

Press Release

"Proteomics is becoming increasingly precise, digital and clinically relevant": An interview with the Congress President of the EuPA | Proteomic Forum 2026

Würzburg. Personalised therapies, artificial intelligence and the analysis of individual cells are revolutionising biomedical research. Proteins also play a key role in this. They reveal what actually happens inside cells and enable researchers to gain new insights into diseases, as well as into the development of new diagnostic and therapeutic options. In this interview, Congress President Dr Stefanie Hauck discusses current developments in proteomics and the key themes of the EuPA | Proteomic Forum 2026, which will take place in Würzburg from 29 November to 3 December.

The EuPA | Proteomic Forum 2026 covers 19 key scientific topics featuring high-calibre international keynote speakers. Where do you see the key trends this year?

Dr. Hauck: The strength of EuPA 2026 lies in the fact that it covers the entire spectrum of modern proteomics. Nevertheless, a few clear focal points can be identified. The fields currently experiencing particularly dynamic development are artificial intelligence in proteomics, computational proteomics and big data, single-cell proteomics, spatially resolved proteomics, as well as multi-omics and systems biology. These themes run like a common thread through the programme. At the same time, we are seeing an increasing focus on medical applications. Sessions on clinical proteomics, cancer proteomics, immunoproteomics and the standardisation of blood proteomics demonstrate that our discipline is moving ever closer to clinical practice.
The overarching trend is this: We are not only measuring more and more proteins, but we are also gaining a better understanding of their function within complex biological systems.

Artificial intelligence, computer-aided proteomics and big data are key topics at the congress. How are these technologies transforming research?

Dr. Hauck: The volume of data generated by modern mass spectrometry today would be almost impossible to analyse without advanced algorithms and AI. Artificial intelligence helps scientists to recognise patterns in highly complex datasets, identify biomarkers and understand biological processes more quickly. The significance of this development is also reflected in dedicated programme themes on 'Artificial Intelligence in Proteomics' and 'Computational Proteomics and Big Data'. But AI does not replace humans. On the contrary: it expands our capabilities. The actual scientific

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Congress president

Dr. Stefanie Hauck

Head of Core Facility Metabolomics and Proteomics (CF-MPC)

Helmholtz Zentrum Munich

Hosting societies

German Society for Proteome Research

www.dgpf.org

Office:

c/o Universitätsmedizin Greifswald
Abt. Funktionelle Genomforschung
Felix-Hausdorff-Str. 8
17475 Greifswald

and

European Proteomics Association

www.eupa.org

Office:

c/o Universitätsmedizin Mainz
Institut für Immunologie,
Gebäude 308A
Langenbeckstr. 1
55131 Mainz

Venue

Congress Centrum Würzburg
Pleichertorstraße
97070 Würzburg

Congress organization

Conventus Congressmanagement & Marketing GmbH
Julian Unger | Andreas Lelle
Carl-Pulfrich-Str. 1 | 07745 Jena
T +49 (0)3641 31 16-330 | -397
M proteomic-forum@conventus.de

Press contact

Johanna Ratz
T: +49 3641 31 16-280

Kerstin Aldenhoff
T: +49 172 3516916

M presse@conventus.de



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questions, the interpretation of the results and the clinical assessment remain a human task. AI is increasingly becoming a powerful tool that supports researchers in making better decisions based on a significantly broader data set.

In the context of systems biology and multi-omics, there is often talk of 'virtual' cells. Will digital twins of humans soon become a reality?

Dr. Hauck: Digital twins of biological systems are no longer the stuff of science fiction. Initial models already exist for individual cells, tissues or specific disease processes. The combination of proteomics, genomics, metabolomics and AI opens up entirely new possibilities. This is precisely why multi-omics and systems biology play an important role in the conference programme. However, we are still a long way from a complete digital twin of a human being. Biological systems are simply too complex and too dynamic for that. Nevertheless, we are moving step by step in this direction. In the field of personalised medicine in particular, digital models could help in the future to predict therapies and optimise them on an individual basis.

Single-cell proteomics is regarded as one of the most dynamic fields of research in the life sciences. How far are we from its use in routine clinical practice?

Dr. Hauck: Single-cell proteomics is undoubtedly one of the most exciting developments of recent years and will therefore have its own dedicated session at EuPA 2026. For the first time, we can analyse the protein composition of individual cells and thus reveal differences that remain hidden in traditional measurements of whole tissues. This is of enormous significance, particularly for cancer research, immunology and developmental biology. At present, single-cell proteomics is primarily a tool for basic research. It provides entirely new insights into the heterogeneity of cells and tissues and helps us to decipher biological mechanisms that remain hidden using conventional methods. The findings derived from this will provide important impetus for precision medicine in the future.

Which conditions could particularly benefit from new proteome-based diagnostic methods?

Dr. Hauck: We currently see the greatest potential in complex conditions where existing diagnostic methods have reached their limits. These include cancer, neurodegenerative diseases such as Alzheimer's or Parkinson's, cardiovascular diseases, inflammatory diseases and infectious diseases. The relevant focal points in the conference programme range from Cancer Proteomics and Clinical Proteomics, through Human Health Insights, to Host-Pathogen Interactions and Virology. Proteins reflect the current biological state of an organism. Consequently, proteome-based tests can often provide information that goes beyond genetic analyses alone. In the long term, we expect more sensitive early diagnoses, more precise patient selection for therapies and better monitoring of disease progression.

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Head of Core Facility Metabolomics and Proteomics (CF-MPC)

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M proteomic-forum@conventus.de

Press contact

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Kerstin Aldenhoff
T: +49 172 3516916

M presse@conventus.de



What are you personally most looking forward to at the EuPA | Proteomic Forum 2026?

Dr. Hauck: The scientific presentations are a highlight, particularly the international keynote speeches from fields such as AI, single-cell analysis, clinical proteomics and systems biology. But what I am most looking forward to is the opportunity for face-to-face discussion. The EuPA brings together researchers from across Europe and far beyond. Often, the crucial ideas emerge not only during the presentations, but in discussions across different disciplines. It is precisely the connection between technology developers, data scientists, clinical researchers and basic scientists that constitutes the strength of our community. When participants return home with new collaborations, new ideas and renewed enthusiasm, that is the greatest success of the conference for me.

Thank you for the interview!

Background: The EuPA and the Proteomic Forum are among the most important European conferences on proteomics. They bring together academia, clinical practice, and industry. Each year, the latest research findings and technological innovations in proteomics are discussed.

All information and the conference program can be found at: https://proteomic-forum.com/

Journalists are cordially invited to the conference! We look forward to your coverage. We'd be happy to put you in touch with contacts for interviews. You can apply for accreditation on the conference website or directly through the press contact.

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