

# Company Overview

## About Us

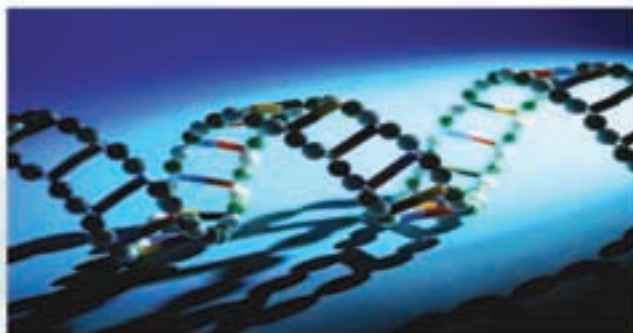
Bruker Daltonics is a leading developer and supplier of mass spectrometers and related accessories for the areas of biochemical, biological, and pharmaceutical research, as well as substance detection and pathogen identification.

Bruker Daltonics is the only major manufacturer with life science mass spectrometry as our primary business. We have one of the broadest sets of mass spectrometry platforms for the research and development of new life science systems and techniques. We have two business groups to reflect our markets: Life Science Systems, and the Substance Detection and Pathogen Identification Division (also referred to as "ABCDE," short for atomic, biological, chemical, drug, and explosive/ environmental detection). Our mass spectrometers are used extensively throughout these markets in a wide variety of applications.

metabolomic and biomarker profiling, and fates) is referred to as "Metabolomics." Thus, continued study of the genome is "Genomics." Combined, Proteomics, Metabolomics, Genomics, and related areas of Drug Discovery, molecular biology, and medical research are now considered among the most important areas of scientific research and discovery within the first part of this new century. Mass spectrometry is ideally suited for many of these areas of research, providing precise sequence information where required,

often with extremely high-throughput. We also offer bioinformatics tools to easily manage the entire process, with on-line research and advanced data management.

### Mass Spectrometry and Substance Detection and Pathogen Identification



### About Mass Spectrometers

Mass spectrometers are precision instruments used to identify molecules and their composition. These molecules can range in size from "small" molecules such as drugs (with molecular weights under 1,000 Daltons), to large proteins (with molecular weights of 10,000 Daltons or greater). The extreme versatility and sensitivity of mass spectrometers makes them perfect for the study of biological and related compounds.

### Mass Spectrometry and the Life Sciences

Mass spectrometry has become recognized as a primary tool for the study of the life sciences. The completion of the Human Genome Project has recently shifted attention to research of the proteome. The study of the proteome, how genes express proteins and their related compounds, as well as how these proteins function, is referred to as "Proteomics." Similarly, the study of the metabolites which result from these activities (including the study of disease pathways,

Substance detection and pathogen identification devices can be used for anti-terrorism, law enforcement, field detection of chemical and biological agents, radiation, illegal drugs and trace explosives, as well as facilities monitoring. Law enforcement agencies, emergency response, and government defense agencies use our portable or fixed detection and identification systems, many of which are based on the same mass spectrometry technology as our life science systems.

Life Science systems represented approximately 74% of our revenues in 2001, and were based on four main technology platforms. These are Matrix Assisted Laser Desorption Ionization (MALDI) Time of Flight (TOF) mass spectrometry, ElectroSpray Ionization (ESI) TOF mass spectrometry, Fourier Transform mass spectrometry (FTMS), and Ion Trap mass spectrometry (ITMS).



# Company Overview

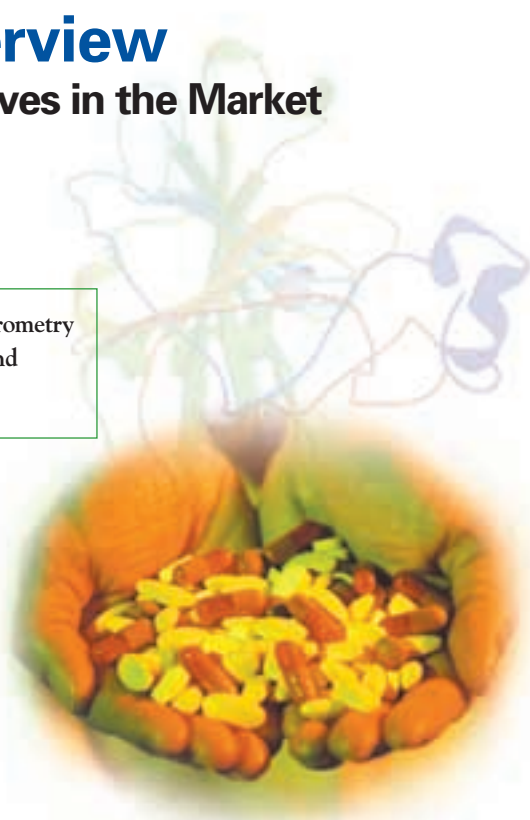
## Where We See Ourselves in the Market

Our goal is to grow our position as a leading provider of mass spectrometry and related solutions for the life sciences and substance detection and pathogen identification markets.



