

GeDiPNet Cluster 587 -- 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 23:21:09

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Acyl chain remodeling of DAG and TAG	Reactome	1	PNPLA3	7	7	245.10	4.074e-3	3.169e-2
Regulation of IFNA signaling	Reactome	1	IFNA1	24	7	71.49	1.391e-2	6.943e-2
TRAF6 mediated IRF7 activation	Reactome	1	IFNA1	29	7	59.16	1.678e-2	7.755e-2
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	Reactome	1	MEN1	32	7	53.62	1.851e-2	8.204e-2
RHO GTPases activate IQGAPs	Reactome	1	MEN1	32	7	53.62	1.851e-2	8.204e-2
Deactivation of the beta-catenin transactivating complex	Reactome	1	MEN1	42	7	40.85	2.423e-2	9.576e-2
Autoimmune thyroid disease	KEGG	1	IFNA1	54	7	31.77	3.106e-2	1.102e-1
Glycerolipid metabolism	KEGG	1	PNPLA3	64	7	26.81	3.672e-2	1.213e-1
Interferon alpha/beta signaling	Reactome	1	IFNA1	67	7	25.61	3.841e-2	1.246e-1
RIG-I-like receptor signaling pathway	KEGG	1	IFNA1	72	7	23.83	4.123e-2	1.295e-1
Gastric acid secretion	KEGG	1	SST	76	7	22.58	4.347e-2	1.336e-1
Cytosolic DNA-sensing pathway	KEGG	1	IFNA1	83	7	20.67	4.740e-2	1.405e-1
Formation of the beta-catenin:TCF transactivating complex	Reactome	1	MEN1	88	7	19.50	5.019e-2	1.451e-1
Factors involved in megakaryocyte development and platelet production	Reactome	1	IFNA1	99	7	17.33	5.631e-2	1.550e-1
Peptide ligand-binding receptors	Reactome	1	SST	106	7	16.19	6.018e-2	1.607e-1