

# BSgenome.Vvinifera.URGI.IGGP12Xv2

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BSgenome.Vvinifera.URGI.IGGP12Xv2

*Full reference nuclear genome sequences for Vitis vinifera subsp. vinifera PN40024 (IGGP version 12Xv2)*

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## Description

Full reference nuclear genome sequences for *Vitis vinifera* subsp. *vinifera* PN40024 (derived from Pinot Noir and close to homozygosity after 6-9 rounds of selfing) as assembled by the IGGP (version 12Xv2) and available at the URGI (INRA)

## Note

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

[https://urgi.versailles.inra.fr/download/vitis/12Xv2\\_grapevine\\_genome\\_assembly.fa.gz](https://urgi.versailles.inra.fr/download/vitis/12Xv2_grapevine_genome_assembly.fa.gz)

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

## Author(s)

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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.Vvinifera.URGI.IGGP12Xv2
genome <- BSgenome.Vvinifera.URGI.IGGP12Xv2
head(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

\*Topic **data**

BSgenome.Vvinifera.URGI.IGGP12Xv2,  
[1](#)

\*Topic **package**

BSgenome.Vvinifera.URGI.IGGP12Xv2,  
[1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Vvinifera.URGI.IGGP12Xv2, [1](#)

BSgenome.Vvinifera.URGI.IGGP12Xv2-package  
(BSgenome.Vvinifera.URGI.IGGP12Xv2),  
[1](#)

BSgenomeForge, [1](#)

DNAStrng, [1](#)

Vvinifera

(BSgenome.Vvinifera.URGI.IGGP12Xv2),  
[1](#)