

Analysis of Proteins by Mass Spectrometry

We can run the following ESI-MS analysis (ASL rates/analysis):

1) intact protein (up to 80kDa).

Please provide sample in 10mM NH₄OAc. No Tris, HEPES, or other organic buffers, and the protein must have been desalted (minimal Na⁺ or K⁺). An easy way to desalt is to precipitate protein with acetone and wash multiple times with deionized water prior to dissolving in ammonium acetate. We need around 50uL of a 50 uM protein.

You will get a full scan ESI-MS spectra and the deconvoluted monoisotopic mass of your protein sample.

2) Gas-phase (top-down) sequencing of protein: please consult LC-MS manager.

3) protein digests (in-gel or in solution)

Please provide us with the protease-digested samples in 10mM NH₄OAc. No Tris, HEPES, or other organic buffers, and the protein must have been desalted (minimal Na⁺ or K⁺). An easy way to desalt is to precipitate protein with acetone and wash multiple times with deionized water prior to dissolving in ammonium acetate. Do this prior to protein digestion. We can also give you a working digestion protocol (if needed). Please don't use Sigma trypsin, only use MS-grade proteases (like the ones sold by Promega or Pierce) . Please show us a picture of the gel band (prior to digestion) or 50 uL digests (protein starting concentration: at least 20u M)

- Protein digestion can be done in-house at a higher price (P3,500).

You will get a full scan ESI-MS spectra and the deconvoluted monoisotopic masses (and/or peak list) of all the peptides in your sample.

For those who want MS/MS data, please provide please consult LC-MS manager.

- Analysis price only covers the cost of running the samples and generating a mass spectra. The client is responsible for mass spectral data analysis (protein identification, sequencing, and assigning fragmentation).
- If client does not know how to analyze MS data, he/she should ask ASL for a list of chemists who can interpret data. Chemists will charge consultation fees (based on degree and level of difficulty of spectral analysis)