GUIDELINES AND INFORMATION FOR CUSTOMERS OF CFMP ZMBH

Title: Intact Protein Mass Determination by LC ESI-MS

Authors: Nicole Lübbehusen, Marcin Luzarowski

Reviewed by: Thomas Ruppert

Last updated: 29.01.2023

Contact information: n.luebbehusen@zmbh.uni-heidelberg.de

m.luzarowski@zmbh.uni-heidelberg.de

Contents

1. Short description

The whole mass determination is a method that allows for accurately determining the mass of a protein within a simple mixture. It serves to confirm the integrity of a protein after purification or to identify post-translational modifications. A relatively pure protein undergoes online desalting using a trap column and is then injected under denaturing conditions into the mass spectrometer.

2. During initial meeting inform us about

- Do you already have an iLab account?
- What is the size of your protein or what molecular weight do you expect? (if possible provide us with the amino acid sequence)
- Protein concentration
- Is the protein glycosylated or otherwise modified?
- Do you have detergents in the sample buffer?

3. Sample preparation

- If really needed, use only little amount of detergent, otherwise the LC-MS system will not work. So far, we have successfully tested the following detergents at given concentration:
    - Tween ≤ 0.05%.
- Submit pure proteins (should be determined with the help of SDS page in your lab).
- Bring around 100 pmol/measurement of your protein.

4. General information

- We will provide you the results within 4 weeks from the sample submission