Our future growth is based on important global trends which have long-term implications, including the completion of the Human Genome Project, the opportunities of the post-genomic era, the acceleration of drug discovery, and a need for greater security. In the aftermath of 9/11, there is a recognized need for more portable, faster, and more sensitive methods of chemical and biological substance detection for many applications. We believe we can meet these needs, and we will continue to develop state-of-the-art instrumentation in this area.

We are at the dawn of a new era, in which our customers are beginning to find cures and responses to many diseases previously thought to be unapproachable. New advances in proteomics, genomics, drug discovery, and related areas have already saved lives and brought new hope. Our new products, such as the **ultraflex™ TOF/TOF** and the **BioTOF™ Q** tandem mass spectrometers, represent major advances in our customers' abilities to make critical breakthroughs in these areas of study. Similarly, our **Proteineer™ Suite** of products automates the preparation of proteins from gel separation to preparation on microarrays, increasing efficiency of analysis and bioinformatic knowledge gain.




We recognize the need to continually develop new platforms and applications. We will continue to integrate our technologies across new and existing platforms and provide new levels of automation in sample preparation and processing – with bioinformatics to make the management of the resulting high volumes of data and information easy and powerful. To this end, we will seek to improve upon and increase our strategic alliances and pursue acquisitions and other methods of business growth and development wherever applicable. We will continue to leverage our intellectual property, and we will maintain high standards of scientific integrity throughout our endeavors.

*Bruker Daltonics was incorporated in Massachusetts, as Bruker Federal Systems Corporation. In February 2000, we reincorporated in Delaware as Bruker Daltonics Inc. On August 4, 2000 we became a publicly traded company.*



# To Our Shareholders

Much has been written about healthcare, scientific, and economic trends, as well as the events of the past year and how our lives have changed. Bruker Daltonics has performed very well during this challenging year and is committed to meeting the new challenges presented in 2002, and to do our part in helping agencies, companies, and others in building a healthier future.



With the completion of the sequencing of the human genome, the next step is to understand the function of these genes on an individual basis. Consequently, the study of genetic variation and of the proteins encoded by these genes has become of paramount importance. Both the areas of the actual gene expression (“expression proteomics”) and determination of the functionalities of the expressed proteins (“functional proteomics”) are tremendous in scope as well as scale. Our exciting new **Proteineer** Suite of products has been specifically created to address these challenges: Proteineer integrates our complete line of **MALDI-TOF**, **ESI-Ion Trap**, and **ESI-Q-q TOF** mass spectrometer systems, a complete range of automated sampling, preparation, and handling robotics, and a full suite of bioinformatics software for easy data processing and analysis.



Our new tandem mass spectrometers, the **BioTOF Q (Q-q-TOF)** and the **ultraflex TOF/TOF**, have literally changed the way in which we think about mass spectrometry. The **ultraflex TOF/TOF** performs initial high-throughput screening using **MALDI-TOF** analysis, and then on the same sample, provides ultra-high sensitivity analysis via **MALDI-TOF/TOF** for extremely detailed protein characterization.

We continue to be the leader in **FTMS**, with a commitment to more automated **FTMS** systems.

For all of our life science mass spectrometry systems, the areas of proteomics and pharmacogenomics (the study of the efficacy, pharmacology, and toxicity of drugs) have been prime growth areas, and we look for that trend to continue in the coming year. We continue our drive to create more powerful and flexible systems and to make our mass spectrometers more automated and easier to use.

For the full year 2001, new life science systems bookings increased by more than 25% when compared to the full year 2000. Our total revenues in 2001 were approximately \$93 million, up from \$76 million in 2000. For the full year 2001, our life science systems bookings growth was led by **MALDI-TOF**, which includes **MALDI-TOF/TOF**, with more than 40% growth. **Ion Trap** mass spectrometry (**ITMS**) grew more than 30% for all **ITMS** unit bookings sold either directly by us or via our strategic **ITMS** partner **Agilent Technologies**.

**Frank H. Laukien, Ph.D.**  
Chairman, President  
and Chief Executive Officer of  
Bruker Daltonics Inc.

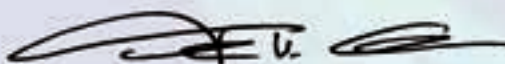
For the year 2002, we are optimistic that demand for our products, many of which are still in the early product ramp-up phase, will continue to grow at a rapid pace. During 2002, we anticipate several significant new product introductions, which should contribute to our growth objectives.

We continued our collaborative efforts in the life sciences by forging new strategic alliances with Integrative Proteomics, Biacore International, GeneFormatics, and Intrinsic Bioprobes. These are in addition to our ongoing agreements with Sequenom, Agilent, GeneProt, and Variagenics. These alliances benefit us greatly from new applications of their technologies, and in many cases, their sales and marketing efforts.

