

GeDiPNet Cluster 129 -- 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 17:44:29

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Neurexins and neuroligins	Reactome	4	NLGN4X, DLG3, CASK, NLGN3	32	106	14.16	1.704e-4	3.447e-3
Sodium/Proton exchangers	Reactome	2	SLC9A7, SLC9A6	9	106	25.18	2.668e-3	2.829e-2
Processing of Capped Intron-Containing Pre-mRNA	Reactome	3	RBMX, HNRNPH1, HNRNPH2	37	106	9.19	4.176e-3	3.885e-2
mRNA Splicing - Major Pathway	Reactome	6	CSTF2, RBMX, UPF3B, HNRNPH1, HNRNPH2, PQBP1	183	106	3.71	5.593e-3	4.714e-2
Rho GTPase cycle	Reactome	5	ARHGEF9, ARHGEF6, GDI1, FGD1, OPHN1	138	106	4.11	7.474e-3	5.688e-2
Defective SLC9A6 causes X-linked, syndromic mental retardation,, Christianson type (MRXSCH)	Reactome	1	SLC9A6	1	106	113.30	8.826e-3	6.364e-2
Defective MAOA causes Brunner syndrome (BRUNS)	Reactome	1	MAOA	1	106	113.30	8.826e-3	6.364e-2
Loss of MECP2 binding ability to 5hmC-DNA	Reactome	1	MECP2	1	106	113.30	8.826e-3	6.364e-2
Defective SLC35A2 causes congenital disorder of glycosylation 2M (CDG2M)	Reactome	1	SLC35A2	1	106	113.30	8.826e-3	6.364e-2
Trafficking of GluR2-containing AMPA receptors	Reactome	2	TSPAN7, GRIA3	17	106	13.33	9.626e-3	6.709e-2
NRAGE signals death through JNK	Reactome	3	ARHGEF9, ARHGEF6, FGD1	55	106	6.18	1.258e-2	7.845e-2
Receptor-type tyrosine-protein phosphatases	Reactome	2	SLITRK2, IL1RAPL1	20	106	11.33	1.322e-2	8.070e-2
mRNA 3'-end processing	Reactome	3	CSTF2, THOC2, UPF3B	58	106	5.86	1.451e-2	8.539e-2
Synaptic adhesion-like molecules	Reactome	2	DLG3, GRIA3	21	106	10.79	1.453e-2	8.539e-2
Unblocking of NMDA receptors, glutamate binding and activation	Reactome	2	DLG3, GRIA3	22	106	10.30	1.589e-2	9.017e-2