

GeDiPNet Cluster 423 -- 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 15:34:47

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Highly calcium permeable nicotinic acetylcholine receptors	Reactome	3	CHRNA2, CHRNA4, CHRNB2	9	12	333.61	6.381e-8	4.429e-6
Highly calcium permeable postsynaptic nicotinic acetylcholine receptors	Reactome	3	CHRNA2, CHRNA4, CHRNB2	12	12	250.21	1.668e-7	1.019e-5
Nicotine addiction	KEGG	3	CHRNA4, CHRNB2, GABRG2	41	12	73.23	7.953e-6	2.769e-4
Neuroactive ligand-receptor interaction	KEGG	5	CHRNA2, CHRNA4, CHRNB2, CRH, GABRG2	370	12	13.52	1.790e-5	5.458e-4
Highly sodium permeable postsynaptic acetylcholine nicotinic receptors	Reactome	2	CHRNA4, CHRNB2	7	12	285.95	1.917e-5	5.784e-4
Amino acids regulate mTORC1	Reactome	2	DEPDC5, ATP6V0C	55	12	36.39	1.320e-3	1.670e-2
Cholinergic synapse	KEGG	2	CHRNA4, CHRNB2	115	12	17.41	5.634e-3	4.741e-2
Synthesis of UDP-N-acetyl-glucosamine	Reactome	1	AMDHD2	8	12	125.10	7.968e-3	5.956e-2
Bicarbonate transporters	Reactome	1	SLC4A10	10	12	100.08	9.951e-3	6.820e-2
GABA receptor activation	Reactome	1	GABRG2	16	12	62.55	1.588e-2	9.016e-2
Class B/2 (Secretin family receptors)	Reactome	1	CRH	18	12	55.60	1.785e-2	9.668e-2
Chemical carcinogenesis - receptor activation	KEGG	2	CHRNA4, CHRNB2	215	12	9.31	1.871e-2	9.904e-2
Ion channel transport	Reactome	1	ATP6V0C	24	12	41.70	2.373e-2	1.132e-1
Insulin receptor recycling	Reactome	1	ATP6V0C	26	12	38.49	2.568e-2	1.182e-1
Collecting duct acid secretion	KEGG	1	ATP6V0C	28	12	35.74	2.763e-2	1.234e-1