# **Resource Summary Report**

Generated by <u>dkNET</u> on May 10, 2025

# **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

Funding:

Resource Name: GLiMMPS

Resource ID: SCR\_001787

Alternate IDs: OMICS\_01947

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250420T014039+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: <u>SciCrunch Registry</u>

## **Usage and Citation Metrics**

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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