Resource Summary Report

Generated by NIF on Apr 25, 2025

SeqSaw

RRID:SCR_009185
Type: Tool

Proper Citation

SeqSaw (RRID:SCR_009185)

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

Funding:

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: 20250420T014451+0000

Ratings and Alerts

No rating or validation information has been found for SeqSaw.

No alerts have been found for SeqSaw.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.