

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

IDBA-UD

RRID:SCR_011912

Type: Tool

Proper Citation

IDBA-UD (RRID:SCR_011912)

Resource Information

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

Proper Citation: IDBA-UD (RRID:SCR_011912)

Description: Software for an iterative De Bruijn Graph De Novo Assembler for Short Reads Sequencing data with Highly Uneven Sequencing Depth.

Abbreviations: IDBA-UD

Resource Type: software resource

Defining Citation: [PMID:22495754](#), [DOI:10.1093/bioinformatics/bts174](#)

Availability: Acknowledgement requested

Resource Name: IDBA-UD

Resource ID: SCR_011912

Alternate IDs: OMICS_01423

Alternate URLs: <https://sources.debian.org/src/idba/>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260725T190723+0000

Ratings and Alerts

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

No alerts have been found for IDBA-UD.

Data and Source Information

Usage and Citation Metrics

We found 505 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Festa F, et al. (2025) A multi-disciplinary approach to identify spillover interfaces of bat coronaviruses to pig farms in Italy. PloS one, 20(10), e0332117.

Veseli I, et al. (2025) Microbes with higher metabolic independence are enriched in human gut microbiomes under stress. eLife, 12.

Wu DG, et al. (2025) Comparative metagenomics of tropical reef fishes show conserved core gut functions across hosts and diets with diet-related functional gene enrichments. Applied and environmental microbiology, 91(2), e0222924.

Snopková K, et al. (2025) *Pseudomonas rossensis* sp. nov., a novel psychrotolerant species produces antimicrobial agents targeting resistant clinical isolates of *Pseudomonas aeruginosa*. Current research in microbial sciences, 8, 100353.

Li S, et al. (2025) Association between gut microbiota and short-chain fatty acids in children with obesity. Scientific reports, 15(1), 483.

Cervantes-Echeverría M, et al. (2025) Human-derived fecal virome transplantation (FVT) reshapes the murine gut microbiota and virome, enhancing glucose regulation. PloS one, 20(12), e0337760.

Ma M, et al. (2025) Symbiotic solutions for colony nutrition: Conserved nitrogen recycling within the bacterial pouch of *Tetraponera* ants. Proceedings of the National Academy of Sciences of the United States of America, 122(44), e2514882122.

He Z, et al. (2025) A Review of the Psyllid Genus *Epipsylla* (Hemiptera, Psyllidae) from the Chinese Mainland with Phylogenetic Considerations and the Description of a New Species. Insects, 16(1).

Bechtold EK, et al. (2025) Metabolic interactions underpinning high methane fluxes across terrestrial freshwater wetlands. Nature communications, 16(1), 944.

Kashchenko G, et al. (2025) Investigating Aerobic Hive Microflora: Role of Surface Microbiome of *Apis Mellifera*. Biology, 14(1).

Li N, et al. (2025) Culture-dependent and -independent analyses reveal unique community structure and function in the external mycelial cortices of *Ophiocordyceps sinensis*. BMC microbiology, 25(1), 78.

Chrzastek K, et al. (2025) Whole-Genome Shotgun Sequencing from Chicken Clinical Tracheal Samples for Bacterial and Novel Bacteriophage Identification. Veterinary sciences, 12(2).

Ribeyre Z, et al. (2025) De novo transcriptome assembly and discovery of drought-responsive genes in white spruce (*Picea glauca*). *PloS one*, 20(1), e0316661.

Hai C, et al. (2025) Loss of Myostatin Alters Gut Microbiota and Carbohydrate Metabolism to Influence the Gut-Muscle Axis in Cattle. *Veterinary sciences*, 12(6).

Pinto D, et al. (2025) Genomic survey reveals no detectable bacteriophage activity in *Mycobacterium bovis* across a large population. *FEMS microbiology ecology*, 101(8).

Mérel V, et al. (2025) Relaxed Purifying Selection is Associated with an Accumulation of Transposable Elements in Flies. *Molecular biology and evolution*, 42(6).

Watanabe S, et al. (2025) Lubiprostone in chronic kidney disease: Insights into mitochondrial function and polyamines from a randomized phase 2 clinical trial. *Science advances*, 11(35), eadw3934.

Wu J, et al. (2025) Metagenomic analysis of microbial community dynamics in konjac rhizosphere during soft rot disease progression. *Applied microbiology and biotechnology*, 109(1), 212.

Olsson S, et al. (2025) De novo assembled nuclear, chloroplast, and mitochondrial genomes show high intraspecific variation in the tropical rainforest species *Symphonia globulifera*. *G3 (Bethesda, Md.)*, 15(11).

Yue Z, et al. (2025) CNPS.cycle: streamlining shotgun metagenomic data analysis for biogeochemical cycles. *mSystems*, 10(11), e0102125.