

BSgenome.Gmax.NCBI.Gmv40

August 20, 2025

BSgenome.Gmax.NCBI.Gmv40

Full genome sequences for Glycine max (Gmv40)

Description

Full genome sequences for Glycine max as provided by NCBI (assembly Gmv40, assembly accession GCF_000004515.5) and stored in Biostrings objects.

Note

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

GCF_000004515.6_Glycine_max_v4.0_genomic.fna.gz from https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF_000004515.6_Glycine_max_v4.0_genomic.fna.gz

See [?BSgenomeForge](#) and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the **BSgenome** software package for how to make a BSgenome data package.

Author(s)

person("Deisiany", "Ferreira Neres", email = "deisianyufg@gmail.com", role = c("aut", "cre"))

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.Gmax.NCBI.Gmv40
genome <- BSgenome.Gmax.NCBI.Gmv40
head(seqlengths(genome))
```

```
## -----
## 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")
```

Index

* **data**

BSgenome.Gmax.NCBI.Gmv40, [1](#)

* **package**

BSgenome.Gmax.NCBI.Gmv40, [1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Gmax.NCBI.Gmv40, [1](#)

BSgenome.Gmax.NCBI.Gmv40-package
(BSgenome.Gmax.NCBI.Gmv40), [1](#)

BSgenomeForge, [1](#)

DNAString, [1](#)

Gmax (BSgenome.Gmax.NCBI.Gmv40), [1](#)