

GeDiPNet Cluster 485 -- 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 00:02:54

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	14	122.55	1.139e-4	2.104e-3
Mitochondrial translation elongation	Reactome	3	ERAL1, DAP3, MRPL49	85	14	30.28	1.177e-4	2.152e-3
Mitochondrial translation termination	Reactome	3	ERAL1, DAP3, MRPL49	87	14	29.58	1.262e-4	2.275e-3
Aminoacyl-tRNA biosynthesis	KEGG	2	LARS2, HARS2	66	14	26.00	2.594e-3	2.298e-2
rRNA processing in the mitochondrion	Reactome	1	PRORP	4	14	214.46	4.655e-3	3.479e-2
tRNA processing in the mitochondrion	Reactome	1	PRORP	5	14	171.57	5.816e-3	4.033e-2
tRNA modification in the mitochondrion	Reactome	1	PRORP	6	14	142.98	6.975e-3	4.528e-2
Beta-oxidation of pristanoyl-CoA	Reactome	1	HSD17B4	9	14	95.32	1.045e-2	5.837e-2
Beta-oxidation of very long chain fatty acids	Reactome	1	HSD17B4	11	14	77.99	1.275e-2	6.573e-2
alpha-linolenic acid (ALA) metabolism	Reactome	1	HSD17B4	13	14	65.99	1.506e-2	7.270e-2
Primary bile acid biosynthesis	KEGG	1	HSD17B4	17	14	50.46	1.965e-2	8.492e-2
Elastic fibre formation	Reactome	1	FBN1	18	14	47.66	2.079e-2	8.765e-2
Cholesterol biosynthesis	Reactome	1	GGPS1	21	14	40.85	2.422e-2	9.574e-2
Terpenoid backbone biosynthesis	KEGG	1	GGPS1	23	14	37.30	2.649e-2	1.008e-1
Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol	Reactome	1	HSD17B4	24	14	35.74	2.763e-2	1.031e-1