

# BSgenome.Amellifera.NCBI.AmelHAV3.1

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BSgenome.Amellifera.NCBI.AmelHAV3.1

*Full genome sequences for Apis mellifera (Amel\_HAV3.1)*

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## Description

Full genome sequences for *Apis mellifera* as provided by NCBI (assembly Amel\_HAV3.1, assembly accession GCF\_003254395.2) and stored in Biostrings objects.

## Note

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

GCF\_003254395.2\_Amel\_HAV3.1\_genomic.fna.gz from <https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/003>

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.NCBI.AmelHAV3.1
genome <- BSgenome.Amellifera.NCBI.AmelHAV3.1
head(seqlengths(genome))
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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