

Resource Summary Report

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SpliceGrapher

RRID:SCR_006657

Type: Tool

Proper Citation

SpliceGrapher (RRID:SCR_006657)

Resource Information

URL: <http://sourceforge.net/projects/splicegrapher/>

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Description: Software that predicts alternative splicing patterns and produces splice graphs that capture in a single structure the ways a gene's exons may be assembled. It enhances gene models using evidence from next-generation sequencing and EST alignments.

Abbreviations: SpliceGrapher

Resource Type: software resource

Defining Citation: [PMID:22293517](#)

Resource Name: SpliceGrapher

Resource ID: SCR_006657

Alternate IDs: OMICS_01266

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260801T190314+0000

Ratings and Alerts

No rating or validation information has been found for SpliceGrapher.

No alerts have been found for SpliceGrapher.

Data and Source Information

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Daoud A, et al. (2025) The role of chromatin state in intron retention: A case study in leveraging large scale deep learning models. PLoS computational biology, 21(1), e1012755.

Pootakham W, et al. (2024) A chromosome-level reference genome assembly and a full-length transcriptome assembly of the giant freshwater prawn (*Macrobrachium rosenbergii*). G3 (Bethesda, Md.), 14(9).

Wang Y, et al. (2021) Global Survey of the Full-Length Cabbage Transcriptome (*Brassica oleracea* Var. *capitata* L.) Reveals Key Alternative Splicing Events Involved in Growth and Disease Response. International journal of molecular sciences, 22(19).

Ding Y, et al. (2020) Alternative splicing in tea plants was extensively triggered by drought, heat and their combined stresses. PeerJ, 8, e8258.

Abdel-Ghany SE, et al. (2020) Transcriptome Analysis of Drought-Resistant and Drought-Sensitive Sorghum (*Sorghum bicolor*) Genotypes in Response to PEG-Induced Drought Stress. International journal of molecular sciences, 21(3).

Wang Z, et al. (2020) Multi-omics sequencing provides insight into floral transition in *Catalpa bungei*. C.A. Mey. BMC genomics, 21(1), 508.

Li Y, et al. (2019) Functional identification of lncRNAs in sweet cherry (*Prunus avium*) pollen tubes via transcriptome analysis using single-molecule long-read sequencing. Horticulture research, 6, 135.

Zuo C, et al. (2018) Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. Biotechnology for biofuels, 11, 170.

Liu B, et al. (2018) Chloride intracellular channel 1 (CLIC1) contributes to modulation of cyclic AMP-activated whole-cell chloride currents in human bronchial epithelial cells. Physiological reports, 6(2).

Xie SQ, et al. (2018) ISODB: A Comprehensive Database of Full-Length Isoforms Generated by Iso-Seq. International journal of genomics, 2018, 9207637.

Wang J, et al. (2018) Comparative transcriptome analysis reveals molecular response to salinity stress of salt-tolerant and sensitive genotypes of indica rice at seedling stage. Scientific reports, 8(1), 2085.

Kuosmanen A, et al. (2018) Evaluating approaches to find exon chains based on long reads. Briefings in bioinformatics, 19(3), 404.

Ullah F, et al. (2018) Exploring the relationship between intron retention and chromatin accessibility in plants. *BMC genomics*, 19(1), 21.

Piriyapongsa J, et al. (2018) Uncovering full-length transcript isoforms of sugarcane cultivar Khon Kaen 3 using single-molecule long-read sequencing. *PeerJ*, 6, e5818.

Scott H, et al. (2017) Recognition memory-induced gene expression in the perirhinal cortex: A transcriptomic analysis. *Behavioural brain research*, 328, 1.

Chen SY, et al. (2017) A transcriptome atlas of rabbit revealed by PacBio single-molecule long-read sequencing. *Scientific reports*, 7(1), 7648.

Zhang S, et al. (2016) Analysis of weighted co-regulatory networks in maize provides insights into new genes and regulatory mechanisms related to inositol phosphate metabolism. *BMC genomics*, 17, 129.

Chen L, et al. (2016) Genome Sequence of the Edible Cultivated Mushroom *Lentinula edodes* (Shiitake) Reveals Insights into Lignocellulose Degradation. *PloS one*, 11(8), e0160336.

Su Y, et al. (2016) Genomic, Transcriptomic, and Proteomic Analysis Provide Insights Into the Cold Adaptation Mechanism of the Obligate Psychrophilic Fungus *Mrakia psychrophila*. *G3 (Bethesda, Md.)*, 6(11), 3603.

Qu J, et al. (2016) Transcriptome Dynamics during Maize Endosperm Development. *PloS one*, 11(10), e0163814.