RB1, ATR, MDM2, TNF, WNT7A, VEGFA	333	32	11.27	8.804e-9	7.829e-7
Stabilization of p53	Reactome	4	TP53, ATM, MDM2, CDKN2A	11	32	136.48	1.352e-8	1.131e-6
Regulation of TP53 Degradation	Reactome	5	TP53, ATM, MTOR, MDM2, CDKN2A	36	32	52.13	3.443e-8	2.569e-6
p53 signaling pathway	KEGG	6	TP53, ATM, CCND1, ATR, MDM2, CDKN2A	75	32	30.03	3.855e-8	2.827e-6
Glioma	KEGG	6	TP53, CCND1, MTOR, RB1, MDM2, CDKN2A	76	32	29.63	4.178e-8	3.034e-6
Pancreatic cancer	KEGG	6	TP53, CCND1, MTOR, RB1, CDKN2A, VEGFA	77	32	29.25	4.523e-8	3.260e-6
Human cytomegalovirus infection	KEGG	8	TP53, CCND1, MTOR, RB1, MDM2, TNF, CDKN2A, VEGFA	226	32	13.29	9.901e-8	6.470e-6
Cell cycle	KEGG	7	TP53, ATM, CCND1, RB1, ATR, MDM2, CDKN2A	158	32	16.63	1.524e-7	9.437e-6
Endocrine resistance	KEGG	6	TP53, CCND1, MTOR, RB1, MDM2, CDKN2A	99	32	22.75	2.052e-7	1.222e-5
Hepatocellular carcinoma	KEGG	7	TP53, CCND1, MTOR, RB1, SMARCA4, CDKN2A, WNT7A	170	32	15.45	2.513e-7	1.459e-5
Proteoglycans in cancer	KEGG	7	TP53, CCND1, MTOR, MDM2, TNF, WNT7A, VEGFA	204	32	12.88	8.640e-7	4.299e-5
Melanoma	KEGG	5	TP53, CCND1, RB1, MDM2, CDKN2A	73	32	25.71	1.280e-6	6.055e-5
Non-small cell lung cancer	KEGG	5	TP53, CCND1, RB1, CDKN2A, FHIT	73	32	25.71	1.280e-6	6.055e-5