

Early Cancer Institute Summer Programme 2026 Project Details

The Early Cancer Institute Summer Programme 2026 will give five Master's degree students the opportunity to work on a research project within one of our [research groups](#). The five projects available are detailed below. On the application form please select two of the five projects – note that your choices will not be ranked and successful applicants may be offered either of the projects they choose.

The project leads have specified the preferred subject(s) of study for applicants to that project. Please bear this in mind when making your application.

Project details

Project title: Early detection of leukaemia gatekeepers using self-collected blood samples

Supervisor/Research Group: Aristi Damaskou (Caroline Watson's Group)

Project summary: Acute myeloid leukaemia (AML) is an aggressive blood cancer with poor survival rates. Recent studies show that the “seeds” of AML are “sown” years before diagnosis, and that some individuals are more likely to develop AML than others. Monitoring this high-risk population for early signs of leukaemia could represent an invaluable opportunity for early detection and disease prevention or interception.

While several common AML mutations can also be found in the blood of healthy older individuals, others are leukaemia-specific and, as their acquisition is quickly followed by disease presentation, they are considered critical “gatekeepers” in leukaemia development. This project aims to adapt molecular assays to detect leukaemia gatekeeper mutations in self-collected blood samples, which provide a non-invasive, inexpensive and scalable alternative to venepuncture. Successful development of this platform may open the door for large-scale screening in the high-risk population and enable early detection that could improve AML survival.

Proposed student activities: The student undertaking this project will develop a broad range of practical, analytical and interpersonal skills. In the first instance, they will be provided with relevant literature and encouraged to engage with it, to build a solid theoretical understanding of the project. They will be trained for several wet-lab techniques including cell culture, nucleic acid extraction, reverse transcription and qPCR. During the assay optimisation phase, the student will be encouraged to conduct independent online research/literature review to contribute effectively to experimental design. They will also learn how to analyse and visualise qPCR data. Finally, the student will have the chance to develop their communication skills by presenting their findings at the group lab meeting at the end of the programme.

Skills: Literature review, cell culture, DNA/RNA extraction, RT-qPCR, data analysis, project design and management, problem-solving, communication and presentation skills

Preferred student background(s): Biological sciences

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Project title: Investigating neurodevelopmental reprogramming as an early driver and predictor of aggressive prostate cancer

Supervisor/Research Group: Henson Lee Yu (Harveer Dev's Group)

Project summary: Prostate cancer affects one in eight men. While most typically arise as adenocarcinomas that respond to androgen deprivation therapies, a subset evolves into castration-resistant cancers, with 10-30% further transdifferentiating into lethal neuroendocrine prostate cancer (NEPC). In our lab, analysis of methylation profiles of early localised adenocarcinomas revealed early neurodevelopmental gene dysregulation. Corroboration with single-cell and spatial transcriptomic data show enrichment of these signatures in highly proliferative luminal cells and are predictive of poorer progression-free survival. In another work, we show that benign prostate epithelia acquire metastatic potential and neuroendocrine-like features following PTEN–CTNNA1 loss. These findings suggest that early tumours already harbour neuroendocrine-like programs.

In this project, the student will analyse publicly available methylation and transcriptomic datasets from metastatic and NEPC samples to determine which early features persist. They will also assess whether these biomarkers are detectable in plasma methylation profiles and correlate them with severity and risk of progression.

Proposed student activities: The project will provide the student with broad experience in cancer epigenomics and multi-omic data analyses. They will learn to critically assess relevant literature, analyse publicly available datasets, and gain proficiency in computational tools (bash scripting and R) for DNA methylation, and single cell / spatial transcriptomic profiling. The student will also work with internal methylation and transcription datasets from early prostate cancers, integrating these with public resources to derive robust insights in tumour biology.

In addition, they will also have the opportunity to participate in wet lab experiments including sample processing, DNA extraction, and perform methylation sequencing of blood samples, to enable exploration of neurodevelopmental reprogramming signatures in circulating tumour DNA. Through direct involvement in our ongoing efforts to define early molecular markers of lethal prostate cancer, the student will contribute to research with clear translational relevance.

Preferred student background(s): Biological sciences, Computational / data science

Project title: Translating a multiplex protein assay on the capsule sponge into a bedside diagnostic test for oesophageal disease

Supervisor/Research Group: Ahsen Ustaoglu (Rebecca Fitzgerald's Group); Dr Yunzhao (Trevor) Wu – Klenerman Group, Department of Chemistry

Project summary: Early detection of oesophageal adenocarcinoma(OAC) will facilitate curative treatments with fewer side-effects for a major public health priority. The Fitzgerald lab has developed a first-in-class non-endoscopic capsule-sponge test to screen, diagnose and monitor Barrett's oesophagus(BO), a pre-cancerous condition. Eosinophilic oesophagitis(EoE) is a chronic allergic disease of the oesophagus defined by symptoms of dysphagia and/or food impaction with increasing prevalence.

