# Package ‘AssessORFData’

July 24, 2025

**Type** Package

**Title** Data and Files for the AssessORF Package

**Version** 1.27.0

**Date** 2019-04-07

**Description** This package provides access to mapping and results objects generated by the AssessORF package, as well as the genome sequences for the strains corresponding to those objects.

**Depends** R (>= 3.5.0), RSQLite (>= 1.1)

**Imports** DECIPHER, utils

**Suggests** AssessORF, BiocStyle, knitr, rmarkdown

**biocViews** OrganismData, Bacillus_subtilis_Data, Escherichia_coli_Data, Pseudomonas_aeruginosa_Data, Staphylococcus_aureus_Data, Genome, Proteome, SequencingData

**License** GPL-3

**Encoding** UTF-8

**LazyData** FALSE

**NeedsCompilation** no

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

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# Contents

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`AP1` `Assessment` *Objects for* Streptococcus pyogenes *strain AP1*

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Streptococcus pyogenes* strain AP1

## Usage

```
data(AP1_PreSaved_DataMapObj)
data(AP1_PreSaved_ResultsObj_GenBank)
data(AP1_PreSaved_ResultsObj_GeneMarkS2)
data(AP1_PreSaved_ResultsObj_Glimmer)
data(AP1_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'AP1_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'AP1_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'AP1_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'AP1_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'AP1_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: AP1
- `Species`: S. pyogenes

## Mapping object

The mapping object, 'AP1_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD006345. The related genomes used to determine evolutionary conservation all came from the family, Streptococcaceae exculding anomalous genomes and non-complete *Streptococcus pneumoniae* genomes. Links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'AP1_PreSaved_ResultsObj_GenBank', 'AP1_PreSaved_ResultsObj_GeneMarkS2', 'AP1_PreSaved_ResultsObj_Glimmer', and 'AP1_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("AP1", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD006345`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/CP007537.1`

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# `AssessORF_StrainIDs` *Vector of strain IDs used in the package*

## Description

Vector of strain IDs, which describes the strains for which the package has data

## Usage

```
data(AssessORF_StrainIDs)
```

## Format

Character vector of length 26

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# `ATCC11842` `Assessment` *Objects for* Lactobacillus delbrueckii *subsp.* bulgaricus *strain ATCC 11842*

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Lactobacillus delbrueckii* subsp. *bulgaricus* strain ATCC 11842

## Usage

```
data(ATCC11842_PreSaved_DataMapObj)
data(ATCC11842_PreSaved_ResultsObj_GenBank)
data(ATCC11842_PreSaved_ResultsObj_GeneMarkS2)
data(ATCC11842_PreSaved_ResultsObj_Glimmer)
data(ATCC11842_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'ATCC11842_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'ATCC11842_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'ATCC11842_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'ATCC11842_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'ATCC11842_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: ATCC11842
- `Species`: L. delbrueckii bulgaricus

## Mapping object

The mapping object, 'ATCC11842_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD006551. The related genomes used to determine evolutionary conservation all came from the genus Lactobacillus, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'ATCC11842_PreSaved_ResultsObj_GenBank', 'ATCC11842_PreSaved_ResultsObj_GeneMarkS 'ATCC11842_PreSaved_ResultsObj_Glimmer', and 'ATCC11842_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("ATCC11842", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD006551

NCBI's Genome Browser: https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/

GenBank record: https://www.ncbi.nlm.nih.gov/nuccore/NC_008054.1

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`ATCC13032` `Assessment` *Objects for* Corynebacterium glutamicum *strain ATCC 13032*

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### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Corynebacterium glutamicum* strain ATCC 13032

### Usage

```
data(ATCC13032_PreSaved_DataMapObj)
data(ATCC13032_PreSaved_ResultsObj_GenBank)
data(ATCC13032_PreSaved_ResultsObj_GeneMarkS2)
data(ATCC13032_PreSaved_ResultsObj_Glimmer)
data(ATCC13032_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

### Details

'ATCC13032_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'ATCC13032_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'ATCC13032_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'ATCC13032_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'ATCC13032_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: ATCC13032
- `Species`: C. glutamicum

### Mapping object

The mapping object, 'ATCC13032_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD005812. The related genomes used to determine evolutionary conservation came from the genera Corynebacterium, Dietzia, and Tsukamurella, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'ATCC13032_PreSaved_ResultsObj_GenBank', 'ATCC13032_PreSaved_ResultsObj_GeneMarkS 'ATCC13032_PreSaved_ResultsObj_Glimmer', and 'ATCC13032_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("ATCC13032", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD005812`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/BA000036.3`

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# `ATCC17978` `Assessment` *Objects for* Acinetobacter baumannii *strain ATCC 17978*

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Acinetobacter baumannii* strain ATCC 17978

## Usage

```
data(ATCC17978_PreSaved_DataMapObj)
data(ATCC17978_PreSaved_ResultsObj_GenBank)
data(ATCC17978_PreSaved_ResultsObj_GeneMarkS2)
data(ATCC17978_PreSaved_ResultsObj_Glimmer)
data(ATCC17978_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'ATCC17978_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'ATCC17978_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'ATCC17978_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'ATCC17978_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'ATCC17978_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: ATCC17978
- `Species`: A. baumannii

