

Resource Summary Report

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U12DB: The U12 Intron Database

RRID:SCR_013410

Type: Tool

Proper Citation

U12DB: The U12 Intron Database (RRID:SCR_013410)

Resource Information

URL: <http://genome.imim.es/cgi-bin/u12db/u12db.cgi>

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Description: This is a searchable database of U12-type introns. U12-type introns are spliced by the U12-dependent spliceosome and are present in the genomes of many higher eukaryotic lineages including plants, chordates and some invertebrates. Investigations into the evolution and mechanism of U12-depending splicing would be facilitated by access to a catalog of such introns. However, due to their relatively recent discovery and a systematic bias against recognition of non-canonical splice sites in general, the introns defined by U12-type splice sites are under-represented in genome annotations. Such under-representation compounds the already difficult problem of determining gene structures. It also impedes attempts to study these introns genome-wide or phylum-wide. The resource described here, the U12 Intron Database (U12DB), aims to catalog the U12 introns of completely sequenced eukaryotic genomes and associate orthologous introns with each other. Two pathways for the removal of eukaryotic spliceosomal introns exist: a major pathway that is dependent on the main U2 snRNA-containing spliceosome and a minor pathway that is dependent on the low abundance U12 snRNA-containing spliceosome. The two spliceosomes share only one snRNA, U5, but have many of the same protein components in common. They are distinguished mainly by the splice signal sequences in the pre-mRNA to which they bind. U12 consensus sequences for the donor site, RTATCCTTT, and branch point, TTCCTTRAY, are highly conserved and distinct from the U2 consensi. The two spliceosomes also differ in the order of spliceosomal assembly. U11 and U12 form a dimer which then recognizes the donor site and branch point simultaneously, whereas U1 and U2 recognize these sites independently before associating. Computational scans for U12 introns have previously been performed for human (Levine and Durbin, 2001) and Arabidopsis (Zhu and Brendel, 2003). Both scans used similar methodology, essentially predicting introns and confirming them using alignment to expressed sequence. We extended this approach to 20 genomes using spliced alignment of sequence flanking known introns or transcript-confirmed intron predictions to the genomic sequence of orthologous genes. Details can be found in forthcoming article in the Nucleic Acids Research database issue.

Synonyms: U12DB

Resource Type: database, data or information resource

Resource Name: U12DB: The U12 Intron Database

Resource ID: SCR_013410

Alternate IDs: nif-0000-03600

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260808T190432+0000

Ratings and Alerts

No rating or validation information has been found for U12DB: The U12 Intron Database.

No alerts have been found for U12DB: The U12 Intron Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Moyer DC, et al. (2020) Comprehensive database and evolutionary dynamics of U12-type introns. Nucleic acids research, 48(13), 7066.

Bai Y, et al. (2017) Identification of genome-wide non-canonical spliced regions and analysis of biological functions for spliced sequences using Read-Split-Fly. BMC bioinformatics, 18(Suppl 11), 382.

Janice J, et al. (2012) U12-type spliceosomal introns of Insecta. International journal of biological sciences, 8(3), 344.

Alioto TS, et al. (2007) U12DB: a database of orthologous U12-type spliceosomal introns. Nucleic acids research, 35(Database issue), D110.