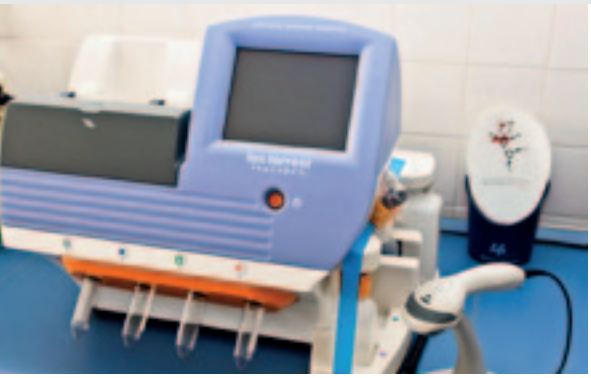
CLIP GENOMICS



ABOUT US

The CLIP Genomics is a part of Childhood Leukaemia Investigation Prague (CLIP), which has been founded in 1996 to promote the research and diagnostics of childhood leukaemia in the Czech Republic. The group has a broad expertise in the diagnostics and research of childhood hematologic malignancies, bone marrow failure syndromes and immunodeficiencies.

The strongest part of the group is a tight connection to the clinical department resulting in a direct application of developed methods into the diagnostic and treatment algorithms (e.g. the minimal residual disease (MRD) monitoring or flow cytometry diagnostics).

The CLIP Genomics group was formed in 2013 in response to the rapid development of high-throughput genomic methods, mainly the next generation sequencing (NGS) technologies.

We have a broad expertise in various high-throughput methods, including whole-exome, transcriptome, amplicon or methylome NGS and whole-genome SNP analysis. We analyse leukaemia samples in treatment-refractory patients to discover actionable targets for personalised therapy.

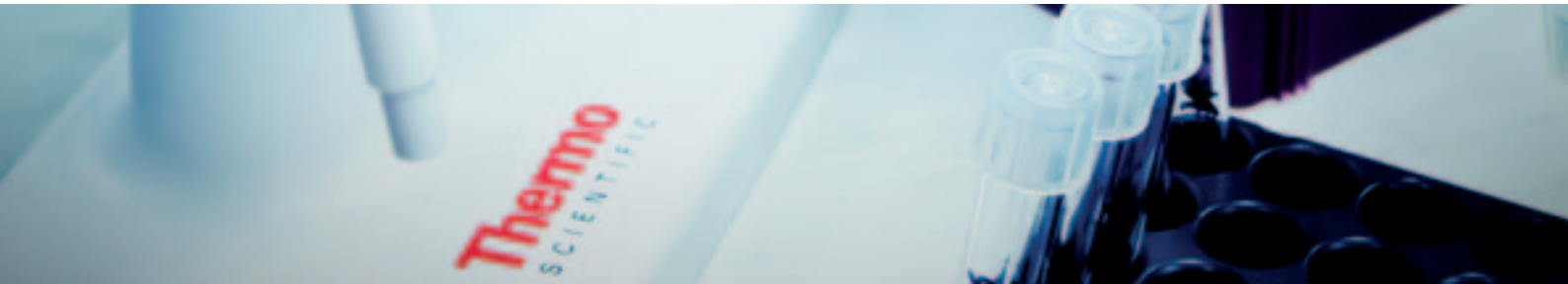
We also use NGS to discover underlying mutations in patients with immunodeficiencies, autoimmunity and bone marrow failure syndromes. We have a high-throughput NextSeq500 (Illumina) sequencer for large-scale projects and a desktop Ion Torrent PGM (Thermo Fisher) machine for projects using amplicon sequencing for mutational and MRD analysis in cancer. The crucial part of all high-throughput methods is the bioinformatics analysis. Our bioinformatics team develops and maintains data analysis pipelines for various applications.

OUR TEAM

Mgr. Alena Dobiášová
Mgr. Karel Fišer, Ph.D.
MUDr. Eva Froňková, Ph.D.
MUDr. Michaela Kotrová
MUDr. Markéta Kubričanová-Žaliová, Ph.D.
Mgr. Martina Slámová
Mgr. Jan Stuchlý
prof. MUDr. Jan Trka, Ph.D.

ACHIEVEMENTS

Publications in peer-reviewed and high-impact journals (Blood, Leukaemia, Journal of Clinical Oncology, Haematologica, Journal of Immunology etc.). Results are regularly presented as lectures on leading conferences in the field (American Society of Haematology meeting, European Haematology Association meeting).



SECOND FACULTY OF MEDICINE
CHARLES UNIVERSITY

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WE OFFER

NGS data analysis service
We offer bioinformatic analysis of next generation sequencing data from all current NGS platforms. From your primary data we will create well-ordered and easily accessible results. Our working group has an adequate hardware for the analysis of large-scale NGS data. Our specialists have both mathematical and biological education which ensures a comprehensive approach to the results.

Amplicon/exome sequencing – variant analysis
- DNA sequencing of selected parts of the genome (amplicons) or all exons of protein-coding genes

Transcriptome sequencing (mRNA-Seq)
- mRNA-sequencing for gene expression analysis

Methylome sequencing (RRBS) - sequencing of GpG-rich areas and their broader neighbourhood for the assessment of DNA methylation

Chromatin immunoprecipitation sequencing (ChIP-Seq) - sequencing of DNA after chromatin immunoprecipitation for the DNA-protein analysis

NGS data analysis courses
We organize regular NGS data analysis courses for both academy and industry participants covering all the process including data interpretation

ACHIEVEMENTS

We are members of the Euroclonality-NGS Consortium which cooperates in the development of NGS-based tools for antigen receptor repertoire analysis and minimal residual disease detection in lymphoproliferative disorders. We are also members of International Berlin-Frankfurt-Münster Group, leading community in the field of acute lymphoblastic leukaemia treatment. The group facilitates the direct transfer of new technologies into the diagnostic and stratification algorithms in childhood ALL.

CONTACT

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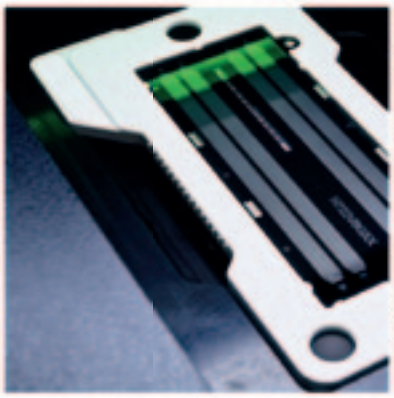
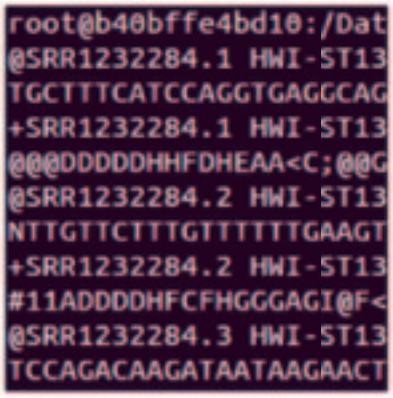

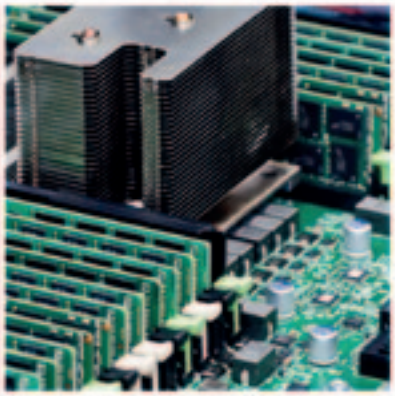

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