## Mapping object

The mapping object, 'ATCC17978_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The proteomics data was generated in-house and collected as part of the work for the AssessORF paper. The raw mass spectra data can be found at ProteomeXchange dataset PXD012539. The related genomes used to determine evolutionary conservation all came from the genus Acinetobacter, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'ATCC17978_PreSaved_ResultsObj_GenBank', 'ATCC17978_PreSaved_ResultsObj_GeneMarkS
'ATCC17978_PreSaved_ResultsObj_Glimmer', and 'ATCC17978_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("ATCC17978", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD012539`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/CP000521.1`

---

# `ATCC700084` Assessment *Objects for* Mycobacterium smegmatis *strain ATCC 700084*

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Mycobacterium smegmatis* strain ATCC 700084

## Usage

```
data(ATCC700084_PreSaved_DataMapObj)
data(ATCC700084_PreSaved_ResultsObj_GenBank)
data(ATCC700084_PreSaved_ResultsObj_GeneMarkS2)
data(ATCC700084_PreSaved_ResultsObj_Glimmer)
data(ATCC700084_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'ATCC700084_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'ATCC700084_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'ATCC700084_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'ATCC700084_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'ATCC700084_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: ATCC700084
- `Species`: M. smegmatis

## Mapping object

The mapping object, 'ATCC700084_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD003500. The related genomes used to determine evolutionary conservation all came from the genus Mycobacterium, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'ATCC700084_PreSaved_ResultsObj_GenBank', 'ATCC700084_PreSaved_ResultsObj_GeneMar
'ATCC700084_PreSaved_ResultsObj_Glimmer', and 'ATCC700084_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("ATCC700084", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine. Please note that there is no genome sequence available for strain ATCC 700084 so the reference genome from strain MC2 155 was used instead.

### Source

Proteomcis data: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD003500

NCBI's Genome Browser: https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/

GenBank record: https://www.ncbi.nlm.nih.gov/nuccore/NC_008596.1

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## `BW25113` `Assessment` *Objects for* Escherichia coli *strain BW25113*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Escherichia coli* strain BW25113

### Usage

```
data(BW25113_PreSaved_DataMapObj)
data(BW25113_PreSaved_ResultsObj_GenBank)
data(BW25113_PreSaved_ResultsObj_GeneMarkS2)
data(BW25113_PreSaved_ResultsObj_Glimmer)
data(BW25113_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

### Details

'BW25113_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'BW25113_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'BW25113_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'BW25113_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'BW25113_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: BW25113
- `Species`: E. coli

### Mapping object

The mapping object, 'BW25113_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD000498. The related genomes used to determine evolutionary conservation all came from the genus Escherichia, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'BW25113_PreSaved_ResultsObj_GenBank', 'BW25113_PreSaved_ResultsObj_GeneMarkS2', 'BW25113_PreSaved_ResultsObj_Glimmer', and 'BW25113_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("BW25113", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD000498`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/NZ_CP009273.1`

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`CCMP1375` `Assessment` *Objects for* Prochlorococcus marinus *subsp.* marinus *strain CCMP1375*

---

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Prochlorococcus marinus* subsp. *marinus* strain CCMP1375

## Usage

```
data(CCMP1375_PreSaved_DataMapObj)
data(CCMP1375_PreSaved_ResultsObj_GenBank)
data(CCMP1375_PreSaved_ResultsObj_GeneMarkS2)
data(CCMP1375_PreSaved_ResultsObj_Glimmer)
data(CCMP1375_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'CCMP1375_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'CCMP1375_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'CCMP1375_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'CCMP1375_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'CCMP1375_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: CCMP1375
- `Species`: P. marinus

## Mapping object

The mapping object, 'CCMP1375_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD005745. The related genomes used to determine evolutionary conservation all came from the order Synechococcales, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, ’CCMP1375_PreSaved_ResultsObj_GenBank’, ’CCMP1375_PreSaved_ResultsObj_GeneMarkS2 ’CCMP1375_PreSaved_ResultsObj_Glimmer’, and ’CCMP1375_PreSaved_ResultsObj_Prodigal’, store how much evidence there is supporting or against each gene in a set of predicted genes for the strain’s genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain’s genome

Use `SaveGenomeToPath("CCMP1375", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD005745`

NCBI’s Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/NC_005042.1`

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## `CECT5344` Assessment *Objects for* Pseudomonas pseudoalcaligenes *strain CECT 5344*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Pseudomonas pseudoalcaligenes* strain CECT 5344

### Usage

```
data(CECT5344_PreSaved_DataMapObj)
data(CECT5344_PreSaved_ResultsObj_GenBank)
data(CECT5344_PreSaved_ResultsObj_GeneMarkS2)
data(CECT5344_PreSaved_ResultsObj_Glimmer)
data(CECT5344_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'CECT5344_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'CECT5344_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'CECT5344_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'CECT5344_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'CECT5344_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: CECT5344
- `Species`: P. pseudoalcaligenes

