

# 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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**Maintainer** Bioconductor Package Maintainer <maintainer@bioconductor.org>

**Depends** BSgenome (>= 1.54.0)

**Imports** BSgenome

**Suggests**

**License** Artistic-2.0

**organism** Pseudomonas aeruginosa

**common\_name** P. aeruginosa PAO1

**provider** NCBI

**provider\_version** ASM676v1

**release\_date** 2006-07-07

**release\_name** Pseudomonas aeruginosa PAO1 (g-proteobacteria)

**source\_url** [https://www.ncbi.nlm.nih.gov/assembly/GCF\\_000006765.1](https://www.ncbi.nlm.nih.gov/assembly/GCF_000006765.1)

**biocViews** AnnotationData, Genetics, BSgenome, Pseudomonas\_aeruginosa

**NeedsCompilation** no

## R topics documented:

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```
BSgenome.Paeruginosa.NCBI.ASM676v1
```

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

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## 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")
```