

GeDiPNet Cluster 379 -- 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 12:21:45

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
DNA replication	KEGG	3	RNASEH2A, RNASEH2B, RNASEH2C	36	8	125.10	1.371e-6	6.423e-5
Cytosolic DNA-sensing pathway	KEGG	3	ADAR, SAMHD1, TREX1	83	8	54.26	1.738e-5	5.328e-4
Regulation by TREX1	Reactome	1	TREX1	1	8	1501.25	6.661e-4	9.955e-3
Nucleobase catabolism	Reactome	1	SAMHD1	1	8	1501.25	6.661e-4	9.955e-3
Interferon alpha/beta signaling	Reactome	2	ADAR, SAMHD1	67	8	44.81	8.401e-4	1.188e-2
RIG-I-like receptor signaling pathway	KEGG	2	ADAR, IFIH1	72	8	41.70	9.695e-4	1.325e-2
C6 deamination of adenosine	Reactome	1	ADAR	2	8	750.63	1.332e-3	1.681e-2
Formation of editosomes by ADAR proteins	Reactome	1	ADAR	2	8	750.63	1.332e-3	1.681e-2
Measles	KEGG	2	ADAR, IFIH1	139	8	21.60	3.558e-3	3.470e-2
Influenza A	KEGG	2	ADAR, IFIH1	173	8	17.36	5.456e-3	4.639e-2
SLBP independent Processing of Histone Pre-mRNAs	Reactome	1	LSM11	10	8	150.13	6.644e-3	5.278e-2
SLBP Dependent Processing of Replication-Dependent Histone Pre-mRNAs	Reactome	1	LSM11	11	8	136.48	7.306e-3	5.623e-2
NF-kB activation through FADD/RIP-1 pathway mediated by caspase-8 and -10	Reactome	1	IFIH1	12	8	125.10	7.968e-3	5.956e-2
IRF3-mediated induction of type I IFN	Reactome	1	TREX1	13	8	115.48	8.629e-3	6.279e-2
TRAF3-dependent IRF activation pathway	Reactome	1	IFIH1	14	8	107.23	9.290e-3	6.561e-2