

# Package ‘RSeqAn’

May 6, 2024

**Type** Package

**Title** R SeqAn

**Version** 1.24.0

**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\_19

**git\_last\_commit** a882262

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-05-05

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

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

## Contents

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

---

containment_test	<i>containment test</i>
------------------	-------------------------

---

**Description**

containment test

**Usage**

```
containment_test(s1)
```

**Arguments**

s1                   Should be a character string

# Index

containment\_test, [2](#)