NextSeq® Series of Sequencing Systems

Fast, flexible high-throughput desktop sequencers enable a wide range of applications with the accuracy of Illumina SBS technology.

Highlights

- **First High-Throughput Desktop Sequencer**
  Performs whole-genome, exome, transcriptome sequencing and more, today or as your research grows
- **Highly Flexible to Fit Research Demands**
  Supports a broad range of sequencing applications and offers tunable read length and multiple output configurations
- **Fast Turnaround Time**
  Rapid sequencing for time-critical studies ensures that projects are completed in record time
- **Industry-Leading Illumina Chemistry**
  Highly accurate SBS chemistry delivers high-quality results with no homopolymer issues
- **Push-Button Operation and Easy Data Analysis**
  Walk away sample-to-results solution with streamlined informatics performed on premises or in the cloud
- **End-to-End Illumina Scientific Support**
  Illumina scientists and engineers are there every step of the way, providing installation, training, applications, and data analysis support

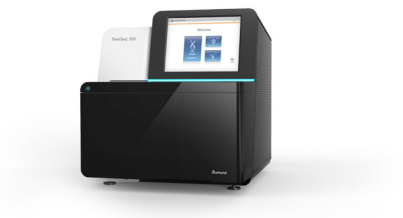
Introduction

A transformative addition to the industry-leading Illumina next-generation sequencing (NGS) system portfolio, the NextSeq 500 System delivers the power of high-throughput sequencing with the simplicity of a desktop sequencer (Figure 1). Its fast, integrated, sample-to-results workflow enables rapid sequencing of exomes, whole genomes, and transcriptomes in a single run, with the flexibility to switch to lower throughput sequencing as needed (Figure 2). The system fits seamlessly into research laboratories, with no need for specialized equipment. Illumina scientists are available at every point along the way with support and guidance, enabling researchers to focus on making the next breakthrough discovery.

Enabling New Discoveries

The NextSeq 500 System enables researchers to keep pace with technology, putting them in control of their sequencing projects. This robust, scalable system turns a broad range of high-throughput applications into affordable everyday research tools. The flexible NextSeq 500 System enables researchers to switch quickly from one application to another and configure output based on sample volume and coverage needs. Now, even the smallest laboratory can perform any combination of sequencing applications to advance their studies, supporting faster publication of landmark research.

Figure 1: NextSeq 500 Sequencing System



By leveraging the latest advances in SBS chemistry and the industry's simplest workflow, the NextSeq 500 System delivers high-quality results for whole-genome, exome, or transcriptome sequencing.

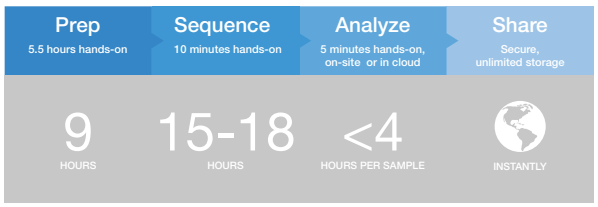
Fast and Easy Workflow

The NextSeq 500 intuitive user interface and load-and-go operation enables researchers to perform more sequencing applications at the highest depth and resolution. It takes less than 10 minutes to load and setup the NextSeq 500 System. While other platforms require several pieces of specialized equipment, the NextSeq 500 System integrates cluster generation and sequencing into a single instrument and offers a seamless transition for onsite or cloud-based data analysis.

Samples prepared using one of the simple, streamlined Illumina library prep kits are loaded into the NextSeq 500 System where sequencing is automated and fast. Data are generated in as little as 12 hours for a 75 cycle sequencing run and less than 30 hours for paired 150 cycle reads.

By employing the Illumina industry-leading sequencing by synthesis (SBS) chemistry and file format conventions, the NextSeq 500 System

Figure 2: NextSeq 500 System Sample-to-Answer Workflow*



The simple NextSeq 500 workflow delivers highly accurate sequencing data.

* Times vary by experiment and assay type. Details shown are for an mRNA expression profiling experiment assuming 2 × 75 bp on instrument, analysis results include differential expression and identification of alternative transcripts.

Table 1: Unprecedented Flexibility for Multiple Applications

Application	High Output Flow Cell Configuration		Mid Output Flow Cell Configuration	
	No. of Samples	Time	No. of Samples	Time
Gene Expression Profiling > 10 M Reads 1 × 75 bp	40	11 hours	N/A	N/A
mRNA-Seq > 40 M Reads 2 × 75 bp	10	18 hours	3	15 hours
Enrichment Panel 12 Mb Region > 20× coverage at > 95% targets	N/A	N/A	20	26 hours
Whole-Exome Sequencing > 90% at > 10× coverage	9	18 hours	3	15 hours
Human Whole-Genome Sequencing 3 GB Genome > 30× coverage 2 × 150 bp	1	29 hours	N/A	N/A

offers customers access to the broadest ecosystem of established protocols, workflows, data sets, and data analysis tools.

