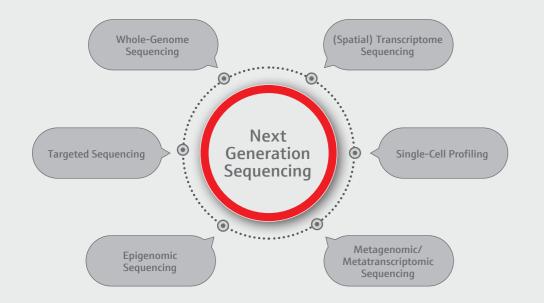
Trust in Your NGS Library Preparation

Next Generation Sequencing (NGS) technologies have revolutionized the field of genomics by performing massive parallel sequencing of millions of DNA fragments.

This powerful technology has paved the way for breakthroughs in several areas of biology, including genomics, personalized medicine and evolutionary biology. NGS enables to study whole genomes or transcriptomes, identify sequence variants or even single cells and to uncover new insights into the structure, function, and variation of genomes.

A critical step for successful NGS results is the sequencing library preparation, which generates a pool of sequencing

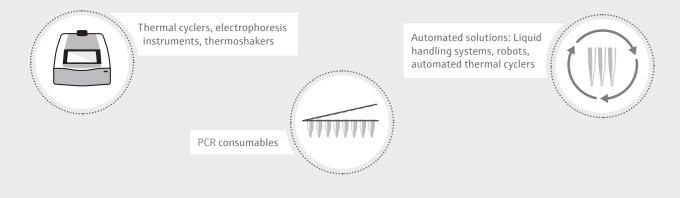
fragments from RNA or DNA samples in a format suitable for sequencing. The quality of the library preparation directly impacts the downstream analysis and interpretation of NGS data. By carefully constructing sequencing libraries, researchers can maximize the yield of usable sequencing data, minimize technical biases or artifacts that can occur during the sequencing process and increase sequencing coverage for vulnerable sample material.



NGS Library Preparation: From Sample to Library

DNA library preparation involves a series of steps with enzymatic incubations, including DNA/RNA fragmentation, cDNA synthesis, adapter ligation, and amplification. Also, additional control measures for fragment size validation and library quantification are part of the workflow.

With Analytik Jena instruments, you can be sure to create DNA libraries that fully meet the demands of your desired sequencing technology.



Learn More

Discover your Next Generation Sequencing Library Preparation solutions: From manual workflows to modular automation, achieving excellence for all throughputs. We recommend the following products from our portfolio.



** z = Different sizes

Headquarter

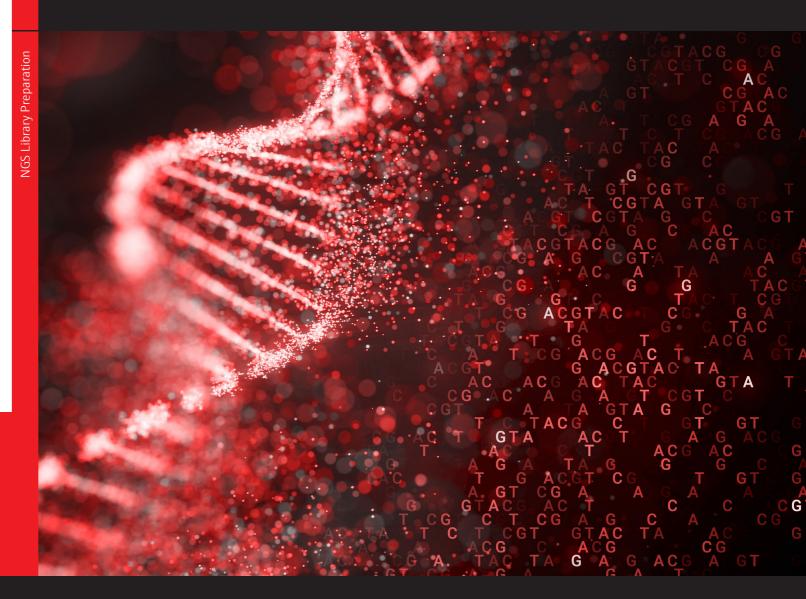
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Pictures: Analytik Jena GmbH+Co. KG

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Subjects to changes in design and scope of delivery as well as further technical development.

The Foundation for Your Next Generation Sequencing







Enhance Your Library Preparation Process

Why should you rely on Analytik Jena instruments?

