illumina

MiSeq[™] i100 Series

Powerful, fast, and simple sequencing for oncology research

Access meaningful insights for all your oncology research by identifying key mutations, such as gene fusions, copy number alterations, and other genomic aberrations that underlie tumorigenesis.

The MiSeq i100 Series is here.





Gain more genomic insights and discovery power than you ever thought possible

Rapidly uncover insights in your lab

Using the MiSeg 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, fast results

Industry-standard accuracy ready when you are: obtain results quickly with ~4-15.5 hour run times.

Designed for efficient lab operations with reliable results



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Intuitive interface for easy navigation

Easy onboarding for new users and applications



Maximized walk-away time throughout the workflow—saving time, resources, and money



The MiSeq i100 Series brings a new level of flexibility to labs of all sizes

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 faster than ever

Powered by XLEAP-SBS[™] 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 Runs as fast as four hours7

Accurate, efficient analysis Onboard DRAGEN[™] 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

Oncology focused workflows are available and 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 results with access to data sets in BaseSpace[™] 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 HHHH 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





"Now we can save time unpacking and save on waste. And it helps planning for the sequencing runs because we don't have to think two days before to get a kit out of the freezer. The room-temperature storage really is a game-changer."

> - Geneviève Donpierre Team Leader, NGS Sequencing, Genome Quebec





Bring more possibilities to your lab

Learn how the simplicity and flexibility of the MiSeq i100 Series from Illumina enables oncology research to gain insights and answers with unbelievable speed and accuracy.

What will you discover next?

Illumina.com/MiSeqi100



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

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¹ Estimated throughputs are based on noted experimental parameters. Optimal parameters should be determined empirically.

² Based on 100K DNA fragments (200K total reads) per sample using 16S rRNA sequencing
³ Based on 2.3M paired end reads per sample using Pillar® oncoReaveal[™] Multi-Cancer CNV + RNA fusion panel
⁴ 50M and 100M flow cells are only available on the MiSeq i100 Plus System and will be available in 2025

⁵ Based on 4.5M paired end reads per sample using Pillar oncoReveal Myeloid panel

⁷ As compared with MiSeq System ⁸ Data calculations on file, Illumina, Inc. 2022

⁹Based on transactional surveys from technical support, service, and field application

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⁶ Based on 33 paired end reads per sample