

Resource Summary Report

Generated by [dkNET](#) on Jul 29, 2026

Illumina: MiniSeq System

RRID:SCR_016378

Type: Tool

Proper Citation

Illumina: MiniSeq System (RRID:SCR_016378)

Resource Information

URL: <https://www.illumina.com/systems/sequencing-platforms/miniseq.html>

Proper Citation: Illumina: MiniSeq System (RRID:SCR_016378)

Description: MiniSeq System to perform range of targeted DNA and RNA applications for low numbers of samples.

Synonyms: MiniSeq, MiniSeq System

Resource Type: instrument resource

Keywords: Illumina, Sequencing System, Instrument Equipment, USEDit,

Availability: Restricted

Specification URL:

https://drive.google.com/file/d/17NMglofv7u_Uz275ve8kKo9kFf3ExTfa/view?usp=drivesdk

Resource Name: Illumina: MiniSeq System

Resource ID: SCR_016378

Alternate IDs: SCR_020136, Model_Number_MiniSeq

Alternate URLs: <https://www.illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/miniseq-system-spec-sheet-m-na-00006/miniseq-system-spec-sheet-m-na-00006.pdf>

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260725T190822+0000

Ratings and Alerts

No rating or validation information has been found for Illumina: MiniSeq System.

No alerts have been found for Illumina: MiniSeq System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Frias-De-Diego A, et al. (2025) Influence of Sequencing Technology on Pangenome-Level Analysis and Detection of Antimicrobial Resistance Genes in ESKAPE Pathogens. Open forum infectious diseases, 12(4), ofaf183.

Hwang GH, et al. (2025) Large DNA deletions occur during DNA repair at 20-fold lower frequency for base editors and prime editors than for Cas9 nucleases. Nature biomedical engineering, 9(1), 79.

Brinkley DM, et al. (2025) Pseudomonads coordinate innate defense against viruses and bacteria with a single regulatory system. Cell host & microbe, 33(8), 1333.

Singh P, et al. (2024) Genomic characterization of Influenza A (H1N1)pdm09 and SARS-CoV-2 from Influenza Like Illness (ILI) and Severe Acute Respiratory Illness (SARI) cases reported between July-December, 2022. Scientific reports, 14(1), 10660.

Yang S, et al. (2024) An Antibody-CRISPR/Cas Conjugate Platform for Target-Specific Delivery and Gene Editing in Cancer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(21), e2308763.

Kim S, et al. (2023) Enhancement of Gene Editing and Base Editing with Therapeutic Ribonucleoproteins through In Vivo Delivery Based on Absorptive Silica Nanoconstruct. Advanced healthcare materials, 12(4), e2201825.

Planini? A, et al. (2023) Characterization of Human Immunodeficiency Virus-1 Transmission Clusters and Transmitted Drug-Resistant Mutations in Croatia from 2019 to 2022. Viruses, 15(12).

Singh P, et al. (2022) Genomic characterization unravelling the causative role of SARS-CoV-2 Delta variant of lineage B.1.617.2 in 2nd wave of COVID-19 pandemic in Chhattisgarh, India. Microbial pathogenesis, 164, 105404.

Song B, et al. (2021) Analysis of NHEJ-Based DNA Repair after CRISPR-Mediated DNA Cleavage. International journal of molecular sciences, 22(12).

Jang HK, et al. (2021) High-purity production and precise editing of DNA base editing ribonucleoproteins. Science advances, 7(35).

Hirabayashi A, et al. (2021) Plasmid analysis of NDM metallo- β -lactamase-producing Enterobacterales isolated in Vietnam. *PloS one*, 16(7), e0231119.

Bak SY, et al. (2021) Quantitative assessment of engineered Cas9 variants for target specificity enhancement by single-molecule reaction pathway analysis. *Nucleic acids research*, 49(19), 11312.

Ducotterd C, et al. (2021) A powerful long metabarcoding method for the determination of complex diets from faecal analysis of the European pond turtle (*Emys orbicularis*, L. 1758). *Molecular ecology resources*, 21(2), 433.

Na YR, et al. (2020) Protein Kinase A Catalytic Subunit Is a Molecular Switch that Promotes the Pro-tumoral Function of Macrophages. *Cell reports*, 31(6), 107643.

Cabibbe AM, et al. (2020) Application of Targeted Next-Generation Sequencing Assay on a Portable Sequencing Platform for Culture-Free Detection of Drug-Resistant Tuberculosis from Clinical Samples. *Journal of clinical microbiology*, 58(10).

Naqib A, et al. (2019) PCR effects of melting temperature adjustment of individual primers in degenerate primer pools. *PeerJ*, 7, e6570.

Akter H, et al. (2019) Novel mutations in actionable breast cancer genes by targeted sequencing in an ethnically homogenous cohort. *BMC medical genetics*, 20(1), 150.

Jo DH, et al. (2019) Long-Term Effects of In Vivo Genome Editing in the Mouse Retina Using *Campylobacter jejuni* Cas9 Expressed via Adeno-Associated Virus. *Molecular therapy : the journal of the American Society of Gene Therapy*, 27(1), 130.

Jarett JK, et al. (2019) Diets with and without edible cricket support a similar level of diversity in the gut microbiome of dogs. *PeerJ*, 7, e7661.

Ge M, et al. (2019) Different next-generation sequencing pipelines based detection of tumor DNA in cerebrospinal fluid of lung adenocarcinoma cancer patients with leptomeningeal metastases. *BMC cancer*, 19(1), 143.