Resource Summary Report

Generated by T1D on Aug 1, 2026

HuRef

RRID:SCR_002952
Type: Tool

Proper Citation

HuRef (RRID:SCR_002952)

Resource Information

URL: https://catalog.coriell.org/1/HuRef

Proper Citation: HuRef (RRID:SCR_002952)

Description: Database for the diploid genome sequence of J. Craig Venter as published in PLoS Biology. Its graphical interface depicts the haploid sequence with SNP and insertion/deletion DNA variants as identified by genome assembly and comparison methods, as well as represents the haplotype blocks from which diploid genome sequence can be inferred and gene annotations.

Synonyms: Human Reference Genome - J. Craig Venter Institute, Human Reference Genome

Resource Type: biomaterial supply resource, material resource

Defining Citation: PMID:19036787, PMID:17803354

Keywords: diploid, human genome, haplotype, j craig venter

Availability: Commercial availability, Available to the scientific community

Resource Name: HuRef

Resource ID: SCR_002952

Alternate IDs: nif-0000-03001

Old URLs: http://huref.jcvi.org

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260801T191045+0000

Ratings and Alerts

No rating or validation information has been found for HuRef.

No alerts have been found for HuRef.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 43 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Warren RL, et al. (2025) ntRoot: computational inference of human ancestry at scale from genomic data. Bioinformatics advances, 5(1), vbaf287.

Wu Z, et al. (2024) Human pangenome analysis of sequences missing from the reference genome reveals their widespread evolutionary, phenotypic, and functional roles. Nucleic acids research, 52(5), 2212.

Ding W, et al. (2024) Adaptive functions of structural variants in human brain development. Science advances, 10(14), eadl4600.

Wang N, et al. (2022) Tool evaluation for the detection of variably sized indels from next generation whole genome and targeted sequencing data. PLoS computational biology, 18(2), e1009269.

Mouliere F, et al. (2021) Fragmentation patterns and personalized sequencing of cell-free DNA in urine and plasma of glioma patients. EMBO molecular medicine, 13(8), e12881.

Lee YG, et al. (2020) Insertion variants missing in the human reference genome are widespread among human populations. BMC biology, 18(1), 167.

Cao X, et al. (2020) Polymorphic mobile element insertions contribute to gene expression and alternative splicing in human tissues. Genome biology, 21(1), 185.

Langley SA, et al. (2019) Haplotypes spanning centromeric regions reveal persistence of large blocks of archaic DNA. eLife, 8.

Zhou A, et al. (2019) Evaluating nanopore sequencing data processing pipelines for structural variation identification. Genome biology, 20(1), 237.

Uralsky LI, et al. (2019) Classification and monomer-by-monomer annotation dataset of suprachromosomal family 1 alpha satellite higher-order repeats in hg38 human genome assembly. Data in brief, 24, 103708.

Ai H, et al. (2018) GenomeLandscaper: Landscape analysis of genome-fingerprints maps assessing chromosome architecture. Scientific reports, 8(1), 1026.

Bazin T, et al. (2018) Microbiota Composition May Predict Anti-Tnf Alpha Response in Spondyloarthritis Patients: an Exploratory Study. Scientific reports, 8(1), 5446.

Jain M, et al. (2018) Linear assembly of a human centromere on the Y chromosome. Nature biotechnology, 36(4), 321.

Zhou B, et al. (2018) Extensive and deep sequencing of the Venter/HuRef genome for developing and benchmarking genome analysis tools. Scientific data, 5, 180261.

Berton MP, et al. (2017) Genomic regions and pathways associated with gastrointestinal parasites resistance in Santa Inês breed adapted to tropical climate. Journal of animal science and biotechnology, 8, 73.

Löytynoja A, et al. (2017) Short template switch events explain mutation clusters in the human genome. Genome research, 27(6), 1039.

Sharbrough J, et al. (2017) The Mitonuclear Dimension of Neanderthal and Denisovan Ancestry in Modern Human Genomes. Genome biology and evolution, 9(6), 1567.

Chen J, et al. (2017) RelocaTE2: a high resolution transposable element insertion site mapping tool for population resequencing. PeerJ, 5, e2942.

Uddin M, et al. (2017) Germline and somatic mutations in STXBP1 with diverse neurodevelopmental phenotypes. Neurology. Genetics, 3(6), e199.

Cho YS, et al. (2016) An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. Nature communications, 7, 13637.