



Figure 4: Storage and Analysis of NextSeq 500 System Data in the BaseSpace Cloud. NextSeq 500 System data can be securely and seamlessly uploaded to the BaseSpace cloud for fast, cost-effective analysis and storage.

Summary

Delivering the highest data quality and accuracy, the NextSeq 500 System WGS Solution enables researchers to characterize and explore whole genomes fully. This high-throughput, desktop sequencer can cost-effectively perform WGS of any species, with a streamlined workflow that minimizes hands-on time. Integrated data analysis in BaseSpace, supplemented with a large collection of commercial and open source software tools, enables researchers to mine the rich NextSeq 500 System WGS data set now and in the future as new discoveries are made.

Learn More

Go to www.illumina.com/applications/sequencing/dna_sequencing/whole_genome_sequencing.ilmn to learn more about the next revolution in WGS.

Join the Illumina Community

With a NextSeq 500 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.

NextSeq 500 System Specifications.

Instrument Configuration

RFID tracking for consumables

Instrument Control Computer (Internal)^a

Base Unit: Dual Intel Xeon ES-2448L 1.8 GHz CPU

Memory: 96 GB RAM

Hard Drive: 750 GB

Operating System: Windows 7 embedded standard

a. 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

WxDxH: 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

NextSeq 500 Sequencing System

Catalog No.

SY-415-1001

Output Kit Name

NextSeq 500 Mid Output Kit (150 cycles)

NextSeq 500 Mid Output Kit (300 cycles)

NextSeq 500 High Output Kit (75 cycles)

NextSeq 500 High Output Kit (150 cycles)

NextSeq 500 High Output Kit (300 cycles)

NextSeq 500 Mid Output v2 Kit (150 cycles)

NextSeq 500 High Output v2 Kit (150 cycles)

NextSeq 500 Mid Output v2 Kit (300 cycles)

NextSeq 500 High Output v2 Kit (300 cycles)

NextSeq 500 High Output v2 Kit (75 cycles)

Catalog No.

FC-404-1001

FC-404-1003

FC-404-1005

FC-404-1002

FC-404-1004

FC-404-2001

FC-404-2002

FC-404-2003

FC-404-2004

FC-404-2005

References

1. Racz C, Petrovski R, Saunders CT, et al. Isaac: ultra-fast whole-genome secondary analysis on Illumina sequencing platforms. *Bioinformatics*. 2013;29:2041-2043.

