

GeDiPNet Cluster 392 -- 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 15:31:35

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective MAOA causes Brunner syndrome (BRUNS)	Reactome	1	MAOA	1	27	444.81	2.248e-3	2.484e-2
Serotonin clearance from the synaptic cleft	Reactome	1	SLC6A4	1	27	444.81	2.248e-3	2.484e-2
Enzymatic degradation of Dopamine by monoamine oxidase	Reactome	1	MAOA	2	27	222.41	4.491e-3	4.079e-2
Metabolism of serotonin	Reactome	1	MAOA	2	27	222.41	4.491e-3	4.079e-2
Biogenic amines are oxidatively deaminated to aldehydes by MAOA and MAOB	Reactome	1	MAOA	2	27	222.41	4.491e-3	4.079e-2
Graft-versus-host disease	KEGG	2	HLA-DQA1, KIR3DS1	45	27	19.77	4.540e-3	4.113e-2
Enzymatic degradation of dopamine by COMT	Reactome	1	MAOA	3	27	148.27	6.730e-3	5.319e-2
Axon guidance	KEGG	3	EPHA7, LRRC4C, TRPC6	183	27	7.29	7.779e-3	5.861e-2
Alcoholism	KEGG	3	CRH, MAOA, NTRK2	188	27	7.10	8.375e-3	6.146e-2
L1CAM interactions	Reactome	1	GAP43	4	27	111.20	8.963e-3	6.417e-2
Activated NTRK2 signals through PLCG1	Reactome	1	NTRK2	4	27	111.20	8.963e-3	6.417e-2
NTRK2 activates RAC1	Reactome	1	NTRK2	5	27	88.96	1.119e-2	7.338e-2
Activated NTRK2 signals through FRS2 and FRS3	Reactome	1	NTRK2	6	27	74.14	1.342e-2	8.136e-2
Antigen processing and presentation	KEGG	2	HLA-DQA1, KIR3DS1	81	27	10.98	1.414e-2	8.407e-2
Aspartate and asparagine metabolism	Reactome	1	SLC25A12	12	27	37.07	2.666e-2	1.207e-1