

# Package ‘TENxIO’

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**Description** Provides a structured S4 approach to importing data files from the 10X pipelines. It mainly supports Single Cell Multiome ATAC + Gene Expression data among other data types. The main Bioconductor data representations used are SingleCellExperiment and RaggedExperiment.

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**Author** Marcel Ramos [aut, cre] (<<https://orcid.org/0000-0002-3242-0582>>)

**Maintainer** Marcel Ramos <marcel.amos@roswellpark.org>

## R topics documented:

TENxFile . . . . .	2
TENxFile-class . . . . .	3
TENxFileList . . . . .	4
TENxFileList-class . . . . .	5
TENxFragments . . . . .	6
TENxFragments-class . . . . .	7
TENxH5 . . . . .	8
TENxH5-class . . . . .	10
TENxIO . . . . .	12
TENxMTX . . . . .	13
TENxMTX-class . . . . .	13
TENxPeaks . . . . .	14
TENxPeaks-class . . . . .	16
TENxTSV-class . . . . .	17

**Index** **19**

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TENxFile	<i>TENxFile constructor function</i>
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### Description

The TENxFile constructor function serves as the auto-recognizer function for 10X files. It can import several different file extensions, namely:

- \* H5 - on-disk HDF5
- \* MTX - matrix market
- \* .tar.gz - compressed tarball

### Usage

```
TENxFile(resource, extension, ...)
```

### Arguments

resource	character(1) The path to the file
extension	character(1) The file extension for the given resource. It can usually be obtained from the file path. An override can be provided especially for ExperimentHub resources where the file extension is removed.
...	Additional inputs to the low level class generator functions

**Details**

**Note** that the example below includes the use of a large ~ 4 GB ExperimentHub resource obtained from the 10X website.

**Value**

A subclass of TENxFile according to the input file extension

**Examples**

```
if (interactive()) {
  ## from ExperimentHub
  hub <- ExperimentHub::ExperimentHub()
  fname <- hub[["EH1039"]]
  TENxFile(fname, extension = "h5", group = "mm10", version = "2")
}
```

---

 TENxFile-class

*TENxFile: General purpose class for 10X files*


---

**Description**

The TENxFile class is the default representation for unrecognized subclasses. It inherits from the BiocFile class and adds a few additional slots. The constructor function can handle typical 10X file types. For more details, see the constructor function documentation.

**Slots**

`extension` `character(1)` The file extension as extracted from the file path or overridden via the `ext` argument in the constructor function.

`colidx` `integer(1)` The column index corresponding to the columns in the file that will subsequently be imported

`rowidx` `integer(1)` The row index corresponding to rows in the file that will subsequently be imported

`remote` `logical(1)` Whether the file exists on the web, i.e., the resource is a URL

`compressed` `logical(1)` Whether the file is compressed with, e.g., `.gz`

---

 TENxFileList

*TENxFileList: Represent groups of files from 10X Genomic*


---

### Description

This constructor function is meant to handle .tar.gz tarball files from 10X Genomics.

### Usage

```
TENxFileList(..., version, compressed = FALSE)
```

### Arguments

...	A single file path, named arguments corresponding to file paths, or a list of named file paths
version	character(1) The version in the tarball. See details.
compressed	logical(1) Whether or not the file provided is compressed, usually as tar.gz (default FALSE)

### Details

These tarballs usually contain three files:

1. matrix.mtx.gz - the counts matrix
2. features.tsv.gz - row metadata usually represented as rowData
3. barcodes.tsv.gz - column names corresponding to cell barcode identifiers If all above files are in the tarball, the import method will provide a SingleCellExperiment. Otherwise, a simple list of imported data is given. Note that version "3" uses 'features.tsv.gz' and version "2" uses 'genes.tsv.gz'. If known, indicate the version argument in the TENxFileList constructor function.

### Value

Either a SingleCellExperiment or a list of imported data

### Examples

```
f1 <- system.file(
  "extdata", "pbmc_granulocyte_sorted_3k_ff_bc_ex_matrix.tar.gz",
  package = "TENxIO", mustWork = TRUE
)

import(TENxFileList(f1))
```

---

TENxFileList-class      *TENxFileList: A list-like representation for TENxFiles*

---

## Description

This class was designed to mainly handle tarballs from 10X Genomics. The typical file extension for these tarballs is `.tar.gz`.

