

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

JuncBASE

RRID:SCR_003103

Type: Tool

Proper Citation

JuncBASE (RRID:SCR_003103)

Resource Information

URL: <http://compbio.berkeley.edu/proj/juncbase/Home.html>

Proper Citation: JuncBASE (RRID:SCR_003103)

Description: Software used to identify and classify alternative splicing events from RNA-Seq data. JuncBASE also uses read counts to quantify the relative expression of each isoform and identifies splice events that are significantly differentially expressed across two or more samples.

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

Keywords: splicing event, splicing events, alternative splicing event, rna seq

Availability: Free, Available for download, Freely available

Resource Name: JuncBASE

Resource ID: SCR_003103

Alternate IDs: OMICS_01335

Alternate URLs: <https://github.com/anbrooks/juncBASE>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132458+0000

Ratings and Alerts

No rating or validation information has been found for JuncBASE.

No alerts have been found for JuncBASE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Soulette CM, et al. (2023) Full-length transcript alterations in human bronchial epithelial cells with U2AF1 S34F mutations. *Life science alliance*, 6(10).

Guo L, et al. (2021) Genetics of white color and iridophoroma in "Lemon Frost" leopard geckos. *PLoS genetics*, 17(6), e1009580.

Robinson EK, et al. (2021) Inflammation drives alternative first exon usage to regulate immune genes including a novel iron-regulated isoform of Aim2. *eLife*, 10.

Silva DBS, et al. (2020) Spliced genes in muscle from Nelore Cattle and their association with carcass and meat quality. *Scientific reports*, 10(1), 14701.

Huang HH, et al. (2020) Proteasome inhibitor-induced modulation reveals the spliceosome as a specific therapeutic vulnerability in multiple myeloma. *Nature communications*, 11(1), 1931.

Yin S, et al. (2019) A Murine Model of Chronic Lymphocytic Leukemia Based on B Cell-Restricted Expression of Sf3b1 Mutation and Atm Deletion. *Cancer cell*, 35(2), 283.

Ling Z, et al. (2019) Evolution of Alternative Splicing in Eudicots. *Frontiers in plant science*, 10, 707.

Huang W, et al. (2019) Changes of alternative splicing in *Arabidopsis thaliana* grown under different CO₂ concentrations. *Gene*, 689, 43.

Masaki S, et al. (2019) Myelodysplastic Syndrome-Associated SRSF2 Mutations Cause Splicing Changes by Altering Binding Motif Sequences. *Frontiers in genetics*, 10, 338.

Ling Y, et al. (2018) Thermoprimering triggers splicing memory in *Arabidopsis*. *Journal of experimental botany*, 69(10), 2659.

Li J, et al. (2018) An alternative splicing switch in FLNB promotes the mesenchymal cell state in human breast cancer. *eLife*, 7.

Shiozawa Y, et al. (2018) Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. *Nature communications*, 9(1), 3649.

Paolella BR, et al. (2017) Copy-number and gene dependency analysis reveals partial copy loss of wild-type SF3B1 as a novel cancer vulnerability. *eLife*, 6.

Kawasawa YI, et al. (2017) Genome-wide profiling of differentially spliced mRNAs in human fetal cortical tissue exposed to alcohol. *Alcohol* (Fayetteville, N.Y.), 62, 1.

AlShareef S, et al. (2017) Herboxidiene triggers splicing repression and abiotic stress responses in plants. *BMC genomics*, 18(1), 260.

Chhibber A, et al. (2017) Transcriptomic variation of pharmacogenes in multiple human tissues and lymphoblastoid cell lines. *The pharmacogenomics journal*, 17(2), 137.

Guan Y, et al. (2017) Functional changes in mRNA expression and alternative pre-mRNA splicing associated with the effects of nutrition on apoptosis and spermatogenesis in the adult testis. *BMC genomics*, 18(1), 64.

Liang G, et al. (2016) Altered microRNA expression and pre-mRNA splicing events reveal new mechanisms associated with early stage *Mycobacterium avium* subspecies paratuberculosis infection. *Scientific reports*, 6, 24964.

Brooks AN, et al. (2015) Regulation of alternative splicing in *Drosophila* by 56 RNA binding proteins. *Genome research*, 25(11), 1771.