

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## SeqSaw

RRID:SCR\_009185

Type: Tool

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### Proper Citation

SeqSaw (RRID:SCR\_009185)

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### Resource Information

**URL:** <http://bioinfo.au.tsinghua.edu.cn/software/seqsaw/>

**Proper Citation:** SeqSaw (RRID:SCR\_009185)

**Description:** A package for mapping of spliced reads and unbiased detection of novel splice junctions from RNA-seq data.

**Abbreviations:** SeqSaw

**Synonyms:** SeqSaw - Short Spliced Sequence Mapping Tool

**Resource Type:** software resource

**Defining Citation:** [PMID:21575597](#)

**Keywords:** bio.tools

**Resource Name:** SeqSaw

**Resource ID:** SCR\_009185

**Alternate IDs:** biotools:seqsaw, OMICS\_01250

**Alternate URLs:** <https://bio.tools/seqsaw>

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20260905T132632+0000

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### Ratings and Alerts

No rating or validation information has been found for SeqSaw.

No alerts have been found for SeqSaw.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.