## Mapping object

The mapping object, 'CECT5344_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD005745. The related genomes used to determine evolutionary conservation all came from the genus Pseudomonas, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'CECT5344_PreSaved_ResultsObj_GenBank', 'CECT5344_PreSaved_ResultsObj_GeneMarkS2', 'CECT5344_PreSaved_ResultsObj_Glimmer', and 'CECT5344_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("CECT5344", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD005745`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/HG916826.1`

---

`CNRZ327` `Assessment` *Objects for* Lactobacillus delbrueckii *subsp.* lactis *strain LBCNRZ327_V11*

---

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Lactobacillus delbrueckii* subsp. *lactis* strain LBCNRZ327_V11

### Usage

```
data(CNRZ327_PreSaved_DataMapObj)
data(CNRZ327_PreSaved_ResultsObj_GenBank)
data(CNRZ327_PreSaved_ResultsObj_GeneMarkS2)
data(CNRZ327_PreSaved_ResultsObj_Glimmer)
data(CNRZ327_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

### Details

'CNRZ327_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'CNRZ327_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'CNRZ327_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'CNRZ327_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'CNRZ327_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: CNRZ327
- `Species`: L. delbrueckii lactis

### Mapping object

The mapping object, 'CNRZ327_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD006551. The related genomes used to determine evolutionary conservation all came from the genus Lactobacillus, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'CNRZ327_PreSaved_ResultsObj_GenBank', 'CNRZ327_PreSaved_ResultsObj_GeneMarkS2', 'CNRZ327_PreSaved_ResultsObj_Glimmer', and 'CNRZ327_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("CNRZ327", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD006551`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/CCDV01000001.1`

---

## COH1 Assessment *Objects for* Streptococcus agalactiae *strain COH1*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Streptococcus agalactiae* strain COH1

### Usage

```
data(COH1_PreSaved_DataMapObj)
data(COH1_PreSaved_ResultsObj_GenBank)
data(COH1_PreSaved_ResultsObj_GeneMarkS2)
data(COH1_PreSaved_ResultsObj_Glimmer)
data(COH1_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'COH1_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'COH1_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'COH1_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'COH1_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'COH1_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: COH1
- `Species`: S. agalactiae

## Mapping object

The mapping object, 'COH1_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The proteomics data was generated in-house and collected as part of the work for the AssessORF paper. The raw mass spectra data can be found at ProteomeXchange dataset PXD012567. The related genomes used to determine evolutionary conservation all came from the family Streptococcaceae, exculding anomalous genomes and non-complete *Streptococcus pneumoniae* genomes. Links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'COH1_PreSaved_ResultsObj_GenBank', 'COH1_PreSaved_ResultsObj_GeneMarkS2', 'COH1_PreSaved_ResultsObj_Glimmer', and 'COH1_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("COH1", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD012567`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/HG939456.1`

---

`D_UW_3_CX` `Assessment` *Objects for* Chlamydia trachomatis *strain D/UW-3/CX*

---

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Chlamydia trachomatis* strain D/UW-3/CX

## Usage

```
data(D_UW_3_CX_PreSaved_DataMapObj)
data(D_UW_3_CX_PreSaved_ResultsObj_GenBank)
data(D_UW_3_CX_PreSaved_ResultsObj_GeneMarkS2)
data(D_UW_3_CX_PreSaved_ResultsObj_Glimmer)
data(D_UW_3_CX_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'D_UW_3_CX_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'D_UW_3_CX_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'D_UW_3_CX_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'D_UW_3_CX_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'D_UW_3_CX_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: D_UW_3_CX
- `Species`: C. trachomatis

## Mapping object

The mapping object, 'D_UW_3_CX_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD003883. The related genomes used to determine evolutionary conservation all came from the phylum Chlamydiae, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'D_UW_3_CX_PreSaved_ResultsObj_GenBank', 'D_UW_3_CX_PreSaved_ResultsObj_GeneMa
'D_UW_3_CX_PreSaved_ResultsObj_Glimmer', and 'D_UW_3_CX_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("D_UW_3_CX", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD003883

NCBI's Genome Browser: https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/

GenBank record: https://www.ncbi.nlm.nih.gov/nuccore/AE001273.1

---

# `EGD_e` `Assessment` *Objects for* Listeria monocytogenes *strain EGD-e*

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Listeria monocytogenes* strain EGD-e

## Usage

```
data(EGD_e_PreSaved_DataMapObj)
data(EGD_e_PreSaved_ResultsObj_GenBank)
data(EGD_e_PreSaved_ResultsObj_GeneMarkS2)
data(EGD_e_PreSaved_ResultsObj_Glimmer)
data(EGD_e_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'EGD_e_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'EGD_e_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'EGD_e_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'EGD_e_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'EGD_e_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: EGD_e
- `Species`: L. monocytogenes