Industry-Leading SBS Chemistry Delivers Highest Accuracy

At the core of the NextSeq 500 System is industry-leading Illumina SBS chemistry—the most widely adopted NGS technology. This proprietary reversible terminator-based method enables the massively parallel sequencing of millions of DNA fragments, detecting single bases as they are incorporated into growing DNA strands. The method virtually eliminates errors and missed calls associated with strings of repeated nucleotides (homopolymers).

Furthermore, the latest evolution in sequencing chemistry—SBS v2 sequencing reagents—enable the NextSeq 500 System to deliver the most accurate human genome, exome, or transcriptome at any coverage level. The NextSeq 500 System with SBS v2 chemistry delivers improved signal intensities and the lowest number of false positives, false negatives, and error rates yet. This exceptional data quality sets Illumina systems apart and gives researchers full confidence in the data generated.

Versatile and Flexible to Support the Widest Range of Applications

The NextSeq 500 System is the right sequencer for any project size and sequencing throughput, providing users with optimal operational efficiency. It is the only desktop sequencing system capable of sequencing a high-coverage (30×) whole human genome in one run. The NextSeq 500 System also delivers a one-day turnaround for a number of popular sequencing applications. With this instrument, researchers can sequence:

- 1–16 exomes/run
- 1–20 transcriptomes/run
- 6–96 targeted panels/run
- 12–40 gene expression profiling samples/run

The NextSeq 500 System is easily configured providing researchers with scalability to handle low to high-throughput project sizes for maximum operational efficiency. Based on sample volume and coverage needs, researchers can choose between two flow cell configurations (High Output and Mid Output), easily shifting from low to higher throughput processing with each sequencing run (Table 1). The NextSeq 500 System provides integrated support for paired-end sequencing, offering user-defined read lengths up to 2 × 150 bp.

The system is supported by the full suite of Illumina library prep and target enrichment solutions, offering library compatibility across the Illumina sequencing portfolio. This allows researchers to scale-up

Figure 3: Illumina NGS Portfolio Makes Sequencing Accessible to All Researchers

HiSeq 2500
Power and efficiency for large-scale genomics.

NextSeq 500
Speed and simplicity for personal-scale genomics.

MiSeq
Speed and simplicity for targeted and small genome sequencing.

Illumina NGS systems offer solutions for every application, sample type, and sequencing scale. Each delivers high data quality and accuracy with flexible throughput and simple, streamlined workflows. Data can be seamlessly compared, exchanged, and analyzed in BaseSpace.

†Q30 = 1 error in 1,000 base calls or an accuracy of 99.9%

studies easily to the higher throughput HiSeq® System or perform follow-up studies on the MiSeq® System (Figure 3).

NextSeq 550 Enables Array Scanning

The NextSeq 550 System combines microarray scanning with the proven and robust NextSeq 500 sequencing system.*† By leveraging microarray scanning on the NextSeq 550 System, researchers have instant access to a powerful, complementary technology for further exploration or confirmation of copy number variants detected through sequencing. With the NextSeq 550 System, the menu of cutting-edge research applications is maximized while the instrument costs are simultaneously minimized. The NextSeq 550 System supports flexible options by enabling a broad range of applications in reproductive, genetic health, and oncology-related research.

Streamlined Bioinformatics

The NextSeq 500 System supports a number of data analysis options. Primary data analyses, including base calling and quality scoring, are performed by integrated instrument computers. Sequencing run data can be run through a wide range of open-source or commercial pipelines developed for Illumina data, or instantly transferred, analyzed, and stored securely in BaseSpace® (Cloud or Onsite), the Illumina genomics computing environment. BaseSpace downstream data analysis includes alignment and variant detection, annotation, visualization, and interpretation.

BaseSpace also includes Illumina-developed data analysis apps for exome, transcriptome, whole-genome, and somatic variant calling. Thanks to Illumina's industry-standard data formats, third-party developers have created a rich ecosystem of commercial and open-source tools for more extensive downstream data analysis.

Summary

The NextSeq 500 and NextSeq 550 Systems are transformative sequencers that enable NGS to become an everyday tool in laboratories worldwide. Incorporating the latest advancements in SBS chemistry, the flexible NextSeq Systems push-button operation and streamlined sample-to-results workflow allow researchers to perform the most popular high-throughput applications in less than a day. Its multiple flow cell and reagent configurations enable low-throughput sequencing as needed, providing researchers with the operating efficiency to handle a range of project sizes.

