

GeDiPNet Cluster 554 -- 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: 2026-10-19 23:20:54

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Scavenging by Class A Receptors	Reactome	3	MSR1, APOB, APOE	11	95	34.48	7.556e-5	1.518e-3
Abacavir transmembrane transport	Reactome	2	SLC22A2, SLC22A3	3	95	84.28	1.848e-4	3.086e-3
Interleukin-4 and Interleukin-13 signaling	Reactome	6	CXCL8, HGF, MCL1, MMP1, PTGS2, TP53	108	95	7.02	2.090e-4	3.399e-3
Transcriptional Regulation by VENTX	Reactome	4	RELA, AGO3, TP53, CDKN2A	38	95	13.31	2.207e-4	3.552e-3
Bladder cancer	KEGG	4	CXCL8, MMP1, TP53, CDKN2A	41	95	12.33	2.973e-4	4.478e-3
Chylomicron clearance	Reactome	2	APOB, APOE	5	95	50.57	6.096e-4	7.795e-3
Lipid and atherosclerosis	KEGG	7	CXCL8, MMP1, PPARG, RELA, APOB, SOD2, TP53	216	95	4.10	1.600e-3	1.616e-2
Chylomicron remodeling	Reactome	2	APOB, APOE	9	95	28.09	2.150e-3	2.009e-2
Chylomicron assembly	Reactome	2	APOB, APOE	9	95	28.09	2.150e-3	2.009e-2
Oncogene Induced Senescence	Reactome	3	AGO3, TP53, CDKN2A	33	95	11.49	2.203e-3	2.045e-2
Detoxification of Reactive Oxygen Species	Reactome	3	GPX3, GPX7, SOD2	34	95	11.15	2.402e-3	2.178e-2
Organic cation transport	Reactome	2	SLC22A2, SLC22A3	10	95	25.28	2.673e-3	2.349e-2
Gastric acid secretion	KEGG	4	GAST, SLC9A1, SST, CFTR	76	95	6.65	3.052e-3	2.575e-2
Stabilization of p53	Reactome	2	TP53, CDKN2A	11	95	22.99	3.251e-3	2.697e-2
Longevity regulating pathway	KEGG	4	PPARG, RELA, SOD2, TP53	90	95	5.62	5.589e-3	3.927e-2