

AXELIOS 1 Platform for Next-Generation Sequencing

Explore the platform that's set to
transform sequencing



Flexibility

Optimized workflows and longer read lengths for diverse use cases; explore beyond the limitations of short reads.¹

Speed

Rapid sequencing and near real-time data processing reduces 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 desired for a wide range of methods and applications; all at a rapid pace.

Introduction

Next-generation sequencing (NGS) has become a universal technology for research in biology, medicine, agriculture, ecology, and biotechnology; enabling the identification, characterization, and quantification of DNA, RNA, epigenetic signatures, and proteins across time and cellular space. Despite incredible advances over the past couple of decades, ever-growing project sizes and increasingly challenging applications continue to demand more flexibility, shorter turnaround times, and greater throughput; all at the requisite accuracy.

The AXELIOS 1 Platform combines Roche's innovative sequencing-by-expansion (SBX) technology with ultra-high throughput nanopore-based sequencing and accelerated data analysis to enable accurate, real-time single-molecule sequencing. SBX addresses a fundamental resolution challenge of nanopore sequencing by converting nucleic acid templates to accurately measurable surrogate Xpandomer molecules.^{2,3} The platform (Figure 1) comprises separate instruments for Xpandomer synthesis and sequencing / analysis to allow for maximum operational flexibility and independent optimization of key processes.

Up to four Xpandomer pools may be synthesized in parallel and queued for sequencing, with one pool per run and up to four runs. Accelerated base calling, as well as FASTQ generation and reference-based alignment for SBX-Duplex sequencing (SBX-D) are performed on integrated compute, in near real time; thereby expediting access to high-accuracy data for downstream analysis. All aspects of the workflow—from synthesis through sequencing run planning, as well as user and data management—are orchestrated off instrument through the AXELIOS 1 Platform Manager Software, via an intuitive user interface.

The AXELIOS 1 Platform offers the appropriate level of accuracy for a wide variety of applications, all with fast turnaround times. Differentiating features include a single, universal platform adaptable to multiple use cases, a reusable sensor module, standardized consumables and reagents, and integrated, accelerated analysis steps—to seamlessly support a diverse range of sample types, read lengths, throughput, and batch sizes. Through this unique combination of flexibility, speed, scalability, and accuracy, the AXELIOS 1 Platform has the potential to redefine the NGS space and marks a new era in next-generation sequencing.



Figure 1. The AXELIOS 1 Platform for next-generation sequencing. The synthesis instrument offers the flexibility to synthesize one to four Xpandomer pools in parallel in up to 4 h, independently from sequencing. The sequencing instrument employs a reusable CMOS-based sensor module and standardized reagents, thereby enabling uninterrupted sequencing of up to four Xpandomer pools in 16 h of sequencing time (not including pre-sequencing setup and post-run clean up). The analysis module provides high-accuracy, near real-time primary / post-primary data analysis (base calling, as well as demultiplexing, intramolecular consensus, and reference-based alignment for SBX-D). The AXELIOS 1 Platform Manager Software provides an intuitive user interface for integrated, off-instrument management of users, synthesis and sequencing orders (runs), and data analysis. The platform supports a wide range of methods through flexible read lengths and tunable throughput (sequencing times and / or batch sizes).

1 platform, endless possibilities

While modern NGS platforms have evolved significantly to support expanding applications, operational compromises remain common. Scaling a lab from mid- to high-throughput capacity, or performing variable read-length applications typically requires maintaining a fragmented ecosystem of distinct sequencing platforms. Furthermore, cost-efficiency is heavily dependent on large batch sizes, and system flexibility depends on a complex inventory of specialized consumables and reagents. In contrast, the AXELIOS 1 Platform offers flexibility, speed, scalability, and accuracy in a single solution with standardized synthesis and sequencing consumables and reagents, and integrated, near real-time analysis (up to alignment for SBX-D).



