

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

Bioparser

RRID:SCR_024065

Type: Tool

Proper Citation

Bioparser (RRID:SCR_024065)

Resource Information

URL: <https://github.com/rvaser/bioparser/>

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Description: Software C++ library for parsing several formats in bioinformatics. C++ header only parsing library for several bioinformatics formats (FASTA/Q, MHAP/PAF/SAM), with support for zlib compressed files.

Synonyms: bioparser, libbioparser-dev

Resource Type: software library, software resource, software toolkit

Keywords: C ++, parsing formats, FASTA/Q, MHAP/PAF/SAM, support for zlib compressed files,

Availability: Free, Available for download, Freely available,

Resource Name: Bioparser

Resource ID: SCR_024065

Alternate URLs: <https://sources.debian.org/src/libbioparser-dev/>

License: MIT License

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260912T200113+0000

Ratings and Alerts

No rating or validation information has been found for Bioparser.

No alerts have been found for Bioparser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Henriques C, et al. (2015) Identification and functional characterization of a novel arginine/ornithine transporter, a member of a cationic amino acid transporter subfamily in the Trypanosoma cruzi genome. Parasites & vectors, 8, 346.

Capriles PV, et al. (2010) Structural modelling and comparative analysis of homologous, analogous and specific proteins from Trypanosoma cruzi versus Homo sapiens: putative drug targets for chagas' disease treatment. BMC genomics, 11, 610.

Beres SB, et al. (2008) Genome sequence of a Lancefield group C Streptococcus zooepidemicus strain causing epidemic nephritis: new information about an old disease. PloS one, 3(8), e3026.