

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 26, 2025

cisRED: cis-regulatory element

RRID:SCR_002098

Type: Tool

Proper Citation

cisRED: cis-regulatory element (RRID:SCR_002098)

Resource Information

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

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Description: Database for conserved sequence motifs identified by genome scale motif discovery, similarity, clustering, co-occurrence and coexpression calculations. Sequence inputs include low-coverage genome sequence data and ENCODE data. The database offers information on atomic motifs, motif groups and patterns. In promoter-based cisRED databases, sequence search regions for motif discovery extend from 1.5 Kb upstream to 200b downstream of a transcription start site, net of most types of repeats and of coding exons. Many transcription factor binding sites are located in such regions. For each target gene's search region, a base set of probabilistic ab initio discovery tools is used, in parallel, to find over-represented atomic motifs. Discovery methods use comparative genomics with over 40 vertebrate input genomes. In ChIP-seq-based cisRED databases, sequence search regions for motif discovery correspond to significant peaks that represent genome-wide sites of protein-DNA binding. Because such peaks occur in a wide range of genic and intergenic locations, ChIP-seq and promoter-based databases are complementary. Currently, motif discovery for ChIP-seq data uses scan-based approaches that make more explicit use of sets of sequences known to be functional transcription factor binding sites, and that consider a wide range of levels of conservation. For the human STAT1 ChIP-seq database search regions in the target species (human) was selected +/- 300 bp around the ChIP-seq peak maximum. Repeats and coding regions were masked. Multiple sequence alignment were used to assemble orthologous input sequences from other species.

Abbreviations: cisRED

Synonyms: cisRED - Databases of genome-wide regulatory module and element predictions

Resource Type: data or information resource, database

Defining Citation: [PMID:16381958](#)

Keywords: atomic motif, conserved sequence motif, motif pattern, regulatory element, motif, atomic, promoter, chip-seq, transcription factor binding site, bio.tools

Funding: Genome Canada ;
BC Cancer Foundation ;
Michael Smith Foundation for Health Research

Availability: Acknowledgement requested

Resource Name: cisRED: cis-regulatory element

Resource ID: SCR_002098

Alternate IDs: nif-0000-02665, biotools:cisred, OMICS_01857

Alternate URLs: <https://bio.tools/cisred>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250426T055518+0000

Ratings and Alerts

No rating or validation information has been found for cisRED: cis-regulatory element.

No alerts have been found for cisRED: cis-regulatory element.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Rezaeian A, et al. (2021) Methylation Status of MTHFR Promoter and Oligozoospermia Risk: An Epigenetic Study and in Silico Analysis. Cell journal, 22(4), 482.

Aden K, et al. (2019) Epithelial RNase H2 Maintains Genome Integrity and Prevents Intestinal Tumorigenesis in Mice. *Gastroenterology*, 156(1), 145.

Lu Q, et al. (2016) AAV-mediated transduction and targeting of retinal bipolar cells with improved mGluR6 promoters in rodents and primates. *Gene therapy*, 23(8-9), 680.

Hajjari M, et al. (2014) Characterizing the Retinoblastoma 1 locus: putative elements for Rb1 regulation by in silico analysis. *Frontiers in genetics*, 5, 2.

Kubota T, et al. (2013) TdIF1 recognizes a specific DNA sequence through its Helix-Turn-Helix and AT-hook motifs to regulate gene transcription. *PloS one*, 8(7), e66710.

Krystkowiak I, et al. (2013) Nencki Genomics Database--Ensembl funcgen enhanced with intersections, user data and genome-wide TFBS motifs. *Database : the journal of biological databases and curation*, 2013, bat069.

Liò P, et al. (2012) Statistical approaches to use a model organism for regulatory sequences annotation of newly sequenced species. *PloS one*, 7(9), e42489.

Mota NR, et al. (2012) Linking dopamine neurotransmission and neurogenesis: The evolutionary history of the NTAD (NCAM1-TTC12-ANKK1-DRD2) gene cluster. *Genetics and molecular biology*, 35(4 (suppl)), 912.

Grishkevich V, et al. (2012) A genomic bias for genotype-environment interactions in *C. elegans*. *Molecular systems biology*, 8, 587.

Labruna G, et al. (2011) Sequence Analysis of the UCP1 Gene in a Severe Obese Population from Southern Italy. *Journal of obesity*, 2011, 269043.

Gruel J, et al. (2011) Simple Shared Motifs (SSM) in conserved region of promoters: a new approach to identify co-regulation patterns. *BMC bioinformatics*, 12, 365.

Engelmann I, et al. (2011) A comprehensive analysis of gene expression changes provoked by bacterial and fungal infection in *C. elegans*. *PloS one*, 6(5), e19055.

Mikula M, et al. (2010) Comprehensive analysis of the palindromic motif TCTCGCGAGA: a regulatory element of the HNRNPK promoter. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 17(4), 245.

Sonnhammer EL, et al. (2005) Genome informatics: taming the avalanche of genomic data. *Genome biology*, 6(1), 301.