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

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

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")
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