

GeDiPNet Cluster 637 -- 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: 2026-10-20 03:30:09. · Rows: 10 · Generated: 2026-10-20 00:03:00

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Regulation of cholesterol biosynthesis by SREBP (SREBF)	Reactome	1	SREBF1	7	1	1715.71	5.828e-4	7.518e-3
NR1H2 & NR1H3 regulate gene expression linked to lipogenesis	Reactome	1	SREBF1	9	1	1334.44	7.494e-4	9.089e-3
RORA activates gene expression	Reactome	1	SREBF1	18	1	667.22	1.499e-3	1.536e-2
Activation of gene expression by SREBF (SREBP)	Reactome	1	SREBF1	42	1	285.95	3.497e-3	2.831e-2
Insulin resistance	KEGG	1	SREBF1	109	1	110.18	9.076e-3	5.365e-2
PPARA activates gene expression	Reactome	1	SREBF1	115	1	104.43	9.575e-3	5.543e-2
AMPK signaling pathway	KEGG	1	SREBF1	122	1	98.44	1.016e-2	5.739e-2
Insulin signaling pathway	KEGG	1	SREBF1	138	1	87.03	1.149e-2	6.195e-2
Alcoholic liver disease	KEGG	1	SREBF1	144	1	83.40	1.199e-2	6.340e-2
Non-alcoholic fatty liver disease	KEGG	1	SREBF1	157	1	76.50	1.307e-2	6.683e-2