

GeDiPNet Cluster 306 -- 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: 2026-10-09 13:03:21

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Th1 and Th2 cell differentiation	KEGG	4	GATA3, IL2RB, NOTCH2, RUNX3	93	15	34.44	4.309e-6	1.629e-4
Primary immunodeficiency	KEGG	2	CIITA, PTPRC	38	15	42.14	9.973e-4	1.340e-2
Allograft rejection	KEGG	2	CD86, IL10	39	15	41.06	1.050e-3	1.394e-2
Interleukin-10 signaling	Reactome	2	CD86, IL10	47	15	34.07	1.524e-3	1.858e-2
Intestinal immune network for IgA production	KEGG	2	CD86, IL10	50	15	32.03	1.723e-3	2.044e-2
Autoimmune thyroid disease	KEGG	2	CD86, IL10	54	15	29.65	2.007e-3	2.284e-2
RUNX3 regulates RUNX1-mediated transcription	Reactome	1	RUNX3	2	15	400.33	2.496e-3	2.680e-2
Inflammatory bowel disease	KEGG	2	GATA3, IL10	66	15	24.26	2.982e-3	3.049e-2
NOTCH2 Activation and Transmission of Signal to the Nucleus	Reactome	1	NOTCH2	3	15	266.89	3.743e-3	3.577e-2
Virion - Adenovirus	KEGG	1	CD86	4	15	200.17	4.987e-3	4.363e-2
RUNX3 regulates BCL2L11 (BIM) transcription	Reactome	1	RUNX3	5	15	160.13	6.230e-3	5.078e-2
RUNX3 Regulates Immune Response and Cell Migration	Reactome	1	RUNX3	5	15	160.13	6.230e-3	5.078e-2
Defective LFNG causes SCDO3	Reactome	1	NOTCH2	5	15	160.13	6.230e-3	5.078e-2
Viral protein interaction with cytokine and cytokine receptor	KEGG	2	IL10, IL2RB	100	15	16.01	6.716e-3	5.336e-2
Pre-NOTCH Processing in Golgi	Reactome	1	NOTCH2	6	15	133.44	7.472e-3	5.710e-2