

Resource Summary Report

Generated by [dkNET](#) on Aug 25, 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: 20260821T194146+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 20 mentions in open access literature.

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

Boudjadi S, et al. (2026) Involvement of the FGF8/FGF Receptor Signaling Pathway in the Maintenance and Progression of Fusion-Positive Rhabdomyosarcoma. *Molecular cancer therapeutics*, 25(3), 493.

Yang J, et al. (2026) GLS1 Orchestrates Exosome-Mediated Tumor-Endothelial Communication to Facilitate Angiogenesis. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(41), e75510.

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*.

Melchiorssen 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.

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

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).

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).