

Resource Summary Report

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EnTAP

RRID:SCR_023010

Type: Tool

Proper Citation

EnTAP (RRID:SCR_023010)

Resource Information

URL: <https://entap.readthedocs.io/en/latest/>

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Description: Software package as eukaryotic non model annotation pipeline.Used for bringing functional annotation to non-model eukaryotic transcriptomes to improve the accuracy, speed, and flexibility of functional gene annotation for de novo assembled transcriptomes in non-model eukaryotes. Addresses fragmentation and related assembly issues that result in inflated transcript estimates and poor annotation rates of protein-coding transcripts.

Synonyms: Eukaryotic Non-Model Transcriptome Annotation Pipeline

Resource Type: software resource, software toolkit

Defining Citation: [DOI:10.1111/1755-0998.13106](https://doi.org/10.1111/1755-0998.13106)

Keywords: functional annotation, non model eukaryotic transcriptomes, functional gene annotation, de novo assembled transcriptomes, non-model eukaryotes, protein-coding transcripts,

Availability: Free, Available for download, Freely available

Resource Name: EnTAP

Resource ID: SCR_023010

Record Creation Time: 20221130T050153+0000

Record Last Update: 20260808T042958+0000

Ratings and Alerts

No rating or validation information has been found for EnTAP.

No alerts have been found for EnTAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Xin G, et al. (2026) The chromosome-scale genome assembly, annotation of *Bischofia polycarpa* (H. Lév.) Airy Shaw, Phyllanthaceae. *Scientific data*, 13(1).

Zadesenets KS, et al. (2026) Mining Differentially Expressed Genes in the Marine Free-Living Flatworm *Macrostomum lignano* Under Aneuploidy-Driven Ploidy Changes. *Cells*, 15(3).

Zamora-Ballesteros C, et al. (2026) Dual RNA-seq analysis reveals differences in defensive lncRNA expression in *Pinus* spp. with varying susceptibility to *Fusarium circinatum*. *BMC plant biology*, 26(1), 326.

Salgado-Roa FC, et al. (2026) Gene Expression and Structural Differences Underpinning Black and White Colouration in Spiders. *Molecular ecology*, 35(12), e70433.

Polinski JM, et al. (2025) Chromosome-level reference genome for the Jonah crab, *Cancer borealis*. *G3 (Bethesda, Md.)*, 15(1).

Torres J, et al. (2025) Draft genome sequence of the glasshouse-potato aphid *Aulacorthum solani*. *G3 (Bethesda, Md.)*, 15(3).

Brady MJ, et al. (2025) Antagonistic kinesin-14s within a single chromosomal drive haplotype. *bioRxiv : the preprint server for biology*.

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.

Hunt DR, et al. (2025) Genome report: first whole genome assembly of *Python regius* (ball python), a model of extreme physiological and metabolic plasticity. *G3 (Bethesda, Md.)*, 15(11).

Park H, et al. (2025) Chromosome-level genome of *Zoysia sinica* in the intertidal zone reveals genomic insights into waterlogging stress adaptation. *The plant genome*, 18(3), e70070.

Robbins MD, et al. (2025) Haplotype-resolved genome assembly of 'Manhattan' perennial ryegrass (*Lolium perenne* L.) and characterization of drought responsive late

embryogenesis abundant genes. BMC genomics, 26(1), 1125.

McEvoy SL, et al. (2024) Profiling genome-wide methylation in two maples: Fine-scale approaches to detection with nanopore technology. Evolutionary applications, 17(4), e13669.

McEvoy SL, et al. (2024) The reference genome of an endangered Asteraceae, *Deinandra increscens* subsp. *villosa*, endemic to the Central Coast of California. G3 (Bethesda, Md.), 14(8).

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. Nature communications, 15(1), 6297.

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.

Vuruputoor VS, et al. (2023) Welcome to the big leaves: Best practices for improving genome annotation in non-model plant genomes. Applications in plant sciences, 11(4), e11533.

Lötter A, et al. (2022) Haplogenome assembly reveals structural variation in *Eucalyptus* interspecific hybrids. GigaScience, 12.

Zamora-Ballesteros C, et al. (2022) Genome-wide identification and characterization of *Fusarium circinatum*-responsive lncRNAs in *Pinus radiata*. BMC genomics, 23(1), 194.

McEvoy SL, et al. (2022) Strategies of tolerance reflected in two North American maple genomes. The Plant journal : for cell and molecular biology, 109(6), 1591.

Marrano A, et al. (2020) High-quality chromosome-scale assembly of the walnut (*Juglans regia* L.) reference genome. GigaScience, 9(5).