

GeDiPNet Cluster 165 -- 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: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-10 07:00:54

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Voltage gated Potassium channels	Reactome	2	KCNQ2, KCNQ3	43	12	46.55	8.078e-4	1.196e-2
Phase 0 - rapid depolarisation	Reactome	2	SCN2A, SCN8A	44	12	45.49	8.458e-4	1.232e-2
Thyroid hormone synthesis	KEGG	2	ATP1A2, CGA	75	12	26.69	2.439e-3	2.735e-2
Cholinergic synapse	KEGG	2	KCNQ2, KCNQ3	115	12	17.41	5.634e-3	4.911e-2
Mineralocorticoid biosynthesis	Reactome	1	CGA	6	12	166.81	5.981e-3	5.107e-2
Thyroxine biosynthesis	Reactome	1	CGA	7	12	142.98	6.975e-3	5.637e-2
Highly calcium permeable nicotinic acetylcholine receptors	Reactome	1	CHRNA2	9	12	111.20	8.960e-3	6.622e-2
Reactions specific to the complex N-glycan synthesis pathway	Reactome	1	CGA	10	12	100.08	9.951e-3	7.054e-2
Androgen biosynthesis	Reactome	1	CGA	11	12	90.98	1.094e-2	7.498e-2
Glycoprotein hormones	Reactome	1	CGA	12	12	83.40	1.193e-2	7.898e-2
Hormone ligand-binding receptors	Reactome	1	CGA	12	12	83.40	1.193e-2	7.898e-2
Highly calcium permeable postsynaptic nicotinic acetylcholine receptors	Reactome	1	CHRNA2	12	12	83.40	1.193e-2	7.898e-2
TFAP2 (AP-2) family regulates transcription of growth factors and their receptors	Reactome	1	CGA	15	12	66.72	1.489e-2	9.000e-2
cAMP signaling pathway	KEGG	2	ATP1A2, CGA	226	12	8.86	2.055e-2	1.086e-1
Proximal tubule bicarbonate reclamation	KEGG	1	ATP1A2	23	12	43.51	2.275e-2	1.150e-1