Fraunhofer IGB

Fraunhofer Institute for Interfacial Engineering and Biotechnology IGB

Next-Generation Sequencing

From wet lab to dry lab – complete sample analysis

www.igb.fraunhofer.de/en/ngs

Progress in science depends on new techniques, new discoveries and new ideas, probably in that order.«

Sydney Brenner

Sequencing technologies – the next generation

The rapid development of high-throughput sequencing technologies (next-generation sequencing, NGS) are reducing costs while increasing capacity. This has opened up completely new dimensions in nucleic acid analytics and revolutionized countless areas of life sciences research. These new technologies are now making it possible to sequence several hundred million fragments simultaneously, not just isolated fragments as in the past.

At the Fraunhofer Institute for Interfacial Engineering and Biotechnology IGB, we use NGS technologies to focus on a wide range of scientific and application-oriented challenges. Projects cover, for example, de-novo sequencing of industrially or medically relevant bacterial and fungal strains, analyses of transcription profiles, identification of relevant genes – e.g., for an early diagnosis of tumor diseases –, and screening for diagnostic biomarkers.

From wet lab to dry lab

NGS competences for a complete analysis

We are pleased to provide you with a one-stop shop, covering the complete workflow from sample preparation to sequencing and bioinformatics. We are happy to help you with a specific question in the short term or stand by your side as a reliable partner for a long-term project. The combination of state-of-the-art equipment (Illumina NextSeq2000, Illumina MiniSeq, Oxford Nanopore MinION, QIAcube, Biomek FX etc.) with our long-standing expertise in the field of NGS gives you access to a large variety of protocols and analyses to meet your individual needs.

Sequencing with Illumina NextSeq 2000

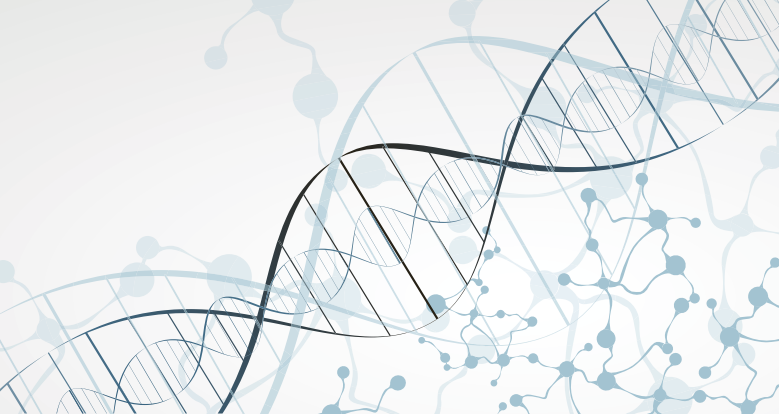
	Max. read length	Reads / flow cell
High output run mode	2 × 150 bases	1,1 bn
Rapid run mode	2 × 150 bases	400 mio

Sample preparation

- DNA/RNA extraction established for various materials
  - Fungi and bacteria from pure cultures or directly from their biocenosis
  - Animal and plant tissues (incl. FFPE)
  - Blood, stool and environmental samples

- Comprehensive repertoire of specific protocols available
  - DNA-Seq: whole genome shotgun (WGS), 16S amplicons, enrichments
  - RNA-Seq: polyA+, small RNA, ncRNA, strand specificity, rRNA- and/or globin-depletions
  - Automation on Biomek FXP

Capacity / flow cell	Advantages
330 gb	Universally applicable, high throughput
120 gb	Rapid data delivery time



Bioinformatic analysis

- De-novo genome assemblies
- Gene annotation based on in-silico predictions or on RNA-Seq data
- Reference mapping and variance calling
- Differential gene expression analyses
- Metagenome and metatranscriptome analyses
- Biomarker screening

Apart from previously established standard protocols and analyses, we also pursue individual solutions to achieve the best results possible. If you want to use our sequencing capacities exclusively, you can also send us your ready-to-load DNA libraries. We sequence these with the desired coverage and immediately deliver the raw data. All sample preparation steps and sequencing runs are validated and will be carried out according to strict SOPs. Processing times vary between two and eight weeks, depending on the project content.

Projects tailored to your individual needs

We are well equipped to answer any of your questions, please contact us at any time by e-mail or telephone. Based on our considerable experience, we believe that the best results are achieved by joint planning of the project. Therefore, our scientists coordinate the projects in close communication with you and assist you throughout the whole project phase – from initial quality assessment of starting material to delivery of the final report. We look forward to supporting you.

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