

Voyager-DE™ PRO Workstation

Matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry is a proven technology for the structural analysis of organic and inorganic compounds. Applied Biosystems MALDI-TOF mass spectrometers are the industry standard for superior spectral quality and industry leaders in technical innovations.

The Voyager-DE™ PRO Workstation is a compact benchtop MALDI-TOF mass spectrometer that includes a linear and reflector analyzer, easy-to-use instrument software, and unique analysis tools that help you to quickly master a wide range of biological challenges.

Linear and reflector operations provide the high performance specifications required to complete protein identification studies, synthetic peptide validation experiments, and small molecule and polymer analysis, all in a single instrument platform.

The reflecting ion mirror boosts resolution and mass accuracy and allows post-source decay (PSD) experiments so that you can obtain valuable peptide sequencing information. Additional structural information is also available by using the collision-induced dissociation (CID) option for enhanced fragmentation.

Instrument Hardware:

- Patented Delayed Extraction® technology.
- 1.30-m effective path length, reflector mode.
- 100x video camera with dedicated monitor for magnified view of sample spot and laser position.



Figure 1. Applied Biosystems Voyager-DE™ PRO Workstation with data station.

- 337-nm nitrogen laser producing 3-ns pulses at repetition to 20 Hz.
- 4,000-step variable laser intensity with neutral-density filter.
- Negative ion operation.
- Ion acceleration between +25 kV and -20 kV.
- Low mass gate filters matrix ion interference.
- Automatic vacuum system with two air-cooled turbomolecular pumps.

Data System Hardware (Minimum):

- 733-MHz Pentium III (minimum) processor.
- 256 MB system RAM.
- 4 MB video RAM.
- 30-GB hard drive.
- On-board network card.
- 17 x 40 CD-ROM drive.
- Integrated 3COM ethernet adapter.
- 19" high-resolution color monitor.
- Microsoft® Windows NT® operating platform.
- Includes Microsoft® Office 2000.

Installation Requirements:

- Dedicated circuit: 20 A at 120 V (60 Hz) or 10 A at 230 V (50 Hz).
- No need for water cooling or compressed air.
- Footprint: 165 cm high x 64 cm wide x 69 cm deep.
- Weight: approx. 159 kg (350 lbs), excluding data station.

Mass Accuracy:

Linear Mode, External Calibration:

- $\leq \pm 0.05\%$ for angiotensin [1,296.6853] and myoglobin [16,952.5].

Reflector Mode, External Calibration:

- $\leq \pm 0.01\%$ for ACTH 18–39 [m/z 2,565.1989].
- $\leq \pm 0.01\%$ for *E. coli* thioredoxin [m/z 11,674.4].

Mass Resolution:

Linear Resolution:

- $\geq 2,500$ for angiotensin (m/z 1,296).
- $\geq 1,000$ for myoglobin (m/z 16,952).
- ≥ 80 for BSA (m/z 66,431).

Reflector Resolution:

- $\geq 10,000$ for insulin (m/z 5,734).

Sensitivity:**Reflector Mode:**

S/N ≥ 10 for 5 fmol of neurotensin (m/z 1,672. 918), a minor component, in a mixture of low-mass peptides.

Linear Mode:

S/N ≥ 20 for 5 fmol of neurotensin (m/z 1,672. 918), a minor component, in a mixture of low mass peptides.

Post-Source Delay Mass Accuracy:

$\leq \pm 0.2$ m/z using histidine fragment of angiotensin (110.07 monoisotopic).

System Software:

Voyager™ 5 Software provides high-throughput acquisition and automated peak detection. The user-friendly instrument control panel lets you display and customize configuration settings and acquisition commands simultaneously. Exclusive data processing algorithms with an integrated macro capability let you access the unique performance enhancing analysis tools of the Data Explorer® Analysis Software.

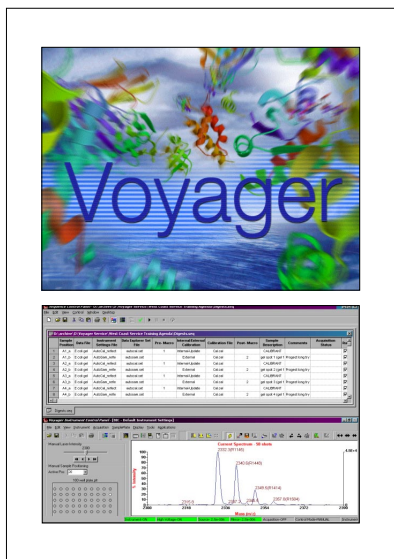


Figure 2. Voyager™ 5 Software for high-throughput acquisition and automated peak detection.

Optional Accessories:**The Proteomics Solution 1™ (PS1)**

Data Station for automated database searching is a powerful application software package that enables optimization and throughput of your peptide mass fingerprinting experiments. The PS1 Software is installed on a high-performance computer system and includes a Microsoft® Access database for complete sample tracking, report generation, and results querying for confident protein identification.

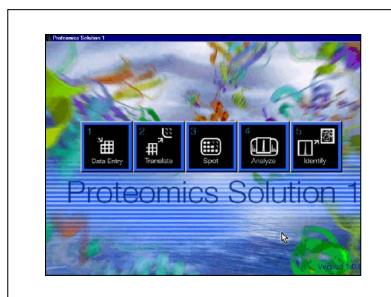


Figure 3. Proteomics Solution 1™ Software for peptide mass fingerprinting.

PS1 Advanced Results Browser (ARB)

simplifies the results of your PS1 peptide mass fingerprinting experiment. The software provides comparative analysis tools for quick evaluation of protein identification results and relative quantitation information. It evaluates expressed protein levels in diseased and non-diseased state samples that have been labeled using the Isotope Coded Affinity Tag Reagent.



Figure 4. PS1 Advanced Results Browser.

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Printed in the USA, 07/2002
Publication115DA02-01