

# BSgenome.Hsapiens.NCBI.T2T.CHM13v2.0

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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)

The Bioconductor Dev Team

## 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
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## 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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