Resource Summary Report

Generated by dkNET on May 5, 2025

CTCFBSDB

RRID:SCR_002279
Type: Tool

Proper Citation

CTCFBSDB (RRID:SCR_002279)

Resource Information

URL: http://insulatordb.uthsc.edu/

Proper Citation: CTCFBSDB (RRID:SCR_002279)

Description: A comprehensive collection of experimentally determined and computationally predicted CCCTC-binding factor (CTCF) binding sites (CTCFBS) from the literature. The database is designed to facilitate the studies on insulators and their roles in demarcating functional genomic domains. The CTCFBS Prediction Tool allows users to scan sequences for the single best match to CTCF position weight matrices. Currently (March 2014), the database contains almost 15 million experimentally determined CTCF binding sites across several species. CTCF binding sites were collected from published papers containing CTCF binding sites identified using ChIPSeq or similar methods, data from the ENCODE project, and a set of approximately 100 manually curated binding sites identified by low-throughput experiments. Users can browse insulator sequence features, function annotations, genomic contexts including histone methylation profiles, flanking gene expression patterns and orthologous regions in other mammalian genomes. Users can also retrieve data by text search, sequence search and genomic range search.

Abbreviations: CTCFBSDB, CTCFBSDB 2.0

Synonyms: CTCFBSDB: a CTCF binding site database for characterization of vertebrate genomic insulators, CTCFBSDB 2.0: A database for CTCF binding sites and genome organization

Resource Type: data analysis service, database, analysis service resource, production service resource, data or information resource, service resource

Defining Citation: PMID:23193294, PMID:17981843

Keywords: cctc-binding factor, ctcf, ctcf binding site, insulator, genomic insulator, genome, binding site, FASEB list

Funding:

Resource Name: CTCFBSDB

Resource ID: SCR_002279

Alternate IDs: nif-0000-02703, OMICS_00530

Old URLs: http://insulatordb.utmem.edu/

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250505T053412+0000

Ratings and Alerts

No rating or validation information has been found for CTCFBSDB.

No alerts have been found for CTCFBSDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 61 mentions in open access literature.

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

Costagli S, et al. (2024) De Novo Genome Assembly at Chromosome-Scale of Hermetia illucens (Diptera Stratiomyidae) via PacBio and Omni-C Proximity Ligation Technology. Insects, 15(2).

Iurlaro M, et al. (2024) Systematic assessment of ISWI subunits shows that NURF creates local accessibility for CTCF. Nature genetics, 56(6), 1203.

Tritto V, et al. (2024) Genetic/epigenetic effects in NF1 microdeletion syndrome: beyond the haploinsufficiency, looking at the contribution of not deleted genes. Human genetics, 143(6), 775.

da Silva Santos R, et al. (2024) Hypomethylation at H19DMR in penile squamous cell carcinoma is not related to HPV infection. Epigenetics, 19(1), 2305081.

Nakamura M, et al. (2024) Unraveling the DNA methylation landscape in dog blood across breeds. BMC genomics, 25(1), 1089.

Kwak Y, et al. (2023) Chromosomal-level assembly of Bactericera cockerelli reveals rampant gene family expansions impacting genome structure, function and insect-microbe-plant-interactions. Molecular ecology resources, 23(1), 233.

Lavretsky P, et al. (2023) Chromosomal-level reference genome of a wild North American mallard (Anas platyrhynchos). G3 (Bethesda, Md.), 13(10).

Fang H, et al. (2023) CTCF-mediated insulation and chromatin environment modulate Car5b escape from X inactivation. bioRxiv : the preprint server for biology.

Pokharel K, et al. (2023) Whole-genome sequencing provides novel insights into the evolutionary history and genetic adaptation of reindeer populations in northern Eurasia. Scientific reports, 13(1), 23019.

Hintermann A, et al. (2022) Developmental and evolutionary comparative analysis of a regulatory landscape in mouse and chicken. Development (Cambridge, England), 149(12).

Wu Z, et al. (2022) cccDNA Surrogate MC-HBV-Based Screen Identifies Cohesin Complex as a Novel HBV Restriction Factor. Cellular and molecular gastroenterology and hepatology, 14(6), 1177.

Kostiniuk D, et al. (2022) Methylation pattern of polymorphically imprinted nc886 is not conserved across mammalia. PloS one, 17(3), e0261481.

Zhabotynsky V, et al. (2022) eQTL mapping using allele-specific count data is computationally feasible, powerful, and provides individual-specific estimates of genetic effects. PLoS genetics, 18(3), e1010076.

Ottema S, et al. (2021) The leukemic oncogene EVI1 hijacks a MYC super-enhancer by CTCF-facilitated loops. Nature communications, 12(1), 5679.

D'Arienzo V, et al. (2021) The CCCTC-binding factor CTCF represses hepatitis B virus enhancer I and regulates viral transcription. Cellular microbiology, 23(2), e13274.

Amândio AR, et al. (2021) Sequential in cis mutagenesis in vivo reveals various functions for CTCF sites at the mouse HoxD cluster. Genes & development, 35(21-22), 1490.

Beccari L, et al. (2021) Dbx2 regulation in limbs suggests interTAD sharing of enhancers. Developmental dynamics : an official publication of the American Association of Anatomists, 250(9), 1280.

Willemin A, et al. (2021) Induction of a chromatin boundary in vivo upon insertion of a TAD border. PLoS genetics, 17(7), e1009691.

Jian X, et al. (2021) Large parental differences in chromatin organization in pancreatic beta cell line explaining diabetes susceptibility effects. Nature communications, 12(1), 4338.

Qazi S, et al. (2021) In silico approach to understand the epigenetic mechanism of SARS-CoV-2 and its impact on the environment. Virusdisease, 32(2), 286.