Resource Summary Report

Generated by RRID on Apr 9, 2025

EID: Exon-Intron Database

RRID:SCR_002469
Type: Tool

Proper Citation

EID: Exon-Intron Database (RRID:SCR_002469)

Resource Information

URL: http://bpg.utoledo.edu/~afedorov/lab/eid.html

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Description: Data sets of protein-coding intron-containing genes that contain gene information from humans, mice, rats, and other eukaryotes, as well as genes from species whose genomes have not been completely sequenced. This is a comprehensive and convenient dataset of sequences for computational biologists who study exon-intron gene structures and pre-mRNA splicing. The database is derived from GenBank release 112, and it contains protein-coding genes that harbor introns, along with extensive descriptions of each gene and its DNA and protein sequences, as well as splice motif information. They have created subdatabases of genes whose intron positions have been experimentally determined. The collection also contains data on untranslated regions of gene sequences and intron-less genes. For species with entirely sequenced genomes, species-specific databases have been generated. A novel Mammalian Orthologous Intron Database (MOID) has been introduced which includes the full set of introns that come from orthologous genes that have the same positions relative to the reading frames.

Abbreviations: EID

Synonyms: The Exon-Intron Database, Exon-Intron Database

Resource Type: data or information resource, data set

Defining Citation: PMID:16772261, PMID:10592221

Keywords: eukaryote genome, exon, exon-intro, gene structure, genome splicing, intron, ortholog, fasta, gene, protein-coding gene, splice, motif, gene prediction, structure, coding region

Funding:

Availability: Acknowledgement requested

Resource Name: EID: Exon-Intron Database

Resource ID: SCR_002469

Alternate IDs: OMICS_01886, nif-0000-02793

Alternate URLs: http://www.utoledo.edu/med/depts/bioinfo/database.html

Old URLs: http://www.meduohio.edu/bioinfo/eid/, http://mcb.harvard.edu/gilbert/EID

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250407T215322+0000

Ratings and Alerts

No rating or validation information has been found for EID: Exon-Intron Database.

No alerts have been found for EID: Exon-Intron Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Tilli TM, et al. (2016) A strategy to identify housekeeping genes suitable for analysis in breast cancer diseases. BMC genomics, 17(1), 639.

Carels N, et al. (2015) A computational strategy to select optimized protein targets for drug development toward the control of cancer diseases. PloS one, 10(1), e0115054.

Carels N, et al. (2015) An Interpretation of the Ancestral Codon from Miller's Amino Acids and Nucleotide Correlations in Modern Coding Sequences. Bioinformatics and biology insights, 9, 37.

Jiang N, et al. (2014) Conserved and divergent patterns of DNA methylation in higher vertebrates. Genome biology and evolution, 6(11), 2998.

Hill AE, et al. (2014) Longevity and plasticity of CFTR provide an argument for noncanonical SNP organization in hominid DNA. PloS one, 9(10), e109186.

Deng J, et al. (2014) Human metapneumovirus infection induces significant changes in small noncoding RNA expression in airway epithelial cells. Molecular therapy. Nucleic acids, 3(5), e163.

Akkuratov EE, et al. (2014) Bioinformatics analysis of plant orthologous introns: identification of an intronic tRNA-like sequence. Gene, 548(1), 81.

Nabiyouni M, et al. (2013) Vertebrate codon bias indicates a highly GC-rich ancestral genome. Gene, 519(1), 113.

Carels N, et al. (2013) A Statistical Method without Training Step for the Classification of Coding Frame in Transcriptome Sequences. Bioinformatics and biology insights, 7, 35.

Mahdi RN, et al. (2012) Codon usage bias as a function of generation time and life expectancy. Bioinformation, 8(3), 158.

Chor B, et al. (2009) Genomic DNA k-mer spectra: models and modalities. Genome biology, 10(10), R108.