Resource Summary Report

Generated by NIF on Apr 17, 2025

PrimerSeq

RRID:SCR_003295
Type: Tool

Proper Citation

PrimerSeq (RRID:SCR_003295)

Resource Information

URL: http://primerseq.sourceforge.net/

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Description: Software that designs RT-PCR primers that evaluate alternative splicing events by incorporating RNA-Seq data. It is particularly advantageous for designing a large number of primers for validating alternative splicing events found in RNA-Seq data. It incorporates RNA-Seq data in the design process to weight exons by their read counts. Essentially, the RNA-Seq data allows primers to be placed using actually expressed transcripts. This could be for a particular cell line or experimental condition, rather than using annotations that incorporate transcripts that are not expressed for the data. Alternatively, you can design primers that are always on constitutive exons. PrimerSeq does not limit the use of gene annotations and can be used for a wide array of species.

Abbreviations: PrimerSeq

Synonyms: Primer Seek in RNA-Seq

Resource Type: software resource

Defining Citation: PMID:24747190

Keywords: primer, rna-seq, rt-pcr, windows, mac os x, bio.tools

Funding:

Availability: Apache License

Resource Name: PrimerSeq

Resource ID: SCR_003295

Alternate IDs: biotools:primerseq, OMICS_02328

Alternate URLs: https://bio.tools/primerseq

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250410T064955+0000

Ratings and Alerts

No rating or validation information has been found for PrimerSeq.

No alerts have been found for PrimerSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Dillingham CM, et al. (2024) KDM3A and KDM3B Maintain Naive Pluripotency Through the Regulation of Alternative Splicing. bioRxiv : the preprint server for biology.

Mohammadi MA, et al. (2021) Genome-wide transcriptome analysis of the early developmental stages of Echinococcus granulosus protoscoleces reveals extensive alternative splicing events in the spliceosome pathway. Parasites & vectors, 14(1), 574.

Kiegle EA, et al. (2018) A Genomic View of Alternative Splicing of Long Non-coding RNAs during Rice Seed Development Reveals Extensive Splicing and lncRNA Gene Families. Frontiers in plant science, 9, 115.

He R, et al. (2017) H3K4 demethylase KDM5B regulates global dynamics of transcription elongation and alternative splicing in embryonic stem cells. Nucleic acids research, 45(11), 6427.

Kim YG, et al. (2016) Transcriptome sequencing of gingival biopsies from chronic periodontitis patients reveals novel gene expression and splicing patterns. Human genomics, 10(1), 28.

Lin JC, et al. (2015) Impacts of Alternative Splicing Events on the Differentiation of

Adipocytes. International journal of molecular sciences, 16(9), 22169.

Fradkin JE, et al. (2013) Diabetes research: a perspective from the National Institute of Diabetes and Digestive and Kidney Diseases. Diabetes, 62(2), 320.