## Usage

```
## S4 method for signature 'TENxFileList'
path(object, ...)

## S4 method for signature 'TENxFileList'
decompress(manager, con, ...)

## S4 method for signature 'TENxFileList,ANY,ANY'
import(con, format, text, ...)
```

## Arguments

<code>object</code>	An object containing paths. Even though it will typically contain a single path, object can actually contain an arbitrary number of paths.
<code>...</code>	Additional arguments, for use in specific methods.
<code>manager</code>	A ConnectionManager internal instance; currently not used.
<code>con</code>	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a <a href="#">BiocFile</a> derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
<code>format</code>	The format of the output. If missing and <code>con</code> is a file name, the format is derived from the file extension. This argument is unnecessary when <code>con</code> is a derivative of <a href="#">BiocFile</a> .
<code>text</code>	If <code>con</code> is missing, this can be a character vector directly providing the string data to import.

## Details

These tarballs usually contain three files:

1. `matrix.mtx.gz` - the counts matrix
2. `features.tsv.gz` - row metadata usually represented as `rowData`
3. `barcodes.tsv.gz` - column names corresponding to cell barcode identifiers Note that version '2' includes `genes.tsv.gz` instead of `features.tsv.gz` in version '3'.

**Value**

A TENxFileList class object

**Functions**

- `path(TENxFileList)`: Obtain file paths for all files in the object as a vector
- `decompress(TENxFileList)`: An intermediate method for decompressing (via `untar`) the contents of a `.tar.gz` file list
- `import(con = TENxFileList, format = ANY, text = ANY)`: Recursively import files within a `TENxFileList`

**Slots**

`listData list()` The data in list format

`extension character()` A vector of file extensions for each file

`compressed logical(1)` Whether the file is compressed as `.tar.gz`

`version character(1)` The version number of the tarball usually either '2' or '3'

---

TENxFragments

*TENxFragments: Import fragments files from 10X*

---

**Description**

TENxFragments: Import fragments files from 10X

**Usage**

```
TENxFragments(resource, yieldSize = 200, which = GRanges(), ...)
```

**Arguments**

<code>resource</code>	<code>character(1)</code> The file path to the fragments resource, usually a compressed tabix file with extension <code>.tsv.gz</code> .
<code>yieldSize</code>	<code>numeric()</code> The number of records to read by default, 200 records will be imported. A warning will be emitted if not modified.
<code>which</code>	<code>GRanges()</code> A <code>GRanges</code> indicating the regions of interest. This get sent to <code>RSamtools</code> as the <code>param</code> input.
<code>...</code>	Further arguments to the class generator function (currently not used)

**Value**

A `RaggedExperiment` object class

## Examples

```
fr <- system.file(
  "extdata", "pbmc_3k_atac_ex_fragments.tsv.gz",
  package = "TENxIO", mustWork = TRUE
)

tfr <- TENxFragments(fr)

fra <- import(tfr)
```

---

TENxFragments-class    *TENxFragments: A class to represent fragments data as GRanges*

---

## Description

This class is designed to work mainly with `fragments.tsv.gz` files from 10x pipelines.

## Usage

```
## S4 method for signature 'TENxFragments,ANY,ANY'
import(con, format, text, ...)
```

## Arguments

<code>con</code>	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a <a href="#">BiocFile</a> derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
<code>format</code>	The format of the output. If missing and <code>con</code> is a file name, the format is derived from the file extension. This argument is unnecessary when <code>con</code> is a derivative of <a href="#">BiocFile</a> .
<code>text</code>	If <code>con</code> is missing, this can be a character vector directly providing the string data to import.
<code>...</code>	Parameters to pass to the format-specific method.

## Details

Fragments data from 10x can be quite large. In order to speed up the initial exploration of the data, we use a default of **200** records for loading. Users can change this default value by specifying a new one via the `yieldSize` argument in the constructor function.

## Value

A `TENxFragments` class object

**Methods (by generic)**

- `import(con = TENxFragments, format = ANY, text = ANY)`: Import method for representing fragments.tsv.gz data from 10x via Rsamtools and RaggedExperiment

**Slots**

`which GRanges()` A GRanges indicating the regions of interest. This get sent to RSamtools as the param input.

