

# Package ‘alabaster.vcf’

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**Title** Save and Load Variant Data to/from File

**Version** 1.7.0

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**Description** Save variant calling SummarizedExperiment to file and load them back as VCF objects.  
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** alabaster.base, VariantAnnotation

**Imports** methods, S4Vectors, alabaster.se, alabaster.string, Rsamtools

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

**RoxygenNote** 7.2.3

**VignetteBuilder** knitr

**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)>

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readVCF	<i>Read a VCF object from disk</i>
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### Description

Read a [VCF](#) object from its on-disk representation.

### Usage

```
readVCF(path, metadata, ...)
```

### Arguments

path	String containing a path to a directory, usually generated by the <a href="#">saveObject</a> method for <a href="#">VCF</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

A [VCF](#) object.

### Author(s)

Aaron Lun

### See Also

[saveObject](#), [VCF-method](#), to save VCF objects to disk.

### Examples

```
f1 <- system.file("extdata", "structural.vcf", package="VariantAnnotation")
vcf <- readVcf(f1)

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

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saveObject, VCF-method *Save a VCF object to disk*

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**Description**

Save a [VCF](#) object to its on-disk representation, namely a VCF file with the same contents.

**Usage**

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

**Arguments**

x	Any instance of a <a href="#">VCF</a> class or one of its subclasses.
path	String containing the path to a directory in which to save x.
...	Further arguments to pass to specific methods.

**Value**

x is saved to file inside path, and NULL is returned.

**Author(s)**

Aaron Lun

**See Also**

[readVCF](#), to read a VCF object back to the R session.

**Examples**

```
f1 <- system.file("extdata", "structural.vcf", package="VariantAnnotation")  
vcf <- readVcf(f1)
```

```
tmp <- tempfile()  
saveObject(vcf, tmp)
```

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