## Mapping object

The mapping object, 'EGD_e_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD000890. The related genomes used to determine evolutionary conservation all came from the genus Listeria, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'EGD_e_PreSaved_ResultsObj_GenBank', 'EGD_e_PreSaved_ResultsObj_GeneMarkS2', 'EGD_e_PreSaved_ResultsObj_Glimmer', and 'EGD_e_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("EGD_e", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD000890`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/NC_003210.1`

---

`GetDataMapObj` *Get a Data Map Object*

---

### Description

Gets and returns the data map object for a specific strain

### Usage

```
GetDataMapObj(strainID)
```

### Arguments

| | |
|---|---|
| `strainID` | Character string corresponding to the strain identifier. |

### Details

`GetDataMapObj` returns an object of class `Assessment` and subclass `DataMap` corresponding to the given strain ID. The given strain ID must be a part of the AssessORF set, and there is no partial matching. Otherwise, the function will error.

### Value

An object of class `Assessment` and subclass `DataMap`

### Examples

```
mapObj <- GetDataMapObj("MGAS5005")
```

---

`GetGeneSources` *Get the Gene Sources*

---

### Description

Returns the list of gene sources used in making the results objects

### Usage

```
GetGeneSources()
```

### Details

`GetGeneSources` returns the list of gene sources (programs and databases) used in making the results objects in the AssessORF set.

### Value

A character vector where each element corresponds to a single gene source

## Examples

```
geneSourceSet <- GetGeneSources()
```

---

# `GetResultsObj` *Get a Results Object*

## Description

Gets and returns the results object for a specific strain-gene source combo

## Usage

```
GetResultsObj(strainID, geneSource = "Prodigal")
```

## Arguments

| | |
|---|---|
| `strainID` | Character string corresponding to the strain identifier. |
| `geneSource` | Character string corresponding to the gene source. |

## Details

`GetDataMapObj` returns an object of class `Assessment` and subclass `Results` corresponding to the given strain ID and the given gene source. The given strain ID must be a part of the AssessORF set, and there is no partial matching. Otherwise, the function will error. The given gene source must also be a part of the AssessORF set, but the function ignores case when checking if the given gene source is a part of the set.

## Value

An object of class `Assessment` and subclass `Results`

## Examples

```
resObj1 <- GetResultsObj("MGAS5005", "Prodigal")
resObj2 <- GetResultsObj("MGAS5005", "GenBank")
resObj3 <- GetResultsObj("MGAS5005", "GeneMarkS2")
resObj4 <- GetResultsObj("MGAS5005", "Glimmer")
```

---

## `GetStrainIDs` *Get the Strain Identifiers*

---

### Description

Returns the list of strain identifiers for which the package has data

### Usage

```
GetStrainIDs()
```

### Details

`GetStrainIDs` returns the list of strains in the AssessORF set. This function is a shorter alternative to `data("AssessORF_StrainIDs")`.

### Value

A character vector where each element corresponds to a single strain identifier

### Examples

```
allStrainIDs <- GetStrainIDs()
```

---

## `H37Rv` `Assessment` *Objects for* Mycobacterium tuberculosis *strain H37Rv*

---

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Mycobacterium tuberculosis* strain H37Rv

### Usage

```
data(H37Rv_PreSaved_DataMapObj)
data(H37Rv_PreSaved_ResultsObj_GenBank)
data(H37Rv_PreSaved_ResultsObj_GeneMarkS2)
data(H37Rv_PreSaved_ResultsObj_Glimmer)
data(H37Rv_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'H37Rv_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'H37Rv_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'H37Rv_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'H37Rv_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'H37Rv_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: H37Rv
- `Species`: M. tuberculosis

## Mapping object

The mapping object, 'H37Rv_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD006117. The related genomes used to determine evolutionary conservation all came from the genus Mycobacterium, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'H37Rv_PreSaved_ResultsObj_GenBank', 'H37Rv_PreSaved_ResultsObj_GeneMarkS2', 'H37Rv_PreSaved_ResultsObj_Glimmer', and 'H37Rv_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("H37Rv", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD006117

NCBI's Genome Browser: https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/

GenBank record: https://www.ncbi.nlm.nih.gov/nuccore/AL123456.3

## `HG001` `Assessment` *Objects for* Staphylococcus aureus *subsp.* aureus *strain HG001*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Staphylococcus aureus* subsp. *aureus* strain HG001

### Usage

```
data(HG001_PreSaved_DataMapObj)
data(HG001_PreSaved_ResultsObj_GenBank)
data(HG001_PreSaved_ResultsObj_GeneMarkS2)
data(HG001_PreSaved_ResultsObj_Glimmer)
data(HG001_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

### Details

'HG001_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'HG001_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'HG001_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'HG001_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'HG001_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: HG001
- `Species`: S. aureus

