



Utrecht University

Biomolecular Mass Spectrometry and Proteomics

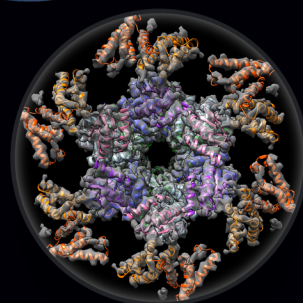
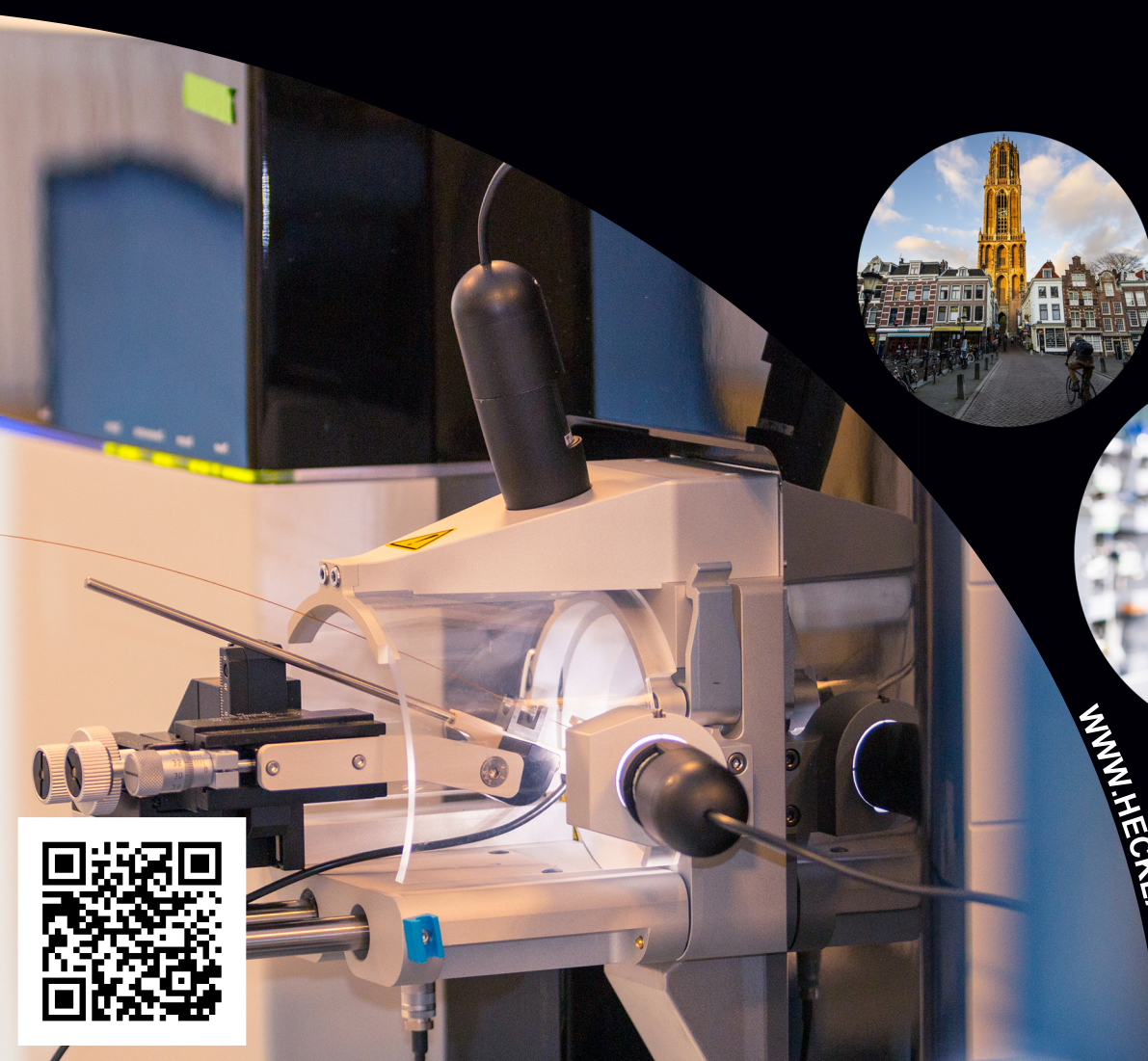
Five Post-doctoral and three PhD Vacancies

