Info Sheet: **Mass determination**

Mass analysis of intact proteins / Protein-metal complexes

General description:

Depending on the size of the molecule to be analyzed and the complexity of the sample (heterogeneity and matrix), either MALDI- or ESI- mass spectrometry (MS) is applied. Highly purified proteins will result in much simpler analysis strategies, while complex mixtures often demand for chromatographic separation or additional purification steps.

The workflow consists of:

- (Optional) Sample clean-up (TCA precipitation / filtration / desalting / deglycosylation)
- (Optional) protein reduction / alkylation
- (LC) ESI-MS or MALDI-MS
- Data analysis
    - deconvolution of the acquired mass spectra
    - (optional) annotation, generation of data in other formats
- Report
- Expected turnaround time (after physical arrival of samples):
    - 3-5 days

Requirements and considerations:

- Volume: >5 µl;
- Minimal concentration: 1-5 pmol/µl; optimal concentration: 10-500 pmol/µl
    - rule of thumb concentrations of (mass in kDa) x 1 pmol/µl are optimal
- If possible dilute or dissolve sample in volatile solvents / free of non-volatile buffers, salts, detergents, glycerol, etc.
- Salt and buffer containing samples may be submitted (we will desalt them on ZipTips prior to the analysis). In some cases, SEC cartridges or LC/MS will be used.

Oligonucleotides, Oligosaccharides, Small organic compounds

General description:

The same mass determination workflow can be applied to almost any type of (bio)molecule, including oligonucleotides and oligosaccharides.

Requirements and considerations:

- Please contact us at proteomics@fgcz.ethz.ch before submitting new type of samples.