

GeDiPNet Cluster 244 -- 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 20:15:04

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Respiratory electron transport	Reactome	2	COX1, ND1	83	4	72.35	2.806e-4	5.096e-3
Oxidative phosphorylation	KEGG	2	COX1, ND1	137	4	43.83	7.635e-4	1.109e-2
Diabetic cardiomyopathy	KEGG	2	COX1, ND1	205	4	29.29	1.701e-3	2.025e-2
Chemical carcinogenesis - reactive oxygen species	KEGG	2	COX1, ND1	227	4	26.45	2.081e-3	2.349e-2
Thermogenesis	KEGG	2	COX1, ND1	234	4	25.66	2.210e-3	2.455e-2
Parkinson disease	KEGG	2	COX1, ND1	268	4	22.41	2.890e-3	2.998e-2
Prion disease	KEGG	2	COX1, ND1	275	4	21.84	3.040e-3	3.104e-2
Huntington disease	KEGG	2	COX1, ND1	308	4	19.50	3.801e-3	3.637e-2
Amyotrophic lateral sclerosis	KEGG	2	COX1, ND1	368	4	16.32	5.393e-3	4.601e-2
Alzheimer disease	KEGG	2	COX1, ND1	388	4	15.48	5.982e-3	4.925e-2
Pathways of neurodegeneration - multiple diseases	KEGG	2	COX1, ND1	480	4	12.51	9.065e-3	6.470e-2
Complex I biogenesis	Reactome	1	ND1	55	4	54.59	1.819e-2	9.775e-2
TP53 Regulates Metabolic Genes	Reactome	1	COX1	86	4	34.91	2.834e-2	1.251e-1
Cardiac muscle contraction	KEGG	1	COX1	87	4	34.51	2.867e-2	1.260e-1
Retrograde endocannabinoid signaling	KEGG	1	ND1	149	4	20.15	4.872e-2	1.692e-1