

GeDiPNet Cluster 221 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 12:16:36

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Amyloid fiber formation	Reactome	8	FGA, LYZ, APCS, APP, GSN, TTR, APOA1, B2M	109	19	46.39	2.468e-12	4.674e-10
Post-translational protein phosphorylation	Reactome	4	FGA, APOE, APP, APOA1	108	19	23.41	2.160e-5	6.499e-4
Retinoid metabolism and transport	Reactome	3	APOE, TTR, APOA1	41	19	46.25	3.445e-5	9.521e-4
Platelet degranulation	Reactome	4	FGA, APP, SERPINE1, APOA1	123	19	20.56	3.605e-5	9.872e-4
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	Reactome	4	FGA, APOE, APP, APOA1	125	19	20.23	3.841e-5	1.042e-3
Neutrophil degranulation	Reactome	6	LYZ, DSP, GSN, PSEN1, TTR, B2M	480	19	7.90	6.871e-5	1.671e-3
Chylomicron remodeling	Reactome	2	APOE, APOA1	9	19	140.47	8.480e-5	1.982e-3
Chylomicron assembly	Reactome	2	APOE, APOA1	9	19	140.47	8.480e-5	1.982e-3
HDL remodeling	Reactome	2	APOE, APOA1	10	19	126.42	1.059e-4	2.376e-3
Scavenging by Class A Receptors	Reactome	2	APOE, APOA1	11	19	114.93	1.293e-4	2.789e-3
IL-6-type cytokine receptor ligand interactions	Reactome	2	OSMR, IL31RA	17	19	74.37	3.180e-4	5.700e-3
Nuclear signaling by ERBB4	Reactome	2	APOE, PSEN1	24	19	52.68	6.410e-4	9.880e-3
Cholesterol metabolism	KEGG	2	APOE, APOA1	51	19	24.79	2.887e-3	3.045e-2
ECM proteoglycans	Reactome	2	APP, SERPINE1	51	19	24.79	2.887e-3	3.045e-2
Defective ABCA1 causes Tangier disease	Reactome	1	APOA1	2	19	316.05	3.162e-3	3.236e-2