

Analytical methods used in mass spectrometry (Quality Control)

The quality control analysis is performed by using one of the four in-house analytical methods, depending on the nature of the sample (i.e. number of proteins/peptides, the nature and the molecular weight of the proteins/peptides) and the aim of the analysis (molecular weight measurement or Top-Down sequencing of intact proteins).

The analytical methods were developed on the two time-of-flight (TOF) instruments equipped with either an electrospray (ESI-TOF) or a matrix-assisted laser desorption ionization source (MALDI-TOF) as summarized below:

ESI_m1

The sample is analyzed by LC-ESI TOF MS (LC: liquid chromatography, ESI: electrospray ionization, TOF: time of flight, MS: mass spectrometry) with a desalting step on a trap column and elution in isocratic mode.

Analysis time: 10 min/sample.

Sample type: purified proteins and peptides in solution.

ESI_m2

The sample is analyzed by LC-ESI TOF MS with a desalting step on a trap column and separation step by gradient on a reverse phase column.

Analysis time: 30-45 min/ sample.

Sample type: mixtures of proteins or peptides in solution; protein limited proteolysis samples in solution.

MALDI_m1

The sample is analyzed by MALDI TOF MS (MALDI: Matrix Assisted Laser Desorption Ionization, TOF: Time of Flight, MS: Mass Spectrometry) after a dilution or a desalting step.

Analysis time: 10-20 min/sample.

Sample type: purified proteins and peptides in solution.

MALDI_m2

The sample is analyzed by MALDI TOF/TOF MS after a dilution or a desalting step by applying the in-source decay (ISD) sequencing method.

Analysis time: 10-20 min/sample.

Sample type: purified proteins and peptides in solution.