

Resource Summary Report

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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 processing software, software application, data analysis software, 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: 20260731T042842+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 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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

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

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

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.

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

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.

Audoux J, et al. (2017) DE-kupl: exhaustive capture of biological variation in RNA-seq data through k-mer decomposition. Genome biology, 18(1), 243.