

GeDiPNet Cluster 292 -- 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 04:51:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Lectin pathway of complement activation	Reactome	3	COLEC10, COLEC11, MASP1	8	8	562.97	1.085e-8	9.360e-7
Initial triggering of complement	Reactome	3	COLEC10, COLEC11, MASP1	17	8	264.93	1.313e-7	8.294e-6
Scavenging by Class A Receptors	Reactome	2	COLEC11, MASP1	11	8	272.95	2.129e-5	6.294e-4
Defective SLC26A2 causes chondrodysplasias	Reactome	1	SLC26A2	1	8	1501.25	6.661e-4	9.955e-3
Ficolins bind to repetitive carbohydrate structures on the target cell surface	Reactome	1	MASP1	5	8	300.25	3.327e-3	3.313e-2
FasL/ CD95L signaling	Reactome	1	FADD	5	8	300.25	3.327e-3	3.313e-2
Transport and synthesis of PAPS	Reactome	1	SLC26A2	6	8	250.21	3.991e-3	3.767e-2
TLR3-mediated TICAM1-dependent programmed cell death	Reactome	1	FADD	6	8	250.21	3.991e-3	3.767e-2
FGFR1b ligand binding and activation	Reactome	1	FGF3	6	8	250.21	3.991e-3	3.767e-2
TRAIL signaling	Reactome	1	FADD	8	8	187.66	5.318e-3	4.557e-2
Multifunctional anion exchangers	Reactome	1	SLC26A2	9	8	166.81	5.981e-3	4.925e-2
TRIF-mediated programmed cell death	Reactome	1	FADD	10	8	150.13	6.644e-3	5.278e-2
FGFR2b ligand binding and activation	Reactome	1	FGF3	10	8	150.13	6.644e-3	5.278e-2
Regulation by c-FLIP	Reactome	1	FADD	11	8	136.48	7.306e-3	5.623e-2
CASP8 activity is inhibited	Reactome	1	FADD	11	8	136.48	7.306e-3	5.623e-2