

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 toolkit, software resource

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: 20260803T040835+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 [NIF](#) .

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).

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

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

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.

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

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

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

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.

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).

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.

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.

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).