Flexibility

- Designed for robust human whole genome sequencing (WGS) across diverse research applications including germline analysis, somatic mutation profiling (FFPE samples), liquid biopsy research (cfDNA samples), bulk and single-cell RNA-seq (gene expression, isoform detection), and multi-omic studies⁴
- Multiple research workflows for different needs; capable of generating longer reads of up to ~1500 bp (with a distribution from ~200 bp to ~1500 bp) under appropriate sample and library prep conditions
- Reusable sensor module supports up to 20 sequencing runs, performed individually or as uninterrupted, queued runs
- Accessible and customizable XOOS tools,⁵ optimized specifically for SBX data, to support a broad range of samples, variant types, and applications



Speed

- Ultra-fast nanopore sequencing without compromising accuracy
- Sequence up to sixteen human genomes in as little as 5.5 h, with the capability of scaling to 64 genomes in a day.
- Near real-time base calling—as well as demultiplexing, intramolecular consensus, and reference-based alignment (for SBX-D) in parallel with sequencing—expedites time-to-data for downstream analysis



Scalability

- Modular hardware comprising individually procurable instruments enable streamlined operations and reduce the capital expense to scale
- Variable batch sizes: pool 1 – 16 samples per run for human germline WGS at ~30x median deduplicated concordant duplex base coverage, or exploit higher multiplexing capabilities for other applications, depending on coverage requirements
- Maximize instrument utilization and scalability by processing 1 – 4 library pools simultaneously during Xpandomer synthesis, and queue up to four independent Xpandomer pools for sequential, automated sequencing runs
- Tunable sequencing times (~15 min to 4 h) allow users to calibrate run duration based on desired coverage depth and / or sample urgency



Accuracy

- Select the sequencing workflow tailored to the accuracy requirements of your application
- Average concordant duplex base accuracy of ~Q38⁴ for duplex (SBX-D) sequencing (e.g., human germline WGS)
- High accuracy across major variant classes, with robust SNV and indel F1 scores⁴



Review the three-step AXELIOS 1 workflow

The three-step AXELIOS 1 workflow is outlined in Figure 2. Library preparation protocols and reagents are sample- and / or method-specific, whereas the same instrumentation, consumables, and reagents are used for sequencing and synthesis across methods. Near real-time on-instrument analysis produces industry standard file formats to support compatibility with downstream analysis, including XOOS analysis tools (Figure 3). Workflow inputs, outputs, and processes are orchestrated via the AXELIOS 1 Platform Manager Software.

