

GeDiPNet Cluster 507 -- 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 00:03:14

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Stabilization of p53	Reactome	2	CDKN2A, TP53	11	5	436.73	7.615e-6	2.329e-4
SUMOylation of transcription factors	Reactome	2	CDKN2A, TP53	18	5	266.89	2.116e-5	5.461e-4
Hepatocellular carcinoma	KEGG	3	CDKN2A, TP53, WNT7A	170	5	42.39	2.729e-5	6.726e-4
Oncogene Induced Senescence	Reactome	2	CDKN2A, TP53	33	5	145.58	7.284e-5	1.474e-3
Regulation of TP53 Degradation	Reactome	2	CDKN2A, TP53	36	5	133.44	8.687e-5	1.698e-3
Transcriptional Regulation by VENTX	Reactome	2	CDKN2A, TP53	38	5	126.42	9.690e-5	1.849e-3
Bladder cancer	KEGG	2	CDKN2A, TP53	41	5	117.17	1.130e-4	2.093e-3
Basal cell carcinoma	KEGG	2	TP53, WNT7A	63	5	76.25	2.681e-4	4.132e-3
Melanoma	KEGG	2	CDKN2A, TP53	73	5	65.81	3.601e-4	5.182e-3
Non-small cell lung cancer	KEGG	2	CDKN2A, TP53	73	5	65.81	3.601e-4	5.182e-3
Platinum drug resistance	KEGG	2	CDKN2A, TP53	75	5	64.05	3.801e-4	5.403e-3
p53 signaling pathway	KEGG	2	CDKN2A, TP53	75	5	64.05	3.801e-4	5.403e-3
Glioma	KEGG	2	CDKN2A, TP53	76	5	63.21	3.904e-4	5.517e-3
Pancreatic cancer	KEGG	2	CDKN2A, TP53	77	5	62.39	4.007e-4	5.629e-3
Chronic myeloid leukemia	KEGG	2	CDKN2A, TP53	77	5	62.39	4.007e-4	5.629e-3