Resource Summary Report

Generated by NIF on Apr 20, 2025

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: database, data or information resource

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

Alternate URLs: http://www.oreganno.org/

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250420T015600+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 74 mentions in open access literature.

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

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.

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.

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.

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.

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.

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

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

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

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.

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

Kircher M, et al. (2022) Systematic assays and resources for the functional annotation of non-coding variants. Medizinische Genetik : Mitteilungsblatt des Berufsverbandes Medizinische Genetik e.V, 34(4), 275.

Wooldridge TB, et al. (2022) An enhancer of Agouti contributes to parallel evolution of cryptically colored beach mice. Proceedings of the National Academy of Sciences of the United States of America, 119(27), e2202862119.

Wu T, et al. (2022) Coupling high-throughput mapping with proteomics analysis delineates

cis-regulatory elements at high resolution. Nucleic acids research, 50(1), e5.

Altman MC, et al. (2021) Inducible expression quantitative trait locus analysis of the MUC5AC gene in asthma in urban populations of children. The Journal of allergy and clinical immunology, 148(6), 1505.

Wanowska E, et al. (2021) A chromatin-associated splicing isoform of OIP5-AS1 acts in cis to regulate the OIP5 oncogene. RNA biology, 18(11), 1834.

Schwartz JR, et al. (2021) The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature communications, 12(1), 985.

Porter HL, et al. (2021) Many chronological aging clocks can be found throughout the epigenome: Implications for quantifying biological aging. Aging cell, 20(11), e13492.