About the author

Arthur Declercq started his academic journey in Biomedical Sciences in 2016. In 2018 he got selected for the honours program in life sciences focused on: "Optimization of CD4+ T cells infection with varicella- zoster virus in vitro"

During his MSc he got the opportunity to combine his interest in immunology with his passion for programming through the development of AI-models for enhanced epitope identification, a project he continued as Predoctoral Researcher within CompOmics at VIB-UGent Center for Medical Biotechnology. He contributed to several tools such as MS^{2}PIP, MS^{2}Rescore, TIMS^{2}Rescore and developed his own epitope prediction tool MHC-3PO. With his contributions to MS^{2}Rescore and its benefits to identify potential vaccine candidates he won the PhD innovation café in 2023.

Funding

Ground control

PROMOTOR
Prof. Dr. Lennart Martens   VIB - *Ghent University*

CO-PROMOTOR
Prof. Dr. Francis Impens   VIB - *Ghent University*

MENTOR
Dr. Ralf Gabriels   VIB - *Ghent University*

Mission Crew

CHAIR
Prof. Dr. Jo Vandesompele   *Ghent University*

COMMITTEE SECRETARY
Dr. An Staes   VIB - *Ghent University*

JURY MEMBER
Dr. Susan Klaeger   *Genentech Inc*

JURY MEMBER
Prof. Dr. Sven Nahnsen   *Tübingen University*

JURY MEMBER
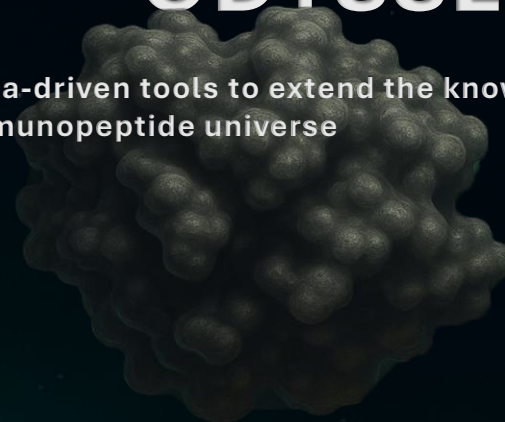Dr. Fabien Henri Thery   VIB - *Ghent University*

JURY MEMBER
Prof. Dr. Bart Mesuere   *Ghent University*

EPITOPE ODYSSEY

Data-driven tools to extend the known immunopeptide universe

Arthur Declercq

Thesis submitted to fulfill the requirements for the degree of Doctor in Health Sciences
2024-2025

VIB-UGENT CENTER FOR MEDICAL BIOTECHNOLOGY   FACULTY OF MEDICINE AND HEALTH SCIENCES   GHENT UNIVERSITY   CompOmics

Summary

Just as astronomers map the stars to understand the universe, scientists map proteins to understand life. Proteins are the workhorses of our cells, carrying out the countless processes that keep us alive. Studying them—proteomics—has transformed biology and medicine, by revealing how our bodies function, why diseases arise, and how therapies can overcome them.

Within proteomics, a key branch called immunopeptidomics, investigates small protein fragments called epitopes. These fragments are displayed on the surface of every cell, acting as signals for the immune system to detect infections, mutations, or cancers. Identifying epitopes is therefore essential for designing effective vaccines and personalized immunotherapies.

My PhD focused on developing AI-powered tools to help identify these epitopes more easily. I worked on MS^{2}PIP, which predicts how epitopes fragment in mass spectrometers, and MS^{2}Rescore, which uses these spectrum predictions and other prediction tools to boost epitope discovery.

I expanded this work with TIMS^{2}Rescore, tailored to newer instruments such as timsTOF, which not only boosts the discovery of epitopes but also helps reveal proteins circulating in the blood and gut. Most recently, I created MHC-3PO, a deep-learning model that can predict likely epitopes—including chemically modified ones—directly from protein sequence.

Together, these tools help expand the epitope landscape, bringing us closer to better vaccines, improved immunotherapies, and a deeper understanding of how our immune system protects us.

Key publications

- Declercq, A. et al. (2022). MS2Rescore boosts immunopeptide identification. Mol Cell Proteomics.
- Declercq, A. et al. (2023). Updated MS2PIP web server for proteomics. Nucleic Acids Res.
- Buur, L.M. & Declercq, A. et al. (2023). MS2Rescore 3.0: modular platform for peptide IDs. J Proteome Res.
- Declercq, A. & Devreese, R. et al. (2025). TIMS2Rescore: optimized rescoring pipeline. J Proteome Res.

Contact

AD Arthur Declercq

✉ Arthur.Declercq@UGent.be

in linkedin.com/in/arthur-declercq

🌐 arthurdeclercq.bio

github.com/ArthurDeclercq

iD orcid.org/0000-0002-9376-1399

Take home messages

1. Epitopes are tiny protein fragments on every cell surface that help the immune system distinguish healthy cells from infected or cancer cells

2. With advanced software, we can identify these epitopes more precisely and reliably.

3. These epitopes provide actionable targets for pathogen vaccines and personalised cancer treatments.