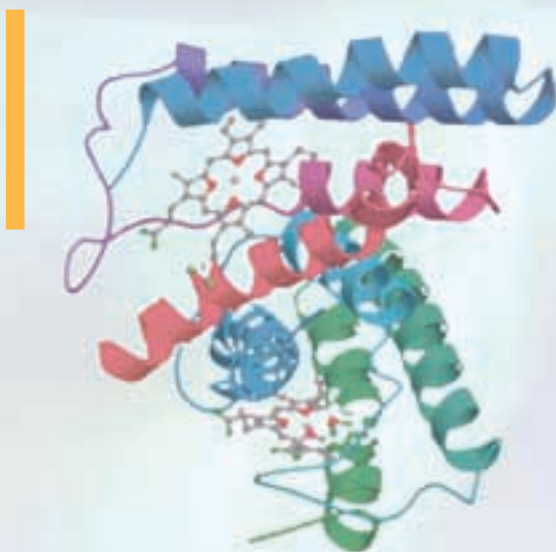
In other important developments of 2001, Bruker Daltonics and Thermo Finnigan Corporation announced a comprehensive settlement agreement in our litigation in the U.S. and Europe. The worldwide settlement agreement provides for the dismissal of all pending suits, the waiving of all damages, and a framework of licensing and arbitration for potential future patent disputes between the companies in the field of Ion Trap mass spectrometry (ITMS).

In September, 2001, our substance detection and pathogen identification (ABCDE) division received a major contract for \$10 million. The Chemical Biological Mass Spectrometers (CBMS) are primarily used for the detection of biological warfare agents, and are an integral part of the Army's Biological Integrated Detection System (BIDS). We began an increased market-awareness campaign of our ABCDE products in 2001; these products represented 10% of our fiscal year-end 2001 revenue.

In 2002, we expect to occupy our new U.S. headquarters and to complete expansion of our Bremen, Germany facility, both of which are equipped with state-of-the-art manufacturing and demonstration facilities. We believe that the demand for life science solutions and substance detection and pathogen identification products will continue to grow, as will our position as a technological leader for these markets.



Frank H. Laukien, Ph.D.  
President and Chief Executive Officer



# Corporate Officers



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Vice President of  
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Jochen Franzen, Ph.D.  
Managing Director of  
Bruker Daltonik GmbH



Dieter Koch, Ph.D.  
Managing Director of  
Bruker Daltonik GmbH  
Managing Director of  
Bruker Saxonian Analytik GmbH;  
Director of  
Bruker Daltonics Inc.



Hans-Jakob Baum  
Vice-General Manager of  
Bruker Daltonik GmbH  
Managing Director of  
Bruker Saxonian Analytik GmbH

## Management Team

**Frank H. Laukien, Ph.D.**  
Chairman, President, and  
Chief Executive Officer

**Dieter Koch, Ph.D.**  
Managing Director of  
Bruker Daltonik GmbH;  
Managing Director of  
Bruker Saxonian Analytik GmbH

**Jochen Franzen, Ph.D.**  
Managing Director

**Hans-Jakob Baum**  
Vice-General Manager  
of Bruker Daltonik GmbH  
and Managing Director  
of Bruker Saxonian  
Analytik GmbH

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Vice President

**Gary Kruppa, Ph.D.\***  
Vice President

**Ulrich Giessman, Ph.D.**  
Vice President

**John J. Hulburt, CPA**  
Chief Financial Officer  
and Treasurer

## Board of Directors

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**Dieter Koch, Ph.D.**  
Director

**M. Christopher Canavan, Jr.**  
Director

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Environmental Molecular  
Sciences Laboratory; former  
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University of Warwick's Institute  
for Mass Spectrometry; Professor  
and Chairman of the  
Department of Chemistry

**Günther Heinrich, Ph.D.**  
Chief Executive Officer and  
President of EPIDAUROS AG

## Corporate Information

**Independent Auditors**  
Ernst & Young LLP  
200 Clarendon Street  
Boston, MA 02116

**Legal Counsel**  
Hutchins, Wheeler & Dittmar LLP  
101 Federal Street  
Boston, MA 02110

**Transfer Agent**  
American Stock Transfer &  
Trust Company

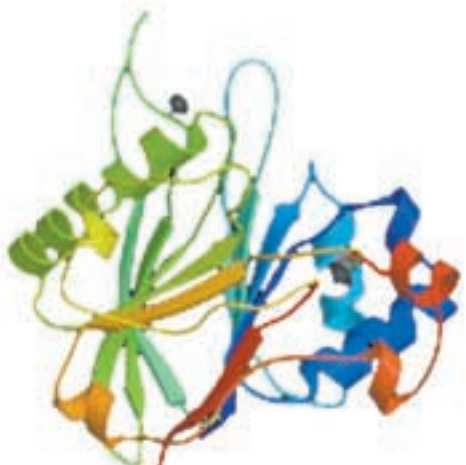


\* Currently on leave of absence and not presently active in the Company.

