

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 20, 2026

Ray Meta

RRID:SCR_011918

Type: Tool

Proper Citation

Ray Meta (RRID:SCR_011918)

Resource Information

URL: <http://denovoassembler.sourceforge.net/>

Proper Citation: Ray Meta (RRID:SCR_011918)

Description: Software for a massively distributed metagenome assembler that is coupled with Ray Communities, which profiles microbiomes based on uniquely-colored k-mers.

Abbreviations: Ray Meta

Resource Type: software resource

Defining Citation: [PMID:23259615](#)

Keywords: c++

Availability: Free

Resource Name: Ray Meta

Resource ID: SCR_011918

Alternate IDs: OMICS_01431

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260919T195221+0000

Ratings and Alerts

No rating or validation information has been found for Ray Meta.

No alerts have been found for Ray Meta.

Data and Source Information

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Jonca J, et al. (2024) Comprehensive phenomic and genomic studies of the species, *Pectobacterium cacticida* and proposal for reclassification as *Alcorniella cacticida* comb. nov. *Frontiers in plant science*, 15, 1323790.

Borowska-Beszta M, et al. (2024) Comparative genomics, pangenomics, and phenomic studies of *Pectobacterium betavascularum* strains isolated from sugar beet, potato, sunflower, and artichoke: insights into pathogenicity, virulence determinants, and adaptation to the host plant. *Frontiers in plant science*, 15, 1352318.

Santiago-Rodriguez TM, et al. (2020) Potential Applications of Human Viral Metagenomics and Reference Materials: Considerations for Current and Future Viruses. *Applied and environmental microbiology*, 86(22).

Álvarez VE, et al. (2020) Crucial Role of the Accessory Genome in the Evolutionary Trajectory of *Acinetobacter baumannii* Global Clone 1. *Frontiers in microbiology*, 11, 342.

Sutton TDS, et al. (2019) Choice of assembly software has a critical impact on virome characterisation. *Microbiome*, 7(1), 12.

Malla MA, et al. (2018) Exploring the Human Microbiome: The Potential Future Role of Next-Generation Sequencing in Disease Diagnosis and Treatment. *Frontiers in immunology*, 9, 2868.

Janouškovec J, et al. (2017) A New Lineage of Eukaryotes Illuminates Early Mitochondrial Genome Reduction. *Current biology : CB*, 27(23), 3717.

Kim HS, et al. (2016) Complete mitochondrial genome of the mangrove killifish *Kryptolebias hermaphroditus* (Cyprinodontiformes, Rivulidae). *Mitochondrial DNA. Part B, Resources*, 1(1), 540.

Escobar-Zepeda A, et al. (2015) The Road to Metagenomics: From Microbiology to DNA Sequencing Technologies and Bioinformatics. *Frontiers in genetics*, 6, 348.

Traglia GM, et al. (2015) Draft Genome Sequence of *Empedobacter* (Formerly *Wautersiella*) *falsenii* comb. nov. Wf282, a Strain Isolated from a Cervical Neck Abscess. *Genome announcements*, 3(2).

Vilacoba E, et al. (2014) Draft Genome Sequence of an International Clonal Lineage 1 *Acinetobacter baumannii* Strain from Argentina. *Genome announcements*, 2(6).

Boisvert S, et al. (2012) Ray Meta: scalable de novo metagenome assembly and profiling. *Genome biology*, 13(12), R122.