

Resource Summary Report

Generated by [NIF](#) on Aug 9, 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: 20260808T190002+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 524 mentions in open access literature.

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

Freitas VC, et al. (2026) First Record of Isolation and Molecular Characterization of Aguas Brancas virus, a New Insect-Specific Virus Found in Brazil. *Viruses*, 18(2).

Arogundade AA, et al. (2026) Exploring sagebrush leaf microbial metagenomes from deep, host-derived sequencing. *Microbiology spectrum*, 14(5), e0219825.

Valdez-Nuñez LF, et al. (2026) Desulfosporosinus and Acididesulfobacillus dominate an acidophilic sulfate-reducing bacteria consortium during acid mine drainage bioremediation. *Applied and environmental microbiology*, 92(5), e0030826.

Conrad RE, et al. (2026) Metagenome-based vertical profiling of the Gulf of Mexico highlights its uniqueness and far-reaching effects of freshwater input. *Applied and environmental microbiology*, 92(2), e0258925.

Vilela C, et al. (2026) Microbial Diversity and Composition Uncovered on Obturator Prosthesis Biofilms: Exploratory Findings from a Pilot Study. *Pathogens (Basel, Switzerland)*, 15(2).

Gangloff V, et al. (2026) Microbial Biofilms Dynamics and Functionality in an Urban Mycobacterium-Dominated Drinking Water Distribution System. *Environmental science & technology*, 60(7), 5242.

Sedaghatkish A, et al. (2026) A contamination-reduced genome of Plasmodiophora brassicae with comprehensive functional annotation. *BMC microbiology*, 26(1), 118.

Xie F, et al. (2026) Genome-resolved metagenomics reveals gastrointestinal microbiome adaptations in sheep responding to fiber- and starch-rich diets. *Animal nutrition (Zhongguo xu mu shou yi xue hui)*, 24, 233.

Wang Y, et al. (2026) Elm Blunervirus 1: A Novel Hexapartite Blunervirus Infecting Ulmus parvifolia in China. *Viruses*, 18(2).

Steininger HM, et al. (2026) Carbohydrate Metabolism Differs in Infants by Asthma-risk Status and is Associated with the Functional Potential of Bacteroides cellulosilyticus. *bioRxiv : the preprint server for biology*.

Feng Y, et al. (2026) A microbial consortium constructed with gut microbes of Chinese native chicken breeds protects chicks against Salmonella infection. *Journal of animal science and biotechnology*, 17(1).

Liu Y, et al. (2026) Metavirome Analysis of Viruses Carried by Dairy Cows in Shaanxi, Gansu and Ningxia, China. *Animals : an open access journal from MDPI*, 16(12).

Yan A, et al. (2026) The developmental trajectory and maturation of the Hulunbuir sheep (*Ovis aries*) microbiome. *Animal microbiome*, 8(1), 10.

Wang SJ, et al. (2026) Mitogenome characteristics of two *Tetragonula* stingless bees (Hymenoptera: Apidae) from Hainan, China. *Journal of insect science* (Online), 26(3).

Li X, et al. (2026) Genomic Characterization and Molecular Detection of a Novel Carlavirus Infecting *Angelica dahurica*: *Angelica carlavirus* Virus. *Microorganisms*, 14(6).

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.

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.

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.