

GeDiPNet Cluster 331 -- 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 08:14:42

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
NF-kappa B signaling pathway	KEGG	3	BCL10, BIRC3, MALT1	105	6	57.19	1.274e-5	4.179e-4
Activation of NF-kappaB in B cells	Reactome	2	BCL10, MALT1	66	6	60.66	4.399e-4	7.370e-3
FCERI mediated NF-kB activation	Reactome	2	BCL10, MALT1	79	6	50.68	6.300e-4	9.738e-3
CLEC7A (Dectin-1) signaling	Reactome	2	BCL10, MALT1	79	6	50.68	6.300e-4	9.738e-3
B cell receptor signaling pathway	KEGG	2	BCL10, MALT1	91	6	43.99	8.351e-4	1.212e-2
Downstream TCR signaling	Reactome	2	BCL10, MALT1	98	6	40.85	9.678e-4	1.357e-2
C-type lectin receptor signaling pathway	KEGG	2	BCL10, MALT1	105	6	38.13	1.110e-3	1.502e-2
T cell receptor signaling pathway	KEGG	2	BCL10, MALT1	122	6	32.81	1.495e-3	1.890e-2
CLEC7A/inflammasome pathway	Reactome	1	MALT1	6	6	333.61	2.994e-3	3.114e-2
Tuberculosis	KEGG	2	BCL10, MALT1	181	6	22.12	3.256e-3	3.302e-2
Attachment of GPI anchor to uPAR	Reactome	1	PIGT	7	6	285.95	3.493e-3	3.476e-2
Regulation of necroptotic cell death	Reactome	1	BIRC3	11	6	181.97	5.484e-3	4.749e-2
Shigellosis	KEGG	2	BCL10, MALT1	250	6	16.01	6.126e-3	5.116e-2
RIPK1-mediated regulated necrosis	Reactome	1	BIRC3	16	6	125.10	7.968e-3	6.070e-2
Transcriptional regulation of pluripotent stem cells	Reactome	1	FOXP1	17	6	117.75	8.465e-3	6.313e-2