

GeDiPNet Cluster 293 -- 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 14:32:37

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cholesterol metabolism	KEGG	5	APOA1, ABCA1, APOB, ANGPTL3, PCSK9	51	8	147.18	6.262e-11	9.372e-9
Defective ABCA1 causes Tangier disease	Reactome	2	APOA1, ABCA1	2	8	1501.25	3.883e-7	2.151e-5
Fat digestion and absorption	KEGG	3	APOA1, ABCA1, APOB	43	8	104.74	2.364e-6	1.018e-4
Scavenging by Class B Receptors	Reactome	2	APOA1, APOB	5	8	600.50	3.879e-6	1.546e-4
HDL assembly	Reactome	2	APOA1, ABCA1	8	8	375.31	1.085e-5	3.593e-4
Chylomicron remodeling	Reactome	2	APOA1, APOB	9	8	333.61	1.395e-5	4.419e-4
Chylomicron assembly	Reactome	2	APOA1, APOB	9	8	333.61	1.395e-5	4.419e-4
Scavenging by Class A Receptors	Reactome	2	APOA1, APOB	11	8	272.95	2.129e-5	6.294e-4
Post-translational protein phosphorylation	Reactome	3	APOA1, APOB, PCSK9	108	8	41.70	3.833e-5	1.025e-3
LDL clearance	Reactome	2	APOB, PCSK9	18	8	166.81	5.909e-5	1.463e-3
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	Reactome	3	APOA1, APOB, PCSK9	125	8	36.03	5.933e-5	1.468e-3
Vitamin digestion and absorption	KEGG	2	APOA1, APOB	26	8	115.48	1.252e-4	2.685e-3
Lipid and atherosclerosis	KEGG	3	APOA1, ABCA1, APOB	216	8	20.85	3.006e-4	5.370e-3
Retinoid metabolism and transport	Reactome	2	APOA1, APOB	41	8	73.23	3.143e-4	5.562e-3
Vitamin E	Reactome	1	TTPA	1	8	1501.25	6.661e-4	9.955e-3