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# MiSeq<sup>™</sup> i100 Series

# Powerful, simple sequencing for microbiology and infectious disease research



Access the simplest, fastest benchtop sequencing system providing highly accurate data for microbiome insights, novel virus tracking, and more.

The MiSeq i100 Series is here.



### Rapidly uncover insights in your lab

### Using the MiSeq i100 Series is as easy as...

#### Simple, intuitive setup

Expedite setup with roomtemperature, no-thaw consumables, and three step sample loading in under 20 minutes.

#### **Efficient workflow**

Sample-to-analysis workflow means less hands-on time and simplified data analysis, which helps reduce the need for bioinformatics expertise.

#### Accurate, same-day results

Industry standard accuracy delivered in a single shift; start sequencing in the morning and complete the run and analysis the same day.

### Designed for efficient lab operations with reliable results



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Intuitive interface for easy navigation

Simplified onboarding for new users and applications



Minimal hands-on time throughout the workflow-saving time, resources, and money



From single pathogen to microbial discovery, the MiSeq i100 Series brings a new level of flexibility for microbiologists in every lab

# More applications enable more possibilities

With multiple reagent kits available, supporting a wide range of throughputs, labs can cost-effectively process samples at any scale.



### Achieve high-quality data in a single shift

Powered by XLEAP-SBS<sup>™</sup> chemistry, our fastest, highest-quality chemistry, sequencing run times are as fast as four hours. And with onboard secondary analysis, results can be generated in a single day.



Improved run times Single shift vs 2.5 days7

Accurate, efficient analysis Onboard DRAGEN<sup>™</sup> software and access to a full suite of cloud-based analysis apps





Now labs of all sizes can bring proven sequencing in house

### Increased accessibility for improved outputs



### Sample-to-analysis workflow solutions

Workflows include library preparation kits, panels, sequencing on the MiSeq i100 Series, and preconfigured DRAGEN secondary analysis.

- Streamline experimental planning with preselected library prep kits and targeted gene panels
- Simplify data analysis with access to preconfigured pipelines, helping reduce need for bioinformatics expertise
- Increase confidence in your data with access to data sets in BaseSpace<sup>™</sup> Sequence Hub



### Room-temperature shipping and storage



XLEAP-SBS reagents help deliver remarkable sustainability and user experience benefits

No dry ice, no cold packs, and no HHH freezer storage required



85% reduction in packaging materials7 and easy disposal for most parts



Simple setup and quick access from shelf storage optimizes uptime with no thawing required





"This instrument will have such a big impact on our microbial profiling and plasma sequencing services. It's going to enable faster sequencing at a lower cost but also really high-quality data."

> - Christopher Noune National Laboratory Operations Manager Australian Genome Research Facility



#### Bring more possibilities to your lab

Learn how the simplicity and flexibility of the MiSeq i100 Series from Illumina enables microbial and infectious disease researchers to gain insights and answers with unbelievable speed and accuracy.

#### What will you discover next?

Illumina.com/MiSegi100





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We are always available for questions, insights, and conversation. Visit us at illumina.com.

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<sup>1</sup> Estimated throughputs are based on noted experimental parameters. Optimal parameters should be determined empirically

<sup>2</sup> Based on 100K DNA fragments (200K total reads) per sample

- <sup>3</sup> Based on 5 Mb genome size, 30x coverage, 2 × 150 bp read length
  <sup>4</sup> 50M and 100M flow cells are only available on the MiSeq i100 Plus System and will be available in 2025
- <sup>5</sup> Based on 4M DNA fragments (8M total reads) per sample

<sup>9</sup>Based on transactional surveys from technical support, service, and field application

 <sup>&</sup>lt;sup>6</sup> Based on 10M DNA fragments (20M total reads) per sample
 <sup>7</sup> As compared with MiSeq System
 <sup>8</sup> Data calculations on file, Illumina, Inc. 2022