BSgenome.Gmax.NCBI.Gmv40

November 17, 2026

`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/GC`

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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