# Market Overview

## Applications: Life Sciences

Mass spectrometers are uniquely suited for the study of biochemistry, biomolecules, and biomolecular processes. The primary areas of interest can perhaps best be divided into three areas, Proteomics, Genomics (including Pharmacogenomics), and Drug Discovery (including Metabolomics). These areas are all very closely related and directly affect each other in many important ways. There are, of course, many other applications in the life sciences to which mass spectrometry is well-suited, but we believe the three areas above currently exhibit the most growth potential.

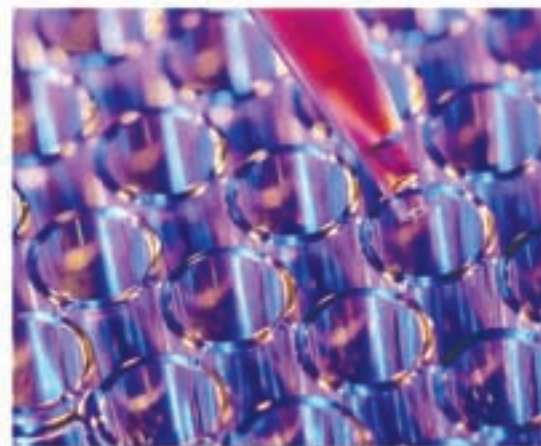


### PROTEOMICS

Now that the human genome has been sequenced, it is necessary to address the proteins that the genes encode. It may seem a relatively straightforward process of identifying the precise proteins expressed by specific genes, but the task has proven more daunting, due to several factors. To put it in a nutshell, very small modifications of proteins may occur during or after expression, simple changes that result in dramatically different activities of the proteins. A phosphorylation here, acetylation or glycosylation there, and the protein may take on an entirely new functionality, in many cases not doing something it was originally expressed to do.

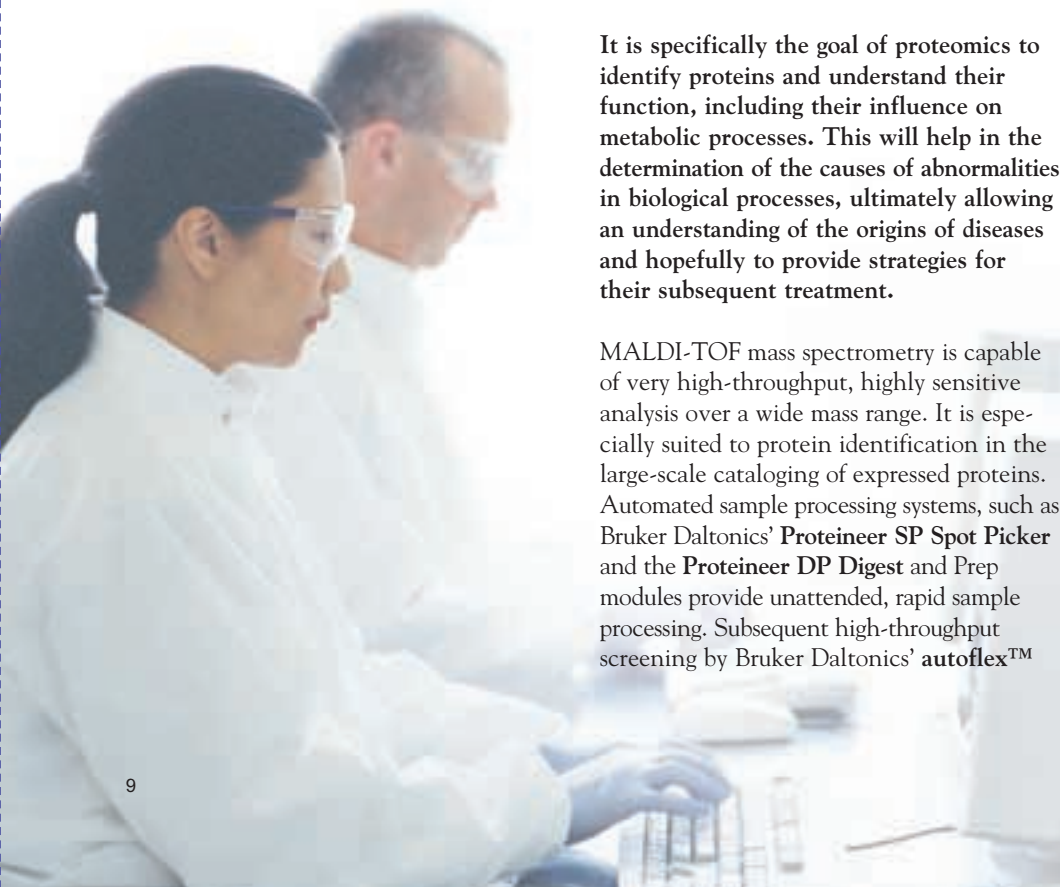
It is specifically the goal of proteomics to identify proteins and understand their function, including their influence on metabolic processes. This will help in the determination of the causes of abnormalities in biological processes, ultimately allowing an understanding of the origins of diseases and hopefully to provide strategies for their subsequent treatment.

