

Resource Summary Report

Generated by [RRID](#) on Aug 7, 2026

Biopieces

RRID:SCR_005783

Type: Tool

Proper Citation

Biopieces (RRID:SCR_005783)

Resource Information

URL: <http://www.biopieces.org>

Proper Citation: Biopieces (RRID:SCR_005783)

Description: A collection of bioinformatics tools that can be pieced together in a very easy and flexible manner to perform both simple and complex tasks. The Biopieces work on a data stream in such a way that the data stream can be passed through several different Biopieces, each performing one specific task: modifying or adding records to the data stream, creating plots, or uploading data to databases and web services. The Biopieces are executed in a command line environment where the data stream is initialized by specific Biopieces which read data from files, databases, or web services, and output records to the data stream that is passed to downstream Biopieces until the data stream is terminated at the end of the analysis. The advantage of the Biopieces is that a user can easily solve simple and complex tasks without having any programming experience. Moreover, since the data format used to pass data between Biopieces is text based, different developers can quickly create new Biopieces in their favorite programming language - and all the Biopieces will maintain compatibility. Finally, templates exist for creating new Biopieces in Perl and Ruby. There are currently ~190 Biopieces (March 2014).

Abbreviations: Biopieces

Synonyms: www.biopieces.org, biopieces - Biopieces is a bioinformatic framework of tools easily used and easily created

Resource Type: source code, software toolkit, software resource

Keywords: bioinformatics, tool, framework, biopieces, language independent, bio.tools, FASEB list

Funding: Danish Agency for Science Technology and Innovation 272-06-0325

Availability: GNU General Public License, v2

Resource Name: Biopieces

Resource ID: SCR_005783

Alternate IDs: nlx_149253, biotools:biopieces, OMICS_01036

Alternate URLs: <http://code.google.com/p/biopieces/>, <https://bio.tools/biopieces>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260807T042624+0000

Ratings and Alerts

No rating or validation information has been found for Biopieces.

No alerts have been found for Biopieces.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Oliveira AER, et al. (2020) Gene expression network analyses during infection with virulent and avirulent *Trypanosoma cruzi* strains unveil a role for fibroblasts in neutrophil recruitment and activation. *PLoS pathogens*, 16(8), e1008781.

Mandal MK, et al. (2020) Elucidation of resistance signaling and identification of powdery mildew resistant mapping loci (ClAPMR2) during watermelon-*Podosphaera xanthii* interaction using RNA-Seq and whole-genome resequencing approach. *Scientific reports*, 10(1), 14038.

Nielsen BLH, et al. (2019) n-3 PUFA biosynthesis by the copepod *Apocyclops royi* documented using fatty acid profile analysis and gene expression analysis. *Biology open*, 8(2).

Jørgensen TS, et al. (2019) The Whole Genome Sequence and mRNA Transcriptome of the Tropical Cyclopoid Copepod *Apocyclops royi*. *G3 (Bethesda, Md.)*, 9(5), 1295.

Guerra FP, et al. (2019) Exome resequencing and GWAS for growth, ecophysiology, and chemical and metabolomic composition of wood of *Populus trichocarpa*. *BMC genomics*, 20(1), 875.

Jørgensen TS, et al. (2019) The Genome and mRNA Transcriptome of the Cosmopolitan Calanoid Copepod *Acartia tonsa* Dana Improve the Understanding of Copepod Genome

Size Evolution. *Genome biology and evolution*, 11(5), 1440.

Blau K, et al. (2019) Manure and Doxycycline Affect the Bacterial Community and Its Resistome in Lettuce Rhizosphere and Bulk Soil. *Frontiers in microbiology*, 10, 725.

Stokholm J, et al. (2018) Maturation of the gut microbiome and risk of asthma in childhood. *Nature communications*, 9(1), 141.

Callejas-Hernández F, et al. (2018) Genomic assemblies of newly sequenced *Trypanosoma cruzi* strains reveal new genomic expansion and greater complexity. *Scientific reports*, 8(1), 14631.

Parras-Moltó M, et al. (2018) Evaluation of bias induced by viral enrichment and random amplification protocols in metagenomic surveys of saliva DNA viruses. *Microbiome*, 6(1), 119.

Bürckert JP, et al. (2018) High-throughput sequencing of murine immunoglobulin heavy chain repertoires using single side unique molecular identifiers on an Ion Torrent PGM. *Oncotarget*, 9(54), 30225.

Gómez-Manjón I, et al. (2018) Noninvasive Prenatal Testing: Comparison of Two Mappers and Influence in the Diagnostic Yield. *BioMed research international*, 2018, 9498140.

Jacquioud S, et al. (2018) Long-term soil metal exposure impaired temporal variation in microbial metatranscriptomes and enriched active phages. *Microbiome*, 6(1), 223.

Kanfra X, et al. (2018) Free-Living Nematodes Together With Associated Microbes Play an Essential Role in Apple Replant Disease. *Frontiers in plant science*, 9, 1666.

Bradford LM, et al. (2018) Transcriptome-Stable Isotope Probing Provides Targeted Functional and Taxonomic Insights Into Microaerobic Pollutant-Degrading Aquifer Microbiota. *Frontiers in microbiology*, 9, 2696.

Belew AT, et al. (2017) Comparative transcriptome profiling of virulent and non-virulent *Trypanosoma cruzi* underlines the role of surface proteins during infection. *PLoS pathogens*, 13(12), e1006767.

Sverrild A, et al. (2017) Eosinophilic airway inflammation in asthmatic patients is associated with an altered airway microbiome. *The Journal of allergy and clinical immunology*, 140(2), 407.

Curtis HJ, et al. (2017) Knockdown and replacement therapy mediated by artificial mirtrons in spinocerebellar ataxia 7. *Nucleic acids research*, 45(13), 7870.

Elhady A, et al. (2017) Microbiomes associated with infective stages of root-knot and lesion nematodes in soil. *PloS one*, 12(5), e0177145.

Jurburg SD, et al. (2017) Autogenic succession and deterministic recovery following disturbance in soil bacterial communities. *Scientific reports*, 7, 45691.