`yieldSize numeric()` The number of records to read by default, 200 records will be imported. A warning will be emitted if not modified.

---

 TENxH5

---

*TENxH5: Represent H5 files from 10X*


---

**Description**

This constructor function was developed using the PBMC 3K dataset from 10X Genomics (version 3). Other versions are supported and input arguments `version` and `group` can be overridden.

**Usage**

```
TENxH5(resource, version, group, ranges, rowidx, colidx, ...)
```

**Arguments**

<code>resource</code>	<code>character(1)</code> The path to the file
<code>version</code>	<code>character(1)</code> There are currently two recognized versions associated with 10X data, either version "2" or "3". See details for more information.
<code>group</code>	<code>character(1)</code> The HDF5 group embedded within the file structure, this is usually either the "matrix" or "outs" group but other groups are supported as well (e.g., "mm10").
<code>ranges</code>	<code>character(1)</code> The HDF5 internal folder location embedded within the file that points to the ranged data information, e.g., "/features/interval". Set to <code>NA_character_</code> if range information is not present.
<code>rowidx, colidx</code>	<code>numeric()</code> A vector of indices corresponding to either rows or columns that will dictate the data imported from the file. The indices will be passed on to the <code>[</code> method of the <code>TENxMatrix</code> representation.
<code>...</code>	Additional inputs to the low level class generator functions

## Details

The various TENxH5 methods including `rowData` and `rowRanges`, provide a snapshot of the data using a length 12 head and tail subset for efficiency. In contrast, methods such as `dimnames` and `dim` give a full view of the dimensions of the data. The `show` method provides relevant information regarding the dimensions of the data including metadata such as `rowData` and "Type" column, if available. The term "projection" refers to the data class that will be provided once the data file is imported.

An additional `ref` argument can be provided when the file contains multiple `feature_type` in the file or "Type" in the `rowData`. By default, the most frequent type is represented.

For data that do not contain genomic coordinate information, one can set the `ranges` argument to `NA_character_`.

The data version "3" mainly includes a "matrix" group and "interval" information within the file. Version "2" data does not include ranged-based information and has a different directory structure compared to version "3". See the internal data.frame: `TENxIO::h5.version.map` for a map of fields and their corresponding file locations within the H5 file. This map is used to create the `rowData` structure from the file.

## Value

Usually, a `SingleCellExperiment` instance

## See Also

import section in [TENxH5](#)

## Examples

```
h5f <- system.file(
  "extdata", "pbmc_granulocyte_ff_bc_ex.h5",
  package = "TENxIO", mustWork = TRUE
)

TENxH5(h5f)

import(TENxH5(h5f))

h5f <- system.file(
  "extdata", "10k_pbmc_ATACv2_f_bc_ex.h5",
  package = "TENxIO", mustWork = TRUE
)

## Optional ref input, most frequent Type used by default
th5 <- TENxH5(h5f, ranges = "/features/id", ref = "Peaks")
th5
TENxH5(h5f, ranges = "/features/id")
import(th5)
```

TENxH5-class

*TENxH5: The HDF5 file representation class for 10X Data***Description**

This class is designed to work with 10x Single Cell datasets. It was developed using the PBMC 3k 10X dataset from the CellRanger v2 pipeline.

**Usage**

```
## S4 method for signature 'TENxH5'
rowData(x, use.names = TRUE, ...)

## S4 method for signature 'TENxH5'
dim(x)

## S4 method for signature 'TENxH5'
dimnames(x)

## S4 method for signature 'TENxH5'
genome(x)

## S4 method for signature 'TENxH5'
rowRanges(x, ...)

## S4 method for signature 'TENxH5,ANY,ANY'
import(con, format, text, ...)

## S4 method for signature 'TENxH5'
show(object)
```

