Resource Summary Report

Generated by T1D on Jul 31, 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: NHGRI U54 HG 004558;
Beta Cell Consortium

Availability: Free, Freely available

Resource Name: RegulomeDB

Resource ID: SCR_017905

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260731T043016+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 123 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

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.

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.

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.

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.

Lai J, et al. (2025) Association between polymorphisms of the adenylate cyclase 3 gene rs2241759 and the effect of high-intensity interval training on blood lipid profiles. PeerJ, 13, e19271.

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

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.

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

Liu Y, et al. (2025) Novel genetic variants in the NLRP3 inflammasome-related PANX1 and APP genes predict survival of patients with hepatitis B virus-related hepatocellular carcinoma. Clinical & translational oncology : official publication of the Federation of Spanish Oncology Societies and of the National Cancer Institute of Mexico, 27(2), 630.

Shi W, et al. (2024) Association of single nucleotide polymorphisms in ITLN1 gene with ischemic stroke risk in Xi'an population, Shaanxi province. PeerJ, 12, e16934.

Chen H, et al. (2024) Additional prognostic value of polymorphisms within the 3'-untranslated region of programmed cell death pathway genes in early-stage breast cancer. Frontiers in immunology, 15, 1284579.

Tang W, et al. (2024) Association of leptin receptor polymorphisms with susceptibility of non-small cell lung cancer: Evidence from 2249 subjects. Cancer medicine, 13(8), e7178.

Lu G, et al. (2024) Potentially functional variants of INPP5D and EXOSC3 in immunity B cell-related genes are associated with non-small cell lung cancer survival. Frontiers in immunology, 15, 1440454.

Nagarajan P, et al. (2024) A Large-Scale Genome-Wide Study of Gene-Sleep Duration Interactions for Blood Pressure in 811,405 Individuals from Diverse Populations. medRxiv : the preprint server for health sciences.

Guo M, et al. (2024) Genetic variants in C1GALT1 are associated with gastric cancer risk by influencing immune infiltration. Journal of biomedical research, 38(4), 348.

Lu G, et al. (2024) Genetic variants of LRRC8C, OAS2, and CCL25 in the T cell exhaustion-related genes are associated with non-small cell lung cancer survival. Frontiers in immunology, 15, 1455927.

Guo M, et al. (2024) Genetic variants in hypoxia-inducible factor pathway are associated with colorectal cancer risk and immune infiltration. Journal of cellular and molecular medicine, 28(1), e18019.

Fan L, et al. (2024) Genetic variant in a BaP-activated super-enhancer increases prostate cancer risk by promoting AhR-mediated FAM227A expression. Journal of biomedical research, 38(2), 149.

Tjader NP, et al. (2024) Association of ESR1 Germline Variants with TP53 Somatic Variants in Breast Tumors in a Genome-wide Study. Cancer research communications, 4(6), 1597.

Wang H, et al. (2024) Potentially functional variants of ERRFI1 in hypoxia-related genes predict survival of non-small cell lung cancer patients. Cancer medicine, 13(15), e70073.