

NEXT GENERATION SEQUENCING

WHAT WE DO

Sequence them all!

All organisms rely on nucleic acid molecules (DNA or RNA) as medium for short and long-term storage of genomic information. This feature explains the fast adoption of Next Generation Sequencing (NGS) as a standard technology across all basic and applied research areas of biology. The VBCF NGS facility has helped to unravel genomes and transcriptomes from a multitude of model and non-model organisms over the past seven years. Wasps and Lipizzaner horses (for scientists of the University of Vienna and Veterinary University of Vienna), axolotl and zebrafish (Institute of Molecular Pathology), mouse and human (Institute for Molecular Biotechnology), widespread and exotic plants (Gregor Mendel Institute), depict a few examples.

Genomics' most versatile tool

With more than 150 protocols available, Next Generation Sequencing enables not only analysis of genomes and transcriptomes but allows capturing of any nucleic acid molecule of interest (mRNA, circular RNA, mitochondrial DNA, nascent RNA, etc.) as well as interactions between them (Protein-DNA, DNA-RNA, Protein-RNA, etc.).

This unrivalled flexibility is currently applied by more than 100 scientists from the Vienna BioCenter campus to shed light into the complex network of molecular architecture, trafficking and cellular signalling cascades. Meinrad Busslinger, senior scientist at the Institute of Molecular Pathology, has been one of the earliest adopters of NGS in our campus. In a very productive collaboration, he has employed a series of sequencing protocols with substantial and crucial help of the VBCF NGS facility, leading to a refined understanding of B- and T-cell activities described in over twenty publications in high ranked scientific journals.

SERVICES AND METHODOLOGIES

The goal of the Next Generation Sequencing Core Facility is to provide cutting edge next generation DNA sequencing technology to its users. Next Generation Sequencing has become a key analysis method for a large number of biological research areas. The capacity to expand analysis from more or less defined genomic regions to genome wide studies has boosted the pace of research discovery and enabled researchers to obtain a global view on biological processes.



Loading a cBot clustering system



Starting a run on an Illumina HiSeq 2500 sequencer



PacBio Sequel sequencer

OUR SERVICES IN 2019:

- Selected library preparation protocols including single cell techniques
- Sequencing on Illumina sequencing platforms
- Sequencing on PacBio Sequel system
- Nanopore Sequencing
- Standardized bioinformatic analyses

WE PROVIDE

- Expertise and advice on project strategy and analysis
- Access to state-of-the-art technology
- High quality and cost-effective services

EQUIPMENT

The VBCF NGS unit is committed to offer its users the best suitable equipment to meet their sequencing needs. Currently we apply different platforms covering a broad range of throughput, read length, flexibility and scalability options:

- Illumina NovaSeq
- Illumina HiSeq 2500
- Illumina NextSeq
- Illumina MiSeq
- Illumina iSeq
- PacBio Sequel
- ONT MinION



VBCF NGS Team

CONTACT AND LOCATION

**Next Generation Sequencing
Vienna BioCenter Core Facilities (VBCF)**

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<https://www.viennabiocenter.org/facilities/next-generation-sequencing/>
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