

GeDiPNet Cluster 448 -- 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 23:18:19

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
sphinganine biosynthetic process	GO:0046511	2	SPTLC2, SPTLC1	2	6	3114.50	8.591e-8	1.113e-5
positive regulation of lipophagy	GO:1904504	2	SPTLC2, SPTLC1	5	6	1245.80	8.588e-7	7.549e-5
sphingomyelin biosynthetic process	GO:0006686	2	SPTLC2, SPTLC1	11	6	566.27	4.719e-6	3.030e-4
sphingosine biosynthetic process	GO:0046512	2	SPTLC2, SPTLC1	16	6	389.31	1.029e-5	5.556e-4
ceramide biosynthetic process	GO:0046513	2	SPTLC2, SPTLC1	41	6	151.93	7.006e-5	2.373e-3
sphingolipid biosynthetic process	GO:0030148	2	SPTLC2, SPTLC1	45	6	138.42	8.453e-5	2.729e-3
sphingolipid metabolic process	GO:0006665	2	SPTLC2, SPTLC1	59	6	105.58	1.458e-4	4.050e-3
regulation of acetylcholine secretion, neurotransmission	GO:0014056	1	CHRNA3	1	6	3114.50	3.211e-4	7.044e-3
regulation of fat cell apoptotic process	GO:1904649	1	SPTLC1	1	6	3114.50	3.211e-4	7.044e-3
amide biosynthetic process	GO:0043604	1	SPTLC1	2	6	1557.25	6.421e-4	1.113e-2
tRNA wobble base 5-methoxycarbonylmethyl-2-thiouridinylation	GO:0002926	1	ELP1	3	6	1038.17	9.630e-4	1.423e-2
synaptic transmission involved in micturition	GO:0060084	1	CHRNA3	4	6	778.63	1.284e-3	1.669e-2
regulation of erythrocyte differentiation	GO:0045646	1	P4HTM	6	6	519.08	1.925e-3	2.069e-2
response to acetylcholine	GO:1905144	1	CHRNA3	8	6	389.31	2.566e-3	2.402e-2
behavioral response to nicotine	GO:0035095	1	CHRNA3	9	6	346.06	2.887e-3	2.555e-2