Resource Summary Report

Generated by NIF on Aug 30, 2026

asSeq

RRID:SCR_001625
Type: Tool

Proper Citation

asSeq (RRID:SCR_001625)

Resource Information

URL: http://bios.unc.edu/~weisun/software/asSeq.htm

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Description: Software that establishes a statistical framework for future developments of eQTL (expression quantitative trait locus) mapping methods using RNA-seq data (e.g., linkage-based eQTL mapping), and the joint study of multiple genetic markers and/or multiple genes. This R package has been submitted to R/bioconductor. It will be available on bioconductor soon. It is recommended to install this R package from bioconductor. You can also install this R package from the source code by yourself. Since the R package contains C code, a C complier is required for installation. With both R and appropriate c complier installed, this R package can be installed using the following command (in Mac Terminal window or Windows command window) R CMD INSTALL asSeq

Abbreviations: asSeq

Resource Type: data analysis software, data processing software, software application, software resource, source code

Defining Citation: PMID:21838806

Keywords: r, rna-seq, expression quantitative trait locus, total read count, allele-specific expression, allele-specific gene expression, gene expression quantitative trait locus, rna isoform, gene expression, genetic marker, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: asSeq

Resource ID: SCR_001625

Alternate IDs: OMICS_01948, nlx_153893, biotools:asseq

Alternate URLs: https://bio.tools/asseq

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260829T182104+0000

Ratings and Alerts

No rating or validation information has been found for asSeq.

No alerts have been found for asSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Yang MG, et al. (2022) Characterization of sequence determinants of enhancer function using natural genetic variation. eLife, 11.

Gori I, et al. (2021) Mutations in SKI in Shprintzen-Goldberg syndrome lead to attenuated TGF-?? responses through SKI stabilization. eLife, 10.

Zou J, et al. (2019) Leveraging allelic imbalance to refine fine-mapping for eQTL studies. PLoS genetics, 15(12), e1008481.

Zhang Q, et al. (2016) The chromatin remodeler DDM1 promotes hybrid vigor by regulating salicylic acid metabolism. Cell discovery, 2, 16027.

Wang W, et al. (2015) Allele-specific copy-number discovery from whole-genome and whole-exome sequencing. Nucleic acids research, 43(14), e90.

Zhang R, et al. (2014) Quantifying RNA allelic ratios by microfluidic multiplex PCR and sequencing. Nature methods, 11(1), 51.