

GeDiPNet Cluster 597 -- 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: 2026-10-19 23:19:04

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
carnitine shuttle	GO:0006853	2	CPT1A, CPT2	4	3	3114.50	1.031e-7	1.303e-5
carnitine metabolic process	GO:0009437	2	CPT1A, CPT2	8	3	1557.25	4.810e-7	4.720e-5
long-chain fatty acid metabolic process	GO:0001676	2	CPT1A, CPT2	29	3	429.59	6.970e-6	4.106e-4
fatty acid beta-oxidation	GO:0006635	2	CPT1A, CPT2	48	3	259.54	1.935e-5	9.004e-4
fatty acid metabolic process	GO:0006631	2	CPT1A, CPT2	211	3	59.04	3.778e-4	7.859e-3
response to tetrachloromethane	GO:1904772	1	CPT1A	3	3	2076.33	4.816e-4	9.241e-3
regulation of fatty acid oxidation	GO:0046320	1	CPT1A	5	3	1245.80	8.025e-4	1.283e-2
aflatoxin metabolic process	GO:0046222	1	CPT1A	7	3	889.86	1.123e-3	1.550e-2
positive regulation of fatty acid beta-oxidation	GO:0032000	1	CPT1A	10	3	622.90	1.605e-3	1.885e-2
response to alkaloid	GO:0043279	1	CPT1A	11	3	566.27	1.765e-3	1.990e-2
cellular response to fatty acid	GO:0071398	1	CPT1A	24	3	259.54	3.848e-3	2.937e-2
eating behavior	GO:0042755	1	CPT1A	26	3	239.58	4.168e-3	3.062e-2
liver regeneration	GO:0097421	1	CPT1A	29	3	214.79	4.649e-3	3.237e-2
cytoplasmic pattern recognition receptor signaling pathway	GO:0002753	1	CPT1A	33	3	188.76	5.289e-3	3.427e-2
positive regulation of innate immune response	GO:0045089	1	CPT1A	36	3	173.03	5.769e-3	3.561e-2