

Resource Summary Report

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PacBio: Sequel System

RRID:SCR_017989

Type: Tool

Proper Citation

PacBio: Sequel System (RRID:SCR_017989)

Resource Information

URL: <https://www.pacb.com/blog/introducing-the-sequel-system-the-scalable-platform-for-smrt-sequencing/>

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Description: Single Molecule, Real-Time sequencer by Pacific Biosciences. System provides higher throughput, more scalability, reduced footprint and lower sequencing project costs compared to PacBio RS II System, while maintaining benefits of SMRT technology. Ideal for projects such as generating high quality, whole genome de novo assemblies for larger genomes, such as human, plants, and animals. Provides characterization of wide variety of genomic variation types, including those in complex regions not accessible with short-read or synthetic long-range sequencing technologies, while simultaneously revealing epigenetic information.

Synonyms: PacBio Sequel™ System, Sequel System

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_017989.pdf

Resource Name: PacBio: Sequel System

Resource ID: SCR_017989

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

Record Creation Time: 20220129T080338+0000

Ratings and Alerts

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

No alerts have been found for PacBio: Sequel System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

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).

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

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.

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.

Herliana L, et al. (2023) A chromosome-level genome assembly of *Plantago ovata*. *Scientific reports*, 13(1), 1528.

Bernot JP, et al. (2022) Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle *Pollicipes pollicipes*. *GigaScience*, 11.

Mu X, et al. (2022) Identification of candidate sex-specific genomic regions in male and female Asian arowana genomes. *GigaScience*, 11.

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. *GigaScience*, 12.

Wang J, et al. (2022) Chromosome-level genome assembly of the Pacific geoduck *Panopea generosa* reveals major inter- and intrachromosomal rearrangements and substantial expansion of the copine gene family. *GigaScience*, 12.

Lu X, et al. (2022) A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. *GigaScience*, 11.

Palmada-Flores M, et al. (2022) A high-quality, long-read genome assembly of the endangered ring-tailed lemur (*Lemur catta*). *GigaScience*, 11.

Yang Y, et al. (2022) Chromosome-level genome assembly of the shuttles hopfish, *Periophthalmus modestus*. *GigaScience*, 11(1).

Liu P, et al. (2022) The assembled and annotated genome of the masked palm civet (*Paguma larvata*). *GigaScience*, 11.

He X, et al. (2022) The whole-genome assembly of an endangered Salicaceae species: *Chosenia arbutifolia* (Pall.) A. Skv. *GigaScience*, 11.

Saenko SV, et al. (2021) The draft genome sequence of the grove snail *Cepaea nemoralis*. *G3* (Bethesda, Md.), 11(2).

Li J, et al. (2021) A new duck genome reveals conserved and convergently evolved chromosome architectures of birds and mammals. *GigaScience*, 10(1).

Jin S, et al. (2021) A chromosome-level genome assembly of the oriental river prawn, *Macrobrachium nipponense*. *GigaScience*, 10(1).

Xu M, et al. (2021) Accurate haplotype-resolved assembly reveals the origin of structural variants for human trios. *Bioinformatics* (Oxford, England), 37(15), 2095.

Hilsdorf AWS, et al. (2021) Genome assembly and annotation of the tambaqui (*Colossoma macropomum*): an emblematic fish of the Amazon River Basin. *GigaByte* (Hong Kong, China), 2021, gigabyte29.

Sharma P, et al. (2021) Improvements in the sequencing and assembly of plant genomes. *GigaByte* (Hong Kong, China), 2021, gigabyte24.