

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

Yeast Intron Database

RRID:SCR_007144

Type: Tool

Proper Citation

Yeast Intron Database (RRID:SCR_007144)

Resource Information

URL: http://compbio.soe.ucsc.edu/yeast_introns.html

Proper Citation: Yeast Intron Database (RRID:SCR_007144)

Description: Database of information about the spliceosomal introns of the yeast *Saccharomyces cerevisiae*. Listed are known spliceosomal introns in the yeast genome and the splice sites actually used are documented. Through the use of microarrays designed to monitor splicing, they are beginning to identify and analyze splice site context in terms of the nature and activities of the trans-acting factors that mediate splice site recognition. In version 3.0, expression data that relates to the efficiency of splicing relative to other processes in strains of yeast lacking nonessential splicing factors is included. These data are displayed on each intron page for browsing and can be downloaded for other types of analysis.

Abbreviations: Yeast Intron Database

Synonyms: Ares lab Yeast Intron Database

Resource Type: data or information resource, database

Defining Citation: [PMID:11988574](#)

Keywords: intron, spliceosomal, splicing, genome, intron splice signal, sequence, splice site

Funding: W. M. Keck Foundation ;
Packard Foundation ;
NIH

Availability: The community can contribute to this resource

Resource Name: Yeast Intron Database

Resource ID: SCR_007144

Alternate IDs: nif-0000-03649, OMICS_01890

Alternate URLs: http://www.cse.ucsc.edu/research/compbio/yeast_introns.html

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260905T133138+0000

Ratings and Alerts

No rating or validation information has been found for Yeast Intron Database.

No alerts have been found for Yeast Intron Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Barrass JD, et al. (2015) Transcriptome-wide RNA processing kinetics revealed using extremely short 4tU labeling. Genome biology, 16, 282.

Ladd AN, et al. (2002) Finding signals that regulate alternative splicing in the post-genomic era. Genome biology, 3(11), reviews0008.