

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

Meta-IDBA

RRID:SCR_011913

Type: Tool

Proper Citation

Meta-IDBA (RRID:SCR_011913)

Resource Information

URL: <http://i.cs.hku.hk/~alse/hkubrg/projects/metaidba/>

Proper Citation: Meta-IDBA (RRID:SCR_011913)

Description: Software for an iterative De Bruijn Graph De Novo short read assembler specially designed for de novo metagenomic assembly. (Please note that MetaIDBA is out of maintainance now, we recommend using IDBA-UD instead which generally performs better.)

Abbreviations: Meta-IDBA

Resource Type: software resource

Defining Citation: [PMID:21685107](#)

Availability: Acknowledgement requested

Resource Name: Meta-IDBA

Resource ID: SCR_011913

Alternate IDs: OMICS_01425

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260725T190724+0000

Ratings and Alerts

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

No alerts have been found for Meta-IDBA.

Data and Source Information

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Gökdemir F?, et al. (2022) Metagenomics Next Generation Sequencing (mNGS): An Exciting Tool for Early and Accurate Diagnostic of Fungal Pathogens in Plants. Journal of fungi (Basel, Switzerland), 8(11).

Vollmers J, et al. (2017) Comparing and Evaluating Metagenome Assembly Tools from a Microbiologist's Perspective - Not Only Size Matters! PloS one, 12(1), e0169662.

Yao W, et al. (2015) Exploring the rice dispensable genome using a metagenome-like assembly strategy. Genome biology, 16, 187.

Kumar S, et al. (2015) Metagenomics: Retrospect and Prospects in High Throughput Age. Biotechnology research international, 2015, 121735.

García-López R, et al. (2015) Fragmentation and Coverage Variation in Viral Metagenome Assemblies, and Their Effect in Diversity Calculations. Frontiers in bioengineering and biotechnology, 3, 141.

Seok HS, et al. (2014) Estimating the composition of species in metagenomes by clustering of next-generation read sequences. Methods (San Diego, Calif.), 69(3), 213.

Treangen TJ, et al. (2013) MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. Genome biology, 14(1), R2.

Ruby JG, et al. (2013) PRICE: software for the targeted assembly of components of (Meta) genomic sequence data. G3 (Bethesda, Md.), 3(5), 865.

Peng Y, et al. (2011) Meta-IDBA: a de Novo assembler for metagenomic data. Bioinformatics (Oxford, England), 27(13), i94.