# **Resource Summary Report**

Generated by dkNET on Apr 30, 2025

# **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

**Funding:** 

Resource Name: IDBA-Tran

Resource ID: SCR\_011891

Alternate IDs: OMICS\_01318

**Record Creation Time:** 20220129T080307+0000

Record Last Update: 20250420T014601+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 23 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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.

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

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

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) Mitochondrial genomes of stick insects (Phasmatodea) and phylogenetic considerations. PloS one, 15(10), e0240186.

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.

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.

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

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

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).

Oliphant A, et al. (2018) Transcriptomic analysis of crustacean neuropeptide signaling during the moult cycle in the green shore crab, Carcinus maenas. BMC genomics, 19(1), 711.

Herlitze I, et al. (2018) Molecular modularity and asymmetry of the molluscan mantle revealed by a gene expression atlas. GigaScience, 7(6).

Richter S, et al. (2017) Comparative analyses of glycerotoxin expression unveil a novel structural organization of the bloodworm venom system. BMC evolutionary biology, 17(1), 64.