

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

## 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:** 20260905T132532+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 [PRECISE-TBI](#) .

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.