

# Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

## Spanki

RRID:SCR\_004469

Type: Tool

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### Proper Citation

Spanki (RRID:SCR\_004469)

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### 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:** 20260815T182253+0000

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### Ratings and Alerts

No rating or validation information has been found for Spanki.

No alerts have been found for Spanki.

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### 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 [NIF](#) .

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

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

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.