

GeDiPNet Cluster 184 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 14:46:30

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
protein oxidation	GO:0018158	1	APOA1	3	5	1245.80	8.025e-4	1.336e-2
peptidyl-methionine modification	GO:0018206	1	APOA1	3	5	1245.80	8.025e-4	1.336e-2
thyroid hormone catabolic process	GO:0042404	1	DIO1	3	5	1245.80	8.025e-4	1.336e-2
positive regulation of phospholipid efflux	GO:1902995	1	APOA1	4	5	934.35	1.070e-3	1.602e-2
regulation of intestinal cholesterol absorption	GO:0030300	1	APOA1	4	5	934.35	1.070e-3	1.602e-2
negative regulation of glomerular filtration	GO:0003105	1	TTR	4	5	934.35	1.070e-3	1.602e-2
cellular response to calcium ion starvation	GO:0072732	1	ALB	4	5	934.35	1.070e-3	1.602e-2
acylglycerol homeostasis	GO:0055090	1	APOA1	5	5	747.48	1.337e-3	1.833e-2
cellular response to lipoprotein particle stimulus	GO:0071402	1	APOA1	5	5	747.48	1.337e-3	1.833e-2
lipoprotein biosynthetic process	GO:0042158	1	APOA1	6	5	622.90	1.605e-3	2.035e-2
negative regulation of very-low-density lipoprotein particle remodeling	GO:0010903	1	APOA1	6	5	622.90	1.605e-3	2.035e-2
cholesterol import	GO:0070508	1	APOA1	6	5	622.90	1.605e-3	2.035e-2
purine nucleobase metabolic process	GO:0006144	1	TTR	7	5	533.91	1.872e-3	2.238e-2
positive regulation of cholesterol metabolic process	GO:0090205	1	APOA1	7	5	533.91	1.872e-3	2.238e-2
negative regulation of cytokine production involved in immune response	GO:0002719	1	APOA1	7	5	533.91	1.872e-3	2.238e-2