

# Package ‘RSeqAn’

April 15, 2020

**Type** Package

**Title** R SeqAn

**Version** 1.6.0

**Description** Headers and some wrapper functions from the SeqAn C++ library for ease of usage in R.

**License** BSD\_3\_clause + file LICENSE

**BugReports** <https://github.com/compbiocore/RSeqAn/issues>

**LinkingTo** Rcpp

**Imports** Rcpp

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**biocViews** Infrastructure, Software

**RoxygenNote** 6.1.0

**git\_url** <https://git.bioconductor.org/packages/RSeqAn>

**git\_branch** RELEASE\_3\_10

**git\_last\_commit** de2b9d9

**git\_last\_commit\_date** 2019-10-29

**Date/Publication** 2020-04-14

**Author** August Guang [aut, cre]

**Maintainer** August Guang <[august.guang@gmail.com](mailto:august.guang@gmail.com)>

## R topics documented:

containment_test . . . . .	2
<b>Index</b>	<b>3</b>

containment\_test      *containment test*

---

**Description**

containment test

**Usage**

containment\_test(s1)

**Arguments**

s1                      Should be a character string

# Index

containment\_test, [2](#)