CLIP Genomics

Childhood Leukaemia Investigation Prague

 # Genomics
 # Immunodeficiency, cytometry
 # Bioinformatics
 # Leukemia
 # CLIP

Offer

NGS Data Analysis Service

- We offer bioinformatic analysis of next generation sequencing data from all current NGS platforms.
- 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) for gene expression analysis
- Methylome sequencing (RRBS) of GpG-rich areas and their neighbourhood for the assessment of DNA methylation
- Chromatin immunoprecipitation sequencing (ChIP-Seq) – 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.

Know-how & Technologies

- 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.
- 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).
- Our bioinformatics team develops and maintains data analysis pipelines for various applications.

"From your primary data we will create well-ordered and easily accessible results."

Research Area & Excellence

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 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.
- The crucial part of all high-throughput methods is the bioinformatics analysis.

Team Members

- 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

Key Research Equipment

We have a high-throughput NextSeq500 (Illumina) sequencer for large-scale projects and a desktop Ion Torrent PGM (Thermo Fisher) machine for projects analysing amplicon sequencing for mutational and MRD analysis in cancer.

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.
- 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.

"We facilitate the direct transfer of new technologies into the diagnostic and stratification algorithms in childhood all."

Are you interested in this expertise?

Please contact CPPT UK
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Experts and their Department

Prof. MUDr. Jan Trka, Ph.D
Department of Paediatric Haematology and Oncology

Klíčová slova

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 # Immunodeficience, cytometrie
 # Bioinformatika
 # Leukemie
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