BSgenome.Hsapiens.NCBI.T2T.CHM13v2.0

November 11, 2026

`BSgenome.Hsapiens.NCBI.T2T.CHM13v2.0`
T2T-CHM13v2.0 assembly (Homo sapiens) wrapped in a BSgenome object

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Description

The T2T-CHM13v2.0 assembly (accession GCA_009914755.4), as submitted to NCBI by the T2T Consortium, and wrapped in a BSgenome object. Companion paper: "The complete sequence of a human genome" by Nurk S, Koren S, Rhie A, Rautiainen M, et al. Science, 2022.

Note

This BSgenome data package was made from the following source data files:

`GCA_009914755.4_T2T-CHM13v2.0_genomic.fna.gz` from `https://ftp.ncbi.nlm.nih.gov/genomes/all/GCA/009/9`

See `?BSgenomeForge` and the BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the **BSgenome** software package for how to make a BSgenome data package.

Author(s)

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See Also

- BSgenome objects and the `available.genomes` function in the **BSgenome** software package.
- DNAString objects in the **Biostrings** package.
- The BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the **BSgenome** software package for how to make a BSgenome data package.

Examples

```
BSgenome.Hsapiens.NCBI.T2T.CHM13v2.0
genome <- BSgenome.Hsapiens.NCBI.T2T.CHM13v2.0
head(seqlengths(genome))
genome[["1"]]

## ---------------------------------------------------------------------
## Genome-wide motif searching
## ---------------------------------------------------------------------
## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostrings and the BSgenome data packages:
if (interactive())
    vignette("GenomeSearching", package="BSgenome")
```

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