

# GUIDELINES AND INFORMATION FOR CUSTOMERS OF CFMP ZMBH

## Title: Intact Protein Mass Determination by LC ESI-MS

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### 1. PURPOSE

This document describes the recommendations regarding sample preparation and submission to Core Facility for Mass Spectrometry and Proteomics for **intact protein mass determination**.

### 2. DURING INITIAL MEETING INFORM US ABOUT

- Do you already have iLab account?  
[https://hmls.corefacilities.org/service\\_center/show\\_external/3564?name=core-facility-for-mass-spectrometry-proteomics](https://hmls.corefacilities.org/service_center/show_external/3564?name=core-facility-for-mass-spectrometry-proteomics)
- 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. RECOMMENDATIONS

- Use detergent/free buffer! Glycerol must be less than 5%.
- If it is not possible to keep the protein in solution without detergent, use only very low amounts of detergents, because they heavily interfere with chromatographic separation. At the moment we have successfully tested the following concentrations so far: Tween  $\leq$  0.05%.
- Submit pure proteins (can be checked by you with help of SDS page).
- 100ul are needed for a single analysis. Protein concentration: 100pmol/100ul (5ug/100ul of a 50kD protein)
- *Freshly prepared samples? Storage on ice?*

### 4. GENERAL INFORMATION

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

- Your samples will be analyzed using a 35 min isocratic separation method (50€/sample (internal); 62,5€/sample (external)).