**Arguments**

x	A TENxH5 object
use.names	For rowData: Like <code>mcols(x)</code> , by default <code>rowData(x)</code> propagates the rownames of x to the returned <code>DataFrame</code> object (note that for a <code>SummarizedExperiment</code> object, the rownames are also the names i.e. <code>rownames(x)</code> is always the same as <code>names(x)</code> ). Setting <code>use.names=FALSE</code> suppresses this propagation i.e. it returns a <code>DataFrame</code> object with no rownames. Use this when <code>rowData(x)</code> fails, which can happen when the rownames contain NAs (because the rownames of a <code>SummarizedExperiment</code> object can contain NAs, but the rownames of a <code>DataFrame</code> object cannot). For <code>combineRows</code> and <code>combineCols</code> : See <code>Combining</code> section below.
...	For assay, arguments in ... are forwarded to assays. For <code>rbind</code> , <code>cbind</code> , ... contains <code>SummarizedExperiment</code> objects to be combined. For other accessors, ignored.

con	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a <a href="#">BiocFile</a> derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
format	The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of <a href="#">BiocFile</a> .
text	If con is missing, this can be a character vector directly providing the string data to import.
object	A TENxH5 class object

### Details

The data version "3" mainly includes a "matrix" group and "interval" information within the file. Version "2" data does not include ranged-based information and has a different directory structure compared to version "3". See the internal data, frame: `TENxIO::h5.version.map` for a map of fields and their corresponding file locations within the H5 file. This map is used to create the `rowData` structure from the file.

### Value

A TENxH5 class object

### Methods (by generic)

- `rowData(TENxH5)`: Generate the `rowData` ad hoc from a TENxH5 file
- `dim(TENxH5)`: Get the dimensions of the data as stored in the file
- `dimnames(TENxH5)`: Get the dimension names from the file
- `genome(TENxH5)`: Read genome string from file
- `rowRanges(TENxH5)`: Read interval data and represent as `GRanges`
- `import(con = TENxH5, format = ANY, text = ANY)`: Import TENxH5 data as a `SingleCell-Experiment`; see section below
- `show(TENxH5)`: Display a snapshot of the contents within a TENxH5 file before import

### Slots

`version` `character(1)` There are currently two recognized versions associated with 10X data, either version "2" or "3". See details for more information.

`group` `character(1)` The HDF5 group embedded within the file structure, this is usually either the "matrix" or "outs" group but other groups are supported as well.

`ranges` `character(1)` The HDF5 internal folder location embedded within the file that points to the ranged data information, e.g., `"/features/interval"`.

**import**

The import method uses `DelayedArray::TENxMatrix` to represent matrix data. Generally, version 3 datasets contain associated genomic coordinates. The associated feature data, as displayed by the `rowData` method, is queried for the "Type" column which will indicate that a `splitAltExps` operation is appropriate. If a `ref` input is provided to the constructor function `TENxH5`, it will be used as the main experiment; otherwise, the most frequent category in the "Type" column will be used. For example, the Multiome ATAC + Gene Expression feature data contains both 'Gene Expression' and 'Peaks' labels in the "Type" column.

**See Also**

[TENxH5](#)

---

TENxIO

*TENxIO: A Bioconductor package for importing 10X Genomics files*

---

**Description**

The package provides file classes based on `BiocIO` for common file extensions found in the 10X Genomics website.

**Supported file types**

Here is a table of supported file and file extensions and their imported classes:

Extension	Class	Imported as
.h5	TENxH5	SingleCellExperiment w/ TENxMatrix
.mtx / .mtx.gz	TENxMTX	SummarizedExperiment w/ dgCMatrx
.tar.gz	TENxFileList	SingleCellExperiment w/ dgCMatrx
peak_annotation.tsv	TENxPeaks	GRanges
fragments.tsv.gz	TENxFragments	RaggedExperiment
.tsv / .tsv.gz	TENxTSV	tibble

**Author(s)**

**Maintainer:** Marcel Ramos <marcel.ramos@roswellpark.org> ([ORCID](#))

**See Also**

Useful links:

- <https://github.com/waldronlab/TENxIO>
- Report bugs at <https://github.com/waldronlab/TENxIO/issues>

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 TENxMTX

*TENxMTX: Represent Matrix Market Format Files from 10X*


---

**Description**

This constructor function accepts `.mtx` and `.mtx.gz` compressed formats for eventual importing. It is mainly used with tarball files from 10X Genomics, where more annotation data is included. Importing solely the `.mtx` format will provide users with a `SummarizedExperiment` with an assay of class `dgCMatrix` from the `Matrix` package. Currently, other formats are not supported but if you'd like to request support for a format, please open an issue on GitHub.

