Package
'BSgenome.Paeruginosa.NCBI.ASM1462v1'

Title Full genome of Pseudomonas aeruginosa UCBPP-PA14

Description Complete Genome

Version 1.0.0

Author Dmytro Strunin

Maintainer Bioconductor Package Maintainer `<maintainer@bioconductor.org>`

Depends R (>= 3.5.0), BSgenome (>= 1.58.0)

Imports BSgenome

Suggests

License Artistic-2.0

organism Pseudomonas aeruginosa

common_name P. aeruginosa PA14

genome ASM1462v1

provider NCBI

release_date 2013-10-06

source_url https://www.ncbi.nlm.nih.gov/assembly/GCF_000014625.1

biocViews AnnotationData, Genetics, BSgenome, Pseudomonas_aeruginosa

NeedsCompilation no

R topics documented:

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Full genome of Pseudomonas aeruginosa UCBPP-PA14

Description

Complete Genome

Note

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

```
-- information not available --
```

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

Author(s)

Dmytro Strunin

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.Paeruginosa.NCBI.ASM1462v1
genome <- BSgenome.Paeruginosa.NCBI.ASM1462v1
head(seqlengths(genome))


## ---------------------------------------------------------------------
## 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")
```