

Resource Summary Report

Generated by [NIF](#) on Aug 11, 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: data analysis software, software application, software resource, sequence analysis software, 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

License: Artistic 2.0

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260811T043546+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 182 mentions in open access literature.

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

Dabak T, et al. (2026) The genetic basis of mimicry in the snowy bumble bee (*Bombus niveatus*) in Anatolia with insights from a color polymorphic gynandromorph. *PLoS genetics*, 22(3), e1012060.

Nguyen HT, et al. (2026) Machine learning-driven identification of virulence determinants in *Borrelia burgdorferi* associated with human dissemination. *PLoS computational biology*, 22(6), e1014407.

Jonsson S, et al. (2026) The dynamic distribution of genetic tandem amplifications in a heteroresistant *Escherichia coli* population revealed by ultra-deep long read sequencing. *Nature communications*, 17(1).

Hamm DC, et al. (2026) KLF18 is a necessary component of the DUX4-initiated transcriptional network and a candidate locus for phenotypic diversity. *Genes & development*, 40(11-12), 873.

Katznelson A, et al. (2026) Basis for lineage-determining pioneer factors targeting distinct repressed chromatin states. *Science advances*, 12(2), eadz7409.

Kiran S, et al. (2026) Segmented filamentous bacteria are worldwide human gut commensals. *Nature communications*, 17(1).

Rao S, et al. (2026) Translational buffering tunes gene expression in mice and humans. *Genome biology*, 27(1).

Zhang H, et al. (2026) Targeting tRNA-dependent tyrosine usage unveils a metabolic vulnerability in hepatocellular carcinoma. *Nature communications*, 17(1).

Dini M, et al. (2026) The detection of three independent benzimidazole resistance mutations in a single *Ancylostoma caninum* population from a Golden Retriever breeding kennel in Sao Paulo, Brazil. *International journal for parasitology. Drugs and drug resistance*, 31, 100643.

Myers A, et al. (2026) HIV-1 BG505 SOSIP immunization induced B cell expansion targeting the 465-glycan hole, with neutralizing antibodies exhibiting distinct binding modes and mechanisms of virus inhibition. *PLoS pathogens*, 22(6), e1014268.

Rock RR, et al. (2026) Female-enriched *Eggerthella lenta* drives neuroinflammation and IFN-?? via host receptor TLR2. *bioRxiv : the preprint server for biology*.

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

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.

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).

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.

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.

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

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.

Scacchetti A, et al. (2025) Pseudouridine selects RNAs for extracellular transport. *bioRxiv* : the preprint server for biology.

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