

Medical University of Gdańsk
is seeking a candidate for the position of

Student – Scholarship Holder (f/m)

within the project entitled "Diagnosis of High-Grade Brain Tumor Using Liquid Biopsy and Machine Learning" (Project No. FENG.02.02-IP.05-0053/24)

Project leader: Dr. Jakub Mieczkowski, Prof. at MUG

The project is carried out under the First Team programme of the Foundation for Polish Science, co-financed by the European Union under Priority 2 of the European Funds for a Modern Economy Programme 2021–2027 (FENG).

THE TASKS OF THE EMPLOYED PERSON WILL INCLUDE:

- support in laboratory work involving the isolation of cfDNA and ctDNA from patients' plasma and urine,
- support in preparing libraries for Oxford Nanopore sequencing,
- assistance with the organisation, documentation and proper handling of biological samples,
- support in the analysis of Oxford Nanopore sequencing data, including DNA methylation patterns and fragment length distributions,
- collaboration with members of the research team in carrying out project-related tasks,
- support in activities related to disseminating information about the project and its results.

REQUIREMENTS:

- student status first- or second-cycle studies in biology, biotechnology, bioinformatics or a related field,
- motivation for scientific work and an interest in interdisciplinary projects,
- flexibility and independence in acquiring new skills,
- experience with Python and R and applications of machine learning and/or laboratory work using molecular biology techniques would be an advantage.

WE OFFER:

- a 3-month scholarship agreement in the amount of PLN 2,500 gross-gross/month, with the possibility of extension, with a maximum contract duration of 18 months,
- the opportunity to gain and expand knowledge in human epigenetics and liquid biopsy,
- mentoring and support from experienced researchers in epigenetics, computational biology and biostatistics,
- work at one of the best medical universities in Poland,
- the opportunity to develop competencies relevant to the position,
- work at the only medical university in Poland with Research University status.

APPLICATION PROCEDURE:

- Interested candidates are requested to submit their application (CV) using the [APPLY](#) button.
- The application deadline is **31 October 2026**.
- Applications submitted after the application deadline but before the job posting closes may also be considered in the recruitment process.
- Please note that only selected candidates will be contacted.

PROJECT DESCRIPTION:

The project focuses on developing analytical tools to identify samples containing circulating tumor DNA (ctDNA) originating from brain tumor cells. The core assumption is that ctDNA fragments differ from background cfDNA in several features, such as length, sequence composition, genomic location, and DNA methylation patterns.

The goal is to create a method capable of detecting whether a given sample contains a mixture of fragments derived from more than one cell population—specifically, whether the distribution of fragment features indicates the presence of tumor-derived DNA.

In practice, this involves applying statistical methods, distribution modeling, and classifiers based on fragment characteristics (e.g., fragment length, position relative to known regulatory elements, methylation probability) to flag samples as ctDNA-positive.

The work includes Oxford Nanopore sequencing data analysis, creation of custom reference datasets, design of fragment-based metrics and classification models, and evaluation of algorithm sensitivity and specificity.

RESEARCH GROUP DESCRIPTION:

The Mieczkowski lab focuses on understanding how chromatin organization and gene regulation shape cellular identity in health and disease. A central aim is to develop computational and experimental tools for characterizing cell states and origins using epigenomic data. The group applies these approaches to liquid biopsy research, particularly in brain tumors, where circulating tumor DNA (ctDNA) is analyzed to detect cancer-specific signatures.

We integrate chromatin accessibility, nucleosome positioning, DNA methylation, and fragmentomics data generated through bulk and single-cell sequencing (e.g. ATAC-seq, ONT methylation, RNA-seq, spatial transcriptomics) to build tumor-agnostic models for ctDNA detection. Our research bridges molecular biology, bioinformatics, and translational medicine to improve non-invasive diagnostics.