* Microarray scanning is only supported on the NextSeq 550 System.
† Microarray scanning enabled Q2 2015 and will include support for the CytoSNP-850k, CytoSNP-12, and Karyomap-12 DNA microarrays.

Join the Illumina Community

With a NextSeq 500 or 550 System in their laboratory, researchers join a worldwide community of over 60,000 scientists using Illumina technology for their research studies. Illumina schedules community events throughout the year, bringing researchers together to share ideas. User group meetings, scientific symposiums, and blog forums provide venues to discuss new research methods and breakthrough studies.

An integral part of the Illumina community is our dedicated service and support team, consisting of more than 300 people worldwide, 75% of whom have advanced degrees. Illumina technical support begins when the NextSeq 500 System is delivered, with Illumina scientists and engineers assisting with system installation and setup, and the training of laboratory personnel. They are there 24/7 globally to answer questions every step of the way, giving researchers the peace of mind to focus on their next research study.

As researchers' needs change, new systems are brought into the laboratory, or new methods are undertaken, the Illumina support and training teams are there to provide assistance. In addition to on-site support, training courses (via webinar or at an Illumina facility) are available to bring laboratory personnel quickly up to speed.

Learn More

Go to www.illumina.com/systems/nextseq-sequencer.ilmn to learn more about the next revolution in sequencing.

NextSeq Series Performance Parameters§

Flow Cell Configuration	Read Length (bp)	Output (Gb)	Run Time	Data Quality	Required Input
High Output Flow Cell Up to 400 M single reads Up to 800 M paired-end reads	2 × 150	100–120	29 hours	> 75% > Q30	100 ng–1 µg with TruSeq® Library Prep Kits
	2 × 75	50–60	18 hours	> 80% > Q30	
	1 × 75	25–30	11 hours	> 80% > Q30	
Mid Output Flow Cell Up to 130 M single reads Up to 260 M paired-end reads	2 × 150	32–39	26 hours	> 75% > Q30	
	2 × 75	16–19	15 hours	> 80% > Q30	

§Total times include cluster generation, sequencing, and base calling on a NextSeq 500 System. Install specifications are based on Illumina PhiX control library at supported cluster densities (between 129 and 165 k/mm^2 clusters passing filter). Actual performance parameters may vary based on sample type, sample quality, and clusters passing filter. The percentage of bases > Q30 is averaged over the entire run.

NextSeq 500 System Specifications

Instrument Configuration
RFID tracking for consumables

Instrument Control Computer (Internal)**
Base Unit: Dual Intel Xeon E5-2448L 1.8 GHz CPU
Memory: 96 GB RAM
Hard Drive: 750 GB
Operating System: Windows 7 embedded standard
**Computer specifications are subject to change.

Operating Environment
Temperature: 19°C to 25°C (22°C ± 3°C)
Humidity: Non-condensing 20%–80% relative humidity
Altitude: Less than 2,000 m (6,500 ft)
Air Quality: Pollution degree rating of II
Ventilation: Up to 2,048 BTU/hr @ 600 W
For Indoor Use Only

Light Emitting Diode (LED)
520 nm, 650 nm; Laser diode: 780 nm, Class IIIb

Dimensions
W×D×H: 58.5 cm × 53.4 cm × 63.5 cm (23.0 in × 21.0 in × 25 in)
Weight: 83 kg (183 lbs)
Crated Weight: 151.5 kg (334 lbs)

Power Requirements
100–120 VAC 15 A
220–240 VAC 10 A

Radio Frequency Identifier (RFID)
Frequency: 13.56 MHz
Power: Supply current 120 mA, RF output power 200 mW

Product Safety and Compliance
NRTL certified IEC 61010-1
CE marked
FCC/IC approved

Ordering Information

System Name	Catalog No.
NextSeq 500 Sequencing System	SY-415-1001
NextSeq 550 System	SY-415-1002

Output Kit Name	
NextSeq 500 Mid Output Kit (150 cycles)	FC-404-1001
NextSeq 500 Mid Output Kit (300 cycles)	FC-404-1003
NextSeq 500 High Output Kit (75 cycles)	FC-404-1005
NextSeq 500 High Output Kit (150 cycles)	FC-404-1002
NextSeq 500 High Output Kit (300 cycles)	FC-404-1004
NextSeq 500 Mid Output Kit v2 (150 cycles)	FC-404-2001
NextSeq 500 Mid Output Kit v2 (300 cycles)	FC-404-2003
NextSeq 500 High Output Kit v2 (75 cycles)	FC-404-2005
NextSeq 500 High Output Kit v2 (150 cycles)	FC-404-2002
NextSeq 500 High Output Kit v2 (300 cycles)	FC-404-2004

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