

# Package ‘alabaster.string’

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**Title** Save and Load Biostrings to/from File

**Version** 1.6.0

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**Description** Save Biostrings objects to file artifacts, and load them back into memory.  
This is a more portable alternative to serialization of such objects into RDS files.  
Each artifact is associated with metadata for further interpretation;  
downstream applications can enrich this metadata with context-specific properties.

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**Depends** Biostrings, alabaster.base

**Imports** utils, methods, S4Vectors

**Suggests** BiocStyle, rmarkdown, knitr, testthat

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

**biocViews** DataImport, DataRepresentation

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**Author** Aaron Lun [aut, cre]

**Maintainer** Aaron Lun <[infinite.monkeys.with.keyboards@gmail.com](mailto:infinite.monkeys.with.keyboards@gmail.com)>

## Contents

readXStringSet . . . . .	2
saveObject,XStringSet-method . . . . .	2
<b>Index</b>	<b>4</b>

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readXStringSet	<i>Read an XStringSet from disk.</i>
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### Description

Read a [XStringSet](#) object from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

### Usage

```
readXStringSet(path, metadata, ...)
```

### Arguments

path	String containing a path to a directory, itself created using the <a href="#">saveObject</a> method for <a href="#">XStringSet</a> objects.
metadata	Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.
...	Further arguments passed to internal <a href="#">altReadObject</a> calls.

### Value

An [XStringSet](#) subclass containing DNA, RNA, protein or custom sequences. This may also be a [QualityScaledDNAStringSet](#) with quality scores.

### See Also

["saveObject,XStringSet-method"](#), to save an [XStringSet](#) to disk.

### Examples

```
library(Biostrings)
stuff <- DNAStringSet(c("AAA", "CC", "G", "TTTT"))

tmp <- tempfile()
saveObject(stuff, tmp)
readObject(tmp)
```

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saveObject,XStringSet-method	<i>Save a XStringSet to disk</i>
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### Description

Save a [XStringSet](#) to its on-disk representation.

### Usage

```
## S4 method for signature 'XStringSet'
saveObject(x, path, ...)
```

**Arguments**

<code>x</code>	A <a href="#">XStringSet</a> or any of its subclasses such as a <a href="#">QualityScaledXStringSet</a> .
<code>path</code>	String containing the path to a directory in which to save <code>x</code> .
<code>...</code>	Further arguments to pass to specific methods.

**Value**

The contents of `x` are saved into a path, and `NULL` is invisibly returned.

**Author(s)**

Aaron Lun

**See Also**

[readXStringSet](#), to read the `XStringSet` back into the R session.

**Examples**

```
library(Biostrings)
stuff <- DNASTringSet(c("AAA", "CC", "G", "TTTT"))

tmp <- tempfile()
saveObject(stuff, tmp)
list.files(tmp, recursive=TRUE)
```

# Index

altReadObject, [2](#)

loadXStringSet (readXStringSet), [2](#)

QualityScaledDNAStrngSet, [2](#)

QualityScaledXStringSet, [3](#)

readObject, [2](#)

readObjectFile, [2](#)

readXStringSet, [2](#), [3](#)

saveObject, [2](#)

saveObject, XStringSet-method, [2](#)

stageObject, XStringSet-method  
    (saveObject, XStringSet-method),  
    [2](#)

XStringSet, [2](#), [3](#)