BSgenome.Vvinifera.URGI.IGGP12Xv0

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`BSgenome.Vvinifera.URGI.IGGP12Xv0`
Full reference nuclear genome sequences for Vitis vinifera subsp. vinifera PN40024 (IGGP version 12Xv0)

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 12Xv0) 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/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)

Timothee Flutre [cre,aut]

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.IGGP12Xv0
genome <- BSgenome.Vvinifera.URGI.IGGP12Xv0
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