**Usage**

```
TENxMTX(resource, compressed = FALSE, ...)
```

**Arguments**

<code>resource</code>	<code>character(1)</code> The path to the file
<code>compressed</code>	<code>logical(1)</code> Whether the resource file is compressed (default <code>FALSE</code> )
<code>...</code>	Additional inputs to the low level class generator functions

**Value**

A `SummarizedExperiment` instance with a `dgCMatrix` in the assay

**Examples**

```
mtxf <- system.file(
  "extdata", "pbmc_3k_ff_bc_ex.mtx",
  package = "TENxIO", mustWork = TRUE
)

con <- TENxMTX(mtxf)

import(con)
```

---

 TENxMTX-class

*TENxMTX: The Matrix Market representation class for 10X Data*


---

**Description**

This class is designed to work with 10x MTX datasets, particularly from the multiome pipelines.

**Usage**

```
## S4 method for signature 'TENxMTX,ANY,ANY'
import(con, format, text, ...)
```

**Arguments**

con	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a <a href="#">BiocFile</a> derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
format	The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of <a href="#">BiocFile</a> .
text	If con is missing, this can be a character vector directly providing the string data to import.
...	Parameters to pass to the format-specific method.

**Details**

The TENxMTX class is a straightforward implementation that allows the user to import a Matrix Market file format using `Matrix::readMM`. Currently, it returns a `SummarizedExperiment` with an internal `dgCMatrix` assay. To request other formats, please open an issue on [GitHub](#).

**Value**

A TENxMTX class object

**Methods (by generic)**

- `import(con = TENxMTX, format = ANY, text = ANY)`: Import method mainly for `mtx.gz` files from 10x

**Slots**

`compressed` `logical(1)` Whether or not the file is in compressed format, usually `gzipped (.gz)`.

---

TENxPeaks

*Import 10x peak annotation files from 10x*

---

**Description**

This constructor function is designed to work with the files denoted with "peak\_annotation" in the file name. These are usually produced as tab separated value files, i.e., `.tsv`.

**Usage**

```
TENxPeaks(resource, extension, ...)
```

**Arguments**

resource	character(1) The path to the file
extension	character(1) The file extension for the given resource. It can usually be obtained from the file path. An override can be provided especially for ExperimentHub resources where the file extension is removed.
...	Additional inputs to the low level class generator functions

**Details**

The output class allows handling of peak data. It can be used in conjunction with the annotation method on a `SingleCellExperiment` to add peak information to the experiment. The ranged data is represented as a `GRanges` class object.

**Value**

A `GRanges` class object of peak locations

**Examples**

```
fi <- system.file(
  "extdata", "pbmc_granulocyte_sorted_3k_ex_atac_peak_annotation.tsv",
  package = "TENxIO", mustWork = TRUE
)
peak_file <- TENxPeaks(fi)
peak_anno <- import(peak_file)
peak_anno

example(TENxH5)

## Add peaks to an existing SCE
## First, import the SCE from an example H5 file
h5f <- system.file(
  "extdata", "pbmc_granulocyte_ff_bc_ex.h5",
  package = "TENxIO", mustWork = TRUE
)
con <- TENxH5(h5f)
sce <- import(con)
## auto-import peaks when using annotation<-
annotation(sce, name = "peak_annotation") <- peak_file
annotation(sce)
```

---

 TENxPeaks-class

*TENxPeaks: The class to represent 10x Peaks files*


---

## Description

This class is designed to work with the files denoted with "peak\_annotation" in the file name. These are usually produced as tab separated value files, i.e., .tsv.

## Usage

```
## S4 method for signature 'TENxPeaks,ANY,ANY'
import(con, format, text, ...)

## S4 replacement method for signature 'SingleCellExperiment,ANY'
annotation(object, ...) <- value

## S4 method for signature 'SingleCellExperiment'
annotation(object, ...)
```

## Arguments

con	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a <a href="#">BiocFile</a> derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
format	The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of <a href="#">BiocFile</a> .
text	If con is missing, this can be a character vector directly providing the string data to import.
...	Parameters to pass to the format-specific method.
object	The object to export.
value	The annotation information to set on object.

