

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

Sage Science: BluePippin system

RRID:SCR_020505

Type: Tool

Proper Citation

Sage Science: BluePippin system (RRID:SCR_020505)

Resource Information

URL: <https://sagescience.com/products/bluepippin/>

Proper Citation: Sage Science: BluePippin system (RRID:SCR_020505)

Description: Used for DNA Size Selection for Next-Gen Sequencing, with Pulsed-Field (100bp ? 50kb).BluePippin has the DNA capabilities of the Pippin Prep, plus the extra benefit of pulsed-field electrophoresis for resolving and collecting high molecular weight DNA. For long-range genomic applications, high-pass filtering allows users to collect all fragments above a size threshold set by the user. Target sizes or ranges of sizes are entered in software, and fractions are collected in buffer. Up to 5 samples/gel cassette may be run, with no possibility of cross contamination.

Resource Type: instrument resource

Keywords: Sage, Automated DNA Size Selector, Instrument Equipment, USEDit

Availability: Commercially available

Resource Name: Sage Science: BluePippin system

Resource ID: SCR_020505

Alternate IDs: Model_Number_BluePippin

Record Creation Time: 20220129T080350+0000

Record Last Update: 20260725T190928+0000

Ratings and Alerts

No rating or validation information has been found for Sage Science: BluePippin system.

No alerts have been found for Sage Science: BluePippin system.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

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

Akagi K, et al. (2023) Intratumoral Heterogeneity and Clonal Evolution Induced by HPV Integration. *Cancer discovery*, 13(4), 910.

Wang Z, et al. (2022) A chromosome-level reference genome of *Ensete glaucum* gives insight into diversity and chromosomal and repetitive sequence evolution in the Musaceae. *GigaScience*, 11.

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).