

Resource Summary Report

Generated by T1D on Aug 3, 2026

Spanki

RRID:SCR_004469

Type: Tool

Proper Citation

Spanki (RRID:SCR_004469)

Resource Information

URL: <https://github.com/dsturg/Spanki>

Proper Citation: Spanki (RRID:SCR_004469)

Description: A set of tools to facilitate analysis of alternative splicing from RNA-SEQ data.

Abbreviations: Spanki

Synonyms: Splicing Analysis Kit

Resource Type: software resource

Defining Citation: [PMID:24209455](#)

Keywords: windows

Resource Name: Spanki

Resource ID: SCR_004469

Alternate IDs: OMICS_01414

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260801T190236+0000

Ratings and Alerts

No rating or validation information has been found for Spanki.

No alerts have been found for Spanki.

Data and Source Information

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Arango D, et al. (2018) Acetylation of Cytidine in mRNA Promotes Translation Efficiency. Cell, 175(7), 1872.

Venturini L, et al. (2018) Leveraging multiple transcriptome assembly methods for improved gene structure annotation. GigaScience, 7(8).

Mei W, et al. (2017) A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. Frontiers in plant science, 8, 694.

Coskran TM, et al. (2017) Induction of endogenous retroelements as a potential mechanism for mouse-specific drug-induced carcinogenicity. PloS one, 12(5), e0176768.

Vleurinck C, et al. (2016) Linking Genes and Brain Development of Honeybee Workers: A Whole-Transcriptome Approach. PloS one, 11(8), e0157980.

Chen ZX, et al. (2014) Comparative validation of the D. melanogaster modENCODE transcriptome annotation. Genome research, 24(7), 1209.

Lee H, et al. (2014) DNA copy number evolution in Drosophila cell lines. Genome biology, 15(8), R70.

Sturgill D, et al. (2013) Design of RNA splicing analysis null models for post hoc filtering of Drosophila head RNA-Seq data with the splicing analysis kit (Spanki). BMC bioinformatics, 14, 320.