

Resource Summary Report

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Trinotate

RRID:SCR_018930

Type: Tool

Proper Citation

Trinotate (RRID:SCR_018930)

Resource Information

URL: <https://github.com/Trinotate/Trinotate.github.io/wiki>

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Description: Software annotation suite designed for automatic functional annotation of transcriptomes, particularly de novo assembled transcriptomes, from model or non-model organisms.

Synonyms: Transcriptome Functional Annotation and Analysis

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Keywords: Automatic functional annotation, transcriptome annotation, de novo assembled transcriptome, model organism, non model organism

Availability: Free, Available for download, Freely available

Resource Name: Trinotate

Resource ID: SCR_018930

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260905T132844+0000

Ratings and Alerts

No rating or validation information has been found for Trinotate.

No alerts have been found for Trinotate.

Data and Source Information

Usage and Citation Metrics

We found 37 mentions in open access literature.

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

Inbar S, et al. (2026) Genetic Basis of Cuticular Hydrocarbon Variation in the Desert Ant *Cataglyphis niger*. *Ecology and evolution*, 16(3), e73108.

Muhammad BL, et al. (2026) Transcriptomic insights into polyketides and toxin biosynthesis genes in freshwater dinoflagellates. *Scientific reports*, 16(1).

Lamichhane B, et al. (2025) Elucidating the enzyme network driving Amaryllidaceae alkaloids biosynthesis in *Leucojum aestivum*. *Plant biotechnology journal*, 23(6), 1988.

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.

Eierman LE, et al. (2025) Exposure to plastic debris alters expression of biomineralization, immune, and stress-related genes in the eastern oyster (*Crassostrea virginica*). *PloS one*, 20(4), e0319165.

Ohm H, et al. (2024) Spatio-temporal transcriptome and storage compound profiles of developing faba bean (*Vicia faba*) seed tissues. *Frontiers in plant science*, 15, 1284997.

Ferreira-Neto JRC, et al. (2024) From Genes to Stress Response: Genomic and Transcriptomic Data Suggest the Significance of the Inositol and Raffinose Family Oligosaccharide Pathways in *Stylosanthes scabra*, Adaptation to the Caatinga Environment. *Plants (Basel, Switzerland)*, 13(13).

Escobar-Sierra C, et al. (2024) Field application of de novo transcriptomic analysis to evaluate the effects of sublethal freshwater salinization on *Gasterosteus aculeatus* in urban streams. *PloS one*, 19(3), e0298213.

Ribeiro RP, et al. (2024) Sex-biased gene expression precedes sexual dimorphism in the agonadal annelid *Platynereis dumerilii*. *bioRxiv : the preprint server for biology*.

Ramirez MD, et al. (2024) Cellular-resolution gene expression mapping reveals organization in the head ganglia of the gastropod, *Berghia stephanieae*. *The Journal of comparative neurology*, 532(6), e25628.

Stenvers VI, et al. (2023) Experimental mining plumes and ocean warming trigger stress in a deep pelagic jellyfish. *Nature communications*, 14(1), 7352.

Chen X, et al. (2023) Deciphering triterpenoid saponin biosynthesis by leveraging transcriptome response to methyl jasmonate elicitation in *Saponaria vaccaria*. *Nature communications*, 14(1), 7101.

Claude SJ, et al. (2023) Comparative Analysis and Identification of Terpene Synthase Genes in *Convallaria keiskei* Leaf, Flower and Root Using RNA-Sequencing Profiling. *Plants* (Basel, Switzerland), 12(15).

García Navarrete T, et al. (2022) Natural variation and improved genome annotation of the emerging biofuel crop field pennycress (*Thlaspi arvense*). *G3* (Bethesda, Md.), 12(6).

Strelin MM, et al. (2022) Delayed differentiation of epidermal cells walls can underlie pedomorphosis in plants: the case of pedomorphic petals in the hummingbird-pollinated *Caipophora hibiscifolia* (Loasaceae, subfam. Loasoideae) species. *EvoDevo*, 13(1), 1.

Hudson J, et al. (2022) Pathogen exposure leads to a transcriptional downregulation of core cellular functions that may dampen the immune response in a macroalga. *Molecular ecology*, 31(12), 3468.

Peel E, et al. (2022) Genome assembly of the numbat (*Myrmecobius fasciatus*), the only termitivorous marsupial. *GigaByte* (Hong Kong, China), 2022, gigabyte47.

Chevignon G, et al. (2022) De Novo Transcriptome Assembly and Analysis of the Flat Oyster Pathogenic Protozoa *Bonamia Ostreae*. *Frontiers in cellular and infection microbiology*, 12, 921136.

Wang ZY, et al. (2022) Isolation disrupts social interactions and destabilizes brain development in bumblebees. *Current biology : CB*, 32(12), 2754.

Castillo H, et al. (2021) *Deinococcus radiodurans* UWO298 Dependence on Background Radiation for Optimal Growth. *Frontiers in genetics*, 12, 644292.