

GeDiPNet Cluster 344 -- 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 05:42:19

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective HK1 causes hexokinase deficiency (HK deficiency)	Reactome	1	HK1	1	48	250.21	3.997e-3	3.823e-2
Acetylation	Reactome	1	NAT2	2	48	125.10	7.978e-3	6.070e-2
Inositol transporters	Reactome	1	SLC2A13	2	48	125.10	7.978e-3	6.070e-2
Mitophagy - animal	KEGG	3	EIF2AK3, SP1, PRKN	105	48	7.15	8.445e-3	6.304e-2
Th17 cell differentiation	KEGG	3	IL2, IL21, IRF4	109	48	6.89	9.353e-3	6.725e-2
TRAF3 deficiency - HSE	Reactome	1	TRAF3	3	48	83.40	1.194e-2	7.793e-2
RUNX2 regulates osteoblast differentiation	Reactome	1	RUNX2	3	48	83.40	1.194e-2	7.793e-2
RUNX2 regulates genes involved in differentiation of myeloid cells	Reactome	1	RUNX2	4	48	62.55	1.589e-2	9.310e-2
Yersinia infection	KEGG	3	CD8B, IL2, MAP2K6	138	48	5.44	1.762e-2	9.880e-2
Measles	KEGG	3	EIF2AK3, IL2, TRAF3	139	48	5.40	1.796e-2	9.992e-2
Alcoholic liver disease	KEGG	3	MAP2K6, TRA2B, TRAF3	144	48	5.21	1.971e-2	1.051e-1
Neomycin, kanamycin and gentamicin biosynthesis	KEGG	1	HK1	5	48	50.04	1.983e-2	1.052e-1
PERK regulates gene expression	Reactome	1	EIF2AK3	5	48	50.04	1.983e-2	1.052e-1
RUNX2 regulates genes involved in cell migration	Reactome	1	RUNX2	5	48	50.04	1.983e-2	1.052e-1
Caffeine metabolism	KEGG	1	NAT2	6	48	41.70	2.375e-2	1.170e-1