### Mapping object

The mapping object, 'HG001_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD000702. The related genomes used to determine evolutionary conservation all came from the genus Staphylococcus, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'HG001_PreSaved_ResultsObj_GenBank', 'HG001_PreSaved_ResultsObj_GeneMarkS2', 'HG001_PreSaved_ResultsObj_Glimmer', and 'HG001_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("HG001", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine. Note that this genome comes from accession CP018205.1, which has the same genome sequence as accession NZ_CP018205.1. Unlike NZ_CP018205.1 however, CP018205.1 does not have any associated GenBank genes.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD000702`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/NZ_CP018205.1`

---

## Houston_1 — Assessment *Objects for* Bartonella henselae *strain Houston-1*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Bartonella henselae* strain Houston-1

### Usage

```
data(Houston_1_PreSaved_DataMapObj)
data(Houston_1_PreSaved_ResultsObj_GenBank)
data(Houston_1_PreSaved_ResultsObj_GeneMarkS2)
data(Houston_1_PreSaved_ResultsObj_Glimmer)
data(Houston_1_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

’Houston_1_PreSaved_DataMapObj’ is an object of subclass `DataMap`.

’Houston_1_PreSaved_ResultsObj_GenBank’ is an object of subclass `Results` with predicted genes from the GenBank database.

’Houston_1_PreSaved_ResultsObj_GeneMarkS2’ is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

’Houston_1_PreSaved_ResultsObj_Glimmer’ is an object of subclass `Results` with predicted genes from the program Glimmer.

’Houston_1_PreSaved_ResultsObj_Prodigal’ is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: Houston_1
- `Species`: B. henselae

## Mapping object

The mapping object, ’Houston_1_PreSaved_DataMapObj’, stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain’s genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD000153. The related genomes used to determine evolutionary conservation came from the families Bartonellaceae, Brucellaceae, Phyllobacteriaceae, Rhizobiaceae. Links to their sequences were downloaded from NCBI’s Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, ’Houston_1_PreSaved_ResultsObj_GenBank’, ’Houston_1_PreSaved_ResultsObj_GeneMarkS2’, ’Houston_1_PreSaved_ResultsObj_Glimmer’, and ’Houston_1_PreSaved_ResultsObj_Prodigal’, store how much evidence there is supporting or against each gene in a set of predicted genes for the strain’s genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain’s genome

Use `SaveGenomeToPath("Houston_1", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD000153`

NCBI’s Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/BX897699.1`

---

`Il1403` `Assessment` *Objects for* Lactococcus lactis *subsp.* lactis *strain Il1403*

---

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Lactococcus lactis* subsp. *lactis* strain Il1403

## Usage

```
data(Il1403_PreSaved_DataMapObj)
data(Il1403_PreSaved_ResultsObj_GenBank)
data(Il1403_PreSaved_ResultsObj_GeneMarkS2)
data(Il1403_PreSaved_ResultsObj_Glimmer)
data(Il1403_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'Il1403_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'Il1403_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'Il1403_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'Il1403_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'Il1403_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: Il1403
- `Species`: L. lactis

## Mapping object

The mapping object, 'Il1403_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD000494. The related genomes used to determine evolutionary conservation all came from the family, Streptococcaceae exculding anomalous genomes and non-complete *Streptococcus pneumoniae* genomes. Links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'Il1403_PreSaved_ResultsObj_GenBank', 'Il1403_PreSaved_ResultsObj_GeneMarkS2', 'Il1403_PreSaved_ResultsObj_Glimmer', and 'Il1403_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("Il1403", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD000494`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/AE005176.1`

---

## `K_12_MG1655` `Assessment` *Objects for* Escherichia coli *strain K-12 substrain MG1655*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Escherichia coli* strain K-12 substrain MG1655

### Usage

```
data(K_12_MG1655_PreSaved_DataMapObj)
data(K_12_MG1655_PreSaved_ResultsObj_GenBank)
data(K_12_MG1655_PreSaved_ResultsObj_GeneMarkS2)
data(K_12_MG1655_PreSaved_ResultsObj_Glimmer)
data(K_12_MG1655_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'K_12_MG1655_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'K_12_MG1655_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'K_12_MG1655_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'K_12_MG1655_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'K_12_MG1655_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: K_12_MG1655
- `Species`: E. coli

## Mapping object

The mapping object, 'K_12_MG1655_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD005901. The related genomes used to determine evolutionary conservation all came from the genus Escherichia, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'K_12_MG1655_PreSaved_ResultsObj_GenBank', 'K_12_MG1655_PreSaved_ResultsObj_Gene 'K_12_MG1655_PreSaved_ResultsObj_Glimmer', and 'K_12_MG1655_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("K_12_MG1655", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD005901`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/CP025268.1`

---

`LAL14_1` `Assessment` *Objects for* Sulfolobus islandicus *strain LAL14/1*

---

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Sulfolobus islandicus* strain LAL14/1

## Usage

```
data(LAL14_1_PreSaved_DataMapObj)
data(LAL14_1_PreSaved_ResultsObj_GenBank)
data(LAL14_1_PreSaved_ResultsObj_GeneMarkS2)
data(LAL14_1_PreSaved_ResultsObj_Glimmer)
data(LAL14_1_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'LAL14_1_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'LAL14_1_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'LAL14_1_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'LAL14_1_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'LAL14_1_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: LAL14_1
- `Species`: S. islandicus

