

Resource Summary Report

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

KisSplice

RRID:SCR_011893

Type: Tool

Proper Citation

KisSplice (RRID:SCR_011893)

Resource Information

URL: <http://kissplice.prabi.fr/>

Proper Citation: KisSplice (RRID:SCR_011893)

Description: Software tool that enables analysis of RNA-seq data with or without reference genome. Local transcriptome assembler for SNPs, indels and AS events.

Abbreviations: KisSplice

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [DOI:10.1186/1471-2105-13-S6-S5](https://doi.org/10.1186/1471-2105-13-S6-S5)

Keywords: RNA-seq data analysis, with reference genome, without reference genome, local transcriptome assembler, SNPs, indels, AS events., bio.tools

Availability: Free, Available for download, Freely available

Resource Name: KisSplice

Resource ID: SCR_011893

Alternate IDs: biotools:KisSplice, OMICS_01321

Alternate URLs: <https://bio.tools/KisSplice>, <https://sources.debian.org/src/kissplice/>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260905T132715+0000

Ratings and Alerts

No rating or validation information has been found for KisSplice.

No alerts have been found for KisSplice.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Bacot T, et al. (2026) Metabolic resistance of the tiger mosquito to pyrethroid insecticides in La Réunion Island likely results from local adaptation. *Genome biology and evolution*, 18(3).

Roces V, et al. (2025) Pra-GE-ATLAS: Empowering Pinus radiata stress and breeding research through a multi-omics database. *Journal of integrative plant biology*, 67(8), 2028.

Dubin A, et al. (2025) Sexual Antagonism and Sex Determination in Three Syngnathid Species Alongside a Male Pregnancy Gradient. *Genome biology and evolution*, 17(7).

Rombaut D, et al. (2024) Accelerated DNA replication fork speed due to loss of R-loops in myelodysplastic syndromes with SF3B1 mutation. *Nature communications*, 15(1), 3016.

Roces V, et al. (2022) Integrative analysis in Pinus revealed long-term heat stress splicing memory. *The Plant journal : for cell and molecular biology*, 112(4), 998.

El Taher A, et al. (2021) Dynamics of sex chromosome evolution in a rapid radiation of cichlid fishes. *Science advances*, 7(36), eabe8215.

Maritim TK, et al. (2021) Multiple-genotypes transcriptional analysis revealed candidate genes and nucleotide variants for improvement of quality characteristics in tea (*Camellia sinensis* (L.) O. Kuntze). *Genomics*, 113(1 Pt 1), 305.

Saud HA, et al. (2021) Molecular mechanisms of embryonic tail development in the self-fertilizing mangrove killifish *Kryptolebias marmoratus*. *Development* (Cambridge, England), 148(24).

Ponnanna K, et al. (2021) Allopatric sibling species pair *Drosophila nasuta nasuta* and *Drosophila nasuta albomicans* exhibit expression divergence in ovarian transcriptomes. *Gene*, 777, 145189.

Madritsch S, et al. (2021) Comparing de novo transcriptome assembly tools in di- and autotetraploid non-model plant species. *BMC bioinformatics*, 22(1), 146.

Tandonnet S, et al. (2020) Molecular basis of resistance to organophosphate insecticides in the New World screw-worm fly. *Parasites & vectors*, 13(1), 562.

Ashraf U, et al. (2020) Influenza virus infection induces widespread alterations of host cell splicing. *NAR genomics and bioinformatics*, 2(4), lqaa095.

Kvist J, et al. (2020) A comprehensive epigenomic analysis of phenotypically distinguishable, genetically identical female and male *Daphnia pulex*. *BMC genomics*, 21(1), 17.

Masclaux FG, et al. (2019) Investigating unexplained genetic variation and its expression in the arbuscular mycorrhizal fungus *Rhizophagus irregularis*: A comparison of whole genome and RAD sequencing data. *PLoS one*, 14(12), e0226497.

Cologne A, et al. (2019) New insights into minor splicing-a transcriptomic analysis of cells derived from TALS patients. *RNA (New York, N.Y.)*, 25(9), 1130.

Zhao H, et al. (2019) Gene expression vs. sequence divergence: comparative transcriptome sequencing among natural *Rhinolophus ferrumequinum* populations with different acoustic phenotypes. *Frontiers in zoology*, 16, 37.

Charrier NP, et al. (2018) Whole body transcriptomes and new insights into the biology of the tick *Ixodes ricinus*. *Parasites & vectors*, 11(1), 364.

Benoit-Pilven C, et al. (2018) Complementarity of assembly-first and mapping-first approaches for alternative splicing annotation and differential analysis from RNAseq data. *Scientific reports*, 8(1), 4307.

Lima L, et al. (2017) Playing hide and seek with repeats in local and global de novo transcriptome assembly of short RNA-seq reads. *Algorithms for molecular biology : AMB*, 12, 2.

Davidson NM, et al. (2017) SuperTranscripts: a data driven reference for analysis and visualisation of transcriptomes. *Genome biology*, 18(1), 148.