

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](#)

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

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: 20260725T190732+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 189 mentions in open access literature.

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

Wang Y, et al. (2025) Surfactin: a novel *Aphis gossypii* killing surfactin produced by *Bacillus australimaris* TRM82479 of Taklamakan Desert origin. *Frontiers in microbiology*, 16, 1559495.

Yang P, et al. (2025) Identification of a novel phage depolymerase against ST11 K64 carbapenem-resistant *Klebsiella pneumoniae* and its therapeutic potential. *Journal of bacteriology*, 207(4), e0038724.

Chen C, et al. (2025) Antibiotic-resistant *Acinetobacter baumannii* can be killed by a combination of bacteriophages and complement. *Medical microbiology and immunology*, 214(1), 40.

Ranta K, et al. (2025) Isolation and characterization of fMGyn-Pae01, a phiKZ-like jumbo phage infecting *Pseudomonas aeruginosa*. *Virology journal*, 22(1), 55.

Ouyang Z, et al. (2025) Differences in virulence and drug resistance between *Clostridioides difficile* ST37 and ST1 isolates. *Virulence*, 16(1), 2502554.

Lin M, et al. (2025) Isolation and identification of a newly discovered broad-spectrum *Acinetobacter baumannii* phage and therapeutic validation against pan-resistant *Acinetobacter baumannii*. *Virologica Sinica*, 40(4), 587.

Li K, et al. (2025) Genomic re-evaluation of clinical isolates reveals a structured *Streptococcus suis* complex. *Journal of clinical microbiology*, 63(12), e0103025.

Ajao YO, et al. (2025) Antibacterial activity of two newly isolated *Bdellovibrio bacteriovorus* strains on *Salmonella enterica* serovars of food safety concern. *Microbiology spectrum*, 13(10), e0086125.

Xu Y, et al. (2025) Genome analysis of viral hemorrhagic septicemia virus isolated from *Paralichthys olivaceus* in China. *Scientific reports*, 15(1), 32976.

Seki M, et al. (2025) Size Distribution and Pathogenic Potential of Culturable Airborne *Clostridium* spp. in a Suburb of Toyama City, Japan. *Microbes and environments*, 40(1).

Huang J, et al. (2025) Multidrug-Resistant *Enterococcus faecalis* from Yak Feces: Isolation, Genomic Characterization and Functional Insights. *Veterinary sciences*, 12(11).

Aguirre-Sánchez JR, et al. (2025) Genetic Characterization of *Staphylococcus aureus* Isolates Associated with Toxic Shock Syndrome Toxin Production: An Epidemiological and Bioinformatics Approach. *Toxins*, 17(9).

Kaufmann H, et al. (2025) Genomic Repertoire of Twenty-Two Novel Vibrionaceae Species Isolated from Marine Sediments. *Microbial ecology*, 88(1), 36.

Hu P, et al. (2025) Isolation and identification of *Klebsiella pneumoniae* phage ϕ K2046: optimizing its antibacterial potential in combination with chlorhexidine. *Antimicrobial resistance and infection control*, 14(1), 42.

Chen H, et al. (2025) Prevalence and Molecular Characterization of Porcine Parvovirus 2 in Southwest China During 2020-2023. *Veterinary sciences*, 12(2).

Mukhopadhyay J, et al. (2025) ϕ Characterization of the mitochondrial genomes for Ophiostomatales and related taxa from various geographic origins and related species: large intron-rich genomes and complex intron arrangements. *IMA fungus*, 16, e159349.

Duan M, et al. (2025) The complete mitochondrial genomes of *Macrostylophora euteles* and *Citellophilus tesquorum sungaris* and the phylogenetics of known Siphonaptera mitogenomes. *Frontiers in veterinary science*, 12, 1558328.

Liu Y, et al. (2025) Isolation, genomic analysis and biocontrol potential of bacteriophage SHY-Vp8 and its endolysin against *Vibrio parahaemolyticus* in shrimp aquaculture. *Virus research*, 361, 199638.

Liu J-p, et al. (2025) Pan-genome classification of the virulence spectrum of *Bartonella* and the variation of heme-binding protein virulence factor in isolates from the Tibetan Plateau. *Microbiology spectrum*, 13(12), e0046525.

Song Y, et al. (2024) Emergence of Lumpy Skin Disease Virus Infection in Yaks, Cattle-Yaks, and Cattle on the Qinghai-Xizang Plateau of China. *Transboundary and emerging diseases*, 2024, 2383886.