Resource Summary Report

Generated by NIF on Apr 16, 2025

LeafCutter

RRID:SCR_017639
Type: Tool

Proper Citation

LeafCutter (RRID:SCR_017639)

Resource Information

URL: https://github.com/davidaknowles/leafcutter/

Proper Citation: LeafCutter (RRID:SCR_017639)

Description: Software tool for identifying and quantifying RNA splicing variation. Used to study sample and population variation in intron splicing. Identifies variable intron splicing events from short read RNA-seq data and finds alternative splicing events of high complexity. Used for detecting differential splicing between sample groups, and for mapping splicing quantitative trait loci (sQTLs).

Resource Type: software resource, data analytics software, data analysis software, software application, data processing software

Defining Citation: PMID:29229983, DOI:10.1038/s41588-017-0004-9

Keywords: Identify, quantitate, RNA, splicing, variation, intron, short, read, RNAseq, data, mapping, trait, loci, sQTL

Funding: CEHG Fellowship ;
Howard Hughes Medical Institute ;
NHGRI HG007036;
NHGRI HG008140;
NHGRI HG009431;
NIMH R01 MH107666

Availability: Free, Available for download, Freely available

Resource Name: LeafCutter

Resource ID: SCR_017639

License: Apache License 2.0

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250416T063831+0000

Ratings and Alerts

No rating or validation information has been found for LeafCutter.

No alerts have been found for LeafCutter.

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 NIF.

Mapel XM, et al. (2024) Molecular quantitative trait loci in reproductive tissues impact male fertility in cattle. Nature communications, 15(1), 674.

Hodonsky CJ, et al. (2024) Multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci. Cell genomics, 4(1), 100465.

Solovyeva EM, et al. (2024) Integrative Proteogenomics for Differential Expression and Splicing Variation in a DM1 Mouse Model. Molecular & cellular proteomics : MCP, 23(1), 100683.

Hazell Pickering S, et al. (2024) Alternative isoform expression of key thermogenic genes in human beige adipocytes. Frontiers in endocrinology, 15, 1395750.

Mehta P, et al. (2024) Reduced protein-coding transcript diversity in severe dengue emphasises the role of alternative splicing. Life science alliance, 7(8).

Ueda MT, et al. (2024) Functional and dynamic profiling of transcript isoforms reveals essential roles of alternative splicing in interferon response. Cell genomics, 4(10), 100654.

Saevarsdottir S, et al. (2024) Start codon variant in LAG3 is associated with decreased LAG-3 expression and increased risk of autoimmune thyroid disease. Nature communications, 15(1), 5748.

Kerimov N, et al. (2023) Systematic visualisation of molecular QTLs reveals variant mechanisms at GWAS loci. bioRxiv : the preprint server for biology.

Real R, et al. (2023) Association between the LRP1B and APOE loci and the development of Parkinson's disease dementia. Brain : a journal of neurology, 146(5), 1873.

Kerimov N, et al. (2023) eQTL Catalogue 2023: New datasets, X chromosome QTLs, and improved detection and visualisation of transcript-level QTLs. PLoS genetics, 19(9), e1010932.

Workman MJ, et al. (2023) Large-scale differentiation of iPSC-derived motor neurons from ALS and control subjects. Neuron, 111(8), 1191.

Kumar R, et al. (2022) Oligonucleotide correction of an intronic TIMMDC1 variant in cells of patients with severe neurodegenerative disorder. NPJ genomic medicine, 7(1), 9.

Kim EY, et al. (2022) Transcriptome-wide changes in gene expression, splicing, and lncRNAs in response to a live attenuated dengue virus vaccine. Cell reports, 38(6), 110341.

Ma XR, et al. (2022) TDP-43 represses cryptic exon inclusion in the FTD-ALS gene UNC13A. Nature, 603(7899), 124.

Sveinbjornsson G, et al. (2022) Multiomics study of nonalcoholic fatty liver disease. Nature genetics, 54(11), 1652.

Lam M, et al. (2021) Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology : official publication of the American College of Neuropsychopharmacology, 46(10), 1788.

Feleke R, et al. (2021) Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body diseases. Acta neuropathologica, 142(3), 449.

Camp FA, et al. (2021) Implications of Antigen Selection on T Cell-Based Immunotherapy. Pharmaceuticals (Basel, Switzerland), 14(10).

Yang HS, et al. (2020) Genetics of Gene Expression in the Aging Human Brain Reveal TDP-43 Proteinopathy Pathophysiology. Neuron, 107(3), 496.

Holmes G, et al. (2020) Integrated Transcriptome and Network Analysis Reveals Spatiotemporal Dynamics of Calvarial Suturogenesis. Cell reports, 32(1), 107871.