

Resource Summary Report

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A5-miseq

RRID:SCR_012148

Type: Tool

Proper Citation

A5-miseq (RRID:SCR_012148)

Resource Information

URL: <http://sourceforge.net/projects/ngopt/>

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Description: Software that produces high quality microbial genome assemblies on a laptop computer without any parameter tuning. A5-miseq does this by automating the process of adapter trimming, quality filtering, error correction, contig and scaffold generation, and detection of misassemblies. Unlike the original A5 pipeline, A5-miseq can use long reads from the Illumina MiSeq, use read pairing information during contig generation, and includes several improvements to read trimming.

Resource Type: software resource

Defining Citation: [PMID:25338718](https://pubmed.ncbi.nlm.nih.gov/25338718/)

Keywords: standalone software, illumina, unix/linux, mac os x, bio.tools

Funding:

Availability: GNU General Public License

Resource Name: A5-miseq

Resource ID: SCR_012148

Alternate IDs: OMICS_06339, biotools:a5-miseq

Alternate URLs: <https://bio.tools/a5-miseq>

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250214T183218+0000

Ratings and Alerts

No rating or validation information has been found for A5-miseq.

No alerts have been found for A5-miseq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 169 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Hu R, et al. (2024) A Chromosomal-Level Genome of *Dermatophagoides farinae*, a Common Allergenic Mite Species. *International journal of genomics*, 2024, 3779688.

Li J, et al. (2024) Isolation, characterization and functional analysis of a bacteriophage targeting *Culex pipiens pallens* resistance-associated *Aeromonas hydrophila*. *Parasites & vectors*, 17(1), 222.

Li S, et al. (2024) Characterization and genomic analysis of a lytic *Stenotrophomonas maltophilia* short-tailed phage A1432 revealed a new genus of the family Mesyzhinovviridae. *Frontiers in microbiology*, 15, 1400700.

Aguirre-Sánchez JR, et al. (2024) Genomic insights of *S. aureus* associated with bovine mastitis in a high livestock activity region of Mexico. *Journal of veterinary science*, 25(4), e42.

Rastegar S, et al. (2024) Characterization of bacteriophage vB_AbaS_SA1 and its synergistic effects with antibiotics against clinical multidrug-resistant *Acinetobacter baumannii* isolates. *Pathogens and disease*, 82.

Wu Q, et al. (2024) Characteristics and whole-genome analysis of a novel *Pseudomonas syringae* pv. tomato bacteriophage D6 isolated from a karst cave. *Virus genes*, 60(3), 295.

Han W, et al. (2024) Characteristic of KPC-12, a KPC Variant Conferring Resistance to Ceftazidime-Avibactam in the Carbapenem-Resistant *Klebsiella pneumoniae* ST11-KL47 Clone Background. *Infection and drug resistance*, 17, 2541.

Feng J, et al. (2024) Genetic epidemiology and plasmid-mediated transmission of *mcr-1* by *Escherichia coli* ST155 from wastewater of long-term care facilities. *Microbiology spectrum*, 12(3), e0370723.

Zhao K, et al. (2024) Genome Analysis for Cholesterol-Lowering Action and Bacteriocin Production of *Lactiplantibacillus plantarum* WLPL21 and ZDY04 from Traditional Chinese Fermented Foods. *Microorganisms*, 12(1).

Wei J, et al. (2024) Influence of specific tobacco endophytic *Bacillus* on tobacco leaf quality enhancement during fermentation. *Frontiers in microbiology*, 15, 1468492.

Gong J, et al. (2024) Genomic Characterization of a Plasmid-Free and Highly Drug-Resistant *Salmonella enterica* Serovar Indiana Isolate in China. *Veterinary sciences*, 11(1).

Zhang Y, et al. (2024) The complete mitochondrial genome and phylogenetic analysis of *Pealius mori* (Hemiptera: Aleyrodidae). *Mitochondrial DNA. Part B, Resources*, 9(7), 856.

Tian X, et al. (2024) Isolation, characterization and therapeutic evaluation of a new *Acinetobacter* virus Abgy202141 lysing *Acinetobacter baumannii*. *Frontiers in microbiology*, 15, 1379400.

Xi H, et al. (2024) Isolation and Characterization of a Lytic Bacteriophage RH-42-1 of *Erwinia amylovora* from Orchard Soil in China. *Viruses*, 16(4).

Tang S, et al. (2024) The complete mitochondrial genome of *Rhipicephalus haemaphysaloides* and its phylogenetic analysis. *Mitochondrial DNA. Part B, Resources*, 9(4), 551.

Shen W, et al. (2024) Characterization of a broad-spectrum antifungal strain, *Streptomyces graminearus* STR-1, against *Magnaporthe oryzae*. *Frontiers in microbiology*, 15, 1298781.

Zhang C, et al. (2024) A tripartite bacterial-fungal-plant symbiosis in the mycorrhiza-shaped microbiome drives plant growth and mycorrhization. *Microbiome*, 12(1), 13.

McDonald JB, et al. (2024) Development of tools for the genetic manipulation of *Campylobacter* and their application to the N-glycosylation system of *Campylobacter hepaticus*, an emerging pathogen of poultry. *mBio*, 15(9), e0110124.

Zhang M, et al. (2024) Complete mitochondrial genome of *Rhopalosiphum maidis* (Hemiptera: Aphididae) and its phylogenetic implications. *Mitochondrial DNA. Part B, Resources*, 9(9), 1227.

Isogai M, et al. (2024) Evaluation of *Klebsiella pneumoniae* pathogenicity through holistic gene content analysis. *Microbial genomics*, 10(9).