

GeDiPNet Cluster 353 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 10:02:31

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Mitochondrial tRNA aminoacylation	Reactome	2	LARS2, HARS2	14	15	114.38	1.314e-4	2.797e-3
Mitochondrial translation elongation	Reactome	3	DAP3, ERAL1, MRPL49	85	15	28.26	1.464e-4	3.053e-3
Mitochondrial translation termination	Reactome	3	DAP3, ERAL1, MRPL49	87	15	27.61	1.569e-4	3.219e-3
Aminoacyl-tRNA biosynthesis	KEGG	2	LARS2, HARS2	66	15	24.26	2.982e-3	3.062e-2
rRNA processing in the mitochondrion	Reactome	1	PRORP	4	15	200.17	4.987e-3	4.365e-2
tRNA processing in the mitochondrion	Reactome	1	PRORP	5	15	160.13	6.230e-3	5.059e-2
tRNA modification in the mitochondrion	Reactome	1	PRORP	6	15	133.44	7.472e-3	5.688e-2
Beta-oxidation of pristanoyl-CoA	Reactome	1	HSD17B4	9	15	88.96	1.119e-2	7.338e-2
Beta-oxidation of very long chain fatty acids	Reactome	1	HSD17B4	11	15	72.79	1.366e-2	8.229e-2
alpha-linolenic acid (ALA) metabolism	Reactome	1	HSD17B4	13	15	61.59	1.612e-2	9.107e-2
Primary bile acid biosynthesis	KEGG	1	HSD17B4	17	15	47.10	2.104e-2	1.058e-1
Elastic fibre formation	Reactome	1	FBN1	18	15	44.48	2.226e-2	1.093e-1
Cholesterol biosynthesis	Reactome	1	GGPS1	21	15	38.13	2.592e-2	1.188e-1
Terpenoid backbone biosynthesis	KEGG	1	GGPS1	23	15	34.81	2.836e-2	1.251e-1
Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol	Reactome	1	HSD17B4	24	15	33.36	2.958e-2	1.279e-1