

Mass Spectrometers

MALDI Micro MX MALDI-TOF (Waters)



The instrument, consisting of a TOF (Time Of Flight) analyzer and a MALDI (Matrix Assisted Laser Desorption Ionization) source provides accurate information on the structure and molecular weight of biomolecules such as peptides, proteins, oligonucleotides and carbohydrates, as well as synthetic polymers. Furthermore, through the PMF (Peptide MassFingerprinting) technique, it enables ultra-fast identification of the proteins separated by 2D electrophoresis. The elute from in situ protein digestion, mixed with the matrix (organic acid), is deposited (1 μ L) on a steel target and left to crystallise before being transferred to the vacuum system. A laser pulse extracts from the target the molecular ions, which are subsequently accelerated by an electrical field and cross the flight tube, enabling, after appropriate calibration, measurement of molecular weight.

ESI-Q-TOF Ultima (Waters)



ESI QTOF MS is a dynamic technique that allows the coupling of the mass spectrometer to a liquid chromatography interface. ESI QTOF MS is used for the sequencing/identification of proteins and/or locating post-translational modifications such as phosphorylation/glycosylation/alkylation etc. Q-Tof Ultima is a quadrupole, orthogonal acceleration time-of-flight tandem mass spectrometer. This instrument is coupled with a CapLC for chromatographic separations and is outfitted with NanoLockSpray technology enabling accurate mass measurement to <5ppm. This instrument can operate in MS mode, allowing an accurate determination of molecular masses, in data-dependent

acquisition mode (DDA) for serial MS/MS acquisition, or can perform selected MS/MS experiments to investigate molecular structure.

6340 ESI Ion Trap (Agilent)



This mass spectrometer is constituted by a chip based nano-chromatography system, interfaced to an ESI source coupled to an Ion Trap analyser. The fragmentation power of ETD is integrated, providing a "softer" mode of fragmentation than classical CID, thus preserving protein labile modifications. ETD and collision induced dissociation (CID) modes of fragmentation from scan to scan help to pinpoint the

precise identity and location of a chemical modification. In addition, neutral-loss triggered auto-MS3 can be used to target specific families of modifications.

LTQ Orbitrap Velos (Thermo Scientific)



LTQ Orbitrap Velos is the next generation mass spectrometers, thanks to its significantly increased sensitivity and scan speed. This is achieved by a vacuum interface using a stacked ring radio frequency ion guide with 10-fold higher transfer efficiency in MS/MS mode and 3–5-fold in full scan spectra, by a dual pressure ion trap configuration, and by reduction of overhead times between scans. The first ion trap efficiently captures and fragments ions at relatively high pressure whereas the second ion trap realizes extremely fast scan speeds at reduced pressure. Ion injection times for MS/MS are predicted from full scans instead of performing automatic gain control scans. Together these improvements routinely enable acquisition of up to ten fragmentation spectra per second. Furthermore, an improved higher-energy collisional dissociation cell with increased ion extraction capabilities was implemented. Higher-collision energy dissociation with high mass accuracy Orbitrap readout is as sensitive as ion trap MS/MS scans in the previous generation of the instrument.

Further, this configuration is supplied with ETD module, which preserves protein labile modifications.

Systems for IEF and 2D PAGE

Ettan™ IPGphor™ 3 IEF System (GE Healthcare)



The Ettan™ IPGphor™ 3 IEF System is a fully integrated isoelectric focusing system optimized to deliver speed and reliability in the first dimension of 2-D electrophoresis. The instrument runs up to 12 IPG strips (7, 11, 13, 18, or 24 cm) simultaneously using Ettan IPGphor Manifold, Ettan IPGphor Manifold Light, or ceramic strip holders. Its lid design allows optimum running with light-sensitive protein samples, such as 2D-DIGE. The Ettan IPGphor 3 Control Software is also available.

Ettan™ DALTwelve Large Vertical System (GE Healthcare)



Ettan DALTwelve System can run simultaneously up to 12 large-format gels in 4 to 6h. The system streamlines performing second-dimension SDS-PAGE separations, increasing productivity while delivering high throughput, resolution, and reproducibility. When used in combination with 24 cm Immobiline™ DryStrip gels, Ettan DALTwelve maximizes the number of discrete, quantifiable protein spots obtainable per large-format gel.

Ettan™ DALSix Large Vertical System (GE Healthcare)



Ettan™ DALSix Electrophoresis Unit runs up to six large format (26×20cm) second-dimension polyacrylamide gels in just 4-5h. The gels accept first dimension 18- or 24-cm Immobiline DryStrip gels (IPG strips) from both Ettan IPGphor™ and Multiphor™ II isoelectric focusing systems. The system components include Ettan DALSix Electrophoresis Unit, Gel Caster and Gradient Maker, an EPS 601 Power Supply, and MultiTemp™ III Thermostatic

Circulator.

Mini and Midi format Electrophoresis Systems (Bio-Rad)



Several mini and midi cells are available for SDS-PAGE, 2D-PAGE, and Western Immunoblotting. Specifically, MiniProtein Tetra Cells and Criterion Cells, plus immunoblotting systems up to 24 cm are present in the laboratory.

