

# Package ‘fastrc’

May 8, 2026

**Title** Fast Reverse Complement of DNA and RNA Sequences

**Version** 0.0.2

**Description** Fast reverse complement of DNA and RNA sequences using a 'C++' lookup table for O(1) per-base complement mapping. Supports full IUPAC ambiguity codes, DNA and RNA modes, case preservation, and NA handling. Much faster than other packages for computing reverse complements of many short sequences such as primers, probes, and, k-mers.

**License** GPL (>= 3)

**Language** en-US

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**LinkingTo** Rcpp

**Imports** Rcpp

**NeedsCompilation** yes

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**Repository** CRAN

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`fast_rc`*Fast Reverse Complement of DNA/RNA Sequences*

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**Description**

Computes the reverse complement of one or more DNA or RNA sequences using a C++ lookup table for O(1) complement mapping. Supports full IUPAC ambiguity codes and preserves case.

**Usage**

```
fast_rc(seqs, type = "DNA")
```

**Arguments**

<code>seqs</code>	A character vector of DNA or RNA sequences.
<code>type</code>	Either "DNA" (A↔T) or "RNA" (A↔U).

**Value**

A character vector of reverse-complemented sequences, with NA values preserved.

**Examples**

```
fast_rc("ATCG")  
fast_rc(c("ATCG", "AAGG", NA))  
fast_rc("AUCG", type = "RNA")
```

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