

Resource Summary Report

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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

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: 20260829T182218+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 [NIF](#) .

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.

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

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

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.

Suv?? 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.