Resource Summary Report

Generated by NIF on Apr 29, 2025

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, data analysis software, software application,

software resource

Defining Citation: DOI:10.1186/1471-2105-13-S6-S5

Keywords: RNA-seg data analysis, with reference genome, without reference genome, local

transcriptome assembler, SNPs, indels, AS events., bio.tools

Funding:

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: 20250428T053638+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 18 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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 candidates genes and nucleotide variants for improvement of quality characteristics in tea (Camellia sinensis (L.) O. Kuntze). Genomics, 113(1 Pt 1), 305.

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).

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

Ashraf U, et al. (2020) Influenza virus infection induces widespread alterations of host cell splicing. NAR genomics and bioinformatics, 2(4), Igaa095.

Tandonnet S, et al. (2020) Molecular basis of resistance to organophosphate insecticides in

the New World screw-worm fly. Parasites & vectors, 13(1), 562.

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.

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.

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.

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.