

# BSgenome.Gmax.NCBI.Gmv40

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BSgenome.Gmax.NCBI.Gmv40

*Full genome sequences for Glycine max (Gmv40)*

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## 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.

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## 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")
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