Resource Summary Report

Generated by dkNET on Sep 12, 2026

RegulomeDB

RRID:SCR_017905
Type: Tool

Proper Citation

RegulomeDB (RRID:SCR_017905)

Resource Information

URL: http://www.regulomedb.org/

Proper Citation: RegulomeDB (RRID:SCR_017905)

Description: Database that annotates SNPs with known and predicted regulatory elements in intergenic regions of H. sapiens genome. Known and predicted regulatory DNA elements include regions of DNAase hypersensitivity, binding sites of transcription factors, and promoter regions that have been biochemically characterized to regulation transcription. Source of these data include public datasets from GEO, ENCODE project, and published literature.

Resource Type: data or information resource, database, service resource

Defining Citation: PMID:22955989

Keywords: Annotate, SNP, regulatory, DNA, element, intergenic, region, human, genome, sequence, DNAase, hypersensitivity, binding, site, transcription, factor, promoter, region, data, FASEB list

Funding: Beta Cell Consortium ;
NHGRI U54 HG 004558

Availability: Free, Freely available

Resource Name: RegulomeDB

Resource ID: SCR_017905

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260912T200218+0000

Ratings and Alerts

No rating or validation information has been found for RegulomeDB.

No alerts have been found for RegulomeDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 161 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Fang X, et al. (2026) The AGPS regulatory variant rs113671272 confers esophageal squamous cell carcinoma susceptibility through allele-specific MEIS3 binding and NF-??B activation in Chinese populations. EBioMedicine, 127, 106249.

Nila NN, et al. (2026) Comprehensive analysis of the deleterious nonsynonymous, non-coding SNPs and cancer variants of human aldo-keto reductase type 1 (AKR1C1) protein and their probable association with disease risk and progression: a computational study. Biochemistry and biophysics reports, 45, 102502.

Blanco FJ, et al. (2026) Redox-Related Genetic and Biological Ageing Signals in Rapid Pain Progression of Knee Osteoarthritis: A Hypothesis-Generating Analysis in the Osteoarthritis Initiative. Antioxidants (Basel, Switzerland), 15(2).

Timasheva Y, et al. (2026) Integrative Analysis of Oxidative Stress and Cellular Senescence Pathways in Chronic Obstructive Pulmonary Disease. Genes, 17(6).

Shchekina VS, et al. (2026) Identifying a Common Autoimmune Gene Core as a Tool for Verifying Biological Significance and Applicability of Polygenic Risk Scores. International journal of molecular sciences, 27(1).

Zhang J, et al. (2026) Association of the FTO gene polymorphism with the features of the clinical course of tuberculosis infection. BMC infectious diseases, 26(1).

Ahmed AM, et al. (2026) Association of NLRP3 Inflammasome rs10754558 Polymorphism with Type 2 Diabetes Mellitus and Its Complications: Clinical and Bioinformatics Study. Diabetes, metabolic syndrome and obesity : targets and therapy, 19, 586787.

Montoya-Delgado IB, et al. (2026) IL4 Gene Variants rs2243250 and rs2243248 and Their Association with Clinical Phenotypes of Severe Asthma in the Mexican Population: In Silico Functional Analysis and Regulatory Implications. International journal of molecular sciences, 27(11).

Tchio C, et al. (2025) ADCY3 Ser107Pro links difficulty awakening in the morning to adiposity through circadian regulation of adipose thermogenesis. bioRxiv : the preprint server for biology.

Al Ghafari M, et al. (2025) Key genes altered in glioblastoma based on bioinformatics (Review). Oncology letters, 29(5), 243.

Lin SY, et al. (2025) Activin A receptor type 1C single nucleotide polymorphisms associated with esophageal squamous cell carcinoma risk in Chinese population. World journal of gastrointestinal oncology, 17(1), 96702.

Mastromoro G, et al. (2025) NUAK2 Pathogenic Variants Are Definitively Associated with Neural Tube Defects in Humans: New Genotype-Phenotype Correlation and Review of the Literature. Diagnostics (Basel, Switzerland), 15(18).

Wei X, et al. (2025) Multi-omics integration analysis of the amino-acid metabolism-related genes identifies putatively causal variants of ACCS associated with hepatitis B virus-related hepatocellular carcinoma survival. BMC cancer, 25(1), 284.

Lou S, et al. (2025) Functional variant at 19q13.3 confers nonsyndromic cleft palate susceptibility by regulating HIF3A. iScience, 28(2), 111829.

Honarpour A, et al. (2025) The First Evidence for the Role of ACVR2A Gene Fetal Genotype in Preeclampsia Susceptibility. Molecular genetics & genomic medicine, 13(2), e70069.

Zhang J, et al. (2025) ULK1 gene polymorphisms and severe tuberculosis in the Chinese Han population: a case-control study. Frontiers in medicine, 12, 1635313.

Ji L, et al. (2025) Identification of Schizophrenia-Risk Regulatory Variant rs1399178 in the Non-coding Region With Its Impact on NRF1 Binding. CNS neuroscience & therapeutics, 31(3), e70275.

Zhao YC, et al. (2025) Gene-Level Analyses of Novel Olfactory-Related Signal from Severe SARS-CoV-2 GWAS Reveal Association with Disease Mortality. COVID, 5(12).

Zhou X, et al. (2025) Characterization of m6A-regulated targets and immune cells in dental caries: insights from multi-omics analysis. European journal of medical research, 30(1), 1258.

Xu X, et al. (2025) The Genetic Risk Score with Variants in PDGFs and PDGFRB for the Risk of Major Cardiovascular Adverse Events in Patients with Coronary Artery Disease. Journal of atherosclerosis and thrombosis, 32(8), 929.