

GeDiPNet Cluster 439 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:53

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Serotonin clearance from the synaptic cleft	Reactome	1	SLC6A4	1	21	571.90	1.749e-3	1.726e-2
Graft-versus-host disease	KEGG	2	HLA-DQA1, KIR3DS1	45	21	25.42	2.755e-3	2.398e-2
Axon guidance	KEGG	3	EPHA7, LRRC4C, TRPC6	183	21	9.38	3.782e-3	3.002e-2
Antigen processing and presentation	KEGG	2	HLA-DQA1, KIR3DS1	81	21	14.12	8.682e-3	5.216e-2
Aspartate and asparagine metabolism	Reactome	1	SLC25A12	12	21	47.66	2.079e-2	8.765e-2
The activation of arylsulfatases	Reactome	1	ARSA	13	21	43.99	2.251e-2	9.162e-2
Elevation of cytosolic Ca2+ levels	Reactome	1	TRPC6	13	21	43.99	2.251e-2	9.162e-2
Keratinization	Reactome	2	KRTAP4-5, KRTAP4-6	152	21	7.53	2.855e-2	1.052e-1
Cell adhesion molecules	KEGG	2	HLA-DQA1, LRRC4C	160	21	7.15	3.138e-2	1.110e-1
Translocation of ZAP-70 to Immunological synapse	Reactome	1	HLA-DQA1	19	21	30.10	3.273e-2	1.138e-1
Effects of PIP2 hydrolysis	Reactome	1	TRPC6	20	21	28.60	3.442e-2	1.168e-1
EPHA-mediated growth cone collapse	Reactome	1	EPHA7	20	21	28.60	3.442e-2	1.168e-1
DAP12 interactions	Reactome	1	KIR3DS1	21	21	27.23	3.611e-2	1.200e-1
Phosphorylation of CD3 and TCR zeta chains	Reactome	1	HLA-DQA1	22	21	26.00	3.780e-2	1.234e-1
EPH-Ephrin signaling	Reactome	1	EPHA7	22	21	26.00	3.780e-2	1.234e-1