

GeDiPNet Cluster 259 -- 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 22:25:05

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Toxoplasmosis	KEGG	4	IL10, IL10RA, IL10RB, TGFB1	112	6	71.49	1.060e-7	6.667e-6
Tuberculosis	KEGG	4	IL10, IL10RA, IL10RB, TGFB1	181	6	44.24	7.312e-7	3.562e-5
Interleukin-10 signaling	Reactome	3	IL10, IL10RA, IL10RB	47	6	127.77	1.114e-6	5.135e-5
Cytokine-cytokine receptor interaction	KEGG	4	IL10, IL10RA, IL10RB, TGFB1	298	6	26.87	5.359e-6	1.943e-4
Viral protein interaction with cytokine and cytokine receptor	KEGG	3	IL10, IL10RA, IL10RB	100	6	60.05	1.100e-5	3.525e-4
JAK-STAT signaling pathway	KEGG	3	IL10, IL10RA, IL10RB	168	6	35.74	5.214e-5	1.282e-3
Human cytomegalovirus infection	KEGG	3	RIPK1, IL10RA, IL10RB	226	6	26.57	1.261e-4	2.627e-3
Intestinal immune network for IgA production	KEGG	2	IL10, TGFB1	50	6	80.07	2.521e-4	4.574e-3
Malaria	KEGG	2	IL10, TGFB1	50	6	80.07	2.521e-4	4.574e-3
Inflammatory bowel disease	KEGG	2	IL10, TGFB1	66	6	60.66	4.399e-4	7.127e-3
Leishmaniasis	KEGG	2	IL10, TGFB1	78	6	51.32	6.142e-4	9.257e-3
Influenza Virus Induced Apoptosis	Reactome	1	TGFB1	2	6	1000.83	9.990e-4	1.340e-2
The IPAF inflammasome	Reactome	1	NLRC4	2	6	1000.83	9.990e-4	1.340e-2
TGFB2 MSI Frameshift Mutants in Cancer	Reactome	1	TGFB1	2	6	1000.83	9.990e-4	1.340e-2
Chagas disease	KEGG	2	IL10, TGFB1	103	6	38.87	1.068e-3	1.413e-2