

GeDiPNet Cluster 233 -- 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: 2026-10-07 21:58:08

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of fatty acid metabolic process	GO:0045922	8	UGT1A1, UGT1A10, UGT1A3, UGT1A4, UGT1A6, UGT1A7, UGT1A8, UGT1A9	11	174	78.11	7.744e-15	5.025e-12
flavone metabolic process	GO:0051552	5	UGT1A1, UGT1A10, UGT1A7, UGT1A8, UGT1A9	5	174	107.40	6.609e-11	1.957e-8
xenobiotic metabolic process	GO:0006805	12	UGT1A1, ABCB1, CYB5B, HNF4A, SULT2A1, UGT1A10, UGT1A3, UGT1A4, UGT1A6, UGT1A7, UGT1A8, UGT1A9	120	174	10.74	1.280e-9	2.720e-7
lipid metabolic process	GO:0006629	28	HMGCR, PLA2G2A, UGT1A1, ASPG, ABCB4, APOE, CYP7A1, DAGLB, FADS1, FADS2, FUT2, FUT3	840	174	3.58	4.185e-9	7.757e-7
steroid metabolic process	GO:0008202	12	HMGCR, UGT1A1, APOE, CYP7A1, SULT2A1, UGT1A3, UGT1A4, UGT1A5, UGT1A8, ABCA1, SREBF1, SULT2B1	135	174	9.55	4.975e-9	9.041e-7
flavonoid metabolic process	GO:0009812	5	UGT1A1, UGT1A3, UGT1A7, UGT1A8, UGT1A9	12	174	44.75	4.964e-8	6.770e-6
triglyceride homeostasis	GO:0070328	6	ABCG8, ABCG5, APOE, GCKR, HNF4A, MLXIPL	38	174	16.96	1.289e-6	1.029e-4
retinoic acid metabolic process	GO:0042573	5	UGT1A1, UGT1A3, UGT1A7, UGT1A8, UGT1A9	25	174	21.48	3.019e-6	2.046e-4
cholesterol homeostasis	GO:0042632	8	ABCG8, ABCG5, APOE, CYP7A1, FGFR4, HNF4A, TTC39B, ABCA1	112	174	7.67	1.004e-5	5.325e-4
lipid transport	GO:0006869	10	ABCG8, ABCB1, ABCB4, ABCG5, APOE, ATP8B1, SLC10A2, VPS13B, VPS13D, CERT1	189	174	5.68	1.134e-5	5.828e-4
lipid homeostasis	GO:0055088	6	ABCB4, APOE, HNF4A, PNPLA3, THADA, CERT1	55	174	11.72	1.187e-5	6.040e-4
liver development	GO:0001889	7	CPS1, HNF1A, HNF1B, UGT1A10, UGT1A7, UGT1A8, UGT1A9	87	174	8.64	1.680e-5	7.944e-4
response to nutrient	GO:0007584	6	ADSL, ABCG8, ABCG5, GIPR, ABCA1, SREBF1	63	174	10.23	2.617e-5	1.119e-3
cholesterol metabolic process	GO:0008203	7	HMGCR, APOE, CYP7A1, SULT2A1, ABCA1, SREBF1, SULT2B1	107	174	7.03	6.413e-5	2.217e-3
negative regulation of intestinal phytosterol absorption	GO:0010949	2	ABCG8, ABCG5	2	174	107.40	8.621e-5	2.771e-3