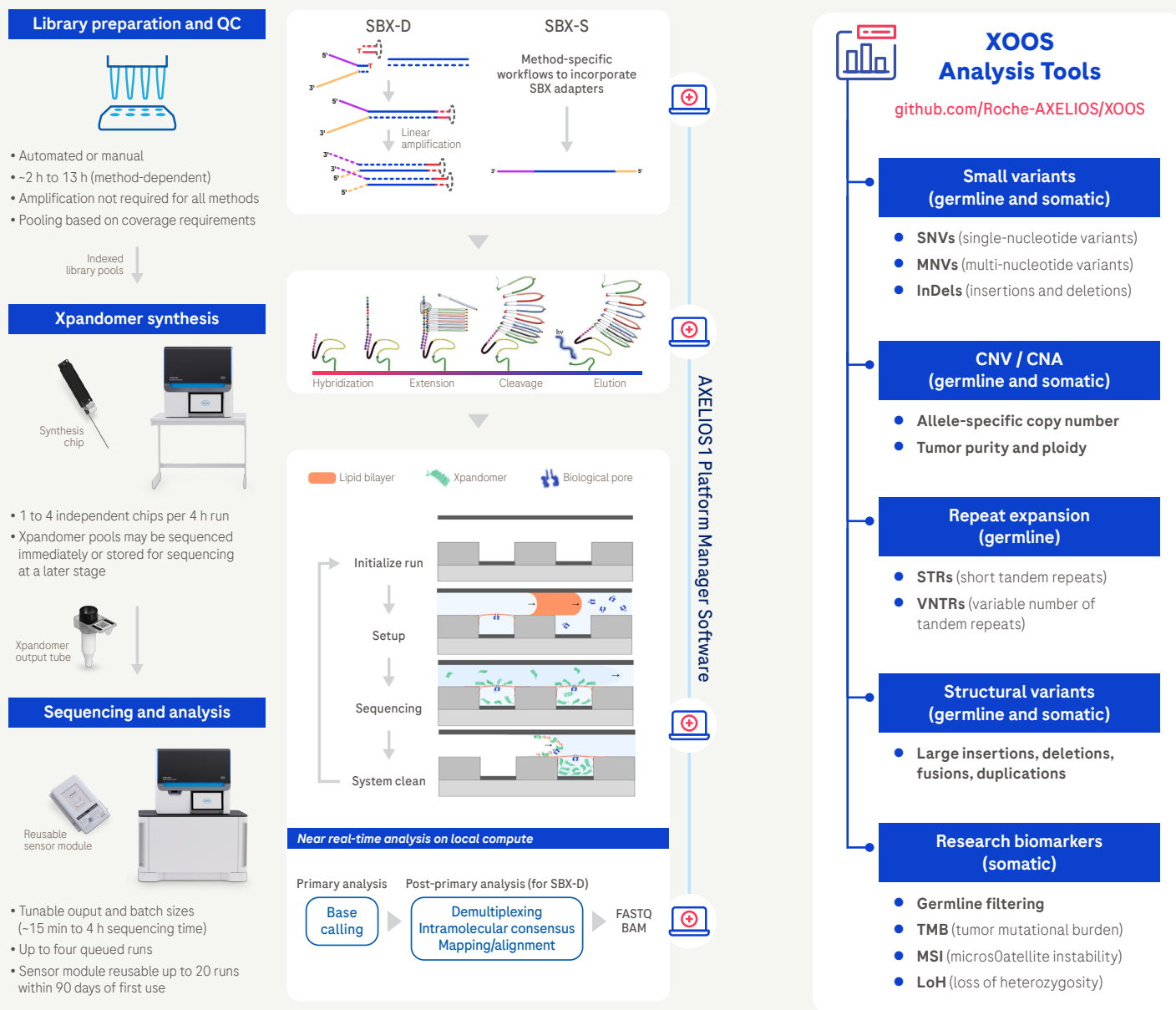


Figure 2. The AXELIOS 1 workflow. Library preparation may be performed manually or using qualified automated liquid handling systems. The library prep workflow depends on whether libraries are prepared for SBX-D or SBX-S sequencing and may include method-specific steps, such as amplification. Fully automated synthesis on the AXELIOS 1 Synthesis Instrument produces sequencing-ready pools of Xpandomer molecules, in output tubes that are the direct input into sequencing. The reusable CMOS sensor module may be used for up to 20 sequencing runs. Base calling on local compute is performed for all sequencing workflows, whereas post-primary analysis steps are currently only performed for SBX-D (e.g., human germline WGS). Synthesis, sequencing, and data analysis processes are described in more detail elsewhere.^{2,3}

Figure 3. Representative view of XOOS analysis tools for downstream analysis. Output files from on-instrument primary / post-primary analysis (final step in Figure 2) are compatible with standalone customizable XOOS software tools (specifically developed and optimized for SBX data), as well as with third-party analysis tools.⁴ Not all XOOS tools and / or features are available at this time.

Explore the flexibility designed to meet your needs

Three unique features of the AXELIOS 1 Platform enable advanced operational flexibility (Figure 4):

- **Independence of key processes and hardware.** Xpandomer pools may be generated completely independently from sequencing.
- **Tunable output and batch sizes.** Xpandomer pools are configured to meet coverage needs and / or urgency, and sequencing times may be adjusted accordingly. With near real-time on-instrument analysis, data is analyzed as and where it is generated; thereby significantly reducing turnaround time.
- **Reusable sensor module.** Fully automated sequencing runs, orchestrated via the AXELIOS 1 Platform Manager Software, may be initiated as and when needed, or queued to execute during off hours.

