

# Package ‘alabaster.string’

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

**Version** 1.8.0

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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

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**biocViews** DataImport, DataRepresentation

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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  
*Save a XStringSet to disk*

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**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

**Author(s)**

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**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)
```

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