Resource Summary Report

Generated by dkNET on Apr 24, 2025

spliceR

RRID:SCR_002280
Type: Tool

Proper Citation

spliceR (RRID:SCR_002280)

Resource Information

URL: http://www.bioconductor.org/packages/2.13/bioc/html/spliceR.html

Proper Citation: spliceR (RRID:SCR_002280)

Description: An easy-to-use R package for classification of alternative splicing and prediction of coding potential from RNA-seq data.

Synonyms: spliceR - Classification of alternative splicing and prediction of coding potential from RNA-seq data

Resource Type: software resource

Defining Citation: PMID:24655717

Keywords: standalone software, unix/linux, mac os x, windows, c, r, differential expression, high throughput sequencing, rna-seq, rna-seq, visualization

Funding:

Availability: GNU General Public License, v2 or greater

Resource Name: spliceR

Resource ID: SCR_002280

Alternate IDs: OMICS_03514

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250420T014057+0000

Ratings and Alerts

No rating or validation information has been found for spliceR.

No alerts have been found for spliceR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Wang M, et al. (2024) Precision Enhancement of CAR-NK Cells through Non-Viral Engineering and Highly Multiplexed Base Editing. bioRxiv : the preprint server for biology.

Bridge J, et al. (2024) Efficient multiplex non-viral engineering and expansion of polyclonal ?? CAR-T cells for immunotherapy. bioRxiv : the preprint server for biology.

Doll RM, et al. (2023) A temperature-tolerant CRISPR base editor mediates highly efficient and precise gene editing in Drosophila. Science advances, 9(35), eadj1568.

Kluesner MG, et al. (2021) CRISPR-Cas9 cytidine and adenosine base editing of splice-sites mediates highly-efficient disruption of proteins in primary and immortalized cells. Nature communications, 12(1), 2437.

Messa L, et al. (2021) Neural Precursor Cells Expanded Inside the 3D Micro-Scaffold Nichoid Present Different Non-Coding RNAs Profiles and Transcript Isoforms Expression: Possible Epigenetic Modulation by 3D Growth. Biomedicines, 9(9).

Louis JM, et al. (2020) TNF-alpha regulates alternative splicing of genes participating in pathways of crucial metabolic syndromes; a transcriptome wide study. Cytokine, 125, 154815.

Kinchesh P, et al. (2019) Reduced respiratory motion artefact in constant TR multi-slice MRI of the mouse. Magnetic resonance imaging, 60, 1.

Webber BR, et al. (2019) Highly efficient multiplex human T cell engineering without double-strand breaks using Cas9 base editors. Nature communications, 10(1), 5222.

Luykx JJ, et al. (2019) Coding and Non-Coding RNA Abnormalities in Bipolar Disorder. Genes, 10(11).

Zhang J, et al. (2019) Knockdown of spliceosome U2AF1 significantly inhibits the

development of human erythroid cells. Journal of cellular and molecular medicine, 23(8), 5076.

Bagwell CE, et al. (2018) Amplicon Sequencing Reveals Microbiological Signatures in Spent Nuclear Fuel Storage Basins. Frontiers in microbiology, 9, 377.

Baek S, et al. (2018) Draft genome sequence of wild Prunus yedoensis reveals massive inter-specific hybridization between sympatric flowering cherries. Genome biology, 19(1), 127.

Huang Y, et al. (2018) SF3B1 deficiency impairs human erythropoiesis via activation of p53 pathway: implications for understanding of ineffective erythropoiesis in MDS. Journal of hematology & oncology, 11(1), 19.

Hauser K, et al. (2018) Predicting resistance of clinical Abl mutations to targeted kinase inhibitors using alchemical free-energy calculations. Communications biology, 1, 70.

De Maio A, et al. (2018) RBM17 Interacts with U2SURP and CHERP to Regulate Expression and Splicing of RNA-Processing Proteins. Cell reports, 25(3), 726.

Sun H, et al. (2017) Deciphering alternative splicing and nonsense-mediated decay modulate expression in primary lymphoid tissues of birds infected with avian pathogenic E. coli (APEC). BMC genetics, 18(1), 21.

Son HG, et al. (2017) RNA surveillance via nonsense-mediated mRNA decay is crucial for longevity in daf-2/insulin/IGF-1 mutant C. elegans. Nature communications, 8, 14749.

Kersemans V, et al. (2017) An efficient and robust MRI-guided radiotherapy planning approach for targeting abdominal organs and tumours in the mouse. PloS one, 12(4), e0176693.

Zhang Y, et al. (2017) MicroRNAs control mRNA fate by compartmentalization based on 3' UTR length in male germ cells. Genome biology, 18(1), 105.

Shao MR, et al. (2017) Stress-responsive pathways and small RNA changes distinguish variable developmental phenotypes caused by MSH1 loss. BMC plant biology, 17(1), 47.