

GeDiPNet Cluster 279 -- 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 21:33:47

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Transcriptional regulation of granulopoiesis	Reactome	2	CEBPA, RXRA	14	43	39.90	1.109e-3	1.465e-2
Regulation of Apoptosis	Reactome	1	OMA1	2	43	139.65	7.148e-3	5.543e-2
Defective Mismatch Repair Associated With MSH6	Reactome	1	MSH6	2	43	139.65	7.148e-3	5.543e-2
Defective Mismatch Repair Associated With MSH2	Reactome	1	MSH6	3	43	93.10	1.070e-2	7.162e-2
NR1H2 & NR1H3 regulate gene expression to limit cholesterol uptake	Reactome	1	RXRA	5	43	55.86	1.778e-2	9.657e-2
NR1H2 & NR1H3 regulate gene expression linked to triglyceride lipolysis in adipose	Reactome	1	RXRA	5	43	55.86	1.778e-2	9.657e-2
NR1H2 & NR1H3 regulate gene expression linked to gluconeogenesis	Reactome	1	RXRA	5	43	55.86	1.778e-2	9.657e-2
Reelin signalling pathway	Reactome	1	DAB1	5	43	55.86	1.778e-2	9.657e-2
Chylomicron clearance	Reactome	1	LIPC	5	43	55.86	1.778e-2	9.657e-2
Transcriptional regulation of white adipocyte differentiation	Reactome	2	CEBPA, RXRA	67	43	8.34	2.390e-2	1.137e-1
Synthesis, secretion, and inactivation of Glucose-dependent Insulinotropic Polypeptide (GIP)	Reactome	1	DPP4	7	43	39.90	2.480e-2	1.158e-1
NR1H2 & NR1H3 regulate gene expression linked to lipogenesis	Reactome	1	RXRA	9	43	31.03	3.178e-2	1.331e-1
NR1H2 & NR1H3 regulate gene expression to control bile acid homeostasis	Reactome	1	RXRA	9	43	31.03	3.178e-2	1.331e-1
Synthesis of pyrophosphates in the cytosol	Reactome	1	PPIP5K2	10	43	27.93	3.525e-2	1.414e-1
Organic cation transport	Reactome	1	SLC22A4	10	43	27.93	3.525e-2	1.414e-1