

GeDiPNet Cluster 603 -- 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: 2026-10-19 22:41:33

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Coronavirus disease - COVID-19	KEGG	2	F13B, IL2	238	5	20.18	3.759e-3	2.986e-2
RUNX1 and FOXP3 control the development of regulatory T lymphocytes (Tregs)	Reactome	1	IL2	10	5	240.20	4.157e-3	3.210e-2
Interleukin-2 signaling	Reactome	1	IL2	12	5	200.17	4.987e-3	3.635e-2
RORA activates gene expression	Reactome	1	TBL1XR1	18	5	133.44	7.473e-3	4.730e-2
Regulation of lipid metabolism by PPARalpha	Reactome	1	TBL1XR1	20	5	120.10	8.300e-3	5.062e-2
Common Pathway of Fibrin Clot Formation	Reactome	1	F13B	22	5	109.18	9.127e-3	5.370e-2
Interleukin receptor SHC signaling	Reactome	1	IL2	27	5	88.96	1.119e-2	6.094e-2
Notch-HLH transcription pathway	Reactome	1	TBL1XR1	28	5	85.79	1.160e-2	6.220e-2
Circadian Clock	Reactome	1	TBL1XR1	28	5	85.79	1.160e-2	6.220e-2
NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	Reactome	1	TBL1XR1	37	5	64.92	1.531e-2	7.347e-2
Allograft rejection	KEGG	1	IL2	39	5	61.59	1.613e-2	7.583e-2
Activation of gene expression by SREBF (SREBP)	Reactome	1	TBL1XR1	42	5	57.19	1.737e-2	7.884e-2
Type I diabetes mellitus	KEGG	1	IL2	44	5	54.59	1.819e-2	8.116e-2
Graft-versus-host disease	KEGG	1	IL2	45	5	53.38	1.860e-2	8.214e-2
Intestinal immune network for IgA production	KEGG	1	IL2	50	5	48.04	2.065e-2	8.746e-2