

A new tool to study human antibody repertoires

Background

The immune system protects us by producing antibodies—proteins made by B cells that can recognize a wide variety of targets. Antibody diversity comes from inherited differences between individuals¹ and from processes inside B cells². Antibody genes are rearranged during B-cell development (V(D)J recombination). Later, as part of an immune response, the genes can accumulate changes through somatic hypermutation, and cells producing better-binding antibodies are selected. Together, these mechanisms create highly diverse antibody repertoires.

Antibody repertoires are shaped by genetics, age, infections, vaccination, and autoimmune disease. Studying repertoires can reveal shared patterns between people and helps us understand adaptive immunity across these contexts³. In infection, characterizing protective antibodies can inform improved vaccine design. In autoimmunity, self-reactive antibodies can contribute to tissue damage and disease. Better characterization of antibody sequences can help identify candidate targets and mechanisms, informing future diagnostics and therapies. *Autoimmune and infectious diseases are major societal health challenges, creating a need for accurate, scalable methods to study antibody repertoires.*

AIRR-seq: reading antibody repertoires

Adaptive Immune Receptor Repertoire sequencing (AIRR-seq) reads antibody sequences expressed by B cells. It allows us to study diversity, track expanded B-cell clones, and examine mutation patterns. However, commonly used approaches capture only parts of the antibody transcript. This can hide important information and make interpretation harder.

Project goal: developing CLAIRR-seq

In this summer project we will develop and test CLAIRR-seq (Capture-based Long-Read Adaptive Immune Receptor Repertoire sequencing). The idea is to capture immunoglobulin transcripts, then amplify and sequence them using Nanopore long-read sequencing (Figure 1).

Full-length antibody transcripts can enable:

- Detecting transcript and constant-region variation, such as alternative isoforms (e.g., membrane-bound vs secreted forms) and potential constant-region allele differences.
- Linking clones to antibody class/subclass (e.g., IgM vs IgG), which matters for antibody effector function and inflammatory potential.

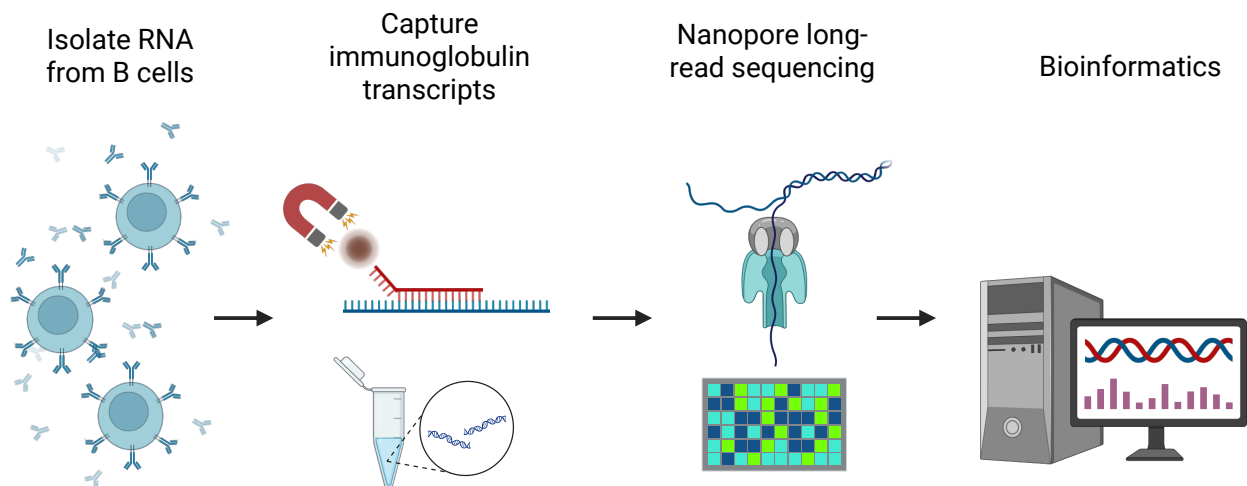


Figure 1. Capture-based Long-Read Adaptive Immune Receptor Repertoire sequencing (CLAIRR-seq).

- Reduced ambiguity, because long reads can reduce the need to infer missing parts of the sequence when similar antibodies look alike.

Interdisciplinary project (wet lab + bioinformatics)

This is an educational, hands-on project combining:

- Molecular biology: contribute to development and optimization of the capture and amplification workflow, generate sequencing libraries and perform basic quality checks.
- Bioinformatics: process and evaluate sequencing data (e.g., sequence completeness, clonotypes, mutation patterns) and compare results to a baseline approach.

What you will learn

You will gain hands-on experience at the interface of immunology, molecular biology, and computational analysis. You will learn core concepts in antibody repertoires and autoimmunity, get practical exposure to long-read sequencing data, and contribute to developing a method that can strengthen studies of immune responses and autoimmune disease.

Research environment and supervision

The summer student will be member of the [Neuroimmunology Research Group](#) at the Institute of Basic Medical Sciences, University of Oslo (UiO). The group currently consists of two postdocs, two PhD students, a research fellow (thesis submitted), a lab engineer, and a professor emeritus. We are equipped with state-of-the-art laboratory facilities, specifically tailored for advanced immunological research and bioinformatics. The summer student will be supervised by the group leader [Andreas Lossius](#) and the research fellow [Mari Gornitzka](#).

References

1. Gornitzka, M. B. et al. Ultra-long sequencing for contiguous haplotype resolution of the human immunoglobulin heavy chain locus. *Genome Res.* 2025. <https://doi.org/10.1101/gr.280400.125>
2. Seyedraoufi, S., Gornitzka, M. B. & Lossius, A. GAT-HeR: Graph-based Accurate Tool for Immunoglobulin HEavy- and Light-chain Reconstruction. 2025. <https://doi.org/10.1101/2025.09.21.677530>
3. Mikocziova, I., Greiff, V. & Sollid, L. M. Immunoglobulin germline gene variation and its impact on human disease. 2021. *Genes Immun.* 2021. <https://doi.org/10.1038/s41435-021-00145-5>