# BSgenome.Vvinifera.URGI.IGGP8X

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`BSgenome.Vvinifera.URGI.IGGP8X`
*Full reference nuclear genome sequences for Vitis vinifera subsp. vinifera PN40024 (IGGP version 8X)*

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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 8X) and available at the URGI (INRA). More details in Jaillon et al (Nature, 2007).

## Note

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

`https://urgi.versailles.inra.fr/download/vitis/VV_chr12x.fsa.zip`

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.IGGP8X
genome <- BSgenome.Vvinifera.URGI.IGGP8X
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")
```

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