MALDI-TOF mass spectrometry is capable of very high-throughput, highly sensitive analysis over a wide mass range. It is especially suited to protein identification in the large-scale cataloging of expressed proteins. Automated sample processing systems, such as Bruker Daltonics' **Proteiner SP Spot Picker** and the **Proteiner DP Digest** and Prep modules provide unattended, rapid sample processing. Subsequent high-throughput screening by Bruker Daltonics' **autoflex™**



MALDI-TOF, complete with the Zymark **Twister™** automated microtiter plate handler, can analyze up to 30,000 samples in one batch.

To determine the function of a protein, one must also determine its properties, including where it functions within a cell, its active binding site(s), and many other issues. Advanced levels of sample analysis for more in-depth structural information on particular proteins are routinely performed with MS/MS. Several technologies from Bruker Daltonics can fulfill this role, with MALDI using the Bruker Daltonics **ultraflex MALDI-TOF/TOF**, or with LS-MS/MS using the **esquire™3000plus ESI-Ion Trap** (and now the BioTOF Q). The **esquire3000plus** provides detailed structural information for individual proteins as they are eluted from an LC separation, with the added benefit of identification of post-translational modifications.





## GENOMICS

Very small changes in single genes may well result in the production of different functionalities in the proteins they express. Single-nucleotide polymorphisms, or SNPs, are minute changes in a gene due to defect or exogenous force that will result in production of proteins with different structure and functionality from the original design.

SNPs can occur in nature, or be intentionally introduced to create new proteins. Pharmaceutical companies often wish to associate groups of SNPs with diseases in their drug development and clinical trials for several purposes. The most obvious is to create new and improve upon existing drugs and to potentially provide “personalized medicines.” However, SNPs may also aid physicians in screening out patients that could have adverse or grave genetic predis-

positions to drugs prior to clinical trials, an issue that in 2001 came to prominence in the news. Screening genetic markers of patients could eventually become a major determining factor in defining the prescription of specific drugs to aid efficacy, in addition to preventing adverse reaction.

Mass spectrometers, in particular the Bruker Daltonics MALDI-TOF **autoflex** and **ultraflex**, are particularly well-suited to the high-throughput detection of SNPs in genes. Large-scale genotyping of this kind is the major pursuit of some of our channel partners, including Sequenom and Variagenics.

The **ultraflex** MALDI-TOF/TOF provides the most sensitive analysis possible, and has the added benefit of using the same microtiter plate that the sample was originally analyzed on during screening. Note that high-throughput screening may also be performed using the **ultraflex** in TOF mode, at the same rate as the **autoflex**. In this way, individual samples may be instantly re-analyzed in TOF/TOF mode when desired. These instruments and their many optional configurations, coupled with our advanced bioinformatics software, are the essence of the Bruker Daltonics **Proteomeer** Suite. For advanced studies including *de novo* peptide sequencing, protein-protein interactions, and protein-ligand interactions, the Bruker Daltonics **BioTOF Q** product provides essential information often not available with MALDI-TOF or ESI-Ion Trap techniques.

## DRUG DISCOVERY

There is a strong relationship between Proteomics and Genomics in modern drug discovery. Mass spectrometers are ideal for these areas of study in that they provide high-throughput, highly precise mass and corresponding structural information throughout the entire analytical process.

In drug discovery, minute changes in the structural makeup of a molecule or precursor can have dramatic effects on the efficacy of the resulting product. Extremely accurate methods of structural determination are required, as incorrect or incomplete determinations can provide useless or even catastrophic results. Bruker Daltonics' APEX FTMS system is capable of providing amongst the most accurate mass determinations of any analytical technique, in relatively short analysis times. It is a key instrument in many pharmaceutical companies for performing complex analysis during the drug development process.

The process of drug discovery also involves the testing of large amounts of materials to rapidly determine small structural differences during the synthesis of new compounds. This area of combinatorial chemistry requires high-throughput, high precision analysis which can be done by a variety of mass spectrometric techniques. Our **esquire3000plus** LC/MS/MS instrument is ideal for the analysis of smaller molecules, including many common drugs. For larger, more complicated complexes, and in the case of complex mixtures (such as racemic isomers and very high molecular weight molecules), the APEX is again the instrument of choice.



Metabolic profiling (“Metabolomics”), the study of the way a drug is metabolized in the body, is another extremely important part of the drug discovery process. Metabolomics gives critical insight into favorable and unfavorable drug fates, which must be taken into account during the design of any new drug. This entire process is usually an *in vivo* study, whereby patients are tested in large populations with various control groups. Typically, LC-MS/MS is done with an instrument such as the **esquire3000plus** as it provides rapid and precise determinations of metabolites with the added facility of easy-to-use bioinformatics software. Similarly, it follows that the testing of drug doping of individuals may be performed with an instrument like the **esquire3000plus**.

# Market Overview

## Applications: **Substance Detection and Pathogen Identification**

Substance detection and pathogen identification are areas of continually growing importance in both defense and civilian areas of application. Bruker Daltonics is a world leader in these markets, with a complete range of atomic, biological, chemical, drug, and explosive/environmental (ABCDE) detection and identification products. These systems make use of many of the same mass spectrometry technologies as our life science instrumentation, in addition to ion mobility spectrometry (IMS), Fourier-transform infrared spectroscopy (FTIR) and others.

