

GeDiPNet Cluster 327 -- 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 18:03:52

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
isoprenoid biosynthetic process	GO:0008299	2	MVK, HMGCR	13	5	574.98	4.462e-6	2.741e-4
sterol biosynthetic process	GO:0016126	2	MVK, HMGCR	31	5	241.12	2.655e-5	1.114e-3
cholesterol biosynthetic process	GO:0006695	2	MVK, HMGCR	39	5	191.66	4.227e-5	1.589e-3
steroid biosynthetic process	GO:0006694	2	MVK, HMGCR	65	5	115.00	1.183e-4	3.434e-3
cholesterol metabolic process	GO:0008203	2	MVK, HMGCR	107	5	69.86	3.212e-4	7.027e-3
steroid metabolic process	GO:0008202	2	MVK, HMGCR	135	5	55.37	5.107e-4	9.698e-3
isopentenyl diphosphate biosynthetic process, mevalonate pathway	GO:0019287	1	MVK	3	5	1245.80	8.025e-4	1.302e-2
positive regulation of myeloid cell differentiation	GO:0045639	1	CSF3	5	5	747.48	1.337e-3	1.795e-2
coenzyme A metabolic process	GO:0015936	1	HMGCR	5	5	747.48	1.337e-3	1.795e-2
granulocyte colony-stimulating factor signaling pathway	GO:0038158	1	CSF3	5	5	747.48	1.337e-3	1.795e-2
cobalamin metabolic process	GO:0009235	1	MMAB	9	5	415.27	2.406e-3	2.497e-2
regulation of SNARE complex assembly	GO:0035542	1	VPS41	12	5	311.45	3.207e-3	2.913e-2
negative regulation of amyloid-beta clearance	GO:1900222	1	HMGCR	12	5	311.45	3.207e-3	2.913e-2
regulation of actin filament organization	GO:0110053	1	CSF3	13	5	287.49	3.474e-3	3.064e-2
protein targeting to vacuole	GO:0006623	1	VPS41	14	5	266.96	3.741e-3	3.178e-2