SEQme – Your partner in Next-Generation Sequencing Services

At SEQme we pride ourselves on providing full solutions in Next-Generation Sequencing (NGS). Our portfolio of services covers all steps of NGS workflow starting from project design and consulting, through DNA/RNA library preparation and sequencing using all major instrument platforms, to standard or customized data analysis pipelines. In addition, we also offer various optimized NGS services such as fast exome sequencing pipeline, targeted sequencing of preselected genes, metagenome analysis or shared NGS runs (ShareSeq). Last but not least, you can join our regular courses or workshops.

A dedicated team of professionals in experiment design and planning, laboratory processes as well as in data analysis pipeline development and execution is able to provide not only services mentioned but also expert consultancy on all steps of the workflow, experiment optimization recommendations, or problem solving suggestions.

When participating at our courses you – as a beginner in the field – gain an overall picture of Next-Generation Sequencing and have the opportunity of directly interacting with our team members, including lab specialists. Should you already be familiar with NGS you can still benefit when joining our data analysis workshops from brushing up your bioinformatics skills or getting a second opinion on procedures and pipelines you have previously mastered in this blossoming field.

As you can see, you can either work with us or learn from us to achieve your scientific, diagnostic or other goals. In any case, when thinking about NGS, rely on us.

Next-Generation Sequencing is a complex and sometimes lengthy process where success of every single step taken inevitably depends on properly performing all preceding steps. Long-term interactions between you as a goal-seeking scientist or physician and us as methodology-focused specialists may lead and in many times has already led to successful method development and optimization where both partners benefit equally.

Give it a try and let us offer our Next-Generation Sequencing services to you for the first time or become our loyal customer and partner to profit most from the long-term cooperation.

Your SEQme team
SEQme - Your partner in DNA sequencing and Real-Time PCR

There are no good or bad, cheap or expensive NGS technologies or platforms, Just as nature is diverse, so are the Next-Generation

Next-Generation Sequencing fleet at SEQme enables

**NovaSeq 6000 (Illumina)**
- Highest sequencing chip capacity
- Single end/Paired end reads, up to 250 bases
- Time to results 4 weeks
- Lowest price per megabase

**Project examples:**
Differential expression analysis; De-novo genome sequencing; Whole genome resequencing of a human genome, etc.

**MiSeq (Illumina)**
- Single end / Paired end reads
- Up to 300 bases
- Output up to 25 million reads per chip
- Time to results 2 weeks
- Target platform for metagenomic studies

**Project examples:**
De-novo sequencing and assembly of approx. 100 Mb genome; Sequencing of amplicons up to 500 bases in length, etc.

**Sequel (Pacific Biosciences)**
- Average read length approx. 12 kb
  - 400,000 reads per chip
  - Longest reads – up to 60 kb, approximate output 8 Gb
  - Circular consensus sequence (CCS) accuracy >99.999%

**Project examples:**
De-novo sequencing and assembly of smaller genomes (< 10 Mb); Long amplicon sequencing, etc.
there are only those more or less appropriate for the task in your mind. Sequencing experiments people conduct to study it.

you achieve your goals without compromise.

MinION / GridION (Oxford Nanopore)
- Amplification-free sequencing
- Longest reads – up to 200 kb
- Output up to 1,5 million reads / 20 Gb per chip
- Read accuracy approx. 95%
- Time to results 4 weeks

Project examples:
De-novo sequencing and assembly, resequencing, etc.

ShareSeq
- Shared Sequencing using Illumina technology
- Single end 100 b, paired end 150 and 250 b
- Customer-defined sequencing capacity, booked in million reads
- Basic data analysis services included
- The lowest cost NGS you can dream about!

Project examples:
De-novo assembly of small genomes; Amplicon mixture resequencing, etc.

Chromium Controller (10x Genomics)
- System for preparation of sequencing libraries
- All fragments originating from one particular molecule (up to 50 kb) have the same barcode, which makes it possible to identify their origin
- Barcoding of up to 750,000 molecules, capable of barcoding every unique polyA RNA molecule originating from a single cell
- Feel free to discuss your projects now!

Project examples:
Perhaps your project can be mentioned here next time…
Standard Data Analysis Services at SEQme

Data analysis forms an inherent part of our Next-Generation Sequencing services. Skilled bioinformaticians discuss your scientific objectives with you and analyze your data regardless of whether these were obtained in our Next-Generation Sequencing lab or not. All data analysis pipelines can also be tailored to your needs as well as to the output of a pilot analysis we may run on your dataset.

