

BSgenome.Amellifera.UCSC.apiMel2

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Full genome sequences for Apis mellifera (UCSC version apiMel2)

Description

Full genome sequences for *Apis mellifera* (Honey Bee) as provided by UCSC (apiMel2, Jan. 2005) and stored in Biostrings objects.

Note

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

GroupFa.zip from <http://hgdownload.cse.ucsc.edu/goldenPath/apiMel2/bigZips/>

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.Amellifera.UCSC.apiMel2
genome <- BSgenome.Amellifera.UCSC.apiMel2
seqlengths(genome)
genome$Group1 # same as genome[["Group1"]]
```

```
## -----
## 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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