

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

Illumina: HiSeq X

RRID:SCR_016385

Type: Tool

Proper Citation

Illumina: HiSeq X (RRID:SCR_016385)

Resource Information

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

Proper Citation: Illumina: HiSeq X (RRID:SCR_016385)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on November 15,2023. Sequencer for whole-genome sequencing. System consists of HiSeq X ultra-high-throughput instruments that deliver over 18,000 human genomes per year.

Synonyms: HiSeq X

Resource Type: instrument resource

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Illumina: HiSeq X

Resource ID: SCR_016385

Alternate IDs: Model_Number_HiSeq X, SCR_020131

Alternate URLs: <https://www.illumina.com/content/dam/illumina-marketing/documents/products/datasheets/datasheet-hiseq-x-ten.pdf>

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260801T190538+0000

Ratings and Alerts

No rating or validation information has been found for Illumina: HiSeq X.

No alerts have been found for Illumina: HiSeq X.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Puzio-Kuter AM, et al. (2025) Restoration of the Tumor Suppressor Function of Y220C-Mutant p53 by Rezatapopt, a Small-Molecule Reactivator. *Cancer discovery*, 15(6), 1159.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. *GigaScience*, 14.

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

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Chen XX, et al. (2025) Microbial dysbiosis with tryptophan metabolites alteration in lower respiratory tract is associated with clinical responses to anti-PD-1 immunotherapy in advanced non-small cell lung cancer. *Cancer immunology, immunotherapy : CII*, 74(4), 140.

Rao WQ, et al. (2025) A Chromosome-level Genome Assembly of the Western Nose-Horned Viper (*Vipera ammodytes ammodytes*). *Genome biology and evolution*, 17(12).

Yoshimura T, et al. (2025) High-Throughput Drug Screening of Clear Cell Ovarian Cancer Organoids Reveals Vulnerability to Proteasome Inhibitors and Dinaciclib and Identifies AGR2 as a Therapeutic Target. *Cancer research communications*, 5(6), 1018.

Xue J, et al. (2025) An HIV fusion-inhibitory lipopeptide provides robust post-exposure prophylaxis and prevents viral reservoir seeding in macaques. *Cell reports*, 44(9), 116228.

Cha J, et al. (2025) 4-1BB+ Tregs and inhibitory progenitor exhausted T cells confer resistance to anti-PD-L1 and anti-CTLA-4 combination therapy. *Cell reports. Medicine*, 6(10), 102408.

Li Q, et al. (2025) Combined Inhibition of XPO1 and DNA Methylation Exerts Synergistic Effects in DLBCL. *Molecular carcinogenesis*.

Zhang C, et al. (2025) Parent-of-origin effects orchestrate transcriptional reprogramming and epigenetic regulation of seedling vigor heterosis in triploid loquat. *Frontiers in plant science*, 16, 1698577.

Lu Y, et al. (2024) Whole-genome sequencing of the invasive golden apple snail *Pomacea canaliculata* from Asia reveals rapid expansion and adaptive evolution. *GigaScience*, 13.

Wang YS, et al. (2024) Chromosome-level genome assemblies of two littorinid marine snails indicate genetic basis of intertidal adaptation and ancient karyotype evolved from bilaterian ancestors. *GigaScience*, 13.

Lavikka K, et al. (2024) Deciphering cancer genomes with GenomeSpy: a grammar-based visualization toolkit. *GigaScience*, 13.

Xiao Y, et al. (2024) Innovative approach for high-throughput exploiting sex-specific markers in Japanese parrotfish *Oplegnathus fasciatus*. *GigaScience*, 13.

Cai L, et al. (2024) The chromosome-scale genome of *Magnolia sinica* (Magnoliaceae) provides insights into the conservation of plant species with extremely small populations (PSESP). *GigaScience*, 13.

Huang Y, et al. (2024) A reference genome of Commelinales provides insights into the commelinids evolution and global spread of water hyacinth (*Pontederia crassipes*). *GigaScience*, 13.

Fan G, et al. (2024) BCL6 confers resistance to HDAC inhibitors in DLBCL. *Biochemical pharmacology*, 227, 116466.

Pirani RM, et al. (2023) A high-quality genome for the slender anole (*Anolis apletophallus*): an emerging model for field studies of tropical ecology and evolution. *G3 (Bethesda, Md.)*, 14(1).