

GeDiPNet Cluster 333 -- 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 04:00:25

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
tRNA processing in the nucleus	Reactome	3	TSEN2, TSEN34, TSEN54	57	11	57.46	1.628e-5	5.028e-4
Dopamine clearance from the synaptic cleft	Reactome	1	SLC6A3	1	11	1091.82	9.159e-4	1.268e-2
Defective SLC6A3 causes Parkinsonism-dystonia infantile (PKDYS)	Reactome	1	SLC6A3	1	11	1091.82	9.159e-4	1.268e-2
SUMOylation of DNA methylation proteins	Reactome	1	DNMT1	4	11	272.95	3.659e-3	3.541e-2
Formation of ATP by chemiosmotic coupling	Reactome	1	ATP5PO	18	11	60.66	1.637e-2	9.168e-2
Cristae formation	Reactome	1	ATP5PO	18	11	60.66	1.637e-2	9.168e-2
Na+/Cl- dependent neurotransmitter transporters	Reactome	1	SLC6A3	19	11	57.46	1.727e-2	9.499e-2
Parkinson disease	KEGG	2	ATP5PO, SLC6A3	268	11	8.15	2.389e-2	1.137e-1
Striated Muscle Contraction	Reactome	1	NEB	36	11	30.33	3.250e-2	1.348e-1
Cocaine addiction	KEGG	1	SLC6A3	49	11	22.28	4.399e-2	1.596e-1
Cysteine and methionine metabolism	KEGG	1	DNMT1	52	11	21.00	4.663e-2	1.648e-1
Amphetamine addiction	KEGG	1	SLC6A3	69	11	15.82	6.144e-2	1.905e-1
Nonhomologous End-Joining (NHEJ)	Reactome	1	RIF1	69	11	15.82	6.144e-2	1.905e-1
PRC2 methylates histones and DNA	Reactome	1	DNMT1	73	11	14.96	6.489e-2	1.965e-1
Pathways of neurodegeneration - multiple diseases	KEGG	2	ATP5PO, SLC6A3	480	11	4.55	6.906e-2	2.030e-1