## Mapping object

The mapping object, 'LAL14_1_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD003074. The related genomes used to determine evolutionary conservation all came from the phylum Crenarchaeota, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'LAL14_1_PreSaved_ResultsObj_GenBank', 'LAL14_1_PreSaved_ResultsObj_GeneMarkS2', 'LAL14_1_PreSaved_ResultsObj_Glimmer', and 'LAL14_1_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("LAL14_1", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD003074`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/CP003928.1`

---

## `MG1363` Assessment *Objects for* Lactococcus lactis *subsp.* cremoris *strain MG1363*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Lactococcus lactis* subsp. *cremoris* strain MG1363

### Usage

```
data(MG1363_PreSaved_DataMapObj)
data(MG1363_PreSaved_ResultsObj_GenBank)
data(MG1363_PreSaved_ResultsObj_GeneMarkS2)
data(MG1363_PreSaved_ResultsObj_Glimmer)
data(MG1363_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'MG1363_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'MG1363_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'MG1363_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'MG1363_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'MG1363_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: MG1363
- `Species`: L. lactis

## Mapping object

The mapping object, 'MG1363_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD011263. The related genomes used to determine evolutionary conservation all came from the family, Streptococcaceae exculding anomalous genomes and non-complete *Streptococcus pneumoniae* genomes. Links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'MG1363_PreSaved_ResultsObj_GenBank', 'MG1363_PreSaved_ResultsObj_GeneMarkS2', 'MG1363_PreSaved_ResultsObj_Glimmer', and 'MG1363_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("MG1363", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD011263

NCBI's Genome Browser: https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/

GenBank record: https://www.ncbi.nlm.nih.gov/nuccore/AM406671.1

---

# `MGAS5005` `Assessment` *Objects for* Streptococcus pyogenes *strain MGAS5005*

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Streptococcus pyogenes* strain MGAS5005

## Usage

```
data(MGAS5005_PreSaved_DataMapObj)
data(MGAS5005_PreSaved_ResultsObj_GenBank)
data(MGAS5005_PreSaved_ResultsObj_GeneMarkS2)
data(MGAS5005_PreSaved_ResultsObj_Glimmer)
data(MGAS5005_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'MGAS5005_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'MGAS5005_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'MGAS5005_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'MGAS5005_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'MGAS5005_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: MGAS5005
- `Species`: S. pyogenes

### Mapping object

The mapping object, 'MGAS5005_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The proteomics data was generated in-house and collected as part of the work for the AssessORF paper. The raw mass spectra data can be found at ProteomeXchange dataset PXD012568. The related genomes used to determine evolutionary conservation all came from the family, Streptococcaceae exculding anomalous genomes and non-complete *Streptococcus pneumoniae* genomes. Links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'MGAS5005_PreSaved_ResultsObj_GenBank', 'MGAS5005_PreSaved_ResultsObj_GeneMarkS
'MGAS5005_PreSaved_ResultsObj_Glimmer', and 'MGAS5005_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("MGAS5005", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD012568`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/CP000017.2`

---

## `NCIB_3610` `Assessment` *Objects for* Bacillus subtilis *subsp.* subtilis *strain NCIB 3610*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Bacillus subtilis* subsp. *subtilis* strain NCIB 3610

## Usage

```
data(NCIB_3610_PreSaved_DataMapObj)
data(NCIB_3610_PreSaved_ResultsObj_GenBank)
data(NCIB_3610_PreSaved_ResultsObj_GeneMarkS2)
data(NCIB_3610_PreSaved_ResultsObj_Glimmer)
data(NCIB_3610_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

’NCIB_3610_PreSaved_DataMapObj’ is an object of subclass `DataMap`.

’NCIB_3610_PreSaved_ResultsObj_GenBank’ is an object of subclass `Results` with predicted genes from the GenBank database.

’NCIB_3610_PreSaved_ResultsObj_GeneMarkS2’ is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

’NCIB_3610_PreSaved_ResultsObj_Glimmer’ is an object of subclass `Results` with predicted genes from the program Glimmer.

’NCIB_3610_PreSaved_ResultsObj_Prodigal’ is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: NCIB_3610
- `Species`: B. subtilis

## Mapping object

The mapping object, ’NCIB_3610_PreSaved_DataMapObj’, stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain’s genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD006444. The related genomes used to determine evolutionary conservation all came from the genus Bacillus, and links to their sequences were downloaded from NCBI’s Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, ’NCIB_3610_PreSaved_ResultsObj_GenBank’, ’NCIB_3610_PreSaved_ResultsObj_GeneMarkS
’NCIB_3610_PreSaved_ResultsObj_Glimmer’, and ’NCIB_3610_PreSaved_ResultsObj_Prodigal’, store how much evidence there is supporting or against each gene in a set of predicted genes for the strain’s genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("NCIB_3610", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD006444`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/NZ_CM000488.1`

---

## `PAO1` `Assessment` *Objects for* Pseudomonas aeruginosa *strain PAO1*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Pseudomonas aeruginosa* strain PAO1

### Usage

