

# BSgenome.Gmax.NCBI.Gmv40

December 11, 2024

---

BSgenome.Gmax.NCBI.Gmv40

*Full genome sequences for Glycine max (Gmv40)*

---

## Description

Full genome sequences for Glycine max as provided by NCBI (assemblyGmv40, 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](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](#)

DNAStrng, [1](#)

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