

# Resource Summary Report

Generated by [RRID](#) on Aug 6, 2026

## [asSeq](#)

RRID:SCR\_001625

Type: Tool

### Proper Citation

asSeq (RRID:SCR\_001625)

### Resource Information

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

**Proper Citation:** asSeq (RRID:SCR\_001625)

**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 compiler is required for installation. With both R and appropriate c compiler 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 processing software, source code, software application, data analysis software, software resource

**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:** 20260806T054326+0000

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## Ratings and Alerts

No rating or validation information has been found for asSeq.

No alerts have been found for asSeq.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.