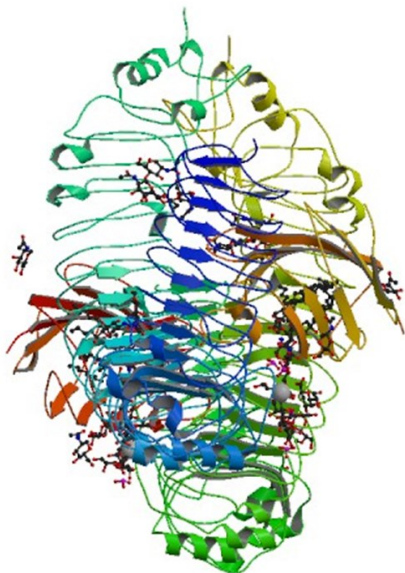


INSTRUMENTATION

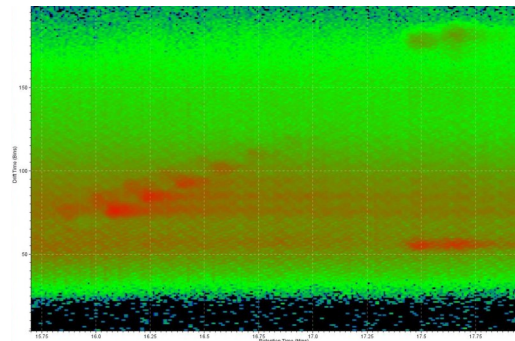
**Ion mobility mass spectrometry -
chromatography - gel electrophoresis**

- Synapt G2 Si / M-Class
- Q-TOF Premier / Ultimate
- MALDI micro-MX
- Esquire 3000 / HP1100
- DIGE / Typhoon / DeCyder
- HP Tower



@CUP 5/2018

Annual Münster Conference on Biomolecule Analysis (for latest information see link on our website)



Core Unit Proteomics

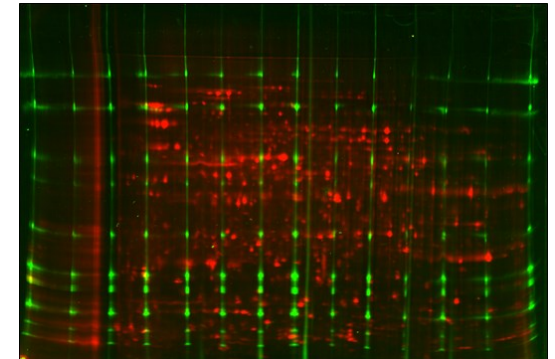
Röntgenstr. 21
48149 Münster

Get in touch for experimental design:

Simone König, Ph.D.
Telefon: 0251-8357164
Fax: 0251-8357255
E-Mail: koenigs@uni-muenster.de
www.medizin.uni-muenster.de/cu-proteomics

Sample submission

cup-sample-submission.uni-muenster.de



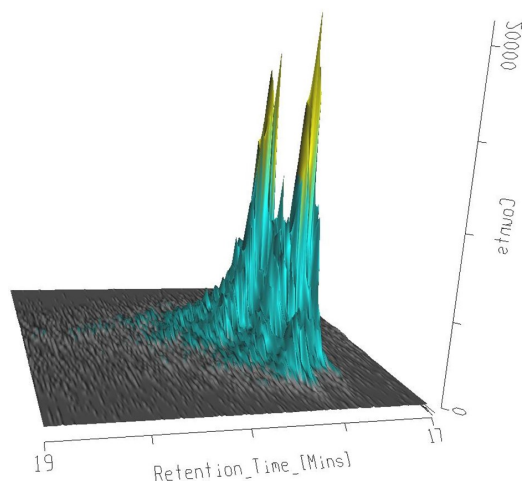
CORE UNIT PROTEOMICS

*Protein identification & quantification
Proteome expression analysis
Biomolecular mass spectrometry*



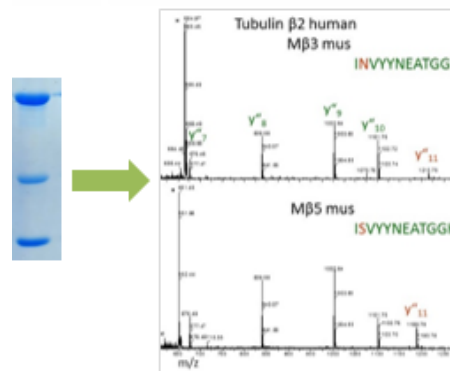
Concept

The Core Unit Proteomics is a technology platform of the IZKF Münster providing analyses based on biomolecular mass spectrometry in conjunction with peripheric techniques such as gel electrophoresis and chromatography. The group offers specialist service and dedicated training courses for the IZKF and other interested parties. Beside routine experiments, research projects are carried out in collaboration.



Portfolio

Biomolecular mass spectrometry: determination of molecular weights, identification of pre-separated (e.g. by gel electrophoresis) proteins



- CID/ETD analysis of protein modifications (phosphorylation and others)
- *De novo* sequencing (e.g. plant proteins)
- TOF-MRM protein quantification
- Cell / tissue preparation
- Substance isolation, separation, depletion, enrichment
- 2D-PAGE with specific and non-specific staining, 2D-DIGE expression analysis, CoFGE standardization
- Chip technology for quality control of protein mixtures
- Isoelectric focusing in the liquid phase for subproteome analysis
- Proteome label-free expression analysis with multivariate statistics and pathway / network analysis
- Protein structure visualization
- Small molecule analysis
- Bioprofiling with principal component and biomarker analysis

Your question?

- What is the difference between my samples?
- Where is my protein modified?
- Which protein did I isolate?
- How much of my protein is present?
- How do I separate my proteins?
- What is the quality of my protein?
- What are the interaction partners of my protein?
- How do I obtain statistically relevant data?

For answers call 0251-8357164.

