

GeDiPNet Cluster 201 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 00:27:02

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	4	APOB, CUBN, PCSK9, ANGPTL3	107	14	49.90	9.731e-7	8.110e-5
cholesterol homeostasis	GO:0042632	3	APOB, PCSK9, ANGPTL3	112	14	35.75	7.270e-5	2.386e-3
lipoprotein transport	GO:0042953	2	APOB, CUBN	20	14	133.48	9.827e-5	2.981e-3
steroid metabolic process	GO:0008202	3	APOB, CUBN, PCSK9	135	14	29.66	1.266e-4	3.612e-3
lipoprotein metabolic process	GO:0042157	2	APOB, PCSK9	26	14	102.68	1.677e-4	4.450e-3
artery morphogenesis	GO:0048844	2	APOB, ANGPTL3	27	14	98.87	1.810e-4	4.713e-3
lipid storage	GO:0019915	2	ANGPTL3, BSCL2	32	14	83.42	2.552e-4	5.995e-3
lipid metabolic process	GO:0006629	5	APOB, CUBN, PCSK9, ANGPTL3, BSCL2	840	14	7.95	2.585e-4	6.055e-3
S-adenosyl-L-methionine transport	GO:0015805	1	SLC25A26	1	14	1334.79	7.492e-4	1.251e-2
macromolecule methylation	GO:0043414	1	SLC25A26	1	14	1334.79	7.492e-4	1.251e-2
mitochondrial S-adenosyl-L-methionine transmembrane transport	GO:1990543	1	SLC25A26	1	14	1334.79	7.492e-4	1.251e-2
low-density lipoprotein receptor particle metabolic process	GO:0032799	1	PCSK9	1	14	1334.79	7.492e-4	1.251e-2
low-density lipoprotein particle receptor catabolic process	GO:0032802	1	PCSK9	1	14	1334.79	7.492e-4	1.251e-2
phospholipid metabolic process	GO:0006644	2	PCSK9, ANGPTL3	66	14	40.45	1.088e-3	1.588e-2
nuclear receptor-mediated bile acid signaling pathway	GO:0038185	1	VDR	2	14	667.39	1.498e-3	1.912e-2