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## **Novel EU-funded collaborative proteomics project to bring proteomics to clinical application**

**Novel proteomic technologies that are so robust and powerful that they can be used in every biological laboratory and in every clinic are expected as results of the currently starting research consortium MSmed. The European Commission is co-funding the project with 3.7 Million Euros for four years starting Dec. 1, 2015 within the research line "Future and Emerging Technologies" under the Horizon 2020 Programme. MSmed will automate workflows in mass spectrometric analysis for proteomics research to prepare them for high-throughput clinical application.**

Proteins are the major functional actors within cells and exert most of the cells' functions. Over the past decade the analysis of the protein inventory of cells and tissues, the „proteome“, has made tremendous progress showing definite promise of mass spectrometry technology in the life sciences. To date proteome analysis is still a specialist technology and has not reached the robustness and availability for large-scale biomedical and clinical applications. In that respect it clearly lags behind genomic technologies that are, however, not applicable to protein based questions.

The MSmed project was initiated to tackle this issue. The vision of project coordinator Matthias Mann is "...to introduce proteome analysis by mass spectrometry as automated routine tool into the clinics". Complementing current genetic methods with direct proteome analysis would allow measuring actual medical parameters as reflected in the patient's proteome rather than solely genetic disposition. Such a paradigm changing approach could transform personalized medicine, revolutionizing medical diagnosis and the assessment of efficacy of medical intervention on an individual basis.





To bring this vision into reality, a team was built around leaders in the proteomics field with a history of successful collaboration. They will bring in a broad range of experiences and expertise to master the various challenges lying ahead. These challenges include the development of novel instrumentation with drastically increased performance, the automation of sample preparation and analysis, the adaptation of analysis protocols to the characteristics of clinical samples, and the development of comprehensive software for extensive in-depth analysis of the large amounts of data obtained.

When successful, MSmed will establish mass spectrometry based proteomics in systems medicine, making all workflows and mass spectrometry platforms available to the community. These workflows will be used as the basis of myriad applications in biomedicine, even in the clinic. This in turn will lead to a new eco-system around improved diagnosis, elucidations of disease mechanisms and drug action.

## The MSmed team

The coordinating Mann group (Novo Nordisk Foundation Center for Protein Research, University of Copenhagen and Max Planck Institute of Biochemistry, Martinsried), the Olsen group (Novo Nordisk Foundation Center for Protein Research, University of Copenhagen), the Cox group (Max Planck Institute of Biochemistry, Martinsried), the Heck group (Utrecht University) and Makarov from the industrial partner Thermo Fisher Scientific, are all leaders in the field and have a longstanding collaboration concerning the improvement of instrumentation in mass spectrometry, with the aim to make it accessible to all researchers. One example is the earlier EU-funded project PROSPECTS, which was also coordinated by Matthias Mann, where Mann, Olsen, Cox and Makarov jointly invented novel technology for in depth quantitative proteomics and the EU-funded project PRIME-XS, coordinated by Albert Heck, wherein amongst others Mann and Olsen participated and jointly provided access to their facilities to researchers in Europe and performed joint research projects.

The coordinating center in Copenhagen brings in expertise in clinical approaches and a network of clinical collaborators. The Heck group (University Utrecht) is a key partner in technology development for novel identification methods to be used in the analysis of modified proteins. The Cox group (Max Planck Institute of Biochemistry, Martinsried) complements the lab expertise with high-end bioinformatics. Together with the Mann group they have developed the most successful and industry standard MaxQuant platform for proteomics research worldwide. Makarov, being the inventor of the leading mass analyser and research director at Thermo Fisher complements the team, and has long standing relationship with all the academic partners. These earlier achievements lend credibility to the future success of the MSmed project.





**Caption:**

The MSMed team. Clockwise: Matthias Mann, Jesper Olsen, Albert Heck, Alexander Makarov und Jürgen Cox (middle).

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