

GeDiPNet Cluster 540 -- 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: 15 · Generated: 2026-10-20 00:02:46

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cholesterol metabolism	KEGG	3	APOB, PCSK9, ANGPTL3	51	7	100.92	2.495e-6	9.116e-5
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	Reactome	3	APOB, MMP1, PCSK9	125	7	41.18	3.737e-5	8.660e-4
LDL clearance	Reactome	2	APOB, PCSK9	18	7	190.63	4.436e-5	9.945e-4
Lipid and atherosclerosis	KEGG	3	APOB, MMP1, PPP3CB	216	7	23.83	1.904e-4	3.160e-3
Degradation of the extracellular matrix	Reactome	2	ELN, MMP1	70	7	49.02	6.901e-4	8.557e-3
Post-translational protein phosphorylation	Reactome	2	APOB, PCSK9	108	7	31.77	1.634e-3	1.642e-2
LDL remodeling	Reactome	1	APOB	3	7	571.90	1.748e-3	1.725e-2
Scavenging by Class H Receptors	Reactome	1	APOB	4	7	428.93	2.330e-3	2.129e-2
Chylomicron clearance	Reactome	1	APOB	5	7	343.14	2.911e-3	2.492e-2
Scavenging by Class B Receptors	Reactome	1	APOB	5	7	343.14	2.911e-3	2.492e-2
VLDL assembly	Reactome	1	APOB	5	7	343.14	2.911e-3	2.492e-2
VLDL clearance	Reactome	1	APOB	5	7	343.14	2.911e-3	2.492e-2
Scavenging by Class F Receptors	Reactome	1	APOB	6	7	285.95	3.493e-3	2.829e-2
Tuberculosis	KEGG	2	PPP3CB, VDR	181	7	18.96	4.513e-3	3.406e-2
NR1H2 & NR1H3 regulate gene expression linked to lipogenesis	Reactome	1	ANGPTL3	9	7	190.63	5.235e-3	3.760e-2