## Details

This class is a straightforward class for handling peak data. It can be used in conjunction with the annotation method on a `SingleCellExperiment` to add peak information to the experiment. The ranged data is represented as a `GRanges` class object.

## Value

A `TENxPeaks` class object

**Functions**

- `import(con = TENxPeaks, format = ANY, text = ANY)`: Import a `peaks_annotation` file from 10x as a `GRanges` representation
- `annotation(object = SingleCellExperiment) <- value`: Replacement method to add annotation data to a `SingleCellExperiment`
- `annotation(SingleCellExperiment)`: Extraction method to obtain annotation data from a `SingleCellExperiment` representation

---

 TENxTSV-class

*TENxTSV: A class to represent 10x tab separated values files*


---

**Description**

This class is general purpose for reading in tabular data from the 10x Genomics website with the `.tsv` file extension. The class also supports compressed files, i.e., those with the `.tsv.gz` extension.

**Usage**

```
## S4 method for signature 'TENxTSV,ANY,ANY'
import(con, format, text, ...)
```

```
TENxTSV(resource, compressed = FALSE, ...)
```

**Arguments**

<code>con</code>	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a <a href="#">BiocFile</a> derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
<code>format</code>	The format of the output. If missing and <code>con</code> is a file name, the format is derived from the file extension. This argument is unnecessary when <code>con</code> is a derivative of <a href="#">BiocFile</a> .
<code>text</code>	If <code>con</code> is missing, this can be a character vector directly providing the string data to import.
<code>...</code>	Parameters to pass to the format-specific method.
<code>resource</code>	character(1) The path to the file
<code>compressed</code>	logical(1) Whether the resource file is compressed (default FALSE)

**Details**

Typical `.tsv` files obtained from the 10X website are compressed and contain information relevant to 'barcodes' and 'features'. Currently, the code only supports files such as `features.tsv.*` and `barcodes.tsv.*`.

**Value**

A TENxTSV class object; a tibble for the import method

**Functions**

- `import(con = TENxTSV, format = ANY, text = ANY)`: General import method for tsv files from 10x; using `readr::read_tsv` and returning a tibble representation

# Index

.TENxFile (TENxFile-class), 3  
.TENxFileList (TENxFileList-class), 5  
.TENxFragments (TENxFragments-class), 7  
.TENxH5 (TENxH5-class), 10  
.TENxMTX (TENxMTX-class), 13  
.TENxPeaks (TENxPeaks-class), 16  
.TENxTSV (TENxTSV-class), 17  
\_PACKAGE (TENxIO), 12

annotation, SingleCellExperiment-method  
(TENxPeaks-class), 16  
annotation<-, SingleCellExperiment, ANY-method  
(TENxPeaks-class), 16

BiocFile, 5, 7, 11, 14, 16, 17

DataFrame, 10  
decompress, TENxFileList-method  
(TENxFileList-class), 5  
dim, TENxH5-method (TENxH5-class), 10  
dimnames, TENxH5-method (TENxH5-class),  
10

genome, TENxH5-method (TENxH5-class), 10

import, TENxFileList, ANY, ANY-method  
(TENxFileList-class), 5  
import, TENxFragments, ANY, ANY-method  
(TENxFragments-class), 7  
import, TENxH5, ANY, ANY-method  
(TENxH5-class), 10  
import, TENxMTX, ANY, ANY-method  
(TENxMTX-class), 13  
import, TENxPeaks, ANY, ANY-method  
(TENxPeaks-class), 16  
import, TENxTSV, ANY, ANY-method  
(TENxTSV-class), 17

mcols, 10

path, TENxFileList-method  
(TENxFileList-class), 5

rowData, TENxH5-method (TENxH5-class), 10  
rowRanges, TENxH5-method (TENxH5-class),  
10

show, TENxH5-method (TENxH5-class), 10

TENxFile, 2  
TENxFile-class, 3  
TENxFileList, 4  
TENxFileList-class, 5  
TENxFragments, 6  
TENxFragments-class, 7  
TENxH5, 8, 9, 12  
TENxH5-class, 10  
TENxIO, 12  
TENxIO-package (TENxIO), 12  
TENxMTX, 13  
TENxMTX-class, 13  
TENxPeaks, 14  
TENxPeaks-class, 16  
TENxTSV (TENxTSV-class), 17  
TENxTSV-class, 17