

Resource Summary Report

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Trans-ABySS

RRID:SCR_013322

Type: Tool

Proper Citation

Trans-ABySS (RRID:SCR_013322)

Resource Information

URL: <http://www.bcgsc.ca/platform/bioinfo/software/trans-abyss>

Proper Citation: Trans-ABySS (RRID:SCR_013322)

Description: A software pipeline for analyzing ABySS-assembled contigs from shotgun transcriptome data.

Abbreviations: Trans-ABySS

Resource Type: software resource

Keywords: bio.tools

Resource Name: Trans-ABySS

Resource ID: SCR_013322

Alternate IDs: OMICS_01326, biotools:trans-abyss

Alternate URLs: <https://bio.tools/trans-abyss/>

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260801T190458+0000

Ratings and Alerts

No rating or validation information has been found for Trans-ABySS.

No alerts have been found for Trans-ABySS.

Data and Source Information

Usage and Citation Metrics

We found 69 mentions in open access literature.

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

Ortiz R, et al. (2025) Skin transcriptomics of invasive Coqui frogs: stress responses, parasite signatures, and antimicrobial peptides. PloS one, 20(7), e0328623.

de Celis M, et al. (2024) Multi-omics framework to reveal the molecular determinants of fermentation performance in wine yeast populations. Microbiome, 12(1), 203.

Johnston CR, et al. (2024) First draft reference genome and annotation of the alternative oil species *Physaria fendleri*. G3 (Bethesda, Md.), 14(9).

Boman J, et al. (2024) Regulatory and evolutionary impact of DNA methylation in two songbird species and their naturally occurring F1 hybrids. BMC biology, 22(1), 124.

Li Y, et al. (2024) Dissection of a rapidly evolving wheat resistance gene cluster by long-read genome sequencing accelerated the cloning of Pm69. Plant communications, 5(1), 100646.

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.

Chen X, et al. (2023) Chemical profile and analysis of biosynthetic pathways and genes of volatile terpenes in *Pityopsis ruthii*, a rare and endangered flowering plant. PloS one, 18(6), e0287524.

Lampe RH, et al. (2023) Short-term acidification promotes diverse iron acquisition and conservation mechanisms in upwelling-associated phytoplankton. Nature communications, 14(1), 7215.

Hempel CA, et al. (2022) Metagenomics versus total RNA sequencing: most accurate data-processing tools, microbial identification accuracy and perspectives for ecological assessments. Nucleic acids research, 50(16), 9279.

Reisle C, et al. (2022) A platform for oncogenomic reporting and interpretation. Nature communications, 13(1), 756.

Foster CSP, et al. (2022) Different Genes are Recruited During Convergent Evolution of Pregnancy and the Placenta. Molecular biology and evolution, 39(4).

Kawato S, et al. (2021) Genome and transcriptome assemblies of the kuruma shrimp, *Marsupenaeus japonicus*. G3 (Bethesda, Md.), 11(11).

Spillane JL, et al. (2021) Signal, bias, and the role of transcriptome assembly quality in phylogenomic inference. BMC ecology and evolution, 21(1), 43.

Docking TR, et al. (2021) A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. *Nature communications*, 12(1), 2474.

Rump MT, et al. (2021) G protein-coupled receptors as candidates for modulation and activation of the chemical senses in decapod crustaceans. *PloS one*, 16(6), e0252066.

Li Y, et al. (2021) Nutrient-imbalanced conditions shift the interplay between zooplankton and gut microbiota. *BMC genomics*, 22(1), 37.

Kozma MT, et al. (2020) Comparison of transcriptomes from two chemosensory organs in four decapod crustaceans reveals hundreds of candidate chemoreceptor proteins. *PloS one*, 15(3), e0230266.

Kozma MT, et al. (2020) Single cell transcriptomes reveal expression patterns of chemoreceptor genes in olfactory sensory neurons of the Caribbean spiny lobster, *Panulirus argus*. *BMC genomics*, 21(1), 649.

Alam MNU, et al. (2020) Short k-mer abundance profiles yield robust machine learning features and accurate classifiers for RNA viruses. *PloS one*, 15(9), e0239381.

Williamson LM, et al. (2019) Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. *Cold Spring Harbor molecular case studies*, 5(3).