

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 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: 20260905T132439+0000

Ratings and Alerts

No rating or validation information has been found for GLiMMPS.

No alerts have been found for GLiMMPS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.