INSTRUMENT USER

ILLUMINA NEXTSEQ 550Dx AND MINISEQ NGS

General Information

Instrument: Illumina NextSeq 550Dx and MiniSeq

Manufacturer: Illumina

Location:

- CRIETT – Circolo Hospital of Varese – Day Center – Microbiology Laboratory
- Viale Borri 56, Varese, Italy
- Floor: 1

Instrument Manager:

- Dr. Angelo Paolo GENONI
  E-mail: angelopaolo.genoni@uninsubria.it
  Telephone: +39 338 9798761

Authorized Users:

Dr. Angelo Paolo Genoni

Training Requirements:
No user training is provided. The instrument is operated exclusively by the technical staff or the instrument manager; direct user access is not permitted.

Internal tickets can be viewed on the intranet page (access with university credentials): https://intranet.uninsubria.it/areadocumenti/ticket-strumenti-criett-utenti-interni

The fee schedule for external users can be viewed on the website: www.uninsubria.it/criett

Acknowledgement in Scientific Publications (see CRIETT Regulations, Article 11): Users are required to acknowledge the use of CRIETT research infrastructure in the acknowledgements section of all scientific publications resulting from work performed with this instrument using the following statement:

"The scientific support from CRIETT centre of University of Insubria (instrument code: XXX) is greatly acknowledged."

Instrument Codes:

- MiniSeq: EP03
- NextSeq 550Dx: EP04

Access Policy

1. Full-Service Access

Eligible users:
Research groups that use the instrument occasionally, external users, or users who do not have qualified personnel.

Access procedure:
Access is provided through the assistance of dedicated technical staff, who are responsible for scheduling, operating the instrument, and performing the sequencing runs.

2. Occasional/Temporary User

Access to the instrument is permitted only under the supervision of the Instrument Manager or an authorized operator.

Description and Features

The Illumina MiniSeq and NextSeq 550Dx are **Next-Generation Sequencing (NGS)** platforms based on **Sequencing by Synthesis (SBS)** technology. This approach enables the simultaneous sequencing of millions of DNA fragments, generating large amounts of genomic data with high throughput and accuracy.

During library preparation, DNA fragments bind to the flow cell surface, where **bridge amplification** generates clonal DNA clusters. Fluorescently labeled nucleotides are then incorporated one base at a time. After each incorporation, the instrument captures an image (imaging) to identify the incorporated nucleotide. The fluorescent label is subsequently removed, allowing the next sequencing cycle to proceed. This process is repeated throughout the run, and the resulting sequence of fluorescent signals is translated into the DNA base sequence (A, T, C, and G).

Technical Specifications

MiniSeq: NextSeq 550dx:

Flow cell configuration[a]	Read length (cycles)	Output (Gb)	Run time[b]	Data quality[c]
High-output kit	300	~ 7.5	~ 24 hours	Q30 > 80%
Up to 25M single reads	150	~ 4	~ 13 hours	Q30 > 85%
Up to 50M paired-end reads	75	~ 2	~ 7 hours	Q30 > 85%
Rapid kit Up to 20M single reads	100	~ 2	< 5 hours	Q30 > 85%
Mid-output kit Up to 8M single reads Up to 16M paired-end reads	300	~ 2.5	~ 17 hours	Q30 > 80%

Configurazione della cella a flusso	Lunghezza lettura	Output	Qualità dei dati
Cella a flusso con output elevato Fino a 400 milioni di letture unidirezionali Fino a 800 milioni di letture paired-end	2 × 150 bp	100-120 Gb	> 75% > Q30
	2 × 75 bp	50-60 Gb	> 80% > Q30
	1 × 75 bp	25-30 Gb	> 80% > Q30
Cella a flusso con output medio Fino a 130 milioni di letture unidirezionali Fino a 260 milioni di letture paired-end	2 × 150 bp	32-39 Gb	> 75% > Q30
	2 × 75 bp	16-19 Gb	> 80% > Q30

⚠ Safety Information

In case of questions, unexpected behavior, or instrument malfunction, contact:

Dr. Angelo Paolo Genoni

Operating Notes

- Instrument reservation is mandatory through the internal booking system.

- Self-service operation is permitted only for trained and registered (authorized) users.
- Any malfunction or technical issue must be reported promptly to CRIETT technical staff.

Materials and Consumables Provided by CRIETT

- 0.2 N NaOH solution for library denaturation
- 2 mL disposable microcentrifuge tubes
- Pipette tips
- Qubit fluorometer for library quantification
- PhiX Control internal sequencing control

Materials and Consumables Provided by the User

- Sequencing library at a known concentration

This version uses terminology consistent with Illumina documentation and international core facility manuals while remaining faithful to the original Italian text.