Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

UnSplicer

RRID:SCR_000226
Type: Tool

Proper Citation

UnSplicer (RRID:SCR_000226)

Resource Information

URL: http://exon.gatech.edu/paul/unsplicer/index.htm

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Description: An RNA-seq alignment program that provides alignment of short reads to a reference genome. The program requires two inputs that are provided by the output of GeneMark-ES: HMM model parameters and ab initio gene predictions. UnSplicer is a sister pipeline to TrueSight.

Resource Type: software resource

Defining Citation: PMID:24259430

Keywords: RNA, sequencing, alignment, short reads, genome, genemark-es, gene prediction

Availability: Free, Available for download, Freely available

Resource Name: UnSplicer

Resource ID: SCR_000226

Alternate IDs: OMICS_01806

Record Creation Time: 20220129T080200+0000

Record Last Update: 20260808T185716+0000

Ratings and Alerts

No rating or validation information has been found for UnSplicer.

No alerts have been found for UnSplicer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Burns PD, et al. (2014) UnSplicer: mapping spliced RNA-Seq reads in compact genomes and filtering noisy splicing. Nucleic acids research, 42(4), e25.