

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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:** 20260905T132715+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 [Kravitz](#) .

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.