

Resource Summary Report

Generated by [RRID](#) on Aug 6, 2026

Illumina: iSeq 100 Sequencing System

RRID:SCR_016377

Type: Tool

Proper Citation

Illumina: iSeq 100 Sequencing System (RRID:SCR_016377)

Resource Information

URL: <https://www.illumina.com/systems/sequencing-platforms/iseq.html>

Proper Citation: Illumina: iSeq 100 Sequencing System (RRID:SCR_016377)

Description: Benchtop next-generation sequencer to sequence DNA and RNA.

Synonyms: iSeq 100, iSeq100

Resource Type: instrument resource

Keywords: Instrument, Equipment, Hardware, Sequencer, Illumina, Sequencing, RNA, DNA

Availability: Restricted

Specification URL: <https://drive.google.com/file/d/1U7-4WcU8rWYVYtkftlShvCofjPAeppR9/view?usp=drivesdk>

Resource Name: Illumina: iSeq 100 Sequencing System

Resource ID: SCR_016377

Alternate IDs: Model_Number_iSeq 100, SCR_020125

Alternate URLs: <https://www.illumina.com/content/dam/illumina-marketing/documents/products/brochures/iseq-brochure-770-2017-038-web.pdf>, <https://www.illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/iseq-100-system-spec-sheet-m-gl-00456/iseq100-system-spec-sheet-m-gl-00456.pdf>

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260801T190538+0000

Ratings and Alerts

No rating or validation information has been found for Illumina: iSeq 100 Sequencing System.

No alerts have been found for Illumina: iSeq 100 Sequencing System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Brinkley DM, et al. (2025) Pseudomonads coordinate innate defense against viruses and bacteria with a single regulatory system. Cell host & microbe, 33(8), 1333.

Motta EVS, et al. (2024) Type VI secretion systems promote intraspecific competition and host interactions in a bee gut symbiont. Proceedings of the National Academy of Sciences of the United States of America, 121(44), e2414882121.

Zhu Y, et al. (2019) qDSB-Seq is a general method for genome-wide quantification of DNA double-strand breaks using sequencing. Nature communications, 10(1), 2313.

Biernacka A, et al. (2018) i-BLESS is an ultra-sensitive method for detection of DNA double-strand breaks. Communications biology, 1, 181.