

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

Spliceosome Database

RRID:SCR_002097

Type: Tool

Proper Citation

Spliceosome Database (RRID:SCR_002097)

Resource Information

URL: <http://spliceosomedb.ucsc.edu/>

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Description: A database of proteins and RNAs that have been identified in various purified splicing complexes. Various names, orthologs and gene identifiers of spliceosome proteins have been cataloged to navigate the complex nomenclature of spliceosome proteins. Links to gene and protein records are also provided for the spliceosome components in other databases. To navigate spliceosome assembly dynamics, tools were created to compare the association of spliceosome proteins with complexes that form at specific stages of spliceosome assembly based on a compendium of mass spectrometry experiments that identified proteins in purified splicing complexes.

Abbreviations: Spliceosome Database

Synonyms: Spliceosome Database - A source of information for the SLPICEOSOME: The large ribonucleoprotein complex responsible for pre-mRNA splicing, Spliceosome Component Database

Resource Type: data or information resource, database

Defining Citation: [PMID:23118483](#)

Keywords: splicing, mass spectrometry, protein, rna, complex, spliceosome, small nuclear rna, structure, dynamics, ortholog, gene

Availability: Free, Freely available

Resource Name: Spliceosome Database

Resource ID: SCR_002097

Alternate IDs: OMICS_01891

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260912T200124+0000

Ratings and Alerts

No rating or validation information has been found for Spliceosome Database.

No alerts have been found for Spliceosome Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Anglada-Girotto M, et al. (2026) Exon inclusion signatures enable accurate estimation of splicing factor activity. Nature communications, 17(1).

Todorow V, et al. (2025) Comparative Analysis of Splicing Alterations in Three Muscular Dystrophies. Biomedicines, 13(3).

Anglada-Girotto M, et al. (2024) Disentangling the splicing factor programs underlying complex molecular phenotypes. bioRxiv : the preprint server for biology.

Zhou AX, et al. (2024) Renal Endothelial Single-Cell Transcriptomics Reveals Spatiotemporal Regulation and Divergent Roles of Differential Gene Transcription and Alternative Splicing in Murine Diabetic Nephropathy. International journal of molecular sciences, 25(8).

Fan W, et al. (2024) m6A-Modified SNRPA Controls Alternative Splicing of ERCC1 Exon 8 to Induce Cisplatin Resistance in Lung Adenocarcinoma. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(47), e2404609.

van der Werf I, et al. (2023) Detection and targeting of splicing deregulation in pediatric acute myeloid leukemia stem cells. Cell reports. Medicine, 4(3), 100962.

Xu S, et al. (2022) Spatial and temporal proteomics reveals the distinct distributions and dynamics of O-GlcNAcylated proteins. Cell reports, 39(11), 110946.

Suzuki JMNG, et al. (2022) A genetic screen in C. elegans reveals roles for KIN17 and PRCC in maintaining 5' splice site identity. PLoS genetics, 18(2), e1010028.

Cartwright-Acar CH, et al. (2022) A forward genetic screen in C. elegans identifies conserved residues of spliceosomal proteins PRP8 and SNRNP200/BRR2 with a role in maintaining 5' splice site identity. Nucleic acids research, 50(20), 11834.

Zhao YJ, et al. (2021) Integrated multi-omics analysis of the clinical relevance and potential regulatory mechanisms of splicing factors in hepatocellular carcinoma. *Bioengineered*, 12(1), 3978.

Dumler JS, et al. (2018) Alternative Splicing of Differentiated Myeloid Cell Transcripts after Infection by *Anaplasma phagocytophilum* Impacts a Selective Group of Cellular Programs. *Frontiers in cellular and infection microbiology*, 8, 14.

Mayerle M, et al. (2017) Genetics and biochemistry remain essential in the structural era of the spliceosome. *Methods (San Diego, Calif.)*, 125, 3.

Chen M, et al. (2016) Transcriptome and long noncoding RNA sequencing of three extracellular vesicle subtypes released from the human colon cancer LIM1863 cell line. *Scientific reports*, 6, 38397.

Singh PK, et al. (2015) LEDGF/p75 interacts with mRNA splicing factors and targets HIV-1 integration to highly spliced genes. *Genes & development*, 29(21), 2287.

Fernández-Suárez XM, et al. (2013) The 2013 Nucleic Acids Research Database Issue and the online molecular biology database collection. *Nucleic acids research*, 41(Database issue), D1.