

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: 20260808T185958+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 202 mentions in open access literature.

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

Wang H, et al. (2026) Isolation and Identification of Pathogens Associated with Fruit Rot of Tamarindusindica L. and Screening for Their Biocontrol Agents. Microorganisms, 14(6).

Badawy S, et al. (2026) Genomic analysis of jumbo coliphage fEgEco12. Archives of virology, 171(5).

Lin Y, et al. (2026) Integrated Genomic and Functional Characterization of Lactiplantibacillus plantarum MS11 Reveals Multifunctional Metabolite Production from a High-Altitude Fermented Dairy Niche. Microorganisms, 14(4).

Chen X, et al. (2026) Mechanisms of Bacillus amyloliquefaciens on alleviating lipopolysaccharide-induced oxidative stress in broilers. Animal nutrition (Zhongguo xu mu shou yi xue hui), 24, 316.

Koroleva A, et al. (2026) Metabolic engineering of doxorubicin biosynthesis through P450-redox partner optimization and structural analysis of DoxA. Nature communications, 17(1).

Slizen V, et al. (2026) Sequence-encoded determinants of regional mutational plasticity: comparative analysis of PE_PGRS genes in Mycobacterium tuberculosis and other bacteria. Scientific reports, 16(1).

Yu S, et al. (2026) Keystone bacterial taxa drive denitrification and N2O emission via adaptive genomic and metabolic strategies in contrasting agricultural soils. Environmental microbiome, 21(1).

Zhang Y, et al. (2026) Characterization of the bacteriophage vB_KpnP_Henu1_3 lytic for K1 Klebsiella pneumoniae and its therapeutic efficacy in Galleria mellonella larvae and mice. Microbiology spectrum, 14(2), e0093125.

Xia M, et al. (2026) Identification and characterization of two novel Acinetobacter species capable of degrading polyester. Microbiology spectrum, 14(5), e0249125.

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.

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.

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.

Su L, et al. (2025) General variation in the *Fusarium* wilt rhizosphere microbiome. *Nature communications*, 17(1), 1017.

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.

Arazi P, et al. (2025) Genomic and functional characterization of a novel lytic phage vB-AbaM-fThrA with anti-biofilm activity against CR-MDR *Acinetobacter baumannii*. *BMC microbiology*, 26(1), 71.

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

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

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