Resource Summary Report

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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/oregano/

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

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NCI K22 CA188163;
NHGRI K99 HG007940;
NHGRI R01 HG008150;
NIMH R01 MH101814;
Pleiades Promoter Project ;
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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: 20260905T133146+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 88 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Sui Y, et al. (2026) Using the linear references from the pangenome to discover missing autism variants. Nature communications, 17(1), 1681.

Queeno SR, et al. (2026) Profiling the epigenomic landscape of late embryonic and adult mouse hind limb muscles. Scientific reports, 16(1).

Felício D, et al. (2026) Retrotransposition Events Shape the Evolution of the Ataxin-3 Gene Family in Primates. Genome biology and evolution, 18(3).

Mack T, et al. (2026) Donor-specific assemblies enhance somatic structural variant detection in complex genomic regions. bioRxiv : the preprint server for biology.

Rozenfeld M, et al. (2026) Template Switching as a Driver of Promoter Evolution in Yeast: Case Study of the GRE2 Gene. Genome biology and evolution, 18(4).

Piñero M, et al. (2026) Genomic evidence for limited entomophagy in ancient Europeans. Science advances, 12(23), eaec6939.

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

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

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

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.

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.

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.

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.

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.

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.

Pivirotto 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.