

GeDiPNet Cluster 565 -- 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 00:02:44

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Interleukin-4 and Interleukin-13 signaling	Reactome	5	IL13, IL23R, IRF4, TYK2, TP53	108	46	12.09	5.477e-5	1.172e-3
Melanin biosynthesis	Reactome	2	SLC45A2, TYR	5	46	104.43	1.425e-4	2.512e-3
Interleukin-23 signaling	Reactome	2	IL23R, TYK2	9	46	58.02	5.079e-4	6.746e-3
Th17 cell differentiation	KEGG	4	IL23R, IL2RA, IRF4, TYK2	109	46	9.58	7.813e-4	9.374e-3
Measles	KEGG	4	IL2RA, TYK2, TP53, TLR2	139	46	7.51	1.924e-3	1.852e-2
Inflammatory bowel disease	KEGG	3	IL13, IL23R, TLR2	66	46	11.87	2.033e-3	1.925e-2
Interferon alpha/beta signaling	Reactome	3	IRF4, TYK2, IRF1	67	46	11.69	2.122e-3	1.988e-2
JAK-STAT signaling pathway	KEGG	4	IL13, IL23R, IL2RA, TYK2	168	46	6.22	3.816e-3	3.024e-2
Herpes simplex virus 1 infection	KEGG	4	TAP2, TYK2, TP53, TLR2	182	46	5.74	5.070e-3	3.681e-2
Th1 and Th2 cell differentiation	KEGG	3	IL13, IL2RA, TYK2	93	46	8.42	5.364e-3	3.821e-2
ER-Phagosome pathway	Reactome	2	TAP2, TLR2	30	46	17.41	5.831e-3	4.038e-2
Epstein-Barr virus infection	KEGG	4	TAP2, TYK2, TP53, TLR2	204	46	5.12	7.556e-3	4.767e-2
Regulation of TP53 Expression	Reactome	1	TP53	2	46	130.54	7.646e-3	4.806e-2
Transcriptional activation of cell cycle inhibitor p21	Reactome	1	TP53	4	46	65.27	1.523e-2	7.322e-2
Toll Like Receptor TLR6:TLR2 Cascade	Reactome	1	TLR2	4	46	65.27	1.523e-2	7.322e-2