

GeDiPNet Cluster 51 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 17:02:54

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Tyrosine metabolism	KEGG	4	MAOA, ADH1B, ADH1C, DBH	36	97	13.76	1.932e-4	3.846e-3
Ethanol oxidation	Reactome	2	ADH1B, ADH1C	12	97	20.64	4.042e-3	3.856e-2
Fatty acid degradation	KEGG	3	ADH1B, ADH1C, GCDH	43	97	8.64	4.988e-3	4.437e-2
Defective MAOA causes Brunner syndrome (BRUNS)	Reactome	1	MAOA	1	97	123.81	8.077e-3	6.127e-2
Norepinephrine Neurotransmitter Release Cycle	Reactome	2	MAOA, SLC18A2	18	97	13.76	9.080e-3	6.600e-2
Na+/Cl- dependent neurotransmitter transporters	Reactome	2	SLC6A1, SLC18A2	19	97	13.03	1.010e-2	7.039e-2
Class A/1 (Rhodopsin-like receptors)	Reactome	2	CNR1, CNR2	19	97	13.03	1.010e-2	7.039e-2
Receptor-type tyrosine-protein phosphatases	Reactome	2	PTPRD, PTPRF	20	97	12.38	1.116e-2	7.504e-2
Interleukin-4 and Interleukin-13 signaling	Reactome	4	MAOA, OPRD1, OPRM1, NOS2	108	97	4.59	1.130e-2	7.544e-2
Synaptic adhesion-like molecules	Reactome	2	PTPRD, PTPRF	21	97	11.79	1.227e-2	7.955e-2
G alpha (i) signalling events	Reactome	6	DRD4, HTR1B, CNR1, OPRD1, OPRM1, CNR2	249	97	2.98	1.541e-2	9.121e-2
Enzymatic degradation of Dopamine by monoamine oxidase	Reactome	1	MAOA	2	97	61.91	1.609e-2	9.392e-2
Metabolism of serotonin	Reactome	1	MAOA	2	97	61.91	1.609e-2	9.392e-2
Biogenic amines are oxidatively deaminated to aldehydes by MAOA and MAOB	Reactome	1	MAOA	2	97	61.91	1.609e-2	9.392e-2
NOTCH4 Activation and Transmission of Signal to the Nucleus	Reactome	1	YWHAZ	2	97	61.91	1.609e-2	9.392e-2