

Resource Summary Report

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BitSeq

RRID:SCR_009904

Type: Tool

Proper Citation

BitSeq (RRID:SCR_009904)

Resource Information

URL: <http://code.google.com/p/bitseq/>

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Description: A software application for inferring expression levels of individual transcripts from sequencing (RNA-Seq) data and estimating differential expression (DE) between conditions.

Abbreviations: BitSeq

Resource Type: software resource

Defining Citation: [DOI:10.1093/bioinformatics/btv483](https://doi.org/10.1093/bioinformatics/btv483), [DOI:10.1093/bioinformatics/bts260](https://doi.org/10.1093/bioinformatics/bts260)

Keywords: bio.tools

Resource Name: BitSeq

Resource ID: SCR_009904

Alternate IDs: , OMICS_01269, biotools:bitseq

Alternate URLs: <https://bio.tools/bitseq>, <https://sources.debian.org/src/bitseq/>,

Record Creation Time: 20220129T080255+0000

Record Last Update: 20260829T182323+0000

Ratings and Alerts

No rating or validation information has been found for BitSeq.

No alerts have been found for BitSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Zhou W, et al. (2025) A fuzzy sequencer for rapid DNA fragment counting and genotyping. *Nature biomedical engineering*, 9(12), 2068.

Li X, et al. (2025) Microbiome Single Cell Atlases Generated with a Commercial Instrument. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(27), e2409338.

Choi YG, et al. (2025) The complete mitochondrial genome of a ground beetle, *Chlaenius naeviger* (Carabidae: Harpalinae: Chlaeniini), from South Korea. *Mitochondrial DNA. Part B, Resources*, 10(3), 224.

Abate A, et al. (2023) Microbiome single cell atlases generated with a commercial instrument. *Research square*.

Warner AD, et al. (2019) The *C. elegans* embryonic transcriptome with tissue, time, and alternative splicing resolution. *Genome research*, 29(6), 1036.

Papastamoulis P, et al. (2018) A Bayesian model selection approach for identifying differentially expressed transcripts from RNA sequencing data. *Journal of the Royal Statistical Society. Series C, Applied statistics*, 67(1), 3.

Baumgartner C, et al. (2018) An ERK-Dependent Feedback Mechanism Prevents Hematopoietic Stem Cell Exhaustion. *Cell stem cell*, 22(6), 879.

Bronowski C, et al. (2017) *Campylobacter jejuni* transcriptome changes during loss of culturability in water. *PloS one*, 12(11), e0188936.

Williams CR, et al. (2017) Empirical assessment of analysis workflows for differential expression analysis of human samples using RNA-Seq. *BMC bioinformatics*, 18(1), 38.

Gatto S, et al. (2017) ICF-specific DNMT3B dysfunction interferes with intragenic regulation of mRNA transcription and alternative splicing. *Nucleic acids research*, 45(10), 5739.

Rendeiro AF, et al. (2016) Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. *Nature communications*, 7, 11938.

Topa H, et al. (2016) Analysis of differential splicing suggests different modes of short-term splicing regulation. *Bioinformatics (Oxford, England)*, 32(12), i147.

??abaj PP, et al. (2016) Sensitivity, specificity, and reproducibility of RNA-Seq differential expression calls. *Biology direct*, 11(1), 66.

Ustianenko D, et al. (2016) TUT-DIS3L2 is a mammalian surveillance pathway for aberrant structured non-coding RNAs. *The EMBO journal*, 35(20), 2179.

Sankar A, et al. (2016) Bayesian identification of bacterial strains from sequencing data. *Microbial genomics*, 2(8), e000075.

Li J, et al. (2016) Single-cell transcriptomes reveal characteristic features of human pancreatic islet cell types. *EMBO reports*, 17(2), 178.

Liu X, et al. (2015) Improving RNA-Seq expression estimation by modeling isoform- and exon-specific read sequencing rate. *BMC bioinformatics*, 16, 332.

Gardiner LJ, et al. (2015) A genome-wide survey of DNA methylation in hexaploid wheat. *Genome biology*, 16, 273.

Kanitz A, et al. (2015) Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. *Genome biology*, 16(1), 150.

, et al. (2014) A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. *Nature biotechnology*, 32(9), 903.