Resource Summary Report

Generated by T1D on Sep 5, 2026

ECgene: Gene Modeling with Alternative Splicing

RRID:SCR_007634
Type: Tool

Proper Citation

ECgene: Gene Modeling with Alternative Splicing (RRID:SCR_007634)

Resource Information

URL: https://omictools.com/ecgene-tool

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Description: Database of functional annotation for alternatively spliced genes. It uses a gene-modeling algorithm that combines the genome-based expressed sequence tag (EST) clustering and graph-theoretic transcript assembly procedures. It contains genome, mRNA, and EST sequence data, as well as a genome browser application. Organisms included in the database are human, dog, chicken, fruit fly, mouse, rhesus, rat, worm, and zebrafish. Annotation is provided for the whole transcriptome, not just the alternatively spliced genes. Several viewers and applications are provided that are useful for the analysis of the transcript structure and gene expression. The summary viewer shows the gene summary and the essence of other annotation programs. The genome browser and the transcript viewer are available for comparing the gene structure of splice variants. Changes in the functional domains by alternative splicing can be seen at a glance in the transcript viewer. Two unique ways of analyzing gene expression is also provided. The SAGE tags deduced from the assembled transcripts are used to delineate quantitative expression patterns from SAGE libraries available publicly. The cDNA libraries of EST sequences in each cluster are used to infer qualitative expression patterns.

Abbreviations: ECgene

Synonyms: ECgene - Genome Annotation for Alternative Splicing

Resource Type: data or information resource, database

Defining Citation: PMID:17132829, PMID:15805497, PMID:15608289

Keywords: est cluster, genome, alternative splicing, splice, gene, mrna, est, annotation, gene modeling, structure, function, gene expression, transcript, genome browser, differential expression, snp

Resource Name: ECgene: Gene Modeling with Alternative Splicing

Resource ID: SCR_007634

Alternate IDs: nif-0000-02780, OMICS_01884

Old URLs: http://genome.ewha.ac.kr/ECgene/

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260904T000237+0000

Ratings and Alerts

No rating or validation information has been found for ECgene: Gene Modeling with Alternative Splicing.

No alerts have been found for ECgene: Gene Modeling with Alternative Splicing.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Sumner JT, et al. (2023) De novo genome assembly and comparative genomics for the colonial ascidian Botrylloides violaceus. G3 (Bethesda, Md.), 13(10).

Pankratova EV, et al. (2016) Different N-terminal isoforms of Oct-1 control expression of distinct sets of genes and their high levels in Namalwa Burkitt's lymphoma cells affect a wide range of cellular processes. Nucleic acids research, 44(19), 9218.

Pappas JJ, et al. (2014) The multidrug resistance 1 gene Abcb1 in brain and placenta: comparative analysis in human and guinea pig. PloS one, 9(10), e111135.

Yang Y, et al. (2014) IQGAP3 promotes EGFR-ERK signaling and the growth and metastasis of lung cancer cells. PloS one, 9(5), e97578.

Lin JC, et al. (2012) TROP2 is epigenetically inactivated and modulates IGF-1R signalling in lung adenocarcinoma. EMBO molecular medicine, 4(6), 472.

Facchin F, et al. (2011) Complexity of bidirectional transcription and alternative splicing at human RCAN3 locus. PloS one, 6(9), e24508.

Wu J, et al. (2010) Testing the coding potential of conserved short genomic sequences. Advances in bioinformatics, 2010, 287070.

Mo F, et al. (2008) A compatible exon-exon junction database for the identification of exon skipping events using tandem mass spectrum data. BMC bioinformatics, 9, 537.

Zhang Q, et al. (2008) A mouse plasma peptide atlas as a resource for disease proteomics. Genome biology, 9(6), R93.

Lv B, et al. (2006) Overexpression of the novel human gene, nuclear apoptosis-inducing factor 1, induces apoptosis. The international journal of biochemistry & cell biology, 38(4), 671.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.

Velagaleti GV, et al. (2005) Position effects due to chromosome breakpoints that map approximately 900 Kb upstream and approximately 1.3 Mb downstream of SOX9 in two patients with campomelic dysplasia. American journal of human genetics, 76(4), 652.