

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: topical portal, portal, data or information resource

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: 20260805T044353+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 62 mentions in open access literature.

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

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 *Phyllobates terribilis*. *GigaByte (Hong Kong, China)*, 2025, gigabyte157.

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.

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.

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

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.

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

Kim CW, et al. (2025) Gut dysbiosis from high-salt diet promotes glioma via propionate-mediated TGF- β activation. *The Journal of experimental medicine*, 222(8).

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*.

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

Masamsetti VP, et al. (2025) Lineage contribution of the mesendoderm progenitors in the gastrulating mouse embryo. *Developmental cell*, 60(14), 1991.

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.

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).

McDaniel JM, et al. (2024) p53R172H and p53R245W Hotspot Mutations Drive Distinct Transcriptomes in Mouse Mammary Tumors Through a Convergent Transcriptional Mediator. *Cancer research communications*, 4(8), 1991.

Edelmann M, et al. (2024) Tumor Vessel Normalization via PFKFB3 Inhibition Alleviates Hypoxia and Increases Tumor Necrosis in Rectal Cancer upon Radiotherapy. *Cancer research communications*, 4(8), 2008.

Wang T, et al. (2024) Isolation and identification of specific *Enterococcus faecalis* phage C-3 and G21-7 against Avian pathogenic *Escherichia coli* and its application to one-day-old geese. *Frontiers in microbiology*, 15, 1385860.

Zheng SM, et al. (2024) MILIP Binding to tRNAs Promotes Protein Synthesis to Drive Triple-Negative Breast Cancer. *Cancer research*, 84(9), 1460.

Gatins R, et al. (2024) Whole genome assembly and annotation of the King Angelfish (*Holocanthus passer*) gives insight into the evolution of marine fishes of the Tropical Eastern Pacific. *GigaByte (Hong Kong, China)*, 2024, gigabyte115.

Boutelle AM, et al. (2024) Integrative multiomic approaches reveal ZMAT3 and p21 as conserved hubs in the p53 tumor suppression network. *bioRxiv : the preprint server for biology*.

Salem M, et al. (2024) Functional annotation of regulatory elements in rainbow trout uncovers roles of the epigenome in genetic selection and genome evolution. *GigaScience*, 13.