

GeDiPNet Cluster 448 -- 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: 12 · Generated: 2026-10-20 00:02:38

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Sphingolipid de novo biosynthesis	Reactome	2	SPTLC2, SPTLC1	43	6	93.10	1.861e-4	3.100e-3
Sphingolipid metabolism	KEGG	2	SPTLC2, SPTLC1	54	6	74.14	2.942e-4	4.444e-3
Sphingolipid signaling pathway	KEGG	2	SPTLC2, SPTLC1	122	6	32.81	1.495e-3	1.536e-2
Highly sodium permeable postsynaptic acetylcholine nicotinic receptors	Reactome	1	CHRNA3	7	6	285.95	3.493e-3	2.829e-2
Highly calcium permeable nicotinic acetylcholine receptors	Reactome	1	CHRNA3	9	6	222.41	4.489e-3	3.394e-2
Highly calcium permeable postsynaptic nicotinic acetylcholine receptors	Reactome	1	CHRNA3	12	6	166.81	5.981e-3	4.097e-2
Activation of Matrix Metalloproteinases	Reactome	1	TPSAB1	33	6	60.66	1.638e-2	7.625e-2
Cholinergic synapse	KEGG	1	CHRNA3	115	6	17.41	5.611e-2	1.547e-1
Influenza A	KEGG	1	TPSAB1	173	6	11.57	8.339e-2	1.942e-1
Chemical carcinogenesis - receptor activation	KEGG	1	CHRNA3	215	6	9.31	1.027e-1	2.195e-1
Neuroactive ligand-receptor interaction	KEGG	1	CHRNA3	370	6	5.41	1.712e-1	3.002e-1
Metabolic pathways	KEGG	2	SPTLC2, SPTLC1	1563	6	2.56	1.779e-1	3.074e-1