Resource Summary Report

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ASAP: the Alternative Splicing Annotation Project

RRID:SCR_003415
Type: Tool

Proper Citation

ASAP: the Alternative Splicing Annotation Project (RRID:SCR_003415)

Resource Information

URL: http://bioinfo.mbi.ucla.edu/ASAP/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on 8/12/13. Database to access and mine alternative splicing information coming from genomics and proteomics based on genome-wide analyses of alternative splicing in human (30 793 alternative splice relationships found) from detailed alignment of expressed sequences onto the genomic sequence. ASAP provides precise gene exon-intron structure, alternative splicing, tissue specificity of alternative splice forms, and protein isoform sequences resulting from alternative splicing. They developed an automated method for discovering human tissue-specific regulation of alternative splicing through a genome-wide analysis of expressed sequence tags (ESTs), which involves classifying human EST libraries according to tissue categories and Bayesian statistical analysis. They use the UniGene clusters of human Expressed Sequence Tags (ESTs) to identify splices. The UniGene EST's are clustered so that a single cluster roughly corresponds to a gene (or at least a part of a gene). A single EST represents a portion of a processed (already spliced) mRNA. A given cluster contains many ESTs, each representing an outcome of a series of splicing events. The ESTs in UniGene contain the different mRNA isoforms transcribed from an alternatively spliced gene. They are not predicting alternative splicing, but locating it based on EST analysis. The discovered splices are further analyzed to determine alternative splicing events. They have identified 6201 alternative splice relationships in human genes, through a genome-wide analysis of expressed sequence tags (ESTs). Starting with 2.1 million human mRNA and EST sequences, they mapped expressed sequences onto the draft human genome sequence and only accepted splices that obeyed the standard splice site consensus. After constructing a tissue list of 46 human tissues with 2 million human ESTs, they generated a database of novel human alternative splices that is four times larger than our previous report, and used Bayesian statistics to compare the relative abundance of every pair of alternative splices in these tissues. Using several statistical criteria for tissue specificity, they have identified 667 tissue-specific alternative splicing relationships and analyzed their distribution in human tissues. They have validated our results by comparison with independent studies. This genome-wide

analysis of tissue specificity of alternative splicing will provide a useful resource to study the tissue-specific functions of transcripts and the association of tissue-specific variants with human diseases.

Abbreviations: ASAP

Synonyms: Alternative Splicing, Alternative Splicing Annotation Project, Alternative Splicing Annotation Project database

Resource Type: data or information resource, database

Defining Citation: PMID:12519958

Keywords: gene, genome, human, isoform, mechanism, metazoa, molecular, mrna, nucleus, process, protein, sequence, splice, tissue specificity, transcription, transcript, alternate splicing, microarray, alternative splicing, biological process, alternatively spliced isoform, contig, cancer, image

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Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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Resource ID: SCR_003415

Alternate IDs: nif-0000-33105

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260919T195640+0000

Ratings and Alerts

No rating or validation information has been found for ASAP: the Alternative Splicing Annotation Project.

No alerts have been found for ASAP: the Alternative Splicing Annotation Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 33 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Gu XH, et al. (2025) Integrated evidence reveals a new subspecies of the genus Seuratascaris (Nematoda: Ascaridomorpha), with characterization of the complete mitochondrial genome. Parasite (Paris, France), 32, 14.

Talaga S, et al. (2025) A DNA barcode library for Culex mosquitoes (Diptera: Culicidae) of South America with the description of two cryptic species of subgenus Melanoconion. PloS one, 20(2), e0310571.

Fathy AT, et al. (2025) Effective removal of heavy metal ions (Pb, Cu, and Cd) from contaminated water by limestone mine wastes. Scientific reports, 15(1), 1680.

El-Serag HB, et al. (2025) HES V2.0 outperforms GALAD for detection of HCC: A phase 3 biomarker study in the United States. Hepatology (Baltimore, Md.), 81(2), 465.

Chen HX, et al. (2025) Integrative evidence reveals a new species of Hysterothylacium (Nematoda: Ascaridoidea), with the characterization of its complete mitochondrial genome. International journal for parasitology. Parasites and wildlife, 26, 101042.

Niu M, et al. (2024) Improving DNA barcoding library of armored scale insects (Hemiptera: Diaspididae) in China. PloS one, 19(5), e0301499.

Bu??i?? N, et al. (2024) A DNA barcode reference library of Croatian mosquitoes (Diptera: Culicidae): implications for identification and delimitation of species, with notes on the distribution of potential vector species. Parasites & vectors, 17(1), 216.

Xia C, et al. (2024) Signal enhancement ratio of multi-phase contrast-enhanced MRI: an imaging biomarker for survival in pancreatic adenocarcinoma. European radiology, 34(11), 7460.

Gu XH, et al. (2024) Morphology and ASAP analysis of the important zoonotic nematode parasite Baylisascaris procyonis (Stefahski and Zarnowski, 1951), with molecular phylogenetic relationships of Baylisascaris species (Nematoda: Ascaridida). Parasitology, 151(2), 200.

Lian P, et al. (2024) Facile Synthesis to Porous TiO2 Nanostructures at Low Temperature for Efficient Visible-Light Degradation of Tetracycline. Nanomaterials (Basel, Switzerland), 14(11).

Schattanek-Wiesmair B, et al. (2024) A DNA barcode library of Austrian geometridae (Lepidoptera) reveals high potential for DNA-based species identification. PloS one, 19(3), e0298025.

Williamson CHD, et al. (2024) ColiSeq: a multiplex amplicon assay that provides strain level resolution of Escherichia coli directly from clinical specimens. Microbiology spectrum, 12(6), e0413923.

Rajani RM, et al. (2024) Selective suppression of oligodendrocyte-derived amyloid beta rescues neuronal dysfunction in Alzheimer's disease. PLoS biology, 22(7), e3002727.

Liu J, et al. (2024) A Cell Cycle-Aware Network for Data Integration and Label Transferring of Single-Cell RNA-Seq and ATAC-Seq. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(31), e2401815.

Parsons DJ, et al. (2024) Predicting genetic biodiversity in salamanders using geographic, climatic, and life history traits. PloS one, 19(10), e0310932.

Knorrn AH, et al. (2024) Gaidropsarus mauritanicus (Gadiformes, Gaidropsaridae) a new three-bearded rockling from a deep-water coral ecosystem with a genetically verified biogeographical distribution of the genus and notes to its ecology and behavior. Journal of fish biology, 105(6), 1643.

Aupalee K, et al. (2024) Reliability of wing morphometrics for species identification of human-biting black flies (Diptera: Simuliidae) in Thailand. Parasites & vectors, 17(1), 508.

Vuataz L, et al. (2024) A comprehensive DNA barcoding reference database for Plecoptera of Switzerland. Scientific reports, 14(1), 6322.

Prelic S, et al. (2024) Innexin expression and localization in the Drosophila antenna indicate gap junction or hemichannel involvement in antennal chemosensory sensilla. Cell and tissue research, 398(1), 35.

Subedi S, et al. (2024) A scalable approach to topic modelling in single-cell data by approximate pseudobulk projection. Life science alliance, 7(10).