

Q-MOP

(Quantitative Model Organism Proteomics)

What is Q-MOP?

The main objective of this initiative is the implementation and further development of advanced targeted quantitative proteomics workflows that allow researchers to study hypothesis-driven research questions in a systems biology context and to capitalize on the differentiating advantages of direct protein profiling over other technologies.

In a first phase, **C-MOP** has comprehensively described the proteomes of a number of model organisms of high relevance for experimental biology: *Arabidopsis thaliana*, *Caenorhabditis elegans* and *Drosophila melanogaster*. Results of this first phase include generation of the most extensive proteomics datasets for these model organisms. These results have spurred the development of novel proteomics technologies and bioinformatics data analysis approaches, as well as the improvement of the genome annotation of these organisms.

In a second phase, the focus of **Q-MOP** is now shifting towards the application of advanced targeted quantitative workflows capable of providing complete quantitative proteomics datasets. Proteins of interest can be detected with a much increased sensitivity and at a higher throughput. These improved proteomics technologies will enable researchers to address fundamental biological problems in a systems biology context.

Specific Aims

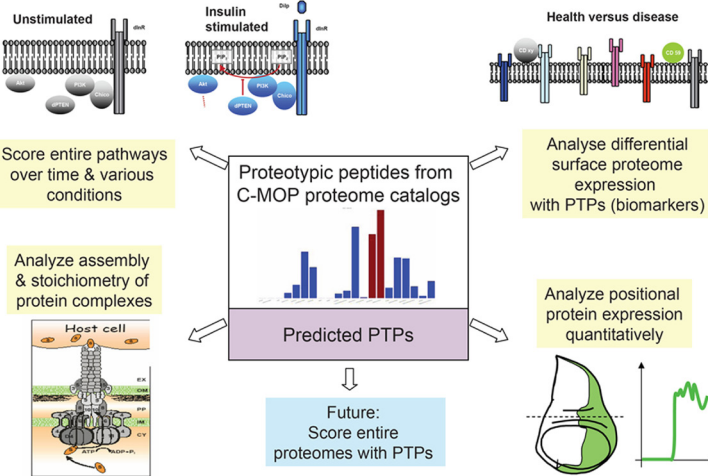
The specific aims of **Q-MOP** are to establish workflows and bioinformatics tools that will allow to quantitatively measure proteins. With these developments complete and quantitative data series for specific protein complexes, signaling pathways or protein networks will be recorded. If required, protein abundance will be determined along with spatio-temporal information, i.e. in a specific subset of cells of a tissue, organ or organism. This allows one to address for instance how the positional information of cells affects their ability to respond to developmental or environmental cues.

To determine protein abundance levels a minimal set of proteotypic peptides (PTPs) that collectively and unambiguously identify this protein is used. For a significant fraction of the proteins of an organism PTPs are experimentally identified during the first phase of proteome analysis. For the proteins that remain unidentified during this initial phase **Q-MOP** is developing, implementing and validating computer-based prediction tools that complete the experimental set of PTPs. A complete PTP list that is based on a significantly improved prediction tool is envisaged to be released soon for the two model organisms *Drosophila melanogaster* and *Caenorhabditis elegans*. In a last step reproducible and robust assays are generated for every PTP and deposited in an open-source atlas.

Q-MOP Minisymposium

Quantitative Proteomics: A Central Technology for Systems Biology

Friday October 30, 2009
University of Zürich
No registration required
Attendance free of charge



Minisymposium

Quantitative Proteomics: A Central Technology for Systems Biology

Friday October 30, 2009
University of Zürich, Irchel
Y15-G-19
Winterthurerstrasse 190
8057 Zürich



Program

Opening of the Mini-symposium

09:40 Joe Jiricny (Head, URPP Systemsbiology, University of Zürich)
09:50 Konrad Basler (Institute of Molecular Biology, University of Zürich)

Scientific Talks Session I:

10:00 Ruedi Aebersold (Institute of Molecular Systems Biology, ETH Zürich)
 “Mapping and Measuring Proteomes”
10:50 Brandon MacLean (University of Washington; Seattle, USA)
 “Software for Targeted Proteomics: Rapid Method Refinement and Quantitative Data Analysis”
11:40 Leigh Anderson (Plasma Proteome Institute; Washington DC, USA)
 “Restructuring the Biomarker Pipeline: Extending the Sensitivity of MS-Based Specific Assays to Cover the Human Proteome”

12:30 Lunch break

Poster Session

13:30 Poster Session and Coffee

Scientific Talks Session II:

14:30 Albert Heck (Department of Biomolecular Mass Spectrometry; Utrecht, The Netherlands)
 “Genome free de novo sequencing using LysN and ETD”
15:20 Aleksey Nesvizhskiy (University of Michigan; Ann Arbor, Michigan, USA)
 “Analysis and statistical validation of large proteomic datasets”
16:10 Christian von Mering (Institute of Molecular Biology, University of Zürich)
 “Optimality and evolution of protein abundance levels in eukaryotes”

Closing remarks / Apéro

17:00 Michael Hengartner (Dean of the Faculty of Science, University of Zürich)
17:15 –19:00 Apéro

University Research Priority Program (URPP)
Systems Biology / Functional Genomics



Universität Zürich