Feel free to inquire about our data analysis services. Examples include:

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Custom Data Analysis Services at SEQme

We know that requirements of each NGS project regarding data analysis may be different and not always are the outcomes of standard data analysis pipelines we do offer sufficient. Therefore, we also offer a project-oriented custom data analysis service. Whether you do not have enough experience in certain areas of data analysis or look for a special bioinformatics pipeline helping to solve your scientific questions we offer our experience and knowledge. Our bioinformaticians can help you with any type of data analysis.
Metagenome genotyping

Next-Generation Sequencing is a very efficient tool when analyzing species in a given environment, commonly referred to as metagenome analysis. NGS has become the approach of choice due to its ability to identify all species in tested samples and is based on sequencing of pre-amplified hypervariable regions (such as 16S, 18S or ITS), traditionally used for species identification, and comparing thus obtained sequences with reference databases.

We apply a well-balanced sequencing strategy in order to achieve desired results.

We recommend and perform:

- Amplicon generation for 1-192 samples, pooling
- 250 b paired-end read sequencing with output >20K reads/sample, demultiplexing, analysis report.
  Optional advanced data analysis services available on request
- For selected primer sets this service is available starting from a single sample
- Time to results: less than 4 weeks

...and you can choose from:

SO-024 - Metagenome analysis, up to 24 samples
Includes Sample QC, Amplicon generation for up to 24 samples using a single primer set, double indexing, library prep + QC, 1x 250 b paired-end sequencing, demultiplexing

SO-048 - Metagenome analysis, up to 48 samples
Includes Sample QC, Amplicon generation for up to 48 samples using a single primer set, double indexing, library prep + QC, 1x 250 b paired-end sequencing, demultiplexing

SO-096 - Metagenome analysis, up to 96 samples
Includes Sample QC, Amplicon generation for up to 96 samples using a single primer set, double indexing, library prep + QC, 1x 250 b paired-end sequencing, demultiplexing

SO-192 - Metagenome analysis, up to 192 samples
Includes Sample QC, Amplicon generation for up to 192 samples using a single primer set, double indexing, library prep + QC, 1x 250 b paired-end sequencing, demultiplexing
We strive to spread our knowledge and advice on the benefits of Next-Generation Sequencing technologies

Next-Generation Sequencing Courses and Workshops at SEQme

We encourage collaboration and the open exploration of ideas. We therefore share our know-how with participants of our courses and workshops focused on mastering laboratory processes and optimizing data analysis pipelines.

All our events are built to meet the needs of beginners as well as advanced laboratory personnel or data analysts using both open-source or commercially available bioinformatical tools.

Starting from…

Next-Generation Sequencing Courses for Beginners, 1 – 2 days

where you will gain a comprehensive resume of NGS technologies and applications, learn not always straightforward experiment planning, understand library preparation and basics of data analysis…

… and going through…

Hands-on Next-generation Sequencing Workshops, 3 – 5 days

guided by our experts you will perform some part of the NGS workflow yourself.

By the way, do not miss the Next-Generation Sequencing data analysis school, organized every year in Prague, where you will spend several fruitful days analyzing NGS data using Linux operating system.

… you can find all our events and their respective dates at www.seqme.eu/courses

Custom Next-Generation Sequencing Courses and Workshops

If your requirements and our portfolio of courses do not match, feel free to get in touch with us and we can tailor the agenda of NGS training to your needs and run it for your group, lab, or department.

All our courses and workshops can be tailored to your needs and organized in your facility!
Workshops and Courses Since 2012
There is nothing more rewarding than a satisfied customer inquiring about our services again...

Testimonials

**Conny L.**, University of Copenhagen, Denmark
*It is an excellent course and I can highly recommend it. You get exactly what you are promised: a theoretical overview of Next-Generation Sequencing. The teachers are experienced and have much knowledge of the topics.*

**Mária Š.**, Institute of Botany, Prague, Czech Republic
*At the planning stage, we have always been presented with a detailed proposal and possible alternatives. SEQme application specialist has a deep knowledge of NGS methodologies and is able to prepare a very efficient and cost-effective sequencing plan, which is not common with company representatives. We have always found affordable but, more importantly, the correct way to carry out our methodically very diverse experiments.*

**Konstantinos P.**, Agricultural University of Athens, Greece
*Microbiome and Metagenome Data analysis workshop is one of the best courses I have attended. Well organized curriculum and excellent instructors.*

**Inga M.**, Department of Zoology, Swedish Museum of Natural History
*Thanks for the great support so far already, this is really an asset.*

You know what you want. We know how to do it.