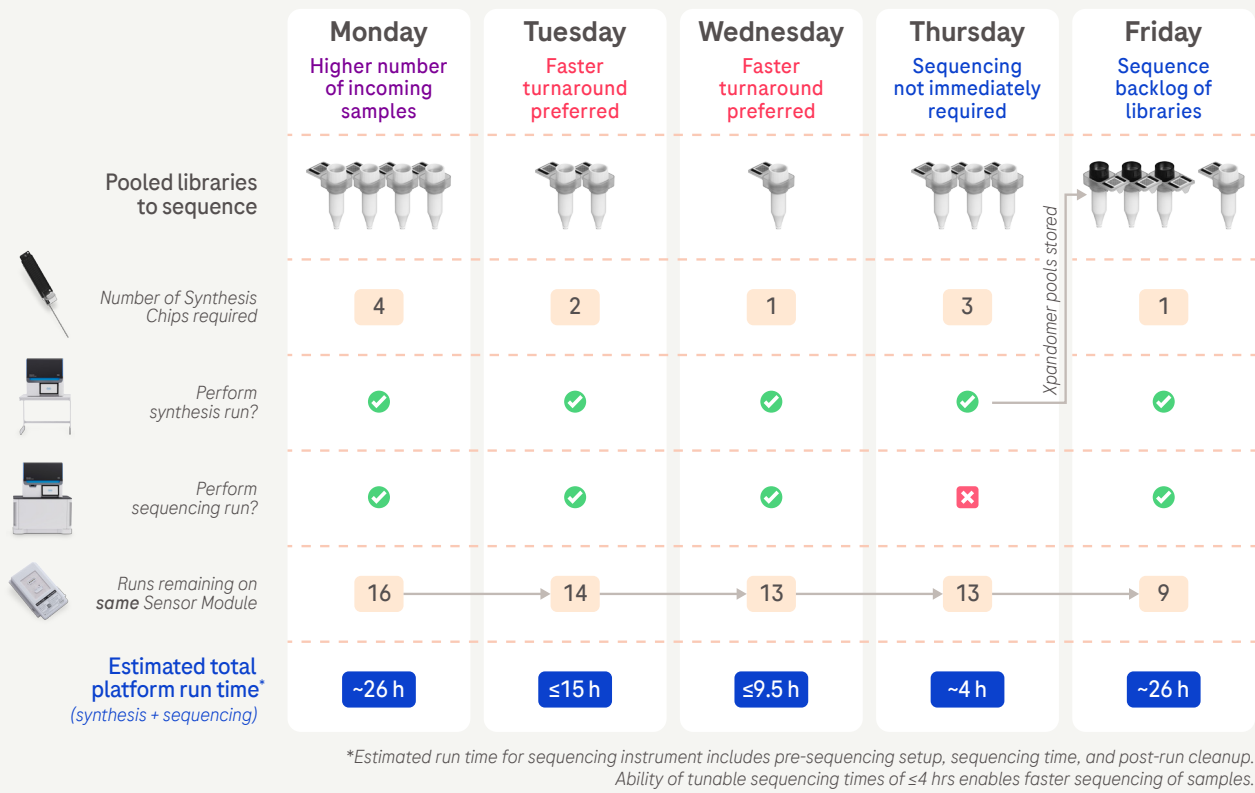


Figure 4. Flexibility in run formats reduces need for batching. Example of how a week may be structured based on sample intake and the ability to perform synthesis and sequencing independently (with variable batch sizes) on the AXELIOS 1 Platform. To illustrate how sample volume impacts daily operations, consider a hypothetical weekly workflow. On a typical Monday, the lab might face a surge of samples requiring same-day sequencing. In contrast, priority samples received on Tuesday and Wednesday may require less than a full 5.5 h run. By Thursday, the lab may choose to defer sequencing entirely—storing the Xpandomers safely overnight to batch them with Friday’s incoming samples for a single, maximized run. Synthesis may be performed earlier or later in the day, depending on when library pools are available for sequencing. Priority samples or those requiring lower data output may be processed shortly after synthesis with fast sequencing times, whereas standard samples may be queued for overnight sequencing. Downstream analysis of sample data may be initiated as soon as a sequencing run is completed and data transferred.