In the Heck group at Utrecht University, a variety of exciting research projects seek motivated researchers to tackle them. The research emphasis is on the development of advanced mass spectrometry based methods for proteomics and structural biology.

The group houses an excellent infrastructure, including a dozen state-of-the-art mass spectrometers, advanced separation technologies, bioinformatics and laboratories for cell culture, biochemistry and molecular biology. The research group is vibrant with over 15 nationalities being present. Utrecht is a great place to be!

More detailed information about the group, these projects and how to apply for them:

- www.hecklab.com/vacancies
- or via c.c.heuzer@uu.nl



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Biomolecular Mass Spectrometry and Proteomics

Five post-doctoral and two PhD positions available in the group of Prof. Dr. Albert Heck

Short description of available positions

Postdocs (minimum of 2 years)

1. Analytical Mass Spectrometry with experience in instrumentation

Further optimization of native mass spectrometry, with the aim to generate even higher sensitivity and resolving power and secondly, optimize workflows for data-integration (e.g. middle-down, top-down and native) for both industrial enzymes and pharmaceutical proteins.

2. Analytical Mass Spectrometry and Proteomics

Quantitative proteomics, analysis of protein interactions and post-translational modifications using state-of-the art quantitative proteomics with an emphasis on the analysis of protein post-translational modifications. Applications will be mostly in virology and immunology.

3. Analytical Mass Spectrometry and Top-down Proteomics

Detailed characterization and de novo sequencing of endogenous antibodies, with the aim to pick up antibodies raised by our immune-system against invasions by pathogens.

4. Mass Spectrometry based Structural Biology

Detailed characterization of proteins involved in the Complement pathway by hybrid mass spectrometry based methods including native mass spectrometry, proteomics, XL-MS and HD-MS.

5. Analytical Mass Spectrometry with experience in engineering

Further optimization of top-down mass spectrometry, notably UV photodissociation and top-down sequencing of proteins and protein complexes. The project will be in collaboration with ThermoFisher Scientific and Maastricht University.

PhD Students (4 year program)

1. Characterization of glycoproteins by hybrid mass spectrometry methods

Development of high-resolution native mass spectrometry methods to characterize the complexity of pharmaceuticals and dairy proteins, including the characterization of isoforms and co-occurring PTMs.

2. Native protein separation methods coupled to native and top-down mass spectrometry

Development of off-line and on-line couple, native separation methods with mass spectrometry, applied to biopharmaceuticals such as IgGs or other antibody-based therapeutics.

3. Analytical Mass Spectrometry and Top-down Proteomics

Detailed characterization and top-down and de novo sequencing of endogenous proteins and protein assemblies, with special emphasis on co-occurring protein isoforms.



Recent illustrative papers

1. Snijder J, et al. (2017) Structures of the cyanobacterial circadian oscillator frozen in a fully assembled state. *Science*. 355:1181-1184.

2. Liepe J, et al. (2016) A large fraction of HLA class I ligands are proteasome-generated spliced peptides. *Science*. 354:354-358.

3. Liu F, Rijkers DT, Post H, Heck AJ. (2015) Proteome-wide profiling of protein assemblies by cross-linking mass spectrometry. *Nature Methods*. 12:1179-84.

4. Hussein SM, et al. (2014) Genome-wide characterization of the routes to pluripotency. *Nature*. 516:198-206.

5. Altelaar AF, Munoz J, & Heck AJ (2013) Next-generation proteomics: towards an integrative view of proteome dynamics. *Nature Review Genetics* 14:35-48.



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