

GeDiPNet Cluster 370 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 07:47:50

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Formation of the beta-catenin:TCF transactivating complex	Reactome	2	EP300, KMT2D	88	9	30.33	1.848e-3	2.150e-2
RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	Reactome	2	EP300, KMT2D	97	9	27.51	2.240e-3	2.482e-2
LRR FLII-interacting protein 1 (LRRFIP1) activates type I IFN production	Reactome	1	EP300	5	9	266.89	3.742e-3	3.593e-2
TNFR1-mediated ceramide production	Reactome	1	TNFRSF1A	6	9	222.41	4.489e-3	4.079e-2
Regulation of FOXO transcriptional activity by acetylation	Reactome	1	EP300	7	9	190.63	5.235e-3	4.504e-2
TNF signaling	Reactome	1	TNFRSF1A	7	9	190.63	5.235e-3	4.504e-2
PI5P Regulates TP53 Acetylation	Reactome	1	EP300	9	9	148.27	6.726e-3	5.319e-2
RUNX3 regulates p14-ARF	Reactome	1	EP300	9	9	148.27	6.726e-3	5.319e-2
Influenza A	KEGG	2	EP300, TNFRSF1A	173	9	15.43	6.949e-3	5.451e-2
Tuberculosis	KEGG	2	EP300, TNFRSF1A	181	9	14.75	7.585e-3	5.754e-2
Regulation of gene expression by Hypoxia-inducible Factor	Reactome	1	EP300	11	9	121.31	8.216e-3	6.072e-2
Kaposi sarcoma-associated herpesvirus infection	KEGG	2	EP300, TNFRSF1A	196	9	13.62	8.846e-3	6.374e-2
Activation of the TFAP2 (AP-2) family of transcription factors	Reactome	1	EP300	12	9	111.20	8.960e-3	6.417e-2
NOTCH1 Intracellular Domain Regulates Transcription	Reactome	1	EP300	13	9	102.65	9.703e-3	6.739e-2
TNFR1-induced proapoptotic signaling	Reactome	1	TNFRSF1A	13	9	102.65	9.703e-3	6.739e-2