GeDiPNet Cluster 649 -- 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: 2026-10-21 12:39:04. · Rows: 15 · Generated: 2026-10-21 08:33:44

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of heart rate by chemical signal	GO:0003062	1	SREBF1	2	1	9343.50	1.070e-4	3.187e-3
negative regulation of triglyceride metabolic process	GO:0090209	1	SREBF1	5	1	3737.40	2.676e-4	6.114e-3
response to fructose	GO:0009750	1	SREBF1	7	1	2669.57	3.746e-4	7.676e-3
regulation of protein targeting to mitochondrion	GO:1903214	1	SREBF1	8	1	2335.88	4.281e-4	8.376e-3
SREBP signaling pathway	GO:0032933	1	SREBF1	9	1	2076.33	4.816e-4	9.070e-3
response to glucagon	GO:0033762	1	SREBF1	10	1	1868.70	5.351e-4	9.696e-3
regulation of fatty acid metabolic process	GO:0019217	1	SREBF1	11	1	1698.82	5.886e-4	1.037e-2
regulation of mitophagy	GO:1901524	1	SREBF1	14	1	1334.79	7.492e-4	1.202e-2
positive regulation of triglyceride biosynthetic process	GO:0010867	1	SREBF1	14	1	1334.79	7.492e-4	1.202e-2
response to fatty acid	GO:0070542	1	SREBF1	18	1	1038.17	9.632e-4	1.398e-2
response to lipid	GO:0033993	1	SREBF1	18	1	1038.17	9.632e-4	1.398e-2
positive regulation of cholesterol biosynthetic process	GO:0045542	1	SREBF1	24	1	778.63	1.284e-3	1.647e-2
cellular response to fatty acid	GO:0071398	1	SREBF1	24	1	778.63	1.284e-3	1.647e-2
response to progesterone	GO:0032570	1	SREBF1	31	1	602.81	1.659e-3	1.897e-2
lipid biosynthetic process	GO:0008610	1	SREBF1	33	1	566.27	1.766e-3	1.956e-2