

GeDiPNet Cluster 185 -- 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 06:19:17

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
HDL remodeling	Reactome	2	APOA1, ALB	10	5	480.40	6.232e-6	2.256e-4
Scavenging of heme from plasma	Reactome	2	APOA1, ALB	13	5	369.54	1.080e-5	3.579e-4
Retinoid metabolism and transport	Reactome	2	TTR, APOA1	41	5	117.17	1.130e-4	2.476e-3
Thyroid hormone synthesis	KEGG	2	TTR, ALB	75	5	64.05	3.801e-4	6.447e-3
Post-translational protein phosphorylation	Reactome	2	APOA1, ALB	108	5	44.48	7.872e-4	1.137e-2
Amyloid fiber formation	Reactome	2	TTR, APOA1	109	5	44.07	8.018e-4	1.153e-2
Defective ABCA1 causes Tangier disease	Reactome	1	APOA1	2	5	1201.00	8.325e-4	1.182e-2
Platelet degranulation	Reactome	2	APOA1, ALB	123	5	39.06	1.020e-3	1.375e-2
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	Reactome	2	APOA1, ALB	125	5	38.43	1.053e-3	1.409e-2
Regulation of thyroid hormone activity	Reactome	1	DIO1	3	5	800.67	1.249e-3	1.600e-2
HDL clearance	Reactome	1	APOA1	5	5	480.40	2.080e-3	2.349e-2
Scavenging by Class B Receptors	Reactome	1	APOA1	5	5	480.40	2.080e-3	2.349e-2
HDL assembly	Reactome	1	APOA1	8	5	300.25	3.327e-3	3.313e-2
Chylomicron remodeling	Reactome	1	APOA1	9	5	266.89	3.742e-3	3.593e-2
Chylomicron assembly	Reactome	1	APOA1	9	5	266.89	3.742e-3	3.593e-2