

Voyager-DE™ STR 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. The Applied Biosystems MALDI-TOF mass spectrometers are the industry standard for superior spectral quality, delivering high resolution, sensitivity, and exceptional mass accuracy.

Linear and reflector operations provide the high-quality 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 provides unparalleled 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.

Innovative designs for ion focusing and fragmentation provide unmatched structural information, giving you the tools you need to characterize complex mixtures and determine molecular weights of low-femtomole samples.

Instrument Hardware:

- Patented Delayed Extraction® technology.
- 2-m effective path length, reflector mode.
- 100x video camera with dedicated monitor for magnified view of sample spot and laser position.
- 337-nm nitrogen laser producing 3-ns pulses at repetition rate to 20 Hz.



Figure 1. Voyager-DE™ STR Workstation.

- 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.

Key Features:

- The ultimate MALDI-TOF system provides the highest quality data.
- Reflectron provides high mass accuracy and PSD.

- Fully automated acquisition and processing of data provides higher throughput.
- Integrated Microsoft® Visual Basic® for Applications (VBA) permits macro recording and customization of processing routines.

Installation Requirements:

- Requires a single-phase 50/60-Hz power source at one of the following voltages: 110 V, 16 A; 120 V, 16 A; 220 V, 10 A; or 240 V, 10 A.
- No need for water cooling or compressed air.
- Footprint: 117 cm high x 239 cm wide x 87 cm deep.
- Weight: approx. 499 kg (1,100 lbs).

Mass Accuracy:

Linear Mode, External Calibration:

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

Reflector Mode, External Calibration:

- $\leq \pm 0.008\%$ for ACTH 18-39 [m/z 2,565.1989].
- $\leq \pm 0.005\%$ for *E. coli* thioredoxin [m/2 1,1674.4] $\pm 0.005\%$ ACTH 18-39.

Mass Resolution:

Reflector Resolution:

- $\geq 20,000$ for insulin (m/z 5,734).
- $\geq 12,000$ for ACTH clips.

Linear Resolution:

- $\geq 3,000$ angiotensin.
- $\geq 3,500$ for ACTH 18–39.
[m/z 2,465.1989].
- $\geq 1,000$ for myoglobin (m/z 16,952).
- ≥ 100 for BSA (m/z 66,431).

Sensitivity:

Routine detection of 5 fmol of neurotensin with a signal to noise ratio $> 80:1$.

Post-Source Decay Mass Accuracy:

≤ 0.2 with default calibration.

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.

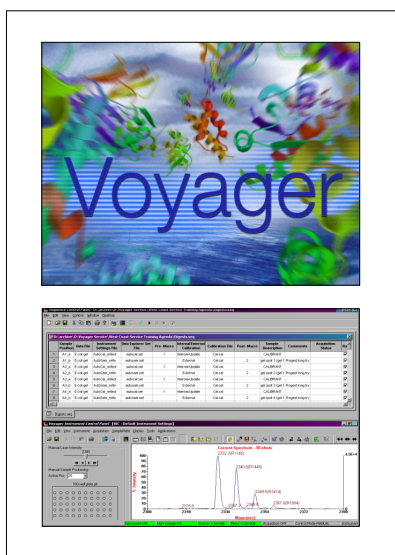


Figure 2. Voyager™ 5 Software for high-throughput acquisition and automated peak detection.

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.

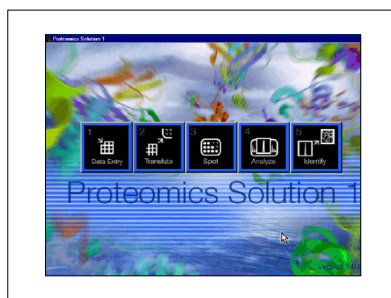


Figure 3. Proteomics Solution 1™ Software for peptide mass fingerprinting.

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.

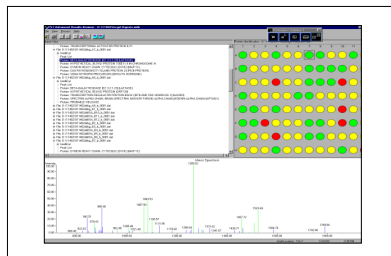


Figure 4. PS1 Advanced Results Browsers.

Worldwide Sales Offices

Applied Biosystems vast distribution and service network, composed of highly trained support and applications personnel, reaches 150 countries on six continents. For international office locations, please call the division headquarters or refer to our Web site at www.appliedbiosystems.com.

Applera is committed to providing the world's leading technology and information for life scientists. Applera Corporation consists of the Applied Biosystems and Celera Genomics businesses.

Headquarters

850 Lincoln Centre Drive
Foster City, CA 94404 USA
Phone: 650.638.5800
Toll Free: 800.345.5224
Fax: 650.638.5884

For Research Use Only.
Not for use in diagnostic procedures.

AB (Design), Applera, Voyager, and Voyager-DE are trademarks and Applied Biosystems, Data Explorer, and Delayed Extraction are registered trademarks of Applera Corporation or its subsidiaries in the US and certain other countries.

Microsoft and Visual Basic are registered trademarks of Microsoft Corporation.

©2002 Applied Biosystems. All rights reserved.
Information subject to change without notice.

Printed in the USA, 07/2002
Publication 115DA03-01