

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

Oases

RRID:SCR_011896

Type: Tool

Proper Citation

Oases (RRID:SCR_011896)

Resource Information

URL: <http://www.ebi.ac.uk/~zerbino/oases/>

Proper Citation: Oases (RRID:SCR_011896)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Software tool as de novo transcriptome assembler designed to produce transcripts from short read sequencing technologies, such as Illumina, SOLiD, or 454 in the absence of any genomic assembly.

Abbreviations: Oases

Resource Type: software resource

Defining Citation: [DOI:10.1093/bioinformatics/bts094](https://doi.org/10.1093/bioinformatics/bts094)

Keywords: bio.tools, transcriptome assembler

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Oases

Resource ID: SCR_011896

Alternate IDs: biotools:oases, OMICS_01322

Alternate URLs: <https://bio.tools/oases>

Old URLs: <https://sources.debian.org/src/oases/>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260725T190726+0000

Ratings and Alerts

No rating or validation information has been found for Oases.

No alerts have been found for Oases.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 289 mentions in open access literature.

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

Jiang Q, et al. (2025) Knowledge status of skin tear prevention and its demographic and occupational influencing factors: A National cross-sectional survey among nurses. *Journal of advanced nursing*, 81(3), 1412.

Hartman I, et al. (2025) Parental communication dynamics with children who stutter: A scoping review. *International journal of language & communication disorders*, 60(1), e13129.

Monjot A, et al. (2025) Metatranscriptomes-based sequence similarity networks uncover genetic signatures within parasitic freshwater microbial eukaryotes. *Microbiome*, 13(1), 43.

Yüceler Kaçmaz H, et al. (2024) The Turkish version of the Skin Tear Knowledge Assessment Instrument (OASES): Validity and reliability study. *International wound journal*, 21(8), e70013.

Daric V, et al. (2024) Genomic Resources and Annotations for a Colonial Ascidian, the Light-Bulb Sea Squirt *Clavelina lepadiformis*. *Genome biology and evolution*, 16(3).

Koene JM, et al. (2024) The genome of the simultaneously hermaphroditic snail *Lymnaea stagnalis* reveals an evolutionary expansion of FMRFamide-like receptors. *Scientific reports*, 14(1), 29213.

Monson C, et al. (2024) In vivo treatment with a non-aromatizable androgen rapidly alters the ovarian transcriptome of previtellogenic secondary growth coho salmon (*Onchorhynchus kisutch*). *PloS one*, 19(10), e0311628.

Andradi-Brown C, et al. (2024) A novel computational pipeline for var gene expression augments the discovery of changes in the *Plasmodium falciparum* transcriptome during transition from in vivo to short-term in vitro culture. *eLife*, 12.

Minařík M, et al. (2024) Identification of multiple transcription factor genes potentially involved in the development of electrosensory versus mechanosensory lateral line organs. *Frontiers in cell and developmental biology*, 12, 1327924.

Tanimoto H, et al. (2024) Gene expression and metabolite levels converge in the thermogenic spadix of skunk cabbage. *Plant physiology*, 195(2), 1561.

Ariffin N, et al. (2024) Proteogenomic Gene Structure Validation in the Pineapple Genome. *Journal of proteome research*, 23(5), 1583.

Theys C, et al. (2024) Localization of stuttering based on causal brain lesions. *Brain : a journal of neurology*, 147(6), 2203.

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.

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. *Cell*, 187(24), 6943.

Chessel A, et al. (2023) RAS-independent ERK activation by constitutively active KSR3 in non-chordate metazoa. *Nature communications*, 14(1), 3970.

Okuno M, et al. (2023) Chromosomal-level assembly of *Tokudaia osimensis*, *Tokudaia tokunoshimensis*, and *Tokudaia muenninki* genomes. *Scientific data*, 10(1), 927.

Kambara K, et al. (2023) Construction of a de novo assembly pipeline using multiple transcriptome data sets from *Cypripedium macranthos* (Orchidaceae). *PloS one*, 18(6), e0286804.

Yamabe T, et al. (2023) Chromosomal-level Genome Assembly of the Coffee Bee Hawk Moth Reveals the Evolution of Chromosomes and the Molecular Basis of Distinct Phenotypes. *Genome biology and evolution*, 15(9).

Schultz CJ, et al. (2022) A targeted bioinformatics approach identifies highly variable cell surface proteins that are unique to Glomeromycotina. *Mycorrhiza*, 32(1), 45.

Ji CY, et al. (2022) Comparative transcriptome profiling of sweetpotato storage roots during curing-mediated wound healing. *Gene*, 833, 146592.