

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

Open Regulatory Annotation Database

RRID:SCR_007835

Type: Tool

Proper Citation

Open Regulatory Annotation Database (RRID:SCR_007835)

Resource Information

URL: <http://www.oreganno.org/oreganno/>

Proper Citation: Open Regulatory Annotation Database (RRID:SCR_007835)

Description: Open source, open access database and literature curation system for community based annotation of experimentally identified DNA regulatory regions, transcription factor binding sites and regulatory variants. Automatically cross referenced against PubMed, Entrez Gene, Ensembl, dbSNP, eVOC: Cell type ontology, and Taxonomy database. Community driven resource for curated regulatory annotation.

Abbreviations: ORegAnno

Synonyms: Open REGulatory ANNOtation, ORegAnno 3.0

Resource Type: data or information resource, database

Defining Citation: [PMID:18006570](#), [PMID:26578589](#)

Keywords: Collection, annotation, curated, experimentally, identified, DNA, regulatory, region, element, transcript, factor, binding, site, regulatory, variant, data, FASEB list

Funding: British Columbia Cancer Foundation ;
Genome Canada ;
Genome British Columbia ;
European Network of Excellence ;
BioSapiens Network of Excellence ;
Research Foundation – Flanders ;
Pleiades Promoter Project ;
Michael Smith Foundation for Health Research ;
Canadian Institutes of Health Research ;
European Molecular Biology Laboratory ;
Marie Curie Early Stage Research Training Fellowship ;
Natural Sciences and Engineering Research Council ;

Swedish Research Council ;
American Cancer Society ;
Edward Mallinckrodt ;
Jr. Foundation ;
NHGRI K99 HG007940;
NHGRI R01 HG008150;
NIMH R01 MH101814;
NCI K22 CA188163

Availability: Free, Freely available

Resource Name: Open Regulatory Annotation Database

Resource ID: SCR_007835

Alternate IDs: nif-0000-03223, r3d100010656

Alternate URLs: <http://www.oreganno.org/>, <https://doi.org/10.17616/R3DG70>

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260804T043343+0000

Ratings and Alerts

No rating or validation information has been found for Open Regulatory Annotation Database.

No alerts have been found for Open Regulatory Annotation Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 81 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#) .

Ahlgren L, et al. (2025) The genomic landscape of relapsed infant and childhood KMT2A-rearranged acute leukemia. Nature communications, 16(1), 8964.

Hu Y, et al. (2025) Accurate Transcription Factor Activity Inference to Decipher Cell Identity from Single-Cell Transcriptomic Data with MetaTF. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(23), e10745.

Garvin MR, et al. (2025) Dysregulation of heterochromatin caused by genomic structural variants may be central to autism spectrum disorder. Frontiers in molecular neuroscience, 18, 1553575.

Sui Y, et al. (2025) Pangenome discovery of missing autism variants. medRxiv : the preprint server for health sciences.

Barker HR, et al. (2025) TFBSFootprinter: a multiomics tool for prediction of transcription factor binding sites in vertebrate species. *Transcription*, 16(2-3), 204.

Shah K, et al. (2025) LncRNA SLNCR phenocopies the E2F1 DNA binding site to promote melanoma progression. *Cell reports*, 44(5), 115608.

Zhang S, et al. (2025) A MGMT Enhancer Variant is Associated with Glioma Susceptibility and Progression. *Cellular and molecular neurobiology*, 45(1), 88.

Fazal S, et al. (2024) RExPRT: a machine learning tool to predict pathogenicity of tandem repeat loci. *Genome biology*, 25(1), 39.

Wieting J, et al. (2024) Sex differences in MAGEL2 gene promoter methylation in high functioning autism - trends from a pilot study using nanopore Cas9 targeted long read sequencing. *BMC medical genomics*, 17(1), 279.

Frett B, et al. (2024) Enhancer-activated RET confers protection against oxidative stress to KMT2A-rearranged acute myeloid leukemia. *Cancer science*, 115(3), 963.

Mei H, et al. (2024) Multi-omics and pathway analyses of genome-wide associations implicate regulation and immunity in verbal declarative memory performance. *Alzheimer's research & therapy*, 16(1), 14.

Ceroni F, et al. (2024) Deletion upstream of MAB21L2 highlights the importance of evolutionarily conserved non-coding sequences for eye development. *Nature communications*, 15(1), 9245.

Swindell WR, et al. (2024) Meta-analysis of differential gene expression in lower motor neurons isolated by laser capture microdissection from post-mortem ALS spinal cords. *Frontiers in genetics*, 15, 1385114.

Buki G, et al. (2023) Correlation between large FBN1 deletions and severe cardiovascular phenotype in Marfan syndrome: Analysis of two novel cases and analytical review of the literature. *Molecular genetics & genomic medicine*, 11(7), e2166.

Pivrotto AM, et al. (2023) Analyses of allele age and fitness impact reveal human beneficial alleles to be older than neutral controls. *bioRxiv : the preprint server for biology*.

Zhang F, et al. (2023) NFATc1 marks articular cartilage progenitors and negatively determines articular chondrocyte differentiation. *eLife*, 12.

Büki G, et al. (2023) Identification of an NF1 Microdeletion with Optical Genome Mapping. *International journal of molecular sciences*, 24(17).

Nappi A, et al. (2023) Loss of p53 activates thyroid hormone via type 2 deiodinase and enhances DNA damage. *Nature communications*, 14(1), 1244.

Meyrueix LP, et al. (2022) Gestational diabetes mellitus placentas exhibit epimutations at placental development genes. *Epigenetics*, 17(13), 2157.

Marion-Poll L, et al. (2022) DNA methylation and hydroxymethylation characterize the identity of D1 and D2 striatal projection neurons. *Communications biology*, 5(1), 1321.