

GeDiPNet Cluster 151 -- 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 08:19:30

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Notch signaling pathway	KEGG	2	DLL3, NOTCH1	62	18	21.52	3.804e-3	3.695e-2
Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	Reactome	1	TFAP2A	3	18	222.41	4.490e-3	4.138e-2
TFAP2 (AP-2) family regulates transcription of other transcription factors	Reactome	1	TFAP2A	4	18	166.81	5.982e-3	5.030e-2
TFAP2 (AP-2) family regulates transcription of cell cycle factors	Reactome	1	TFAP2A	5	18	133.44	7.473e-3	5.806e-2
TFAP2A acts as a transcriptional repressor during retinoic acid induced cell differentiation	Reactome	1	TFAP2A	5	18	133.44	7.473e-3	5.806e-2
Defective LFNG causes SCDO3	Reactome	1	NOTCH1	5	18	133.44	7.473e-3	5.806e-2
Loss of Function of FBXW7 in Cancer and NOTCH1 Signaling	Reactome	1	NOTCH1	5	18	133.44	7.473e-3	5.806e-2
Th1 and Th2 cell differentiation	KEGG	2	DLL3, NOTCH1	93	18	14.35	8.373e-3	6.263e-2
Pre-NOTCH Processing in Golgi	Reactome	1	NOTCH1	6	18	111.20	8.961e-3	6.534e-2
Protein repair	Reactome	1	TXN	6	18	111.20	8.961e-3	6.534e-2
Endocrine resistance	KEGG	2	DLL3, NOTCH1	99	18	13.48	9.444e-3	6.764e-2
Constitutive Signaling by NOTCH1 t(7;9)(NOTCH1:M1580_K2555) Translocation Mutant	Reactome	1	NOTCH1	7	18	95.32	1.045e-2	7.203e-2
Calmodulin induced events	Reactome	1	GRK2	7	18	95.32	1.045e-2	7.203e-2
Metal ion SLC transporters	Reactome	1	SLC31A1	9	18	74.14	1.341e-2	8.370e-2
Negative regulation of activity of TFAP2 (AP-2) family transcription factors	Reactome	1	TFAP2A	9	18	74.14	1.341e-2	8.370e-2