Resource Summary Report

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SpliceSeq

RRID:SCR_005267
Type: Tool

Proper Citation

SpliceSeq (RRID:SCR_005267)

Resource Information

URL: http://bioinformatics.mdanderson.org/main/SpliceSeq:Overview

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Description: A Java application to investigate alternative mRNA splicing patterns in data from high-throughput mRNA sequencing studies. Sequence reads are mapped to splice graphs that unambiguously quantify the inclusion level of each exon and splice junction. The graphs are then traversed to predict the protein isoforms that are likely to result from the observed exon and splice junction reads. UniProt annotations are mapped to each protein isoform to identify potential functional impacts of alternative splicing. This tool may be used on a single RNASeq sample to identify genes with multiple spliceforms, on a pair of samples to identify differential splicing between the two, or on groups of samples to identify statistically significant group level differences in splicing patterns. SpliceSeq can be run from the install page as a java web start application to explore the sequencing data on their server or can be installed locally to analyze your own mRNA-Seq data.

Abbreviations: SpliceSeq

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

Keywords: rna-seq, mrna splicing pattern

Resource Name: SpliceSeq

Resource ID: SCR_005267

Alternate IDs: OMICS_01267

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260905T132532+0000

Ratings and Alerts

No rating or validation information has been found for SpliceSeq.

No alerts have been found for SpliceSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 179 mentions in open access literature.

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

Peng Q, et al. (2026) SRSF9 mediates oncogenic RNA splicing of SLC37A4 via liquid-liquid phase separation to promote oral cancer progression. Journal of advanced research, 79, 505.

Li J, et al. (2026) Multiomics analysis identifies the prognostic significance and biological roles of the HNRNP family in lung adenocarcinoma. Discover oncology, 17(1).

Li D, et al. (2026) SNRPD2-dependency Fuels an Oncogenic Alternative Splicing Repertoire Driving Disease Aggressiveness in Glioma. Cancer genomics & proteomics, 23(2), 169.

Cao B, et al. (2026) CGPA: A Multicontext Cancer Gene Prognosis Atlas. Molecular cancer research : MCR, 24(3), 188.

Zhong B, et al. (2026) Landscape of splicing factors in early-onset gastric cancer reveals SRSF1 as a key driver of oxaliplatin resistance. The Journal of biological chemistry, 302(4), 111279.

Huang X, et al. (2026) Comprehensive bioinformatic analysis reveals TRPM4 as a biomarker for pan-cancer progression and macrophage infiltration. Discover oncology, 17(1).

Li S, et al. (2026) Alternative splicing events show high prognostic values and indicate potential core genes in acute myeloid leukemia. Clinical and experimental medicine, 26(1), 143.

Jia R, et al. (2026) SRSF3 determines Treg cell fate in antitumor immunity and autoimmunity. Science advances, 12(22), eaeh1671.

Wu Q, et al. (2026) Cross-Level Regulatory Interactions Underlying Human Immune Aging. MedComm, 7(7), e70817.

Chen Z, et al. (2025) Comprehensive pan-cancer evaluation of NUP85 prognosis, immune infiltration response, and validation in prostate cancer. Discover oncology, 16(1), 1953.

Ren Y, et al. (2025) Integrated analysis unraveling the immunologic and clinical prognostic values of synaptotagmin like 4 in pan-cancer. Discover oncology, 16(1), 1018.

Huang J, et al. (2025) RUNX2 isoform II protects cancer cells from ferroptosis and apoptosis by promoting PRDX2 expression in oral squamous cell carcinoma. eLife, 13.

Zhu S, et al. (2025) Comprehensive systems biology analysis reveals splicing factor contributions to cutaneous melanoma progression. Scientific reports, 15(1), 9486.

Al Abo M, et al. (2025) Genetic ancestry concordant RNA splicing in prostate cancer involves oncogenic genes and associates with recurrence. NPJ precision oncology, 9(1), 30.

Wu H, et al. (2025) Systematic exploration of prognostic alternative splicing events related to tumor immune microenvironment of Clear Cell Renal Cell Carcinoma. Cancer biomarkers : section A of Disease markers, 42(3), 18758592251317402.

Liu Z, et al. (2025) ACTG1 driven splicing of P4HB gene enhances EMT and bladder cancer progression. NPJ precision oncology, 9(1), 330.

Sun C, et al. (2025) Analysis of SLC genes alternative splicing identifies the SLC7A6 RI isoform as a therapeutic target for colorectal cancer. Cancer science, 116(1), 233.

Brada MD, et al. (2025) AXL and SRC in clear cell renal cell carcinoma: absence of mutations, rare alternative splicing events, but association of protein expression with poor prognosis. The journal of pathology. Clinical research, 11(3), e70028.

Chen M, et al. (2025) Age-related aberrant alternative splicing as a prognostic tool in older breast cancer patients. Communications biology, 9(1), 62.

Ji Y, et al. (2025) Aldolase a in pan-cancer and lung squamous cell carcinoma: prognostic value and macrophage-driven immune suppression unveiled by multi-omics and cohort validation. Cancer cell international, 25(1), 401.