Our systems are designed to be sensitive, field-transportable, easy-to-use, and field-hardened for deployment under virtually any conditions, including at sea, in combat, and in all manner of civilian emergency situations.



# Product Overview

## Life Sciences Mass Spectrometry

Bruker Daltonics offers a number of different mass spectrometry systems for life science applications. Biologically active molecules and related compounds are fundamental structures that can be analyzed with relative ease based on their molecular weight.

Mass spectrometers are complex instruments, but most are based upon simple theories of operation. Basically, a sample is introduced to the system and its molecules are then ionized (electrically charged). The ions are then introduced immediately into some form of mass separation device and subsequently sent to a detector, where they are registered with their intensity. The resultant spectra are then processed with the appropriate software to determine the molecular weight, and whenever possible, chemical structure.

Although they operate on different principles, all mass spectrometers contain, in some format, the following three basic components: (1) Sample introduction and ionization, (2) Mass analyzer, and (3) Detector. Bruker Daltonics systems are designed with several optimized combinations of these components to provide superb performance in a wide range of life science applications, and include a complete range of productivity-enhancing automation systems and bioinformatics software packages.

### MALDI-TOF

Bruker Daltonics has an extensive MALDI-TOF product line, ranging from routine walk-up quality assurance / quality control (QA/QC) to the most advanced proteomics analysis. We also offer important automation and sample handling accessories for the highest possible throughput. MALDI is an extremely rugged, versatile ionization source which permits the analysis of a wide variety of biological materials, especially proteins. Time of Flight employs the simple principle that heavier ions travel slower than lighter ones, so that in the same fixed distance (the TOF tube), heavier items will have longer resulting travel times. Since the masses of ions are fixed in value, it is a relatively simple task for a computer and bioinformatics software to identify ions and their fragment components at the detector.

Bruker Daltonics' **ultraflex**, part of our **Proteiner Suite**, is the most powerful MALDI-TOF proteomics system that we offer. Available in two configurations, **ultraflex TOF** and **ultraflex TOF/TOF**, the system features the Zymark **Twister** 20-plate automated sample handler, designed for 96-, 384-, and 1536-position standard microtiter plates. All configurations include our patented gridless reflectron system. The **ultraflex TOF** is a high-throughput proteomics system that enables characterization of proteins directly following gel processing and deposition onto microtiter plates, eliminating many time-consuming intermediate steps involving liquid-phase work-up.

The **ultraflex TOF/TOF** introduces a second, tandem TOF into the **ultraflex TOF** system. The second TOF adds higher

energy (and subsequently better fragmentation) to the sample analysis via our patented **LIFT™** process. This extra energy results in better sensitivity and higher selectivity (resolution) at the detector.

A complete **ultraflex TOF/TOF** instrument can perform high-throughput screening via peptide mass fingerprinting by initial MALDI-TOF analysis, and then from the same sample, switch to ultra-high sensitivity analysis via MALDI-TOF/TOF for extremely detailed protein characterization.

To identify a protein by peptide mass fingerprinting, the protein is typically digested with an enzyme, which cuts it into smaller pieces (typically 10-50 depending on the size of the protein) called *peptides*. The **ultraflex** can measure

ultraflex TOF/TOF





autoflex

the molecular weight of these peptides with an accuracy of better than 10 ppm (0.001%) in around 10 -15 seconds. The set of these accurate mass measurements is known as the peptide fingerprint, sometimes also called the digest. Having the exact weight of these 10-50 peptides is much more specific than having only the weight of the protein. This information may be sent to a database containing the structural information of thousands of proteins (and also sequences derived from existing genomics databases) which usually gives a 60-80% success rate of protein identification in systems where the genome is known.

However, some proteins are so similar that more information is needed. For these, the **ultraflex** can perform an additional MS/MS fragment analysis on some of the peaks of interest. The TOF/TOF mode allows the analyst to pick a peptide out of the fingerprint, break it into pieces (i.e. fragment it), and measure the weight of these fragments. As before, having the exact weight of 5-20 fragments is much more specific than just having the peptide molecular weight. Adding this information to the database search often identifies the protein. If not, the TOF/TOF analysis can be repeated for other peptides of the fingerprint, on the same digested protein sample. The analysis is very rapid, often taking just seconds to measure the spectrum. The **ultraflex TOF** can be easily upgraded to an **ultraflex TOF/TOF** by Bruker Daltonics.

The **autoflex** is the first MALDI-TOF system specifically designed for ultra-high throughput analysis. Using Bruker Daltonics **MTP™** 1536-position microtiter plates and the Zymark **Twister** 20-plate automated sample handler, the **autoflex** can process over 30,000 samples without operator intervention. Using the same laser and electronics as the **ultraflex TOF**, the **autoflex** provides excellent sensitivity and resolution in a wide variety of life science applications. It is the “work horse” of our MALDI-TOF line, with the best combination of versatility, performance, and price.



omniflex LT

The **autoflex** is available in linear or reflectron configurations for both genomics and proteomics. With features like sample tracking by transponder or barcode, and remote operation and service modules, it is the ideal system for high-throughput proteomics analysis. It is an important part of Bruker Daltonics' **Proteomeer** Suite.

