

Resource Summary Report

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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: 20260905T132715+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 [NIF](#) .

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).