Element Biosciences

Specification Sheet

Element AVITI™ System

Unrivaled combination of cost, quality, and performance that fits any sequencing application at any scale

Highlights

- Flexibility at a lower cost
- Exceptional accuracy and data quality
- Scalability with a complete range of sequencing kits

Introduction

Next-generation sequencing (NGS) has revolutionized the field of genomics, empowering researchers to confront complex scientific questions with an evolving portfolio of technology and tools. Despite these innovations, the cost of benchtop sequencing has remained high, requiring factory-scale throughput to achieve any savings. A compromise on cost is often at the expense of quality and flexibility.

The Element AVITI System reimagines the core components of NGS to offer a benchtop platform that grants access to the genomics ecosystem (Figure 1). Delivering flexible throughput at exceptionally low cost, AVITI saves time and resources without the need to batch or accept lesser quality. Avidity base chemistry (ABC) forms the core of a disruptive design that readily adapts to any application, offering methods that scale from amplicon to whole genome, and from short-read to long.

Scalable experimental design

Whether an experiment requires 2 billion reads per run or 100 million, AVITI enables cost-effective, high-quality sequencing at any scale. Multiple sequencing kit configurations with read lengths of 2 x 75 to 2 x 300 and a full range from high-, medium-, and low-outputs calibrate genomic output without sacrificing cost-effectiveness, even at small scales (Table 1). The cost benefits are similar to a production-scale system without waiting to fill a flow cell or acquire a sufficiently large project.

An alternative to AVITI, the Element AVITI System LT runs both low- and medium-output sequencing kits to offer low-throughput and budget-friendly access to ABC. If future growth and expanded applications require a broader range of throughputs, labs can easily update the AVITI LT to a full-throughput AVITI.

Figure 1. AVITI dramatically reduces sequencing costs and turnaround times while elevating the benchmark for genomic data, all in a compact benchtop format that fits into a variety of spaces.

Novel ABC sequencing

The fundamentals of ABC technology leverage the unique properties of avidites to execute an efficient sequencing reaction and yield highly accurate data. A strong signal-to-noise ratio that persists through high polony densities drives this accuracy.

When a run starts, the library hybridizes to surface primers coating the flow cell. Amplification polymerase then binds to the library and primer duplexes, catalyzing rolling circle amplification (RCA) and generating long DNA strands that include copies of the original library (Figure 2). Each strand forms a polony that contains hundreds of copies of the original library. The polonies hybridize to read-specific sequencing primers.

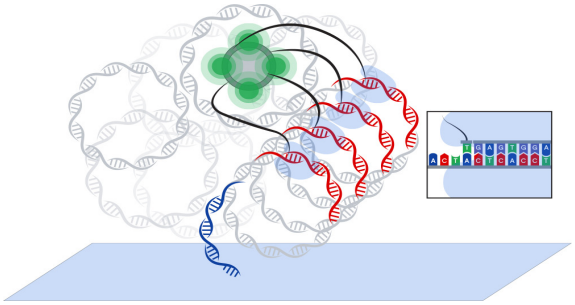

Figure 2. Polymerase binds avidites at the interrogation site. The avidite arms connect to a core that provides a fluorescent signal for detection.

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Kit Configuration	Read Length	Output (Gb)	Read Count[a]	Run Time (hours)[b]	Q30
High output	2 x 300	180	300 million	60	> 85%
	2 x 150	300	1 billion	38	> 90%
	2 x 75	150	1 billion	24	> 90%
Medium output	2 x 300	60	100 million	51	> 85%
	2 x 150	150	500 million	31	> 90%
	2 x 75	75	500 million	20	> 90%
Low output	2 x 150	75	250 million	27	> 90%

[a] Performance metrics, including read counts, are based on sequencing Element libraries. Actual results might differ based on factors, such as library type and preparation.
[b] Individually addressable lanes and other custom recipes can extend run times.

Table 1. AVITI performance metrics

For each cycle, a sequencing polymerase binds an avidite to a polony and primer duplex, and traps a base-specific avidite to the polony. The result forms an extremely tight complex that enables a 100-fold reduction in reagent concentration compared to sequencing-by-synthesis (SBS).[1]

AVITI and ABC reset expectations on quality scores (Q scores), delivering exceptional Q30 accuracy for 2 x 150 sequencing at > 90% and > 85% for 2 x 300 sequencing. AVITI demonstrated higher accuracy compared to legacy sequencing technology. Data showed fewer soft-clipped reads in difficult homopolymer and repeat regions, among other clear advantages.[2,3]

Amplification advantages

RCA uses only the original library as a template to avoid magnifying amplification errors. This method avoids incorporating free index primers into polonies and minimizes index hopping on the flow cell. Additionally, RCA delivers more usable reads due to a low rate of optical duplicates, less than 1 %.

Ordering information

Element AVITI System	880-00001
Element AVITI System LT	880-00003

Summary

AVITI reinvents surface chemistry and data analysis to offer a flexible and cost-effective sequencing platform with exceptional accuracy. Overarching compatibility with standard NGS libraries provides a path to in-house sequencing and accommodates a variety of NGS applications. Multiple kits and abundant software features promote adaptive run setup and analysis to satisfy a spectrum of experiments. AVITI supports your genomic needs.

System specifications

Instrument Configuration	Dual flow cells AVITI Operating Software Ubuntu Core 20.04 LTS operating system
Operating Environment	Temperature: 18°C to 26°C Elevation: < 2000 m Sound level: ≤ 62 db at 3.3 ft
Instrument Dimensions	(H x W x D) 29.5 in x 37.6 in x 28.5 in Weight: 155.1 kg/342 lb
Power Requirements	100–240 VAC at 50/60 Hz, 15 A. 550 W (average)

To learn more, visit elementbiosciences.com/products/aviti

References

1. Arslan, Sinan, Francisco J. Garcia, Minghao Guo, et al., "Sequencing by avidity enables high accuracy with low reagent consumption," Nature Biotechnology (May 2023): https://doi.org/10.1038/s41587-023-01750-7.
2. Semyon Kruglyak, "Measuring the Accuracy of Element AVITI Sequencing Data," Element Biosciences (blog), July 13, 2022, https://www.elementbiosciences.com/blog/measuring-accuracy-element-aviti-sequencing-data.
3. Carroll, Andrew, Alexy Kolesnikov, Daniel E. Cook, et al., "Accurate human genome analysis with Element Avidity sequencing," bioRxiv (August 2023): https://doi.org/10.1101/2023.08.11.553043.

Element Biosciences
Telephone: 619.353.0300
Email: info@elembio.com