BSgenome.Hsapiens.UCSC.hg19

November 11, 2026

`BSgenome.Hsapiens.UCSC.hg19`
Full genome sequences for Homo sapiens (UCSC version hg19, based on GRCh37.p13)

Description

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg19, based on GRCh37.p13) and stored in Biostrings objects.

Note

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

`hg19.2bit, downloaded from https://hgdownload.cse.ucsc.edu/goldenPath/hg19/bigZips/latest/ on March 2`

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.UCSC.hg19
genome <- BSgenome.Hsapiens.UCSC.hg19
head(seqlengths(genome))
genome$chr1  # same as genome[["chr1"]]

## ---------------------------------------------------------------------
## 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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