

Resource Summary Report

Generated by [RRID](#) on Aug 13, 2026

[MeDuSa](#)

RRID:SCR_022058

Type: Tool

Proper Citation

MeDuSa (RRID:SCR_022058)

Resource Information

URL: <http://combo.dbe.unifi.it/medusa>

Proper Citation: MeDuSa (RRID:SCR_022058)

Description: Web server of multi draft based scaffolder. Exploits information obtained from set of genomes from related organisms to determine correct order and orientation of contigs.

Synonyms: Multi-Draft based Scaffolder

Resource Type: software resource, data access protocol, web service

Defining Citation: [PMID:25810435](#)

Keywords: Multi draft based scaffolder, genomes, related organisms, contigs, contigs correct order determination, contigs orientation determination

Availability: Free, Freely available

Resource Name: MeDuSa

Resource ID: SCR_022058

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260813T055227+0000

Ratings and Alerts

No rating or validation information has been found for MeDuSa.

No alerts have been found for MeDuSa.

Data and Source Information

Usage and Citation Metrics

We found 67 mentions in open access literature.

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

Filho CAdC, et al. (2026) A giant virus in a small lake: characterization of a new tropical algal virus expands the geographical and genetic diversity of the Brazilian virosphere. *Journal of virology*, 100(6), e0031826.

Papale AE, et al. (2025) Prefrontal default-mode network interactions with posterior hippocampus during exploration. *bioRxiv : the preprint server for biology*.

Schenk JJ, et al. (2025) Comparative diversification analyses of Hydrangeaceae and Loasaceae reveal complex evolutionary history as species disperse out of Mesoamerica. *American journal of botany*, 112(1), e16455.

Shin JI, et al. (2025) Genomic analysis and pneumococcal population dynamics across PCV implementation in South Korea, 1997-2023. *Microbial genomics*, 11(7).

Paz LN, et al. (2025) Insights into host-pathogen interaction based on the comparison of genomes of leptospira interrogans isolated from dogs, humans, and a rodent in the same epidemiological context: A one health approach. *Heliyon*, 11(1), e41531.

Vander Meersche Y, et al. (2025) PEGASUS: Prediction of MD-derived protein flexibility from sequence. *Protein science : a publication of the Protein Society*, 34(8), e70221.

Jarníková T, et al. (2025) Decreasing importance of carbon-climate feedbacks in the Southern Ocean in a warming climate. *Science advances*, 11(20), eadr3589.

González-Gragera E, et al. (2025) Genomic Characterization of Piscicolin CM22 Produced by Carnobacterium maltaromaticum CM22 Strain Isolated from Salmon (Salmo salar). *Probiotics and antimicrobial proteins*, 17(6), 3826.

Liu Q, et al. (2025) Restoration of intestinal secondary bile acid synthesis: A potential approach to improve pancreatic β cell function in type 1 diabetes. *Cell reports. Medicine*, 6(5), 102130.

Sudheer A, et al. (2025) Comprehensive genomics, probiotic, and antibiofilm potential analysis of Streptococcus thermophilus strains isolated from homemade and commercial dahi. *Scientific reports*, 15(1), 7089.

Aguado Lorenzo V, et al. (2025) Evaluation of NHS Injectable Medicines Guide users' information needs related to the co-infusion of intravenous medicines: user survey and Delphi consensus study. *BMJ open*, 15(5), e094211.

Tu JH, et al. (2025) Single-cell transcriptomic atlas of the chicken cecum reveals cellular responses and state shifts during Eimeria tenella infection. *BMC genomics*, 26(1), 141.

Hossain AA, et al. (2024) DNA glycosylases provide antiviral defence in prokaryotes. *Nature*, 629(8011), 410.

Warmbrunn MV, et al. (2024) Oral histidine affects gut microbiota and MAIT cells improving glycemic control in type 2 diabetes patients. *Gut microbes*, 16(1), 2370616.

Fernández M, et al. (2024) Bacterial Diversity, Metabolic Profiling, and Application Potential of Antarctic Soil Metagenomes. *Current issues in molecular biology*, 46(11), 13165.

Ragozzino C, et al. (2024) Integrated genome and metabolome mining unveiled structure and biosynthesis of novel lipopeptides from a deep-sea *Rhodococcus*. *Microbial biotechnology*, 17(11), e70011.

Tathode MS, et al. (2024) Whole-genome analysis suggesting probiotic potential and safety properties of *Pediococcus pentosaceus* DSPZPP1, a promising LAB strain isolated from traditional fermented sausages of the Basilicata region (Southern Italy). *Frontiers in microbiology*, 15, 1268216.

Maghembe RS, et al. (2024) A sophisticated virulence repertoire and colistin resistance of *Citrobacter freundii* ST150 from a patient with sepsis admitted to ICU in a tertiary care hospital in Uganda, East Africa: Insight from genomic and molecular docking analyses. *Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases*, 120, 105591.

Attaye I, et al. (2024) Oral *Anaerobutyricum soehngenii* augments glycemic control in type 2 diabetes. *iScience*, 27(8), 110455.

Chen L, et al. (2024) Trade-offs between receptor modification and fitness drive host-bacteriophage co-evolution leading to phage extinction or co-existence. *The ISME journal*, 18(1).