Resource Summary Report

Generated by NIF on Apr 27, 2025

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/

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

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

Funding: NSF 0082964;
NSF DGE-9987641;
DOE DEFG0387ER60615

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ASAP: the Alternative Splicing Annotation Project

Resource ID: SCR_003415

Alternate IDs: nif-0000-33105

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250426T055624+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 30 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

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

Buši? 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.

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.

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).

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.

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.

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

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.

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

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

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.

van Eekelen L, et al. (2024) Comparing deep learning and pathologist quantification of cell-level PD-L1 expression in non-small cell lung cancer whole-slide images. Scientific reports, 14(1), 7136.

Duan L, et al. (2024) Machine learning-based pathomics signature of histology slides as a novel prognostic indicator in primary central nervous system lymphoma. Journal of neuro-oncology, 168(2), 283.

Berry CW, et al. (2024) Functional septate junctions between cyst cells are required for survival of transit amplifying male germ cells expressing Bag of marbles. bioRxiv : the preprint server for biology.

Sirach R, et al. (2024) Artificial neural network modelling and experimental investigations of malachite green adsorption on novel carboxymethyl cellulose/?-cyclodextrin/nickel cobaltite composite. Heliyon, 10(13), e33820.

Liu J, et al. (2024) Phylogenetics, Molecular Species Delimitation and Geometric Morphometrics of All Reddish-Brown Species in the Genus Neotriplax Lewis, 1887 (Coleoptera: Erotylidae: Tritomini). Insects, 15(7).