

GeDiPNet Cluster 381 -- 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 10:42:52

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
SMAD2/3 Phosphorylation Motif Mutants in Cancer	Reactome	2	SMAD3, TGFB1	6	51	78.50	2.623e-4	4.829e-3
TGFBR1 KD Mutants in Cancer	Reactome	2	SMAD3, TGFB1	6	51	78.50	2.623e-4	4.829e-3
RUNX3 regulates CDKN1A transcription	Reactome	2	SMAD3, TGFB1	7	51	67.28	3.663e-4	6.266e-3
TGF-beta receptor signaling activates SMADs	Reactome	2	SMAD3, TGFB1	12	51	39.25	1.136e-3	1.494e-2
Downregulation of TGF-beta receptor signaling	Reactome	2	SMAD3, TGFB1	16	51	29.44	2.042e-3	2.317e-2
Integrin cell surface interactions	Reactome	3	COL4A2, KDR, SPP1	81	51	8.72	4.876e-3	4.321e-2
ECM-receptor interaction	KEGG	3	COL4A2, RELN, SPP1	89	51	7.94	6.338e-3	5.112e-2
Rheumatoid arthritis	KEGG	3	CSF1, TGFB1, TNFSF11	95	51	7.44	7.589e-3	5.757e-2
Influenza Virus Induced Apoptosis	Reactome	1	TGFB1	2	51	117.75	8.475e-3	6.198e-2
TGFBR2 MSI Frameshift Mutants in Cancer	Reactome	1	TGFB1	2	51	117.75	8.475e-3	6.198e-2
Signaling by PDGF	Reactome	2	COL4A2, SPP1	33	51	14.27	8.582e-3	6.257e-2
AGE-RAGE signaling pathway in diabetic complications	KEGG	3	COL4A2, SMAD3, TGFB1	101	51	6.99	8.976e-3	6.423e-2
Focal adhesion	KEGG	4	COL4A2, KDR, RELN, SPP1	203	51	4.64	1.066e-2	7.140e-2
Post-translational protein phosphorylation	Reactome	3	AHSG, CSF1, SPP1	108	51	6.54	1.077e-2	7.186e-2
Molecules associated with elastic fibres	Reactome	2	LTBP3, TGFB1	38	51	12.39	1.127e-2	7.364e-2