

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 30, 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 [SPARC SAWG](#) .

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.

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

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.

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.

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.

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

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).

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

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).

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.

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

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

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).

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.

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

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