

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 29, 2026

Trinity

RRID:SCR_013048

Type: Tool

Proper Citation

Trinity (RRID:SCR_013048)

Resource Information

URL: <http://trinityrnaseq.sourceforge.net/>

Proper Citation: Trinity (RRID:SCR_013048)

Description: Software for the efficient and robust de novo reconstruction of transcriptomes from RNA-seq data.

Abbreviations: Trinity

Resource Type: software resource

Defining Citation: [DOI:10.1038/nbt.1883](https://doi.org/10.1038/nbt.1883)

Keywords: bio.tools

Resource Name: Trinity

Resource ID: SCR_013048

Alternate IDs: biotools:trinity, OMICS_01327

Alternate URLs: <https://bio.tools/trinity>, <https://sources.debian.org/src/trinityrnaseq/>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260725T190744+0000

Ratings and Alerts

No rating or validation information has been found for Trinity.

No alerts have been found for Trinity.

Data and Source Information

Usage and Citation Metrics

We found 9576 mentions in open access literature.

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

Wu K, et al. (2026) Deciphering the role of ThHSF1 in the differential expression regulation of laccase isozymes in the white-rot fungus *Trametes hirsuta*. *Microbiology spectrum*, 14(1), e0100425.

Mantzana-Oikonomaki V, et al. (2026) Pigments, Chromatophore Structure, and Gene Expression Underlying Colour Polytypy of a Panamanian Poison Frog. *Molecular ecology*, 35(1), e70214.

Lv X, et al. (2026) *Blautia coccoides*-derived metabolite trimethylamine-N-oxide exacerbates Alzheimer's disease progression via targeting HIF1 α signaling. *Gut microbes*, 18(1), 2605768.

Pronozin AY, et al. (2026) Diversity of lncRNAs in the pan-transcriptome of maize inbred lines. *BMC genomics*, 27(1), 1.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. *Molecular biology and evolution*, 43(1).

Terpis KX, et al. (2025) Multiple plastid losses within photosynthetic stramenopiles revealed by comprehensive phylogenomics. *Current biology : CB*, 35(3), 483.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. *GigaScience*, 14.

Qin H, et al. (2025) The complete genome assembly of *Astragalus membranaceus*: enabling more accurate genetic research. *GigaScience*, 14.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia × blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

Conn T, et al. (2025) Genome assembly and annotation of *Acropora pulchra* from Mo'orea French Polynesia. *GigaByte (Hong Kong, China)*, 2025, gigabyte153.

Winter S, et al. (2025) Chromosome-Level genome assembly and transcriptome analysis of the ural owl, *Strix uralensis* Pallas, 1771. *The Journal of heredity*.

Guest SL, et al. (2025) Myosin 2 drives actin contractility in fast-crawling species outside of the amorphean lineage. *Current biology : CB*, 35(23), 5696.

Graham LA, et al. (2025) Winter-active spiders (*Clubiona*) have a hyperactive antifreeze protein with a unique beta-solenoid fold. *The FEBS journal*.

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Xue HC, et al. (2025) A unified cell atlas of vascular plants reveals cell-type foundational genes and accelerates gene discovery. *Cell*.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.

Huang C, et al. (2025) Impacts of parental genomic divergence in non-syntenic regions on cotton heterosis. *Journal of advanced research*, 73, 15.

Monteiro JPC, et al. (2025) Expression patterns of melanin-related genes are linked to crypsis and conspicuousness in a pumpkin toadlet. *Molecular ecology*, 34(15), e17458.

Miller AK, et al. (2025) Formalin-fixed paraffin-embedded (FFPE) samples help to investigate transcriptomic responses in wildlife disease. *Molecular ecology resources*, 25(5), e13805.