

GeDiPNet Cluster 78 -- 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 07:29:51

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Citric acid cycle (TCA cycle)	Reactome	6	SDHD, SDHA, SDHB, SDHC, DLST, FH	22	38	86.20	4.770e-11	7.410e-9
Citrate cycle (TCA cycle)	KEGG	6	SDHD, SDHA, SDHB, SDHC, DLST, FH	30	38	63.21	3.727e-10	4.689e-8
Tyrosine metabolism	KEGG	6	COMT, DBH, DDC, MAOA, MAOB, TH	36	38	52.68	1.206e-9	1.316e-7
Catecholamine biosynthesis	Reactome	3	DBH, DDC, TH	4	38	237.04	1.166e-7	7.495e-6
Dopaminergic synapse	KEGG	7	AKT1, KIF5B, COMT, DDC, MAOA, MAOB, TH	132	38	16.76	1.569e-7	9.682e-6
Carbon metabolism	KEGG	6	SDHD, SDHA, SDHB, SDHC, DLST, FH	115	38	16.49	1.454e-6	6.755e-5
Parkinson disease	KEGG	8	SDHD, SDHA, SDHB, SDHC, KIF5B, MAOA, MAOB, TH	268	38	9.43	1.516e-6	6.966e-5
Diabetic cardiomyopathy	KEGG	7	SDHD, SDHA, SDHB, SDHC, AKT1, PIK3CA, PTEN	205	38	10.79	3.070e-6	1.268e-4
Chemical carcinogenesis - reactive oxygen species	KEGG	7	SDHD, SDHA, SDHB, SDHC, AKT1, PIK3CA, PTEN	227	38	9.75	6.020e-6	2.202e-4
Tryptophan metabolism	KEGG	4	DDC, MAOA, MAOB, DLST	42	38	30.10	8.749e-6	3.004e-4
Non-alcoholic fatty liver disease	KEGG	6	SDHD, SDHA, SDHB, SDHC, AKT1, PIK3CA	157	38	12.08	8.860e-6	3.038e-4
Enzymatic degradation of Dopamine by monoamine oxidase	Reactome	2	COMT, MAOA	2	38	316.05	9.748e-6	3.283e-4
Biogenic amines are oxidatively deaminated to aldehydes by MAOA and MAOB	Reactome	2	MAOA, MAOB	2	38	316.05	9.748e-6	3.283e-4
Phenylalanine metabolism	KEGG	3	DDC, MAOA, MAOB	16	38	59.26	1.591e-5	4.948e-4
Cocaine addiction	KEGG	4	DDC, MAOA, MAOB, TH	49	38	25.80	1.630e-5	5.033e-4