

GeDiPNet Cluster 55 -- 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 20:15:04

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Synaptic vesicle cycle	KEGG	5	STXBP1, CACNA1A, ATP6V1A, SNAP25, SLC1A3	79	57	13.34	3.472e-5	9.454e-4
GABAergic synapse	KEGG	5	GABRB3, GABRG3, GABBR2, CACNA1A, GPHN	89	57	11.84	6.168e-5	1.513e-3
MECP2 regulates neuronal receptors and channels	Reactome	2	MECP2, PTPN1	4	57	105.35	1.320e-4	2.804e-3
Glutamate Neurotransmitter Release Cycle	Reactome	3	STXBP1, SNAP25, SLC1A3	24	57	26.34	1.911e-4	3.772e-3
Morphine addiction	KEGG	4	GABRB3, GABRG3, GABBR2, CACNA1A	91	57	9.26	8.966e-4	1.250e-2
Nicotine addiction	KEGG	3	GABRB3, GABRG3, CACNA1A	41	57	15.42	9.508e-4	1.306e-2
Phase 0 - rapid depolarisation	Reactome	3	CACNB4, SCN2A, SCN4A	44	57	14.37	1.169e-3	1.526e-2
Presynaptic depolarization and calcium channel opening	Reactome	2	CACNA1A, CACNB4	12	57	35.12	1.417e-3	1.764e-2
GABA synthesis, release, reuptake and degradation	Reactome	2	STXBP1, SNAP25	13	57	32.42	1.669e-3	2.001e-2
GABA receptor activation	Reactome	2	GABRB3, GABRG3	16	57	26.34	2.545e-3	2.729e-2
Acetylcholine Neurotransmitter Release Cycle	Reactome	2	STXBP1, SNAP25	17	57	24.79	2.875e-3	2.986e-2
Serotonin Neurotransmitter Release Cycle	Reactome	2	STXBP1, SNAP25	18	57	23.41	3.225e-3	3.243e-2
Norepinephrine Neurotransmitter Release Cycle	Reactome	2	STXBP1, SNAP25	18	57	23.41	3.225e-3	3.243e-2
Loss of MECP2 binding ability to 5hmC-DNA	Reactome	1	MECP2	1	57	210.70	4.746e-3	4.233e-2
Defective SLC1A3 causes episodic ataxia 6 (EA6)	Reactome	1	SLC1A3	1	57	210.70	4.746e-3	4.233e-2