

GeDiPNet Cluster 361 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 11:42:00

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Regulation by TREX1	Reactome	1	TREX1	1	8	1501.25	6.661e-4	1.017e-2
Defective LFNG causes SCDO3	Reactome	1	NOTCH3	5	8	300.25	3.327e-3	3.351e-2
Pre-NOTCH Processing in Golgi	Reactome	1	NOTCH3	6	8	250.21	3.991e-3	3.823e-2
Ligand-receptor interactions	Reactome	1	GAS1	7	8	214.46	4.655e-3	4.241e-2
Noncanonical activation of NOTCH3	Reactome	1	NOTCH3	8	8	187.66	5.318e-3	4.649e-2
IRF3-mediated induction of type I IFN	Reactome	1	TREX1	13	8	115.48	8.629e-3	6.395e-2
NOTCH3 Intracellular Domain Regulates Transcription	Reactome	1	NOTCH3	18	8	83.40	1.193e-2	7.793e-2
Activation of SMO	Reactome	1	GAS1	18	8	83.40	1.193e-2	7.793e-2
NOTCH3 Activation and Transmission of Signal to the Nucleus	Reactome	1	NOTCH3	19	8	79.01	1.259e-2	8.073e-2
MicroRNAs in cancer	KEGG	2	NOTCH3, PDGFRB	311	8	9.65	1.688e-2	9.628e-2
Notch-HLH transcription pathway	Reactome	1	NOTCH3	28	8	53.62	1.850e-2	1.016e-1
Downstream signal transduction	Reactome	1	PDGFRB	29	8	51.77	1.916e-2	1.035e-1
Human papillomavirus infection	KEGG	2	NOTCH3, PDGFRB	333	8	9.02	1.921e-2	1.037e-1
Pre-NOTCH Transcription and Translation	Reactome	1	NOTCH3	31	8	48.43	2.047e-2	1.072e-1
Signaling by PDGF	Reactome	1	PDGFRB	33	8	45.49	2.178e-2	1.113e-1