SBX-D specifications and estimated throughput⁴

Category	Metric	Value
Performance ^a	SBX-duplex (SBX-D) output (concordant duplex bases per 4 h run)	≥1.8 Tb
	Mean insert length ^b	~230 to 260 bp
	Sequencing time ^c	~15 min to 4 h
	Accuracy ^e (concordant duplex bases)	~Q38
Maximum run time ^d	AXELIOS 1 Synthesis Instrument	~4 h
	AXELIOS 1 Sequencing Instrument	1 run: ~5.5 h
	AXELIOS 1 Sequencing Instrument	4 runs (queued): ~22 h
Throughput	Human genomes per 4 h run (at 30x median deduplicated concordant duplex base coverage)	~16

^a Performance metrics, such as output, mean read length, quality score, etc., can vary based on sample type and quality, library prep conditions, and loading concentration, along with other experimental conditions

^b Includes post-consensus adapter-trimmed full-length and partial duplex reads

^c Sequencing time does not include pre-sequencing setup or post-run cleanup

^d Maximum run time for sequencing instrument includes pre-sequencing setup, sequencing time, and post-run cleanup

^e Based on empirical accuracy calculated using BWA aligned bam files for high-confidence regions of Genome in a Bottle (GIAB) samples



Technical specifications

AXELIOS 1 Synthesis Instrument

Feature	Specification
Dimensions	Width: 780 mm (31 in)
	Height: • 810 mm (32 in) – hood closed • 1250 mm (49 in) – hood open
	Depth: 675 mm (27 in)
Weight	108 kg (238 lb)
Electrical requirements	100 – 120 V AC, 50 / 60 Hz, 15 A (US) 220 – 240 V AC, 50 / 60 Hz, 16 A (EU)
Network requirements	1 Gbps
Operating system	Roche Linux (RLX) – Roche build of Debian

AXELIOS 1 Sequencing Instrument

Feature	Specification
Dimensions	Width: 1380 mm (55 in)
	Height: • 1644 mm (65 in) – hood closed • 2084 mm (82 in) – hood open
	Depth: 760 mm (30 in)
Weight	438 kg (966 lb)
Electrical requirements	2 x 200 – 240 V AC, 50 / 60 Hz, 30 A (US) 2 x 200 – 240 V AC, 50 / 60 Hz, 32 A (EU)
Network requirements	2 x 10 Gbps (recommended dedicated connection)
Operating system	Roche Linux (RLX) – Roche build of Debian

How to order AXELIOS 1

Instruments

Item	Description	Material ID
AXELIOS 1 Synthesis Instrument	AXELIOS 1 Synthesis Instrument	9905502001
AXELIOS 1 Sequencing Instrument	AXELIOS 1 Sequencing Module	9905529001
	AXELIOS 1 Analysis Module	10468360001

