

# Package ‘alabaster.string’

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

**Version** 1.1.1

**Date** 2023-05-01

**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** methods

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

**VignetteBuilder** knitr

**RoxygenNote** 7.2.1

**biocViews** DataImport, DataRepresentation

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loadXStringSet	<i>Load a DNAStringSet</i>
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## Description

Load a [DNAStringSet](#) object, typically from a FASTA or FASTQ file generated by the corresponding [stageObject](#) method.

## Usage

```
loadXStringSet(seq.info, project)
```

## Arguments

seq.info	A named list of metadata for this object.
project	Any argument accepted by the acquisition functions, see <a href="#">?acquireFile</a> . By default, this should be a string containing the path to a staging directory.

## Value

A [DNAStringSet](#) containing DNA sequences. This may also be a [QualityScaledDNAStringSet](#) with quality scores.

## Examples

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

tmp <- tempfile()
dir.create(tmp)
info <- stageObject(stuff, tmp, path="dna_thing")
loadXStringSet(info, project=tmp)
```

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stageObject,XStringSet-method	<i>Stage a XStringSet</i>
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## Description

Stage a XStringSet by saving it to the appropriate file format.

## Usage

```
## S4 method for signature 'XStringSet'
stageObject(x, dir, path, child = FALSE, ...)
```

## Arguments

x	A <a href="#">XStringSet</a> or any of its subclasses, in particular a <a href="#">QualityScaledXStringSet</a> .
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.
...	Further arguments to pass to specific methods.

## Value

A list containing metadata for x. A subdirectory is created at path inside dir and the contents of x are saved to various files within that subdirectory. If x is a QualityScaledXStringSet, a FASTQ file is created instead of a FASTA file.

## Author(s)

Aaron Lun

## Examples

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

tmp <- tempfile()
dir.create(tmp)
stageObject(stuff, tmp, path="dna_thing")
list.files(tmp, recursive=TRUE)
```

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