

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## GLiMMPS

RRID:SCR\_001787

Type: Tool

### Proper Citation

GLiMMPS (RRID:SCR\_001787)

### Resource Information

**URL:** <http://www.mimg.ucla.edu/faculty/xing/glimmps/>

**Proper Citation:** GLiMMPS (RRID:SCR\_001787)

**Description:** Software to characterize the genetic variation of alternative splicing using a robust statistical method for detecting splicing quantitative trait loci (sQTLs) from RNA-seq data. It takes into account the individual variation in sequencing coverage and the noise prevalent in RNA-seq data.

**Abbreviations:** GLiMMPS

**Resource Type:** software resource

**Defining Citation:** [PMID:23876401](#)

**Keywords:** alternative splicing, rna-seq, genetic variation, splicing quantitative trait loci

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** GLiMMPS

**Resource ID:** SCR\_001787

**Alternate IDs:** OMICS\_01947

**Record Creation Time:** 20220129T080209+0000

**Record Last Update:** 20260801T190136+0000

### Ratings and Alerts

No rating or validation information has been found for GLiMMPS.

No alerts have been found for GLiMMPS.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Draper BJ, et al. (2025) Selecting differential splicing methods: Practical considerations for short-read RNA sequencing. F1000Research, 14, 47.

Park E, et al. (2017) Population and allelic variation of A-to-I RNA editing in human transcriptomes. Genome biology, 18(1), 143.