

Resource Summary Report

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Illumina HiSeq 3000/HiSeq 4000 Sequencing System

RRID:SCR_016386

Type: Tool

Proper Citation

Illumina HiSeq 3000/HiSeq 4000 Sequencing System (RRID:SCR_016386)

Resource Information

URL: <https://www.illumina.com/systems/sequencing-platforms/hiseq-3000-4000.html>

Proper Citation: Illumina HiSeq 3000/HiSeq 4000 Sequencing System (RRID:SCR_016386)

Description: Sequencer that uses patterned flow cell technology to provide high-performance sequencing. Perform production-scale, high-throughput exome or transcriptome sequencing projects quickly and economically.

Synonyms: HiSeq 3000, HiSeq 4000, HiSeq 3000/4000

Resource Type: data or information resource, portal, topical portal

Keywords: Illumina, Sequencing System, Instrument Equipment, USEDit,

Availability: Restricted

Resource Name: Illumina HiSeq 3000/HiSeq 4000 Sequencing System

Resource ID: SCR_016386

Alternate IDs: SCR_020127, Model_Number_HiSeq 3000/4000

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260821T194047+0000

Ratings and Alerts

No rating or validation information has been found for Illumina HiSeq 3000/HiSeq 4000 Sequencing System.

No alerts have been found for Illumina HiSeq 3000/HiSeq 4000 Sequencing System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 72 mentions in open access literature.

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

Sherif S, et al. (2026) A Three-Gene Interferon Signature Predicts Sustained Complete Remission in Pediatric AML Patients. *Cancers*, 18(9).

Jiménez-Sánchez A, et al. (2026) Transcriptomic Plasticity Is a Hallmark of Metastatic Pancreatic Cancer. *Cancer research*, 86(7), 1769.

Huerga Encabo H, et al. (2026) Human TET2-Mutant Clonal Hematopoiesis Expansion Is Driven by Distinct Inflammatory Signaling Responses in Stem Cells Versus Myeloid Progeny. *Blood cancer discovery*, 7(2), 287.

Rosenbaum E, et al. (2026) Association of Circulating T Cell and Tumor Microenvironment Profiles with Immune Checkpoint Blockade Outcomes in Sarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1777.

Chang S, et al. (2026) Nascent chain folding status modulates ribosome dynamics and mRNA stability through the ribosome-associated chaperone Zuo1. *Molecular cell*.

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.

Ferreira S, et al. (2026) Inactivation of CDKN2AARF Promotes p53-Independent Remodeling of the PDAC Tumor Microenvironment. *Cancer research*, 86(13), 3109.

Sandoval TA, et al. (2026) Chemoradiation Reprograms Tumor Cells and the Immune Microenvironment in Cervical Cancer. *Cancer research*, 86(7), 1639.

Guercio BJ, et al. (2026) Neoadjuvant Nivolumab with or without Ipilimumab for Cisplatin-Ineligible Patients with Muscle-Invasive Bladder Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(8), 1434.

Suwalska A, et al. (2026) Mutational landscape of normal breast tissues adjacent to invasive breast cancer. *Cell reports. Medicine*, 102543.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phylllobates terribilis*. *GigaByte (Hong Kong, China)*, 2025, gigabyte157.

Crawford KJ, et al. (2025) Targeting FGFR4 abrogates HNF1A-driven metastasis in pancreatic ductal adenocarcinoma. *Molecular cancer*, 24(1), 208.

Ramponi V, et al. (2025) H4K20me3-Mediated Repression of Inflammatory Genes Is a Characteristic and Targetable Vulnerability of Persister Cancer Cells. *Cancer research*, 85(1), 32.

Ault N, et al. (2025) Dynamics of small RNAs in a red-fruited wine grape cultivar infected with Grapevine red blotch virus. *BMC genomics*, 26(1), 417.

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

Zhang L, et al. (2025) A Novel Lytic Salmonella Phage Harboring an Unprecedented Tail-Protein Domain Combination Capable of Lysing Cross-Host-Transmitted Salmonella Strains. *Foods (Basel, Switzerland)*, 14(16).

Nayak PK, et al. (2025) Transcriptome profiling of tendon fibroblasts at the onset of embryonic muscle contraction reveals novel force-responsive genes. *eLife*, 14.

Berger AH, et al. (2025) High-resolution transcriptional impact of AIRE: effects of pathogenic variants p.Arg257Ter, p.Cys311Tyr, and polygenic risk variant p.Arg471Cys. *Frontiers in immunology*, 16, 1572789.

Arenillas C, et al. (2025) Convergent Genetic Adaptation in Human Tumors Developed Under Systemic Hypoxia and in Populations Living at High Altitudes. *Cancer discovery*, 15(5), 1037.

Luo Y, et al. (2025) Single-cell clonal lineage tracing identifies the transcriptional program controlling the cell fate decisions by neoantigen-specific CD8 + T cells. *bioRxiv : the preprint server for biology*.