

AXELIOS

Roche



Be 1 step ahead
with **AXELIOS 1**

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Be 1 step ahead with AXELIOS 1

It's time to join a new era in genomics

Powered by innovative sequencing by expansion (SBX) technology, AXELIOS 1 is the new next in NGS.

From rapid sequencing and near real-time data processing to flexibility and groundbreaking scalability – this game-changing platform is set to advance your science and genomic discovery.

Flexibility

Optimized workflows and longer read lengths for diverse use cases; explore beyond the limitations of short reads.*

Speed

Rapid sequencing and near real-time data processing reduce sequencing time-to-data from days to hours.

Scalability

Tunable sequencing output and batch sizes support seamless scalability, from pilot to production-scale projects.

Accuracy

Achieve the level of accuracy required for a wide range of methods and applications - all at a rapid pace.



Ready to sequence in hours not days?

The speed of both sequencing and data processing mean that you can access data in hours with AXELIOS 1.



1

Standardized instrumentation, consumables, and reagents

Although the sample and/or application may dictate which library prep reagents are used, synthesis and sequencing instrumentation, consumables, and reagents are universal across all applications.

Library preparation & QC

- Automated or manual
- ~2-13 h (method dependent)
- Amplification not required for all methods
- Pooling based on coverage requirements



2

Xpandomer synthesis

- 1-4 independent chips per run
- Xpandomer pools may be sequenced immediately or stored for sequencing at a later stage



3

Sequencing & analysis

- Tunable output and batch sizes (~ 15 min-4 h sequencing time)
- Up to four queued runs in ~ 22 h¹
- Sensor module reusable up to 20 times



Near real-time analysis, industry-standard file types

Near real-time on-instrument analysis produces industry-standard file types, including FASTQs and BAMs.

Combining flexible integrated analysis with powerful XOOS analysis tools, AXELIOS 1 delivers the speed and performance needed to turn high-throughput sequencing data into biological insights.

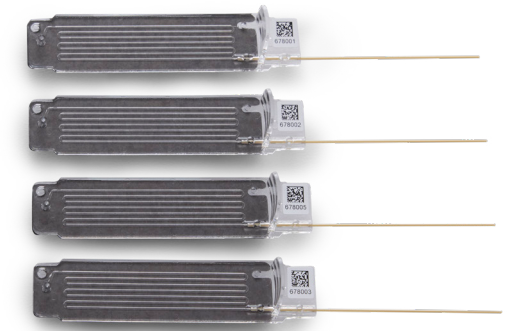
¹Maximum run time for sequencing instrument includes pre-sequencing setup, sequencing time and post-run cleanup.

Get set for the platform that's built for you

From the synthesis chip that supports synthesis of up to four library pools to the reusable sensor module – AXELIOS 1 has been built for you. Its flexibility means you can tailor your sequencing workflow to your needs.

The AXELIOS 1 Synthesis Chip

Transform DNA libraries into high-fidelity Xpandomer molecules through groundbreaking chemistry



- Convert DNA templates into easily measurable Xpandomers to overcome signal-to-noise limitations with the synthesis chip engineered for automated, precise solid-phase synthesis. This conversion ensures single-molecule accuracy without sacrificing speed
- Scale your output by processing up to four library pools in parallel
- Choose from optimized synthesis protocols to support a broad range of sequencing methods

The AXELIOS 1 Sensor Module

Enable rapid sequencing through the reusable sensor module that's at the heart of the platform



- The CMOS-based array is designed for accurate single-molecule sequencing at a staggering scale
- Leverages >8 million independent microwells to execute massively parallel, real-time signal detection, driving exceptional data rates and throughput
- Reusable for up to 20 individual sequencing runs within 90 days of first use. Stored directly on deck for smooth, multi-run convenience

Sequencing to suit your lab

With AXELIOS 1, the
synthesis and sequencing
processes are independent.

**This empowers you to create a
sequencing workflow that's flexible
and adaptable to meet changing needs:**

- Arrange queued Xpandomer pools in sequential order to prioritize time-sensitive samples
- For total workflow autonomy, Xpandomer pools can be sequenced individually or queued for automated, sequential processing on the sequencing instrument with no manual intervention
- Near real-time analysis dramatically reduces the time to data for multiple outputs – including raw reads, consensus reads, and mapped/aligned reads for SBX-D



Specifications for SBX-D germline WGS

Estimated throughput

Human genomes per 4-h run
(at 30x median deduplicated concordant
duplex base coverage)

~16

Tb per 4-h run (duplex)
(concordant duplex bases)

≥1.8

Maximum run time¹

AXELIOS 1 Synthesis Instrument

~ 4 h

AXELIOS 1 Sequencing Instrument

1 run:

~ 5.5 h¹

4 runs (queued):

~ 22 h¹

AXELIOS 1 SBX-D human germline WGS
demonstrated data and internal verification
testing data on file.

¹ Maximum run time for sequencing instrument
includes pre-sequencing setup, sequencing
time and post-run cleanup.

Take the first step together

Get set to join a new tomorrow
with AXELIOS 1.



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**1 community
starts here**