

GeDiPNet Cluster 347 -- 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 16:13:28

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Pyrimidine biosynthesis	Reactome	2	CAD, UMPS	3	5	1601.33	4.159e-7	2.282e-5
Arginine biosynthesis	KEGG	2	CAD, CPS1	23	5	208.87	3.496e-5	9.503e-4
Alanine, aspartate and glutamate metabolism	KEGG	2	CAD, CPS1	37	5	129.84	9.182e-5	2.093e-3
Pyrimidine metabolism	KEGG	2	CAD, UMPS	58	5	82.83	2.271e-4	4.330e-3
Biosynthesis of cofactors	KEGG	2	CAD, UMPS	154	5	31.19	1.593e-3	1.932e-2
HuR (ELAVL1) binds and stabilizes mRNA	Reactome	1	NUP214	8	5	300.25	3.327e-3	3.313e-2
Urea cycle	Reactome	1	CPS1	10	5	240.20	4.157e-3	3.874e-2
Nitrogen metabolism	KEGG	1	CPS1	17	5	141.29	7.059e-3	5.493e-2
Transport of Ribonucleoproteins into the Host Nucleus	Reactome	1	NUP214	31	5	77.48	1.284e-2	7.922e-2
NEP/NS2 Interacts with the Cellular Export Machinery	Reactome	1	NUP214	31	5	77.48	1.284e-2	7.922e-2
Regulation of Glucokinase by Glucokinase Regulatory Protein	Reactome	1	NUP214	31	5	77.48	1.284e-2	7.922e-2
Defective TPR may confer susceptibility towards thyroid papillary carcinoma (TPC)	Reactome	1	NUP214	31	5	77.48	1.284e-2	7.922e-2
Vpr-mediated nuclear import of PICs	Reactome	1	NUP214	33	5	72.79	1.367e-2	8.229e-2
Transport of the SLBP independent Mature mRNA	Reactome	1	NUP214	34	5	70.65	1.408e-2	8.377e-2
SUMOylation of SUMOylation proteins	Reactome	1	NUP214	34	5	70.65	1.408e-2	8.377e-2