

GeDiPNet Cluster 492 -- 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 00:03:21

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Vpr-mediated induction of apoptosis by mitochondrial outer membrane permeabilization	Reactome	1	SLC25A4	3	2	2001.67	4.995e-4	6.672e-3
Transport of nucleosides and free purine and pyrimidine bases across the plasma membrane	Reactome	1	SLC25A4	12	2	500.42	1.997e-3	1.898e-2
Mitochondrial protein import	Reactome	1	SLC25A4	19	2	316.05	3.162e-3	2.643e-2
Spinocerebellar ataxia	KEGG	1	SLC25A4	144	2	41.70	2.384e-2	9.482e-2
Cellular senescence	KEGG	1	SLC25A4	157	2	38.25	2.598e-2	9.970e-2
Necroptosis	KEGG	1	SLC25A4	159	2	37.77	2.630e-2	1.005e-1
cGMP-PKG signaling pathway	KEGG	1	SLC25A4	166	2	36.17	2.745e-2	1.027e-1
Influenza A	KEGG	1	SLC25A4	173	2	34.71	2.860e-2	1.053e-1
Neutrophil extracellular trap formation	KEGG	1	SLC25A4	192	2	31.28	3.172e-2	1.118e-1
Diabetic cardiomyopathy	KEGG	1	SLC25A4	205	2	29.29	3.385e-2	1.159e-1
Human T-cell leukemia virus 1 infection	KEGG	1	SLC25A4	224	2	26.81	3.696e-2	1.216e-1
Chemical carcinogenesis - reactive oxygen species	KEGG	1	SLC25A4	227	2	26.45	3.745e-2	1.228e-1
Calcium signaling pathway	KEGG	1	SLC25A4	254	2	23.64	4.185e-2	1.307e-1
Parkinson disease	KEGG	1	SLC25A4	268	2	22.41	4.413e-2	1.347e-1
Prion disease	KEGG	1	SLC25A4	275	2	21.84	4.527e-2	1.368e-1