

Resource Summary Report

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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: Free, Freely available

Resource Name: cisRED: cis-regulatory element

Resource ID: SCR_002098

Alternate IDs: nif-0000-02665, biotools:cisred, OMICS_01857, r3d100010619

Alternate URLs: <https://bio.tools/cisred>, <https://doi.org/10.17616/R3XK69>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260804T043144+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 [RRID](#) .

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.

Li?? 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.