

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

SpliceSeq

RRID:SCR_005267

Type: Tool

Proper Citation

SpliceSeq (RRID:SCR_005267)

Resource Information

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

Proper Citation: SpliceSeq (RRID:SCR_005267)

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 processing software, software application, data analysis software, 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: 20260731T042707+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 169 mentions in open access literature.

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

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.

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.

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.

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.

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.

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.

Xu Y, et al. (2025) Deciphering the role of CNIH4 in pan-cancer landscapes and its significance in breast cancer progression. Frontiers in genetics, 16, 1536620.

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.

Wang H, et al. (2025) HnRNPR-mediated UPF3B mRNA splicing drives hepatocellular carcinoma metastasis. *Journal of advanced research*, 68, 257.

Wen S, et al. (2024) Identification of macrophage-related genes correlated with prognosis and immunotherapy efficacy in non-small cell lung cancer. *Heliyon*, 10(6), e27170.

Newaz K, et al. (2024) Prognostic importance of splicing-triggered aberrations of protein complex interfaces in cancer. *NAR genomics and bioinformatics*, 6(3), lqae133.

Cho N, et al. (2024) Alternative splicing of PBRM1 mediates resistance to PD-1 blockade therapy in renal cancer. *The EMBO journal*, 43(22), 5421.

Crowl S, et al. (2024) A systematic analysis of the effects of splicing on the diversity of post-translational modifications in protein isoforms. *bioRxiv : the preprint server for biology*.

Li RQ, et al. (2024) CD74 as a prognostic and M1 macrophage infiltration marker in a comprehensive pan-cancer analysis. *Scientific reports*, 14(1), 8125.

Tang Y, et al. (2024) An integrative platform for detection of RNA 2'-O-methylation reveals its broad distribution on mRNA. *Cell reports methods*, 4(3), 100721.

Cheng S, et al. (2024) Landscape analysis of alternative splicing in kidney renal clear cell carcinoma and their clinical significance. *Aging*, 16(11), 10016.

Villagra UMM, et al. (2024) Expression of Truncated Products at the 5'-Terminal Region of RIPK2 and Evolutionary Aspects that Support Their Biological Importance. *Genome biology and evolution*, 16(7).