The **omniflex™** is a bench top, walk-up MALDI-TOF system used for general biology and biochemistry laboratories, drug development, QA/QC, oligonucleotide, and even polymer analysis. It is available in a variety of configurations, including linear or reflectron. The new **omniflex LT** is a lower-cost version of the popular **omniflex**, available only in a discreet linear configuration.

## FTMS

The **APEX FTMS** provides perhaps the most versatility of all mass spectrometric techniques, allowing a tremendous amount of source options. Available sources include MALDI, APcI, NanoElectrospray, FAB/SIMS, EI/CI, and more. The “business end” of the **APEX** is the trapped-ion **Infinity Cell™** located within the center of a superconducting magnet. This patented Bruker Daltonics device has the combined task of trapping, exciting, and detecting analyte ions. The

**APEX** is capable of performing Accurate Mass analysis to sub-ppm levels in many complex matrices. We believe the **APEX FTMS** provides the highest resolution, selectivity, precision, dynamic range, and experimental versatility of any commercially available mass spectrometer.



APEX IV

## ESI-TOF

ElectroSpray Ionization (ESI) with the Bruker Daltonics APOLLO™ source allows the introduction of biological samples into the TOF spectrometer at a neutral pH. This inherently “gentle” method of ionization, followed by TOF analysis, is ideal for the analysis of proteins and non-covalently-bound complexes. The **BioTOF II** is specifically designed for the study of proteins, protein-protein, drug-protein, and protein-ligand interactions. This extremely versatile product can also be used for many genomics applications as well.

The **BioTOF Q** ESI Q-q-TOF adds tandem mass spectrometry (MS/MS) capabilities to the **BioTOF II** system. Tandem mass spectrometry using a Q-q-TOF geometry permits the sensitive and highly accurate determination of molecular fragments in proteomics identification, *de novo* peptide sequencing, complex mixture analysis, and other life science applications. A **BioTOF II** can easily be upgraded to a **BioTOF Q** whenever desired.



APOLLO

## ESI-ION TRAP

The unique orthogonal design of the Agilent ESI source gives Bruker Daltonics' **esquire** series spectrometers outstanding robustness, sensitivity, and reproducibility over a wide range of LC operating conditions. At the heart of the **esquire** systems, our own multipole Ion Trap mass analyzer provides a unique combination of mass range, scan speed, and resolution. Altogether, the **esquire** series ESI-Ion Trap spectrometers provide top-quality analytical performance.

The **esquire3000plus** is the perfect solution for many tasks in proteomics, drug discovery, and LC/MS<sup>n</sup> applications. It is the most advanced LC/MS system for structural characterization and quantitation of complex mixtures in Drug Discovery, Proteomics, Metabolic Profiling, Food Analysis, Environmental Analysis, and Combinatorial Chemistry.

The **esquire2000** system is a more affordable member of the **esquire** family of mass spectrometers geared more to small molecule analysis. With many of the same features as the **esquire3000plus**, it includes automated LC/MS/MS and manual MS<sup>3</sup>, with excellent sensitivity and resolution.

Both the **esquire2000** and **esquire3000plus** are powered by Bruker Daltonics' **HyStar™** software for complete and intuitive LC/MS method development and system control. The **esquire** series mass spectrometers are an integral part of the Bruker Daltonics **Proteineer Suite**.

The **Proteineer SP Spot Picker** enables automated spot picking from 2-D gels into 96- and 384-position microtiter plates. It provides spot picking in less than 7 seconds, with 99.9% reproducibility. The system includes a stainless steel circular cutter, and a transparent safety box to prevent contamination.

The **Proteineer DP Digest & Prep** station subsequently digests and prepares the material from the gel plate for analysis via MALDI-TOF or ESI-Ion Trap. The **Proteineer DP** is based on EMBL-developed digest procedures and is available with a wide range of processing (including dried-droplet, thin-layer, on-target-washing, re-crystallization, and more).

The **MAP™ II** (single-channel) and **MAP II/8** (8-channel) MALDI Automated Prep systems automatically prepare samples for analysis via MALDI-TOF. Automation includes sampling, mixing with the appropriate matrix, and deposition onto MALDI targets with clean-up where necessary.

