

GeDiPNet Cluster 540 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cholesterol metabolic process	GO:0008203	3	APOB, PCSK9, ANGPTL3	107	7	74.85	6.283e-6	3.800e-4
cholesterol homeostasis	GO:0042632	3	APOB, PCSK9, ANGPTL3	112	7	71.51	7.208e-6	4.218e-4
lipoprotein metabolic process	GO:0042157	2	APOB, PCSK9	26	7	205.35	3.892e-5	1.526e-3
artery morphogenesis	GO:0048844	2	APOB, ANGPTL3	27	7	197.75	4.203e-5	1.616e-3
phospholipid metabolic process	GO:0006644	2	PCSK9, ANGPTL3	66	7	80.90	2.551e-4	6.036e-3
low-density lipoprotein receptor particle metabolic process	GO:0032799	1	PCSK9	1	7	2669.57	3.746e-4	7.813e-3
low-density lipoprotein particle receptor catabolic process	GO:0032802	1	PCSK9	1	7	2669.57	3.746e-4	7.813e-3
nuclear receptor-mediated bile acid signaling pathway	GO:0038185	1	VDR	2	7	1334.79	7.491e-4	1.230e-2
negative regulation of phosphate transmembrane transport	GO:2000186	1	VDR	2	7	1334.79	7.491e-4	1.230e-2
regulation of low-density lipoprotein particle receptor catabolic process	GO:0032803	1	PCSK9	2	7	1334.79	7.491e-4	1.230e-2
regulation of chylomicron remodeling	GO:0090318	1	ANGPTL3	2	7	1334.79	7.491e-4	1.230e-2
animal organ morphogenesis	GO:0009887	2	ELN, VDR	130	7	41.07	9.858e-4	1.448e-2
steroid metabolic process	GO:0008202	2	APOB, PCSK9	135	7	39.55	1.062e-3	1.514e-2
positive regulation of low-density lipoprotein particle receptor catabolic process	GO:0032805	1	PCSK9	3	7	889.86	1.123e-3	1.550e-2
negative regulation of signaling	GO:0023057	1	PPP3CB	3	7	889.86	1.123e-3	1.550e-2