Resource Summary Report

Generated by NIF on May 15, 2025

Chromosome 7 Annotation Project

RRID:SCR_007134
Type: Tool

Proper Citation

Chromosome 7 Annotation Project (RRID:SCR_007134)

Resource Information

URL: http://www.chr7.org

Proper Citation: Chromosome 7 Annotation Project (RRID:SCR_007134)

Description: Database containing the DNA sequence and annotation of the entire human chromosome 7, encompassing nearly 158 million nucleotides of DNA and 1917 gene structures, are presented; the most up to date collation of sequence, gene, and other annotations from all databases (eg. Celera published, NCBI, Ensembl, RIKEN, UCSC) as well as unpublished data. To generate a higher order description, additional structural features such as imprinted genes, fragile sites, and segmental duplications were integrated at the level of the DNA sequence with medical genetic data, including 440 chromosome rearrangement breakpoints associated with disease. The objective of this project is to generate a comprehensive description of human chromosome 7 to facilitate biological discovery, disease gene research and medical genetic applications. There are over 360 disease-associated genes or loci on chromosome 7. A major challenge ahead will be to represent chromosome alterations, variants, and polymorphisms and their related phenotypes (or lack thereof), in an accessible way. In addition to being a primary data source, this site serves as a weighing station for testing community ideas and information to produce highly curated data to be submitted to other databases such as NCBI, Ensembl, and UCSC. Therefore, any useful data submitted will be curated and shown in this database. All Chromosome 7 genomic clones (cosmids, BACs, YACs) listed in GBrowser and in other data tables are freely distributed.

Abbreviations: Chromosome 7 Annotation Project

Synonyms: The Chromosome 7 Annotation Project, Chromosome 7 Annotation Project

Resource Type: service resource, data repository, data or information resource, database, storage service resource

Defining Citation: PMID:12690205

Keywords: duplication, gene expression, family, fish, gene, gene annotation, genome, breakpoint, chromosome, chromosome 7, clinical, deletion, disease, dna sequence, human, insertion, inversion, polymorphism, rearrangement, segmental duplication, snp, translocation, annotation, data analysis service, blat, cosmid, bac, yac, biomaterial supply resource, malignant, non malignant, bio.tools

Funding:

Availability: Free, (Genomic clones)

Resource Name: Chromosome 7 Annotation Project

Resource ID: SCR_007134

Alternate IDs: nif-0000-03550, biotools:chr7

Alternate URLs: https://bio.tools/chr7

Record Creation Time: 20220129T080240+0000

Record Last Update: 20250514T061423+0000

Ratings and Alerts

No rating or validation information has been found for Chromosome 7 Annotation Project.

No alerts have been found for Chromosome 7 Annotation Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Poszewiecka B, et al. (2022) TADeus2: a web server facilitating the clinical diagnosis by pathogenicity assessment of structural variations disarranging 3D chromatin structure. Nucleic acids research, 50(W1), W744.

Al-Jawahiri R, et al. (2017) Resources available for autism research in the big data era: a systematic review. PeerJ, 5, e2880.

Lodder EM, et al. (2009) Implication of long-distance regulation of the HOXA cluster in a patient with postaxial polydactyly. Chromosome research : an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology, 17(6), 737.

Marshall CR, et al. (2008) Infantile spasms is associated with deletion of the MAGI2 gene on chromosome 7q11.23-q21.11. American journal of human genetics, 83(1), 106.

Parker-Katiraee L, et al. (2007) Identification of the imprinted KLF14 transcription factor undergoing human-specific accelerated evolution. PLoS genetics, 3(5), e65.

Feuk L, et al. (2006) Absence of a paternally inherited FOXP2 gene in developmental verbal dyspraxia. American journal of human genetics, 79(5), 965.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Feuk L, et al. (2005) Discovery of human inversion polymorphisms by comparative analysis of human and chimpanzee DNA sequence assemblies. PLoS genetics, 1(4), e56.

Nakabayashi K, et al. (2005) Identification of C7orf11 (TTDN1) gene mutations and genetic heterogeneity in nonphotosensitive trichothiodystrophy. American journal of human genetics, 76(3), 510.

Curtiss NP, et al. (2005) Isolation and analysis of candidate myeloid tumor suppressor genes from a commonly deleted segment of 7q22. Genomics, 85(5), 600.

Kendal WS, et al. (2004) A scale invariant clustering of genes on human chromosome 7. BMC evolutionary biology, 4, 3.

Denier C, et al. (2004) Mutations within the MGC4607 gene cause cerebral cavernous malformations. American journal of human genetics, 74(2), 326.

Müller S, et al. (2004) The evolutionary history of human chromosome 7. Genomics, 84(3), 458.