

# Resource Summary Report

Generated by T1D on Jul 29, 2026

## Biostrings

RRID:SCR\_016949

Type: Tool

### Proper Citation

Biostrings (RRID:SCR\_016949)

### Resource Information

**URL:** <https://bioconductor.org/packages/release/bioc/html/Biostrings.html>

**Proper Citation:** Biostrings (RRID:SCR\_016949)

**Description:** Software package for efficient manipulation of biological strings. Memory efficient string containers, string matching algorithms, and other utilities, for fast manipulation of large biological sequences or sets of sequences.

**Resource Type:** software application, data analysis software, sequence analysis software, software resource, data processing software

**Keywords:** manipulation, biological, string, memory, efficient, container, sequence, set, DNA, RNA, protein

**Availability:** Free, Available for download, Freely available

**Resource Name:** Biostrings

**Resource ID:** SCR\_016949

**Alternate URLs:**

[https://web.stanford.edu/class/bios221/labs/biostrings/lab\\_1\\_biostrings.html](https://web.stanford.edu/class/bios221/labs/biostrings/lab_1_biostrings.html)

**License:** Artistic 2.0

**Record Creation Time:** 20220129T080332+0000

**Record Last Update:** 20260729T044425+0000

### Ratings and Alerts

No rating or validation information has been found for Biostrings.

No alerts have been found for Biostrings.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 167 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Tangpeerachaikul A, et al. (2025) Zidesamtinib Selective Targeting of Diverse ROS1 Drug-Resistant Mutations. *Molecular cancer therapeutics*, 24(7), 1005.

Buri MC, et al. (2025) Natural Killer Cell-Mediated Cytotoxicity Shapes the Clonal Evolution of B-cell Leukemia. *Cancer immunology research*, 13(3), 430.

Nakatsu G, et al. (2025) Virulence factor discovery identifies associations between the Fic gene family and Fap2+ fusobacteria in colorectal cancer microbiomes. *mBio*, 16(2), e0373224.

Lacy KD, et al. (2025) Heterozygosity at a conserved candidate sex determination locus is associated with female development in the clonal raider ant (*Ooceraea biroii*). *eLife*, 14.

Carré A, et al. (2025) Interferon- $\gamma$  promotes HLA-B-restricted presentation of conventional and alternative antigens in human pancreatic  $\gamma$ -cells. *Nature communications*, 16(1), 765.

Santolla N, et al. (2025) AI-based antibody design targeting recent H5N1 avian influenza strains. *Computational and structural biotechnology journal*, 27, 2915.

Krawczyk PS, et al. (2025) Re-adenylation by TENT5A enhances efficacy of SARS-CoV-2 mRNA vaccines. *Nature*, 641(8064), 984.

Chabuka L, et al. (2025) Genomic Surveillance of Climate-Amplified Cholera Outbreak, Malawi, 2022-2023. *Emerging infectious diseases*, 31(6), 1090.

Hackmann TJ, et al. (2025) Setting new boundaries of 16S rRNA gene identity for prokaryotic taxonomy. *International journal of systematic and evolutionary microbiology*, 75(4).

Rohan P, et al. (2025) High expression of THY1 is a prognostic marker for gastric Cancer: Deciphering its transcriptional regulation as a component of the Epithelial-mesenchymal transition. *Biochemistry and biophysics reports*, 42, 102050.

Cui T, et al. (2025) Ad5-boosted COVID-19 vaccine reduces symptomatic BA.5 infection via cross-neutralizing antibodies and NK cell immunity. *BMC medicine*, 23(1), 699.

Funikov S, et al. (2025) Analysis of somatic piRNAs in the malaria mosquito *Anopheles coluzzii* reveals atypical classes of genic small RNAs. *RNA biology*, 22(1), 1.

Rao S, et al. (2025) Translational buffering tunes gene expression in mouse and human. *bioRxiv : the preprint server for biology*.

Lacy KD, et al. (2025) Heterozygosity at a conserved candidate sex determination locus is associated with female development in the clonal raider ant (*Ooceraea biroii*). *bioRxiv* : the preprint server for biology.

Bestehorn A, et al. (2025) Cytoplasmic mRNA decay controlling inflammatory gene expression is determined by pre-mRNA fate decision. *Molecular cell*, 85(4), 742.

Trendel J, et al. (2025) The human proteome with direct physical access to DNA. *Cell*, 188(16), 4424.

Johnston J, et al. (2024) Metatranscriptomic Analysis Reveals Synergistic Activities of Comammox and Anammox Bacteria in Full-Scale Attached Growth Nitrogen Removal System. *Environmental science & technology*, 58(29), 13023.

Subramani PG, et al. (2024) Conserved role of hnRNPL in alternative splicing of epigenetic modifiers enables B cell activation. *EMBO reports*, 25(6), 2662.

Shutt-McCabe J, et al. (2024) The plasmid-borne hipBA operon of *Klebsiella michiganensis* encodes a potent plasmid stabilization system. *Journal of applied microbiology*, 135(10).

Chivu AG, et al. (2024) Evolution of promoter-proximal pausing enabled a new layer of transcription control. *bioRxiv* : the preprint server for biology.