

GeDiPNet Cluster 383 -- 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 12:25:04

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
tRNA modification in the nucleus and cytosol	Reactome	1	ADAT3	19	5	126.42	7.886e-3	5.921e-2
Transport of Ribonucleoproteins into the Host Nucleus	Reactome	1	AAAS	31	5	77.48	1.284e-2	7.922e-2
NEP/NS2 Interacts with the Cellular Export Machinery	Reactome	1	AAAS	31	5	77.48	1.284e-2	7.922e-2
Regulation of Glucokinase by Glucokinase Regulatory Protein	Reactome	1	AAAS	31	5	77.48	1.284e-2	7.922e-2
Defective TPR may confer susceptibility towards thyroid papillary carcinoma (TPC)	Reactome	1	AAAS	31	5	77.48	1.284e-2	7.922e-2
Vpr-mediated nuclear import of PICs	Reactome	1	AAAS	33	5	72.79	1.367e-2	8.229e-2
Fructose and mannose metabolism	KEGG	1	GMPPA	34	5	70.65	1.408e-2	8.377e-2
Transport of the SLBP independent Mature mRNA	Reactome	1	AAAS	34	5	70.65	1.408e-2	8.377e-2
SUMOylation of SUMOylation proteins	Reactome	1	AAAS	34	5	70.65	1.408e-2	8.377e-2
Rev-mediated nuclear export of HIV RNA	Reactome	1	AAAS	34	5	70.65	1.408e-2	8.377e-2
Transport of the SLBP Dependant Mature mRNA	Reactome	1	AAAS	35	5	68.63	1.449e-2	8.530e-2
Nuclear Pore Complex (NPC) Disassembly	Reactome	1	AAAS	35	5	68.63	1.449e-2	8.530e-2
Biosynthesis of nucleotide sugars	KEGG	1	GMPPA	37	5	64.92	1.531e-2	8.806e-2
NS1 Mediated Effects on Host Pathways	Reactome	1	AAAS	37	5	64.92	1.531e-2	8.806e-2
Amino sugar and nucleotide sugar metabolism	KEGG	1	GMPPA	38	5	63.21	1.572e-2	8.957e-2