

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: 20260829T182438+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 72 mentions in open access literature.

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

Wang K, et al. (2026) Ontogeny Dictates Oncogenic Potential, Lineage Hierarchy, and Therapy Response in Pediatric Leukemia. *Cancer discovery*, 16(3), 541.

Hulsey CD, et al. (2026) Divergence at the IRX gene cluster underlies extreme trophic polymorphism in a cichlid fish (*Herichthys minckleyi*). *Communications biology*, 9(1).

Liu H, et al. (2026) Long-term outcomes by clinical and molecular risk stratification in patients with medulloblastoma receiving risk-adapted therapy. *Med (New York, N.Y.)*, 7(5), 101076.

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).

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.

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.

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.

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.

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.