```
data(PAO1_PreSaved_DataMapObj)
data(PAO1_PreSaved_ResultsObj_GenBank)
data(PAO1_PreSaved_ResultsObj_GeneMarkS2)
data(PAO1_PreSaved_ResultsObj_Glimmer)
data(PAO1_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

### Details

'PAO1_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'PAO1_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'PAO1_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'PAO1_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'PAO1_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: PAO1
- `Species`: P. aeruginosa

### Mapping object

The mapping object, 'PAO1_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD004560. The related genomes used to determine evolutionary conservation all came from the genus Pseudomonas, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'PAO1_PreSaved_ResultsObj_GenBank', 'PAO1_PreSaved_ResultsObj_GeneMarkS2', 'PAO1_PreSaved_ResultsObj_Glimmer', and 'PAO1_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("PAO1", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD004560`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/AE004091.2`

---

## `SaveGenomeToPath` *Save a Strain's Genome to a Directory*

---

### Description

Saves the genome for a specified strain to a given directory

### Usage

```
SaveGenomeToPath(strainID, filePath)
```

### Arguments

| | |
|---|---|
| `strainID` | Character string corresponding to the strain identifier. |
| `filePath` | Character string corresponding to the path to the file path. Must end in '.fasta'. |

## Details

`SaveGenomeToPath` saves the genome for the specified strain ID to the given file path. If the file specified by the path already exists, it will be overwitten (with a warning). The given strain ID must be a part of the AssessORF set, and there is no partial matching. Otherwise, the function will error.

Note: there is no genome for strain ATCC700084, so a reference genome for the species (strain MC2155) is used instead.

## Value

Invisibly returns `filePath`

## Examples

```
tmpFile <- paste0(tempfile(), ".fasta")
SaveGenomeToPath("MGAS5005", tmpFile)
unlink(tmpFile)
```

---

# `SL1344` `Assessment` *Objects for* Salmonella enterica *subsp.* enterica *serovar Typhimurium strain SL1344*

## Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Salmonella enterica* subsp. *enterica* serovar Typhimurium strain SL1344

## Usage

```
data(SL1344_PreSaved_DataMapObj)
data(SL1344_PreSaved_ResultsObj_GenBank)
data(SL1344_PreSaved_ResultsObj_GeneMarkS2)
data(SL1344_PreSaved_ResultsObj_Glimmer)
data(SL1344_PreSaved_ResultsObj_Prodigal)
```

## Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

'SL1344_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'SL1344_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'SL1344_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'SL1344_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'SL1344_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: SL1344
- `Species`: S. typhimurium

### Mapping object

The mapping object, 'SL1344_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD005579. The related genomes used to determine evolutionary conservation all came from the genus Salmonella, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'SL1344_PreSaved_ResultsObj_GenBank', 'SL1344_PreSaved_ResultsObj_GeneMarkS2', 'SL1344_PreSaved_ResultsObj_Glimmer', and 'SL1344_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("SL1344", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD005579

NCBI's Genome Browser: https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/

GenBank record: https://www.ncbi.nlm.nih.gov/nuccore/FQ312003.1

---

## `Strain10403S` `Assessment` *Objects for* Listeria monocytogenes *strain 10403S*

---

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Listeria monocytogenes* strain 10403S

### Usage

```
data(Strain10403S_PreSaved_DataMapObj)
data(Strain10403S_PreSaved_ResultsObj_GenBank)
data(Strain10403S_PreSaved_ResultsObj_GeneMarkS2)
data(Strain10403S_PreSaved_ResultsObj_Glimmer)
data(Strain10403S_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

### Details

'Strain10403S_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'Strain10403S_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'Strain10403S_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'Strain10403S_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'Strain10403S_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: Strain10403S
- `Species`: L. monocytogenes

### Mapping object

The mapping object, 'Strain10403S_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD010000. The related genomes used to determine evolutionary conservation all came from the genus Listeria, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

### Results objects

The 4 results objects, 'Strain10403S_PreSaved_ResultsObj_GenBank', 'Strain10403S_PreSaved_ResultsObj_GeneMar 'Strain10403S_PreSaved_ResultsObj_Glimmer', and 'Strain10403S_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

### Getting the strain's genome

Use `SaveGenomeToPath("Strain10403S", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

### Source

Proteomcis data: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD010000

NCBI's Genome Browser: https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/

GenBank record: https://www.ncbi.nlm.nih.gov/nuccore/NC_017544.1

---

## `Strain168` `Assessment` *Objects for* Bacillus subtilis *subsp.* subtilis *strain 168*

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Bacillus subtilis* subsp. *subtilis* strain 168

### Usage

```
data(Strain168_PreSaved_DataMapObj)
data(Strain168_PreSaved_ResultsObj_GenBank)
data(Strain168_PreSaved_ResultsObj_GeneMarkS2)
data(Strain168_PreSaved_ResultsObj_Glimmer)
data(Strain168_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

## Details

’Strain168_PreSaved_DataMapObj’ is an object of subclass `DataMap`.

