Resource Summary Report

Generated by dkNET on Apr 23, 2025

Scripture

RRID:SCR_005269
Type: Tool

Proper Citation

Scripture (RRID:SCR_005269)

Resource Information

URL: http://www.broadinstitute.org/software/scripture/

Proper Citation: Scripture (RRID:SCR_005269)

Description: Software for transcriptome reconstruction that relies solely on RNA-Seq reads and an assembled genome to build a transcriptome ab initio. The statistical methods to estimate read coverage significance are also applicable to other sequencing data. Scripture also has modules for ChIP-Seq peak calling.

Abbreviations: Scripture

Resource Type: software resource

Defining Citation: PMID:20436462

Keywords: transcriptome, rna-seq read, genome sequence, bio.tools

Funding:

Resource Name: Scripture

Resource ID: SCR_005269

Alternate IDs: biotools:scripture, OMICS_01265

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

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250420T014247+0000

Ratings and Alerts

No rating or validation information has been found for Scripture.

No alerts have been found for Scripture.

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 dkNET.

Afzal M, et al. (2020) Legume genomics and transcriptomics: From classic breeding to modern technologies. Saudi journal of biological sciences, 27(1), 543.

Mercado CJ, et al. (2020) Identification and characterization of alternative STK39 transcripts within human and mouse kidneys reveals species-specific regulation of blood pressure. Physiological reports, 8(4), e14379.

Zhou C, et al. (2016) Long noncoding RNAs expressed in human hepatic stellate cells form networks with extracellular matrix proteins. Genome medicine, 8(1), 31.

Chen J, et al. (2016) Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. Genome biology, 17, 19.

Suvà ML, et al. (2014) Reconstructing and reprogramming the tumor-propagating potential of glioblastoma stem-like cells. Cell, 157(3), 580.

Boley N, et al. (2014) Genome-guided transcript assembly by integrative analysis of RNA sequence data. Nature biotechnology, 32(4), 341.

Bornstein C, et al. (2014) A negative feedback loop of transcription factors specifies alternative dendritic cell chromatin States. Molecular cell, 56(6), 749.

Zhao X, et al. (2014) FTO-dependent demethylation of N6-methyladenosine regulates mRNA splicing and is required for adipogenesis. Cell research, 24(12), 1403.

Cheng CS, et al. (2013) Semiconductor-based DNA sequencing of histone modification states. Nature communications, 4, 2672.

Zhu J, et al. (2013) Genome-wide chromatin state transitions associated with developmental and environmental cues. Cell, 152(3), 642.

Garber M, et al. (2012) A high-throughput chromatin immunoprecipitation approach reveals

principles of dynamic gene regulation in mammals. Molecular cell, 47(5), 810.