Reagents, consumables, and accessories

Description	Material ID
AXELIOS 1 Synthesis Chip (4-pack)	10112387001
AXELIOS 1 Synthesis Reagent Kit (Box 1 of 2)	10765879001
AXELIOS 1 Synthesis Reagent Kit (Box 2 of 2)	10084278001
AXELIOS 1 Synthesis System Kit	10178469001
AXELIOS 1 Sequencing Kit (Box 1 of 2)	10095954001
AXELIOS 1 Sequencing Kit (Box 2 of 2)	10753781001
AXELIOS 1 Sequencing System Kit	10178477001
AXELIOS 1 Sensor Module	10112450001
AXELIOS 1 Hairpin Adapters (96 HPSIDs)	10756853001
AXELIOS 1 Universal Y-Adapter (96 rxn)	10749725001
AXELIOS 1 Core Library Prep Kit (24 rxn)	10605359001
AXELIOS 1 Library Amplification Kit (24 rxn)	10605367001
AXELIOS 1 Library Quantification Kit (96 rxn)	10605375001
AXELIOS 1 SBX-D Control Kit	10778237001
AXELIOS 1 Adapter Exhaust Duct	10668725001
Analysis Module Power Cable Set US / JPN	10864389001
Analysis Module Power Cable Set INTL	10864397001



1 partnership, ongoing support

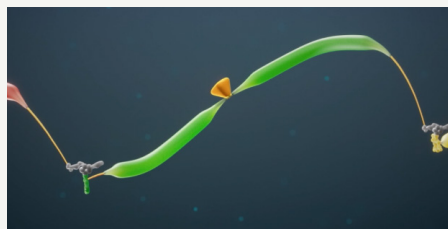
The Roche Diagnostics Support Network is dedicated to ensuring customer success through end-to-end support, aiming to minimize workflow interruptions and improve efficiencies. The Network strives to create and deliver exceptional customer experience through innovative support tools and empowering engagement. Our service spans the entire length of the sales cycle and beyond, ensuring ongoing success with Roche equipment over the life of the partnership.

- **Customer satisfaction:** Roche support has earned a customer satisfaction score (CSAT) of 93% and net promoter score (NPS) of +74.⁷
- **Global footprint:** The Roche Support Network comprises more than 8300 personnel across multiple teams who are committed to supporting customer success. As of 2024, Roche support teams have served more than 670 000 customers, conducted ~800 000 customer visits, supported over 380 000 instruments, and answered >2.8 million customer support calls.⁸
- **Sequencing knowledge:** Roche Diagnostics has established dedicated sequencing-specific support roles, including Field Application Scientists (FASs), Field Service Engineers (FSEs), and bioinformatics specialists with extensive backgrounds in sequencing technologies.

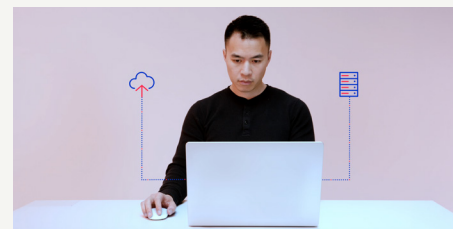
Resources



AXELIOS 1 Solution



SBX technology



Data analysis

Be 1 step ahead with AXELIOS 1

References and disclaimers

1. The technology is capable of generating longer reads of up to ~1500 bp (with a distribution from ~200 bp to ~1500 bp) under appropriate sample and library prep conditions.
 2. Kokoris M, et al. Sequencing by Expansion (SBX) – a novel, high-throughput single-molecule sequencing technology [Preprint]. bioRxiv. 2025 Feb 19. doi: [10.1101/2025.02.19.639056](https://doi.org/10.1101/2025.02.19.639056).
 3. F. Hoffman-La Roche Ltd. Sequencing by expansion (SBX): a fast, flexible, and accurate single-molecule sequencing technology [White paper; cited 2026 June 1]. Available from <https://diagnostics.roche.com/us/en/landing-pages/sequencing-by-expansion-sbx-white-paper.html>.
 4. AXELIOS 1 SBX-D Human Germline WGS demonstrated data and internal verification testing data on file.
 5. Available from github.com/Roche-AXELIOS/XOOS.
 6. Optimization may be needed to obtain desired performance.
 7. Roche Diagnostics Marketing, Commercial & Insights. Results from 35 000+ customer surveys conducted in 2024.
 8. Roche Diagnostics Global Service CRM (REXIS), 2024 operational data.
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