To maximise scalability and accuracy of the capsule sponge test, more quantitative biomarkers that are less reliant on pathology review would be advantageous. Our data suggests that the preservative fluid is a source of secretory proteins which could aid the development of a near bedside test. We have developed an idea that has the potential to transform capsule-sponge testing into a point-of-care diagnostic.

Proposed student activities: This idea involves a multiplex assay which has the ability to quantify soluble proteins released from the cells collected by the capsule sponge into the preservative buffer. These proteins, found in the 'cell-free' supernatant after centrifugation, including novel markers for BO and EoE developed in the Fitzgerald lab. Currently, we are investigating different methods to translate this assay into a clinical test.

In the proposed project, the student will:

- 1) Conduct validation studies using Simoa technology (an ultrasensitive biomarker detection platform) on a smaller panel of proteins to assess whether a simpler method could achieve similar diagnostic performance [Böken, Dorothea et al. Analytical chemistry vol. 97,1 (2025): 290-299]
- 2) Carry out multiplex immunoassays to develop a novel protein biomarker panel to detect eosinophilic oesophagitis and monitor treatment response.

Preferred student background(s): Biological sciences

Project title: Profiling histone expression and modifications in hereditary diffuse gastric cancer

Supervisor/Research Group: Daniel Jacobson and Nandini Karthik (Rebecca Fitzgerald's Group)

Project summary: Hereditary diffuse gastric cancer (HDGC) is a syndrome driven by inherited mutations in the Wnt signalling pathway, most notably CDH1, which accounts for up to 3% of gastric cancers. Patients with germline alterations have significantly increased cancer risk and can opt for a prophylactic total gastrectomy, or regular endoscopic surveillance. This involves identifying 'pale areas', which indicate increased risk of progression. We have shown that cells within these regions, known as 'signet ring' cells, show decreased expression of CDH1 protein, which may be driving cancer progression.

One possible source of this second hit is silencing of CDH1 through epigenetic mechanisms. Promoter hypermethylation often underlies loss of CDH1 expression. However, other epigenetic changes which co-regulate expression, including histone modifications, are poorly understood in HDGC. As epigenetic modifications represent reversible changes that can be targeted using small molecule inhibitors, understanding the epigenetic landscape may allow us to identify viable therapeutic targets.

Proposed student activities: This will be a joint wet/dry-lab project, and the student can hope to gain experience in both settings.

The student will use multiple online datasets to determine whether there is evidence to suggest a role for various epigenetic modifiers, particularly histone modifiers, in CDH1 loss and progression of diffuse gastric cancer. This will include published bulk and single-cell RNA-seq, and ChIP-seq datasets, as well as data from cell lines to identify the most promising potential targets.

Based on this, the student will perform IHC/ IF using antibodies targeting specific modifiers and modifications. They may also use the organoid models established in the lab to functionally validate the role of epigenetic modifiers through studying the presence of histone marks at target loci and silencing or disrupting the activity of these modifiers to examine the effect on organoid viability, growth and differentiation.

The skills which the student may hope to develop will include, but are not limited to: literature review, immunohistochemistry, antibody conjugation, statistical programming in R, analysis of bulk and single-cell RNA-seq in R, data visualisation, presentation skills.

Preferred student background(s): Biological sciences

Project title: Imaging of cancerous tissue using optical coherence tomography (OCT)

Supervisor/Research Group: Matthew Ellis (Danielle Harper's Group)

Project summary: The Harper Lab seeks to apply state-of-the-art optical coherence tomography (OCT) systems for improved biomedical imaging of cancer cells. As a non-destructive label-free technique with up to millimetre imaging depth, OCT has the potential to significantly improve both the speed and quality of biomedical imaging without the need for sample destruction and laborious histology preparation. Being within the ECI allows us to gain access to a wide range of clinically relevant samples across a number of different cancers, where we can use OCT to detect distinguishing features of cancerous tissue and dynamically monitor in vitro tissue models. One particular focus of the project will be using OCT to characterise hereditary diffuse gastric cancer (HDGC) organoids in combination with polarisation microscopy to gain a greater understanding of spindle orientation disruption.

Proposed student activities: The project will involve getting hands on experience with state-of-the-art OCT-imaging techniques for imaging biological samples. The student will learn how to perform image acquisition and processing, in addition to how to handle biological samples. The student will also be encouraged to perform a literature review into the use of OCT for imaging organoids. Depending on the student's interest, there is also the opportunity to get an introduction to working with custom optical setups and learning how to design novel OCT systems.

Preferred student background(s): Biological sciences, Computational / data science, Physics / engineering

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Further information about the Early Cancer Institute may be found on our website www.earlycancer.cam.ac.uk.

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Moderna is pleased to sponsor the Early Cancer Institute Summer Programme, but all research projects and educational activities are conducted independently under the sole direction of the Early Cancer Institute, University of Cambridge.