’Strain168_PreSaved_ResultsObj_GenBank’ is an object of subclass `Results` with predicted genes from the GenBank database.

’Strain168_PreSaved_ResultsObj_GeneMarkS2’ is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

’Strain168_PreSaved_ResultsObj_Glimmer’ is an object of subclass `Results` with predicted genes from the program Glimmer.

’Strain168_PreSaved_ResultsObj_Prodigal’ is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: Strain168
- `Species`: B. subtilis

## Mapping object

The mapping object, ’Strain168_PreSaved_DataMapObj’, stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain’s genome. The raw proteomics mass spectra data came from ProteomeXchange dataset PXD004565. The related genomes used to determine evolutionary conservation all came from the genus Bacillus, and links to their sequences were downloaded from NCBI’s Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, ’Strain168_PreSaved_ResultsObj_GenBank’, ’Strain168_PreSaved_ResultsObj_GeneMarkS2’, ’Strain168_PreSaved_ResultsObj_Glimmer’, and ’Strain168_PreSaved_ResultsObj_Prodigal’, store how much evidence there is supporting or against each gene in a set of predicted genes for the strain’s genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain’s genome

Use `SaveGenomeToPath("Strain168", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD004565`

NCBI’s Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/CM000487.1`

---

## TCH1516 `Assessment` *Objects for* Staphylococcus aureus *subsp.* aureus *strain USA300_TCH1516*

---

### Description

Objects of class `Assessment` and either subclass `DataMap` or subclass `Results` for *Staphylococcus aureus* subsp. *aureus* strain USA300_TCH1516

### Usage

```
data(TCH1516_PreSaved_DataMapObj)
data(TCH1516_PreSaved_ResultsObj_GenBank)
data(TCH1516_PreSaved_ResultsObj_GeneMarkS2)
data(TCH1516_PreSaved_ResultsObj_Glimmer)
data(TCH1516_PreSaved_ResultsObj_Prodigal)
```

### Format

All 5 objects have a list structure. For specifics on what the two types of `Assessment` objects contain, please see the **AssessORF** package.

### Details

'TCH1516_PreSaved_DataMapObj' is an object of subclass `DataMap`.

'TCH1516_PreSaved_ResultsObj_GenBank' is an object of subclass `Results` with predicted genes from the GenBank database.

'TCH1516_PreSaved_ResultsObj_GeneMarkS2' is an object of subclass `Results` with predicted genes from the program GeneMarkS-2.

'TCH1516_PreSaved_ResultsObj_Glimmer' is an object of subclass `Results` with predicted genes from the program Glimmer.

'TCH1516_PreSaved_ResultsObj_Prodigal' is an object of subclass `Results` with predicted genes from the program Prodigal.

For all 5 objects, values of two key identifying list items within each object are listed below.

- `StrainID`: TCH1516
- `Species`: S. aureus

### Mapping object

The mapping object, 'TCH1516_PreSaved_DataMapObj', stores the mapping of proteomics evidence and evolutionary conservation evidence to the strain's genome. The proteomics data was generated in-house and collected as part of the work for the AssessORF paper. The raw mass spectra data can be found at ProteomeXchange dataset PXD012538. The related genomes used to determine evolutionary conservation all came from the genus Staphylococcus, and links to their sequences were downloaded from NCBI's Genome Browser. The object was built using the `MapAssessmentData` function from the **AssessORF** package.

## Results objects

The 4 results objects, 'TCH1516_PreSaved_ResultsObj_GenBank', 'TCH1516_PreSaved_ResultsObj_GeneMarkS2', 'TCH1516_PreSaved_ResultsObj_Glimmer', and 'TCH1516_PreSaved_ResultsObj_Prodigal', store how much evidence there is supporting or against each gene in a set of predicted genes for the strain's genome. The four objects were built using the `AssessGenes` function from the **AssessORF** package, a set of genes, and the mapping object described here.

For the GenBank object, the genes were downloaded from the corresponding record in the GenBank database. For the other three objects, GenemarkS-2 (web server), Prodigal (2.6.3), and Glimmer (3.02) were run at default settings in order to generate the set of predicted genes for the corresponding results object.

The `GeneLeftPos`, `GeneRightPos`, and the `GeneStrand` within each of the four results objects provide positional information on the set of predicted genes used to generate that object.

The `GeneSource` list item within each of the four results objects describes where the predicted genes came from (either "GenBank", "GeneMarkS2", "Glimmer", or "Prodigal" respectively).

## Getting the strain's genome

Use `SaveGenomeToPath("TCH1516", <INSERT FILE PATH HERE>)` to save the genome sequence for the strain to your local machine.

## Source

Proteomcis data: `http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD012538`

NCBI's Genome Browser: `https://www.ncbi.nlm.nih.gov/genome/browse/#!/prokaryotes/`

GenBank record: `https://www.ncbi.nlm.nih.gov/nuccore/CP000730.1`

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