

GeDiPNet Cluster 571 -- 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 00:02:45

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Interleukin-9 signaling	Reactome	1	STAT1	9	1	1334.44	7.494e-4	9.089e-3
Interleukin-21 signaling	Reactome	1	STAT1	10	1	1201.00	8.326e-4	9.853e-3
Interleukin-27 signaling	Reactome	1	STAT1	11	1	1091.82	9.159e-4	1.060e-2
Regulation of IFNG signaling	Reactome	1	STAT1	11	1	1091.82	9.159e-4	1.060e-2
Interleukin-6 signaling	Reactome	1	STAT1	11	1	1091.82	9.159e-4	1.060e-2
Interleukin-35 Signalling	Reactome	1	STAT1	12	1	1000.83	9.992e-4	1.132e-2
Signaling by PDGFRA transmembrane, juxtamembrane and kinase domain mutants	Reactome	1	STAT1	12	1	1000.83	9.992e-4	1.132e-2
Signaling by PDGFRA extracellular domain mutants	Reactome	1	STAT1	12	1	1000.83	9.992e-4	1.132e-2
NOTCH3 Intracellular Domain Regulates Transcription	Reactome	1	STAT1	18	1	667.22	1.499e-3	1.536e-2
Signaling by cytosolic FGFR1 fusion mutants	Reactome	1	STAT1	18	1	667.22	1.499e-3	1.536e-2
Regulation of IFNA signaling	Reactome	1	STAT1	24	1	500.42	1.998e-3	1.898e-2
Interleukin-20 family signaling	Reactome	1	STAT1	25	1	480.40	2.082e-3	1.956e-2
Downstream signal transduction	Reactome	1	STAT1	29	1	414.14	2.415e-3	2.186e-2
Signaling by SCF-KIT	Reactome	1	STAT1	37	1	324.59	3.081e-3	2.594e-2
Inflammatory bowel disease	KEGG	1	STAT1	66	1	181.97	5.495e-3	3.875e-2