

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

Illumina: HiSeq2000 Sequencing System

RRID:SCR_020130

Type: Tool

Proper Citation

Illumina: HiSeq2000 Sequencing System (RRID:SCR_020130)

Resource Information

URL:

https://www.illumina.com/documents/products/datasheets/datasheet_hiseq_systems.pdf

Proper Citation: Illumina: HiSeq2000 Sequencing System (RRID:SCR_020130)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on November 15, 2023. HiSeq 2000 sequencing system for sequencing and fastest data generation rate.

Resource Type: instrument resource

Keywords: Illumina, Genetic Sequencer, Instrument Equipment, USEdit

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Illumina: HiSeq2000 Sequencing System

Resource ID: SCR_020130

Alternate IDs: Model_Number_HiSeq2000, SCR_020132

Alternate URLs: https://support.illumina.com/content/dam/illumina-support/documents/documentation/system_documentation/hiseq2000/hiseq-2000-system-guide-15011190-03.pdf

Record Creation Time: 20220129T080348+0000

Record Last Update: 20260801T190640+0000

Ratings and Alerts

No rating or validation information has been found for Illumina: HiSeq2000 Sequencing System.

No alerts have been found for Illumina: HiSeq2000 Sequencing System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals SIPRR1 control of circadian rhythm and photoperiodic flowering in tomato. GigaScience, 14.

Micoli G, et al. (2025) Decoding the Genomic and Functional Landscape of Emerging Subtypes in Ovarian Cancer. Cancer discovery, 15(11), 2262.

Conticelli D, et al. (2025) AREG and EREG Are Predictive Biomarkers of Response to EGFR Inhibition in Gastroesophageal Cancer. Cancer research, 85(16), 3111.

Kudo-Saito C, et al. (2025) IL33-ST2 axis is a predictive biomarker for anti-PD1 therapeutic efficacy in advanced gastric cancer. Journal of translational medicine, 23(1), 1125.

Yang J, et al. (2025) Blocking the TCA Cycle in Cancer Cells Potentiates CD36+ T-cell-Mediated Antitumor Immunity by Suppressing ER Stress-Associated THBS2 Signaling. Cancer research, 85(11), 2014.

Huang X, et al. (2025) CDK4/6 Inhibition Reverses MEIS2 Suppression of CRL4 CRBN to Enhance Immunomodulatory Drug Therapy in Multiple Myeloma. bioRxiv : the preprint server for biology.

Tang R, et al. (2024) A ghost moth olfactory prototype of the lepidopteran sex communication. GigaScience, 13.

De Bellis C, et al. (2024) Genomic, epigenomic and transcriptomic inter- and intra-tumor heterogeneity in desmoid tumors. Clinical cancer research : an official journal of the American Association for Cancer Research.

Hai L, et al. (2024) A clinically applicable connectivity signature for glioblastoma includes the tumor network driver CHI3L1. Nature communications, 15(1), 968.

Huang LC, et al. (2024) BRCA1 and ELK-1 regulate neural progenitor cell fate in the optic tectum in response to visual experience in Xenopus laevis tadpoles. Proceedings of the National Academy of Sciences of the United States of America, 121(3), e2316542121.

Umeda M, et al. (2024) A new genomic framework to categorize pediatric acute myeloid leukemia. Nature genetics, 56(2), 281.

Umeda M, et al. (2023) Proposal of a new genomic framework for categorization of pediatric acute myeloid leukemia associated with prognosis. Research square.

Melchiorson JU, et al. (2023) Rare heterozygous loss-of-function variants in the human GLP-1 receptor do not associate with cardiometabolic phenotypes. The Journal of clinical endocrinology and metabolism.

Zhang X, et al. (2023) Genome Assembly and Comparative Analysis of the Egg Parasitoid Wasp *Trichogramma dendrolimi* Shed Light on the Composition and Evolution of Olfactory Receptors and Venoms. Insects, 14(2).

Wang X, et al. (2022) Chromosome-level genome and recombination map of the male buffalo. GigaScience, 12.

Smolander OP, et al. (2022) Improved chromosome-level genome assembly of the Glanville fritillary butterfly (*Melitaea cinxia*) integrating Pacific Biosciences long reads and a high-density linkage map. GigaScience, 11(1).

Ta AC, et al. (2022) Temporal and spatial transcriptomic dynamics across brain development in *Xenopus laevis* tadpoles. G3 (Bethesda, Md.), 12(1).

Westfall AK, et al. (2021) A chromosome-level genome assembly for the eastern fence lizard (*Sceloporus undulatus*), a reptile model for physiological and evolutionary ecology. GigaScience, 10(10).