

GeDiPNet Cluster 322 -- 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 11:28:32

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Neurotransmitter receptors and postsynaptic signal transmission	Reactome	2	GLRA1, GLRB	9	6	444.81	7.477e-6	2.627e-4
Defective SLC6A5 causes hyperekplexia 3 (HKPX3)	Reactome	1	SLC6A5	1	6	2001.67	4.996e-4	7.955e-3
Biosynthesis of cofactors	KEGG	2	GPHN, RDH11	154	6	26.00	2.369e-3	2.585e-2
Molybdenum cofactor biosynthesis	Reactome	1	GPHN	6	6	333.61	2.994e-3	3.068e-2
Na+/Cl- dependent neurotransmitter transporters	Reactome	1	SLC6A5	19	6	105.35	9.457e-3	6.631e-2
The canonical retinoid cycle in rods (twilight vision)	Reactome	1	RDH11	20	6	100.08	9.952e-3	6.820e-2
Class I peroxisomal membrane protein import	Reactome	1	ATAD1	20	6	100.08	9.952e-3	6.820e-2
RA biosynthesis pathway	Reactome	1	RDH11	22	6	90.98	1.094e-2	7.246e-2
Neuroactive ligand-receptor interaction	KEGG	2	GLRA1, GLRB	370	6	10.82	1.308e-2	8.009e-2
Folate biosynthesis	KEGG	1	GPHN	28	6	71.49	1.391e-2	8.315e-2
Retinoid metabolism and transport	Reactome	1	RDH11	41	6	48.82	2.031e-2	1.037e-1
Retinol metabolism	KEGG	1	RDH11	68	6	29.44	3.350e-2	1.372e-1
Synaptic vesicle cycle	KEGG	1	SLC6A5	79	6	25.34	3.883e-2	1.493e-1
GABAergic synapse	KEGG	1	GPHN	89	6	22.49	4.366e-2	1.590e-1
Metabolic pathways	KEGG	2	GPHN, RDH11	1563	6	2.56	1.779e-1	3.410e-1