

GeDiPNet Cluster 597 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:54

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Carnitine metabolism	Reactome	2	CPT1A, CPT2	14	3	571.90	3.783e-6	1.301e-4
Fatty acid degradation	KEGG	2	CPT1A, CPT2	43	3	186.20	3.748e-5	8.671e-4
Fatty acid metabolism	KEGG	2	CPT1A, CPT2	57	3	140.47	6.619e-5	1.363e-3
PPAR signaling pathway	KEGG	2	CPT1A, CPT2	76	3	105.35	1.181e-4	2.157e-3
PPARA activates gene expression	Reactome	2	CPT1A, CPT2	115	3	69.62	2.710e-4	4.169e-3
Thermogenesis	KEGG	2	CPT1A, CPT2	234	3	34.22	1.119e-3	1.234e-2
RORA activates gene expression	Reactome	1	CPT1A	18	3	222.41	4.490e-3	3.394e-2
Signaling by Retinoic Acid	Reactome	1	CPT1A	21	3	190.63	5.237e-3	3.760e-2
Adipocytokine signaling pathway	KEGG	1	CPT1A	70	3	57.19	1.739e-2	7.887e-2
Glucagon signaling pathway	KEGG	1	CPT1A	107	3	37.41	2.649e-2	1.008e-1
Insulin resistance	KEGG	1	CPT1A	109	3	36.73	2.698e-2	1.017e-1
AMPK signaling pathway	KEGG	1	CPT1A	122	3	32.81	3.017e-2	1.086e-1
Alcoholic liver disease	KEGG	1	CPT1A	144	3	27.80	3.554e-2	1.190e-1
Efferocytosis	KEGG	1	CPT1A	157	3	25.50	3.871e-2	1.252e-1
Diabetic cardiomyopathy	KEGG	1	CPT2	205	3	19.53	5.034e-2	1.454e-1