

Resource Summary Report

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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: sequence analysis software, data analysis software, software resource, software application, 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: 20260728T043528+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 [nidm-terms](#) .

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- γ promotes HLA-B-restricted presentation of conventional and alternative antigens in human pancreatic γ -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.