

GeDiPNet Cluster 598 -- 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 00:02:57

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycerolipid metabolism	KEGG	2	AGK, TKFC	64	7	53.62	5.770e-4	7.470e-3
Vpr-mediated induction of apoptosis by mitochondrial outer membrane permeabilization	Reactome	1	SLC25A4	3	7	571.90	1.748e-3	1.725e-2
Fructose catabolism	Reactome	1	TKFC	5	7	343.14	2.911e-3	2.492e-2
Glycerophospholipid biosynthesis	Reactome	1	AGK	5	7	343.14	2.911e-3	2.492e-2
FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes	Reactome	1	SOD2	10	7	171.57	5.815e-3	4.033e-2
Transport of nucleosides and free purine and pyrimidine bases across the plasma membrane	Reactome	1	SLC25A4	12	7	142.98	6.975e-3	4.528e-2
Chemical carcinogenesis - reactive oxygen species	KEGG	2	SLC25A4, SOD2	227	7	15.12	7.016e-3	4.546e-2
Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	Reactome	1	SOD2	16	7	107.23	9.291e-3	5.428e-2
DDX58/IFIH1-mediated induction of interferon-alpha/beta	Reactome	1	TKFC	17	7	100.92	9.869e-3	5.651e-2
Mitochondrial protein import	Reactome	1	SLC25A4	19	7	90.30	1.102e-2	6.031e-2
Huntington disease	KEGG	2	SLC25A4, SOD2	308	7	11.14	1.264e-2	6.565e-2
Formation of HIV-1 elongation complex containing HIV-1 Tat	Reactome	1	NELFE	23	7	74.60	1.333e-2	6.766e-2
Formation of the Early Elongation Complex	Reactome	1	NELFE	33	7	51.99	1.908e-2	8.331e-2
Fructose and mannose metabolism	KEGG	1	TKFC	34	7	50.46	1.965e-2	8.493e-2
Detoxification of Reactive Oxygen Species	Reactome	1	SOD2	34	7	50.46	1.965e-2	8.493e-2