

# BSgenome.Osativa.MSU.MSU7

November 6, 2024

---

BSgenome.Osativa.MSU.MSU7

*Oryza sativa full genome (MSU7)*

---

## Description

*Oryza sativa* full genome as provided by MSU (MSU7 Genome Release) and stored in Biostrings objects.

## Note

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

[ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic\\_Projects/o\\_sativa/annotation\\_dbs/pseudomolecu](ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic_Projects/o_sativa/annotation_dbs/pseudomolecu)

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

## Author(s)

Wen Yao <ywhzau@gmail.com>

## See Also

[BSgenome-class](#), [DNASTring-class](#), [available.genomes](#), [BSgenomeForge](#)

## Examples

```
BSgenome.Osativa.MSU.MSU7
genome <- BSgenome.Osativa.MSU.MSU7
seqlengths(genome)
genome$Chr1 # same as genome[["Chr1"]]
```

```
## -----
## 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.Osativa.MSU.MSU7, [1](#)

**\* package**

BSgenome.Osativa.MSU.MSU7, [1](#)

available.genomes, [1](#)

BSgenome-class, [1](#)

BSgenome.Osativa.MSU.MSU7, [1](#)

BSgenome.Osativa.MSU.MSU7-package  
(BSgenome.Osativa.MSU.MSU7), [1](#)

BSgenomeForge, [1](#)

DNASTring-class, [1](#)

Osativa (BSgenome.Osativa.MSU.MSU7), [1](#)