

# BSgenome.Dvirilis.Ensembl.dvircaf1

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BSgenome.Dvirilis.Ensembl.dvircaf1

*Full genome sequences for Drosophila virilis (assembly dvir\_caf1)*

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## Description

Full genome sequences for *Drosophila virilis* (assembly dvir\_caf1, GenBank assembly accession GCA\_000005245.1) as provided by Ensembl and stored in Biostrings objects.

## Note

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

Drosophila\_virilis.dvir\_caf1.dna.toplevel.fa.gz, downloaded from <ftp://ftp.ensemblgenomes.org/pub>

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.Dvirilis.Ensembl.dvircaf1
genome <- BSgenome.Dvirilis.Ensembl.dvircaf1
head(seqlengths(genome))
genome$scaffold_13049 # same as genome[["scaffold_13049"]]
```

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