

Resource Summary Report

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AStalavista

RRID:SCR_001815

Type: Tool

Proper Citation

AStalavista (RRID:SCR_001815)

Resource Information

URL: <http://sammeth.net/confluence/display/ASTA/2+-+Download>

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Description: Tool that extracts and displays alternative splicing (AS) events from a given genomic annotation of exon-intron gene coordinates. By comparing all given transcripts, it detects the variations in their splicing structure and identifies all AS events (like exon skipping, alternate donor, etc) by assigning to each of them an AS code. It provides a visual summary of the AS landscape in the analyzed dataset, the possibility to browse the results on the UCSC website or to download them in GTF or ASTA format. You can use AStalavista for any genome by providing your own annotation set, the identifier of your gene(s) of interest, or analyze the AS landscape of reference annotation datasets like Gencode, RefSeq, Ensembl, FlyBase, etc.

Abbreviations: AStalavista

Synonyms: Alternative Splicing transcriptional landscape visualization tool

Resource Type: data analysis service, service resource, production service resource, software resource, analysis service resource

Defining Citation: [PMID:17485470](#)

Keywords: alternative splicing event, alternative splicing, visualization, genome, transcript

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: AStalavista

Resource ID: SCR_001815

Alternate IDs: OMICS_01943

Alternate URLs: <http://genome.imim.es/astalavista>, <http://genome.crg.es/astalavista/>

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260801T190151+0000

Ratings and Alerts

No rating or validation information has been found for AStalavista.

No alerts have been found for AStalavista.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 83 mentions in open access literature.

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

Wang C, et al. (2025) Genomic-transcriptomic analysis identifies the Syrian hamster as a superior animal model for human diseases. BMC genomics, 26(1), 286.

Yu Z, et al. (2025) Analysis of post-transcriptional regulatory signatures and immune cell subsets in premature ovarian insufficiency based on full-length transcriptome. Scientific reports, 15(1), 5533.

Xu M, et al. (2025) SLC30A4-AS1 Mediates the Senescence of Periodontal Ligament Stem Cells in Inflammatory Environments via the Alternative Splicing of TP53BP1. Cell proliferation, 58(4), e13778.

Yang L, et al. (2025) Dissecting alternative splicing patterns of the Rheum palmatum complex with different contents of medicinal constituents. BMC genomics, 26(1), 855.

Zhang Q, et al. (2024) A Combinatorial Single-Molecule Real-Time and Illumina Sequencing Analysis of Postembryonic Gene Expression in the Asian Citrus Psyllid Diaphorina citri. Insects, 15(6).

Du K, et al. (2024) Maize splicing-mediated mRNA surveillance impeded by sugarcane mosaic virus-coded pathogenic protein Nla-Pro. Science advances, 10(34), eadn3010.

Wang S, et al. (2024) Full-length transcriptome sequencing of Arabidopsis plants provided new insights into the autophagic regulation of photosynthesis. Scientific reports, 14(1), 14588.

Wang N, et al. (2024) FMRP protects breast cancer cells from ferroptosis by promoting SLC7A11 alternative splicing through interacting with hnRNPM. Redox biology, 77, 103382.

Wang Q, et al. (2024) An improved transcriptome annotation reveals asymmetric expression and distinct regulation patterns in allotetraploid common carp. *Communications biology*, 7(1), 1542.

Zong Y, et al. (2024) Comprehensive deciphering the alternative splicing patterns involved in leaf morphogenesis of *Liriodendron chinense*. *BMC plant biology*, 24(1), 250.

E J, et al. (2024) Nanopore-based full-length transcriptome sequencing for understanding the underlying molecular mechanisms of rapid and slow progression of diabetes nephropathy. *BMC medical genomics*, 17(1), 246.

Zheng SY, et al. (2023) A Global Survey of the Full-Length Transcriptome of *Apis mellifera* by Single-Molecule Long-Read Sequencing. *International journal of molecular sciences*, 24(6).

Xue JY, et al. (2023) Comprehensive regulatory networks for tomato organ development based on the genome and RNAome of MicroTom tomato. *Horticulture research*, 10(9), uhad147.

Zeng Z, et al. (2023) The RNAome landscape of tomato during arbuscular mycorrhizal symbiosis reveals an evolving RNA layer symbiotic regulatory network. *Plant communications*, 4(1), 100429.

Bai MZ, et al. (2023) Bioinformatics Analysis of MSH1 Genes of Green Plants: Multiple Parallel Length Expansions, Intron Gains and Losses, Partial Gene Duplications, and Alternative Splicing. *International journal of molecular sciences*, 24(17).

He W, et al. (2022) Full-length transcriptome reconstruction reveals genetic differences in hybrids of *Oryza sativa* and *Oryza punctata* with different ploidy and genome compositions. *BMC plant biology*, 22(1), 131.

Wang L, et al. (2022) Comprehensive analysis of full-length transcriptomes of *Schizothorax prenanti* by single-molecule long-read sequencing. *Genomics*, 114(1), 456.

Jeon J, et al. (2022) Alternative splicing diversifies the transcriptome and proteome of the rice blast fungus during host infection. *RNA biology*, 19(1), 373.

Xuhui L, et al. (2022) Full-length transcriptome analysis of maize root tips reveals the molecular mechanism of cold stress during the seedling stage. *BMC plant biology*, 22(1), 398.

Xing L, et al. (2022) Full-length codling moth transcriptome atlas revealed by single-molecule real-time sequencing. *Genomics*, 114(2), 110299.