Package 'BSgenome.Paeruginosa.NCBI.ASM676v1'

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Title Full genome of Pseudomonas aeruginosa PAO1 (g-proteobacteria)

Description Complete Genome

Version 1.0.0

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Depends R (>= 3.5.0), BSgenome (>= 1.64.0)

Imports BSgenome

Suggests

License Artistic-2.0

organism Pseudomonas aeruginosa (P. aeruginosa PAO1)

common_name P. aeruginosa PA01

genome ASM676v1

provider NCBI

release_date 2006-07-07

source_url https://www.ncbi.nlm.nih.gov/assembly/GCF_000006765.1

biocViews AnnotationData, Genetics, BSgenome, Pseudomonas_aeruginosa

NeedsCompilation no

R topics documented:

BSgenome.Paeruginosa.NCBI.ASM676v1

Full   genome   of   Pseudomonas   aeruginosa   PAO1   (g-proteobacteria)

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.ASM676v1
genome <- BSgenome.Paeruginosa.NCBI.ASM676v1
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")
```

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