

Resource Summary Report

Generated by [dkNET](#) on Aug 17, 2026

PacBio: Sequel II System

RRID:SCR_017990

Type: Tool

Proper Citation

PacBio: Sequel II System (RRID:SCR_017990)

Resource Information

URL: <https://www.pacb.com/technology/hifi-sequencing/sequel-system/>

Proper Citation: PacBio: Sequel II System (RRID:SCR_017990)

Description: Sequencer by Pacific Biosciences. System provides advantages of SMRT Sequencing and now makes it more affordable for all scientists to drive discovery with comprehensive views of genomes and transcriptomes. Generates 8 times more data than original Sequel System. Provides access to highly accurate long reads (HiFi reads). Reduces project time for faster results. Makes sequencing more affordable. Supports range of SMRT Sequencing applications.

Resource Type: instrument resource

Keywords: sequencing machine, hardware, high-throughput sequencing, instrument, equipment

Availability: Restricted

Specification URL: https://raw.githubusercontent.com/SciCrunch/RRID-Instruments/main/PDF/SCR_017990.pdf

Resource Name: PacBio: Sequel II System

Resource ID: SCR_017990

Alternate URLs: <https://www.pacb.com/wp-content/uploads/Operations-Guide-Sequel-II-and-Sequel-Ile-Systems.pdf>

Old URLs: <https://www.pacb.com/products-and-services/sequel-system/latest-system-release/>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260815T182544+0000

Ratings and Alerts

No rating or validation information has been found for PacBio: Sequel II System.

No alerts have been found for PacBio: Sequel II System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 61 mentions in open access literature.

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

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. BMC biology, 24(1).

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus Acanthus Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. GigaScience, 15.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, Carthamus tinctorius L. GigaScience, 15.

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. Cancer research, 86(5), 1300.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. GigaScience, 15.

Chrysostomakis I, et al. (2025) A high-quality reference genome for the Ural Owl (Strix uralensis) enables investigations of cell cultures as a genomic resource for endangered species. GigaScience, 14.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, Protosalanx chinensis. GigaScience, 14.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. GigaScience, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. GigaScience, 14.

Guang X, et al. (2025) Telomere-to-telomere African wild rice (Oryza longistaminata) reference genome reveals segmental and structural variation. GigaScience, 14.

Qin H, et al. (2025) The complete genome assembly of *Astragalus membranaceus*: enabling more accurate genetic research. *GigaScience*, 14.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 231 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. *GigaScience*, 14.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Khan N, et al. (2025) Human Papillomavirus Integration Induces Oncogenic Host Gene Fusions in Oropharyngeal Cancers. *Cancer discovery*, 15(9), 1927.

Bai M, et al. (2024) The telomere-to-telomere (T2T) genome of *Peucedanum praeruptorum* Dunn provides insights into the genome evolution and coumarin biosynthesis. *GigaScience*, 13.