

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 9, 2026

PacBio: RS II Sequencing System

RRID:SCR_017988

Type: Tool

Proper Citation

PacBio: RS II Sequencing System (RRID:SCR_017988)

Resource Information

URL: https://www.msscience.com.au/upload/pages/pacbio/pacbio_rs_ii_brochure.pdf

Proper Citation: PacBio: RS II Sequencing System (RRID:SCR_017988)

Description: Sequencer by Pacific Biosciences. System allows scientists to generate finished genome assemblies, reveal and understand epigenomes, and characterize genomic variation. It achieves longest read lengths and highest consensus accuracy. Finishes microbial genomes and improves assembly of larger organisms with multi-kilobase reads and unbiased coverage regardless of GC content. No amplification is required.

Synonyms: RS II System, RS II Sequencing System

Resource Type: instrument resource

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

Availability: Restricted

Resource Name: PacBio: RS II Sequencing System

Resource ID: SCR_017988

Alternate URLs:

https://www.msscience.com.au/upload/pages/pacbio/pacbio_rs_ii_brochure.pdf

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260808T190056+0000

Ratings and Alerts

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

No alerts have been found for PacBio: RS II Sequencing System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in *Mycobacterium tuberculosis* constitutively generates subpopulations with distinct clinical phenotypes. *iScience*, 29(5), 115045.

Torres MJ, et al. (2023) *Stenotrophomonas goyi* sp. nov., a novel bacterium associated with the alga *Chlamydomonas reinhardtii*. *F1000Research*, 12, 1373.

Yu S, et al. (2023) Resequencing of a Pekin duck breeding population provides insights into the genomic response to short-term artificial selection. *GigaScience*, 12.

Stephens TG, et al. (2022) High-quality genome assemblies from key Hawaiian coral species. *GigaScience*, 11.

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

Smolander OP, et al. (2022) Improved chromosome-level genome assembly of the Glanville fritillary butterfly (*Melitaea cinxia*) integrating Pacific Biosciences long reads and a high-density linkage map. *GigaScience*, 11(1).

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

Warr A, et al. (2020) An improved pig reference genome sequence to enable pig genetics and genomics research. *GigaScience*, 9(6).