Minimized bias made possible by:

- Reduced risk of non-specific amplifications
- No temperature over- and undershoots
- **Optimal yield** made possible by:
- Ensured enzyme activity
- Excluded cross contamination
- Reproducibility made possible by:
- Temperature homogeneity across the whole block



Levarage from PCR expertise for your automated workflow

- With excellent performance for reliable results
- Accurate temperature control
- Space-saving and robust design
- With advanced software designed for automation



Choose your PCR thermal cycler according to your needs

- Biometra TAdvanced for premium performance
- Biometra TRIO for varying applications and throughputs
- Biometra TRobot II: space-saving & robust for optimal automated PCR

... and benefit from

- Consistently high library quality
- Reproducible results across the whole block
- No temperature over- and undershoots to ensure enzyme activity and specific products
- No cross-contamination by reproducible lid pressure
- Compatibility with all common PCR consumables
- High volume capacity with flexible 96 and 384 block format





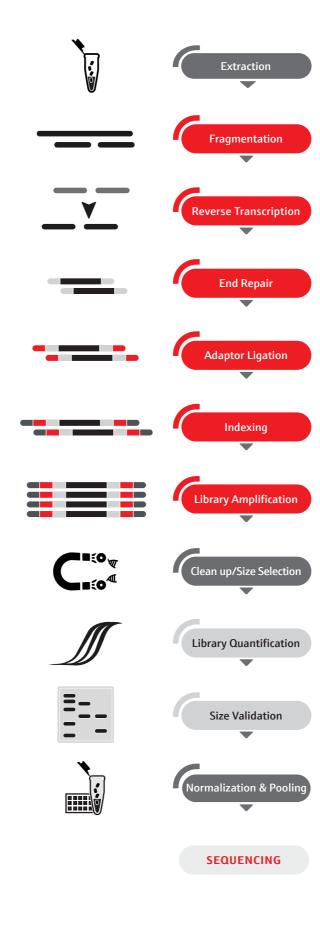


Intuitive software & reliable service

Seamless thermal cycler management & confidence in performance

- Comfortable remote control and online monitoring with the intuitive Biometra TSuite software
- Verified thermal cycler performance with Biometra TMS calibration service

Typical Steps of NGS Library Preparation



Nucleic acid isolation from sample material

Cleaving of DNA or RNA into smaller pieces (< 500 bp) required for short read sequencing

Reverse transcription of sample RNA

Creating blunt ended fragments for library construction

Attachment of binding site for sequencing primers and indexes

Binding of unique index primer to discriminate between samples during sequencing

Amplification of libraries by PCR to increase library yield

Purification of libraries and size selection of fragments

Quantification of the libraries using qPCR

Verification of library integrity and fragment sizes by agarose gel electrophoresis

Standardization for equal and optimal library concentration

Want to Automate Your Workflow?

Elevate your NGS library preparation with automation for efficient, precise pipetting to ensure a seamless, error-free workflow.

Rely on proven liquid handling technology Save valuable space with the modular benchtop pipetting robot CyBio FeliX Expand your personal automation solution any time by connecting automated thermal cyclers and CyBio FeliX via the versatile benchtop robot CyBio Carry CyBio Carry CyBio FeliX

Pipetting robot CyBio FeliX seamlessly manages bead-based procedures like **extraction**, **size selection**, and **clean-up**, while also excelling in normalization, pooling, and **(q)PCR setups**.

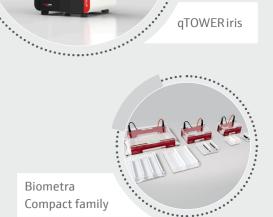
Ensure Library Quality

The determination of library concentrations, fragment size and integrity are essential QC parameters for any NGS sequencing library to ensure precise and adequate input for the sequencing process.

Quantify libraries easy and accurate with our high-precision real-time thermal cyclers

- Highly sensitive detection across a broad range of library concentrations
- Flexible throughput of up to 384 reactions
- Compatibility with all common PCR consumables
- Enhance throughput with qTOWER³ auto: Truly fully automated design for integration into robotic systems





Validate fragment sizes with our gel electrophoresis systems

- Fast and leak-proof gel casting with Biometra Compact Series
- Durable for convenient everyday use
- Wide range of options for different sample throughputs

NEW