

BSgenome.Hsapiens.UCSC.hg17

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Full genome sequences for Homo sapiens (UCSC version hg17)

Description

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg17, May 2004) and stored in Biostrings objects.

Note

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

chromFa.zip, upstream1000.zip, upstream2000.zip, upstream5000.zip
from <http://hgdownload.cse.ucsc.edu/goldenPath/hg17/bigZips/>

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.hg17
genome <- BSgenome.Hsapiens.UCSC.hg17
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## 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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