

GeDiPNet Cluster 402 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-08 23:43:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Loss of MECP2 binding ability to 5hmC-DNA	Reactome	1	MECP2	1	18	667.22	1.499e-3	1.836e-2
Long-term depression	KEGG	2	CACNA1A, RYR1	60	18	22.24	3.567e-3	3.457e-2
Loss of MECP2 binding ability to 5mC-DNA	Reactome	1	MECP2	3	18	222.41	4.490e-3	4.075e-2
MECP2 regulates neuronal receptors and channels	Reactome	1	MECP2	4	18	166.81	5.982e-3	4.934e-2
Calcium signaling pathway	KEGG	3	CACNA1A, PDGFA, RYR1	254	18	7.88	6.030e-3	4.962e-2
Regulation of MECP2 expression and activity	Reactome	1	MECP2	6	18	111.20	8.961e-3	6.459e-2
Hypertrophic cardiomyopathy	KEGG	2	MYH7, TTN	99	18	13.48	9.444e-3	6.688e-2
COPI-mediated anterograde transport	Reactome	2	COG4, DYNC1H1	101	18	13.21	9.814e-3	6.853e-2
Thyroxine biosynthesis	Reactome	1	TPO	7	18	95.32	1.045e-2	7.130e-2
Dilated cardiomyopathy	KEGG	2	MYH7, TTN	105	18	12.71	1.057e-2	7.188e-2
Platelet degranulation	Reactome	2	PDGFA, TTN	123	18	10.85	1.430e-2	8.624e-2
Transcriptional Regulation by MECP2	Reactome	1	MECP2	10	18	66.72	1.489e-2	8.817e-2
Presynaptic depolarization and calcium channel opening	Reactome	1	CACNA1A	12	18	55.60	1.785e-2	9.870e-2
Spinocerebellar ataxia	KEGG	2	CACNA1A, RYR1	144	18	9.27	1.926e-2	1.030e-1
Regulation of insulin secretion	Reactome	1	CACNA1A	16	18	41.70	2.373e-2	1.157e-1