

Specifications

The Naval Research Laboratory requires a Matrix-Assisted Laser Desorption (MALDI) time-of-flight mass spectrometer for research related to the analysis of polymers with high precision per the following specifications.

MALDI Mass Spectrometer Requirements.

A) General

- 1) The instrument must be benchtop in design, having a footprint smaller than 1m x 1m (WxD). The height of the instrument must not exceed 2m.
- 2) The system must include a personal computer for controlling the instrument and its various components with minimal maintenance or attention by the operator.
- 3) Must include a vacuum system with appropriate gauges to monitor the pressure.
- 4) Must include high voltage components with appropriate gauges to monitor the voltage.
- 5) The instrument must have a camera to view the sample during laser irradiation
- 6) An isolation valve must be fitted to the system to allow the target plate to be removed and cleaned without breaking instrument vacuum.

B) Instrument Capabilities

- 1) Must be able to analyze samples by measuring either positive or negative ions and must be able to switch between modes using accompanying software.
- 2) Must be capable of both linear and reflectron time-of-flight mass spectrometry.
- 3) Must be capable of Time Lag Focusing (Delayed Extraction).
- 4) Must have an analog-digital converter with an acquisition rate of at least 2 GHz.
- 5) Must be able to acquire full spectral data at least 10 spectra/sec
- 6) The system must include polymer analysis software for the interpretation of time-of-flight mass spectra of polymers, with the ability to automatically detect the repeat unit, cation and end groups. The software must be capable of calculating the “molecular weight average” and “polydispersity”.
- 7) The system must include protein and peptide processing software, including the ability to identify parent molecules from peptide digests

C) Minimum Performance Specifications

- 1) In linear mode, the instrument must have a resolution of $\geq 2,000$ for a peptide with a m/z of 1600.
- 2) In linear mode, the instrument must have a resolution of ≥ 70 for a protein with a m/z of 66,000.
- 3) In reflectron mode, the instrument must have a resolution of $\geq 10,000$ for a peptide with a m/z of 2,465.
- 4) In linear mode, the instrument must have an RMS error of less than 200 ppm for a protein mixture.
- 5) In reflectron mode, the instrument must have an RMS error of less than 15 ppm for a protein mixture