SERVA HPE™ Tower



The SERVA HPE™ Tower runs four large format (26×20cm) second-dimension polyacrylamide gels in just 4-5h. The instrument consists of four horizontal cooling plates, which are built as movable drawers. The pre-cast gels, which are less than 1 mm thin and film-backed, are protected from light during the run. Instead of buffer chambers as buffer reservoirs fiber wicks are soaked with concentrated buffers and placed between the gel edges and the electrode. The HPE™ Tower is run with an external power supply and a chiller.

Image Acquisition and Analysis

ImageScanner™ III (GE Healthcare)



A highly sensitive flatbed scanner for most common nonfluorescent densitometric applications in the life sciences, especially electrophoresis evaluation. The scanner has a linearity above 3.4 OD, with 16-bit pixel depth, providing accurate quantitation and high sensitivity of very faint images without additional filters.

VersaDocMP 4000 (Bio-Rad)



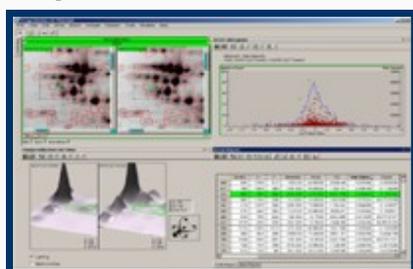
The VersaDoc MP 4000 is the perfect proteomics imager, offering ultimate flexibility with the ability to image chemiluminescent western blots, Coomassie Blue-stained 1-D gels, SYPRO Ruby-stained 2-D gels, and multiplex or multifluorescent samples with a single system. The MP 4000 provides excellent resolution for collecting the finest details of every band and spot. The patented flat fielding technology generates highly uniform data for accurate quantitation across small and large 2-D samples.

DIGE Enabled Typhoon Trio™ Variable Mode Imager



DIGE Enabled Typhoon Trio Imager provides multicolor scanning and optimized detection of CyDye DIGE Fluor dye-labeled proteins. Powerful excitation sources and innovative high quality confocal optics allow sensitive detection of low-abundance targets. The DIGE Enabled Typhoon Trio Imager delivers outstanding linearity, quantitative accuracy, and extremely low limits of detection. Automated multicolor scanning permits detection of multiple samples in the same experiment, which ensures accuracy of analysis, increasing throughput and saving time.

ImageMasterPlatinum and DeCyder (GE Healthcare); PDQuest and QuantityOne (Bio-Rad)



ImageMaster™ 2D Platinum v7.0 offers a flexible interface for the comprehensive visualization, exploration, and analysis of 2-D gel data from non-DIGE technologies. DeCyder™ 2-D Differential Analysis Software (DeCyder 2D) v7.0 is specifically designed for 2-D Fluorescence Difference Gel Electrophoresis (2-D DIGE) analysis and is a key element in the Ettan™ DIGE system. Unlike other 2-D electrophoresis methods, DIGE allows the option of reference to an internal standard for each spot, effectively eliminating gel-to-gel

variation and delivering highly accurate, reproducible, and dependable quantitation. DeCyder 2D applies a gel comparison method that introduces zero statistical error, offering reliable data and analysis for 2-D DIGE experiments. PDQuest software offers powerful comparative gel analysis. Sophisticated analysis tools reveal subtle differences among gels being analyzed (for example, studying the effect of variables such as heat shock, growth media, dose-response, and time course).



Quantity One® is a powerful, flexible software package for imaging and analyzing 1-D electrophoresis gels, dot blots, slot blots, and colonies. Quantity One can quantitate and analyze a wide variety of biological data, including radioactive, chemiluminescent, fluorescent, and color-stained samples acquired from densitometers, phosphor imagers, fluorescent imagers, and gel documentation systems.

Systems for protein extraction quantification handling purification and synthesis

Qiagen TissueLyser



The TissueLyser II simultaneously disrupts multiple biological samples through high-speed shaking in plastic tubes with stainless steel, tungsten carbide, or glass beads. Using the appropriate adapter set, up to 48 or 192 samples can be processed at the same time.

Automated TecanEvo75 liquid handling station



The TecanEvo75 available in our laboratories is a compact liquid handling device configured for handling microtiter plates and for the setup of quantification and analysis methods. A liquid handling and a robotic manipulator arm are present, together with microplate washers, incubators, and readers.

Liberty CEM Microwave Peptide Synthesizer



Peptide synthesizer using microwave energy for the complete peptide synthesis process.

Microwave energy drives biochemical reactions to completion up to 10 times faster than by conventional methods, resulting in peptides of greater purity than can be produced under conventional methods. The Liberty peptide synthesizer's unique utilization of microwave energy gives researchers active in the study of proteins the unprecedented ability to synthesize peptides that were previously inaccessible by conventional synthetic methods. The system is capable of synthesizing up to 12 peptides at scales up to 5 mmol.

AKTA Explorer 10 (GE Healthcare)



ÄKTAexplorer is an FPLC system designed for scouting, development, and optimization of methods for all chromatographic techniques. Flexibility and high levels of automation in combination with reproducibility and reliable operation make it an excellent choice for laboratories involved in method and process development. Scouting, developing, and optimizing methods for all liquid chromatography techniques are the strengths of the ÄKTAexplorer systems. Broad capabilities and flexibility, high levels of automation, simple user interface, and accurate, reproducible, and reliable operation makes it suited for laboratories involved in preproduction method scouting or in developing and optimizing methods.