

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 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: 20260905T133228+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 [PRECISE-TBI](#) .

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.

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

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

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.

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

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.

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.