

Resource Summary Report

Generated by [Kravitz](#) on Sep 18, 2026

IDBA-Tran

RRID:SCR_011891

Type: Tool

Proper Citation

IDBA-Tran (RRID:SCR_011891)

Resource Information

URL: http://i.cs.hku.hk/~alse/hkubrg/projects/idba_tran/

Proper Citation: IDBA-Tran (RRID:SCR_011891)

Description: An iterative De Bruijn Graph De Novo short read assembler for transcriptome.

Abbreviations: IDBA-Tran

Resource Type: software resource

Resource Name: IDBA-Tran

Resource ID: SCR_011891

Alternate IDs: OMICS_01318

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260912T195741+0000

Ratings and Alerts

No rating or validation information has been found for IDBA-Tran.

No alerts have been found for IDBA-Tran.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Boduli? K, et al. (2026) Comprehensive assessment of transcriptome assembly quality using CATS. Nature communications, 17(1).

Neupert S, et al. (2025) Transcriptomics and Neuropeptidomics of the Cockroach *Rhyarobia maderae* to Characterize the Neuropeptide Landscape of the Cockroach's Circadian Clock. Journal of proteome research, 24(11), 5370.

Bouchebti S, et al. (2024) Tolerance and efficient metabolization of extremely high ethanol concentrations by a social wasp. Proceedings of the National Academy of Sciences of the United States of America, 121(44), e2410874121.

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.

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.

Ortiz R, et al. (2021) Pincho: A Modular Approach to High Quality De Novo Transcriptomics. Genes, 12(7).

Voshall A, et al. (2021) A consensus-based ensemble approach to improve transcriptome assembly. BMC bioinformatics, 22(1), 513.

Karmeinski D, et al. (2021) Transcriptomics provides a robust framework for the relationships of the major clades of cladobranch sea slugs (Mollusca, Gastropoda, Heterobranchia), but fails to resolve the position of the enigmatic genus *Embletonia*. BMC ecology and evolution, 21(1), 226.

Shen F, et al. (2020) De novo transcriptome assembly and sex-biased gene expression in the gonads of Amur catfish (*Silurus asotus*). Genomics, 112(3), 2603.

Martin C, et al. (2020) Analysis of Pigment-Dispersing Factor Neuropeptides and Their Receptor in a Velvet Worm. Frontiers in endocrinology, 11, 273.

Bredon M, et al. (2020) Isopod holobionts as promising models for lignocellulose degradation. Biotechnology for biofuels, 13, 49.

Knapik K, et al. (2020) Metatranscriptomic Analysis of Oil-Exposed Seawater Bacterial Communities Archived by an Environmental Sample Processor (ESP). Microorganisms, 8(5).

Song N, et al. (2020) The Mitochondrial Genome of the Phytopathogenic Fungus *Bipolaris sorokiniana* and the Utility of Mitochondrial Genome to Infer Phylogeny of Dothideomycetes. Frontiers in microbiology, 11, 863.

Song N, et al. (2020) Mitochondrial genomes of stick insects (Phasmatodea) and phylogenetic considerations. *PloS one*, 15(10), e0240186.

Liu L, et al. (2019) Identification and Evaluations of Novel Insecticidal Proteins from Plants of the Class Polypodiopsida for Crop Protection against Key Lepidopteran Pests. *Toxins*, 11(7).

Bredon M, et al. (2019) Lignocellulose degradation in isopods: new insights into the adaptation to terrestrial life. *BMC genomics*, 20(1), 462.

Hölzer M, et al. (2019) De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. *GigaScience*, 8(5).

Zhao J, et al. (2019) DTA-SiST: de novo transcriptome assembly by using simplified suffix trees. *BMC bioinformatics*, 20(Suppl 25), 698.

Bushmanova E, et al. (2019) rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. *GigaScience*, 8(9).

Johnson LK, et al. (2019) Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. *GigaScience*, 8(4).