**Proteineer SP, Proteineer DP, and MAP** are all part of the Bruker Daltonics **Proteineer Suite**.



esquire3000plus



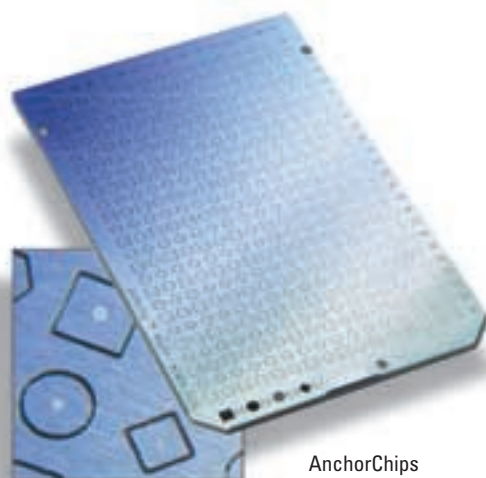
BioTOF Q

## THE PROTEINEER SUITE

Proteomics research often begins in the analytical lab with a 2-D gel electrophoresis separation. Once separated, spots are identified and interesting candidate spots are isolated, removed, and processed for analysis. Large Scale Proteomic analyses often require an initial screening step which aims for the identification of large numbers of proteins. Sample throughput and success rate (the number of positively identified proteins) are key issues to this type of analysis. This task is typically performed via automated MALDI-TOF MS peptide mapping.

Additional MS/MS fragment analyses for further identification and verification can be performed by MALDI-TOF/TOF MS/MS on the same MALDI sample. Additional information can also be obtained by ESI nano-LC/MS/MS, which is slower, but (thanks to the chromatographic separation step included) allows for identification of even the most complex samples and provides high sequence coverage.

Further into Proteomics analysis, relevant candidates must be characterized in greatest possible detail. At this stage, ESI nano-LC/MS/MS provides for a detailed in-depth analysis of the injected sample with high sequence coverage. Information on post-translational modifications can be gained by creating neutral loss traces with regard to the dissociation of phosphate or glycosylation groups from the peptides in the MS/MS process.



AnchorChips

Bruker Daltonics **Proteineer** Suite is designed for all of the above, and will handle proteomics from end-to-end. The process begins with spot picking from a gel and digestion and preparation of the sample, making it ready for analysis. This is all done via our robotics systems, the **Proteineer SP** and **Proteineer DP**, respectively. High-throughput screening continues with the **autoflex MALDI-TOF** or **ultraflex MALDI-TOF/TOF** in TOF mode. Interesting candidates or samples with non-specific search results may then be targeted for additional analysis.

The same MALDI plate can be analyzed using the ultraflex MALDI-TOF/TOF for much more detailed structural information. If separation techniques are ultimately required, the remaining digest sample solution can be processed via LC/MS/MS using the **esquire3000plus** for detailed structural information. The **Proteineer** Suite is designed to be flexible according to the methodology and specific applications required.

*Bruker Daltonics also produces a complete range of aftermarket products for our mass spectrometer systems and related disciplines:*

All Bruker Daltonics MALDI-TOF products may make use of our proprietary **AnchorChip™** microarrays for sample analysis. **AnchorChips** employ patented microfluidics technology that improves sensitivity and dramatically reduces analysis time per sample by concentrating the sample in a precisely-defined location.

**Genopure DS™** purifies double stranded DNA for direct MALDI-TOF MS measurement. PCR products as small as 50 base pairs in length can be processed. Primers, enzymes, salts, and detergents are removed resulting in high-yield double-stranded DNA fragments.

**Genopure Oligo™** purifies single stranded DNA such as oligonucleotides, primer extensions, or sequencing reaction products. Residual reaction components like enzymes, salts, and detergents are removed from the product. Single-stranded DNA is recovered in an elution buffer supplied with the kit.

Bruker Daltonics also has a wide variety of bioinformatics software for data identification, interpretation, and interconnectivity. Products include **BioTools™** biomolecular identification and sequencing software, **MASCOT™** web-enabled protein identification software for protein database connectivity (from Matrix Science), **GenoTools™** SNP interpretation software, and our new **ProteinScape™** powerful bioinformatics and data warehousing package.



genopure

# Product Overview

## Substance Detection and Pathogen Identification

Bruker Daltonics has over 20 years of experience in the development, engineering, and manufacturing of equipment for substance detection and pathogen identification (our ABCDE division). We have an extensive variety of products for a wide range of defense and civilian applications, including soil, water, and air monitoring systems. Many of our systems have been deployed by allied governments worldwide, and are field-proven for durability and performance. These products and others have recently come into the spotlight due to the events of the latter part of 2001. While it is impossible to adequately portray all of our ABCDE products in detail herein, we instead provide brief descriptions and uses of many of our most popular products.

The Chemical Biological Mass Spectrometer (CBMS) is a military ruggedized mobile ion trap mass spectrometer for the identification of chemical warfare agents and the classification biological warfare agents (such as anthrax). The CBMS, equipped with a virtual impactor and pyrolyzer, is capable of detecting and classifying biological warfare agents in three (3) minutes. The CBMS is used in the US Army's Biological Integrated Detection System or BIDS.

The EM 640/640S is a mobile mass spectrometer for fast on-site detection of hazardous compounds from air, soil, and liquids. The rugged GC/MS system is designed for fast and simple on-site assessment of chemical catastrophes and environmental accidents involving organic compounds.

The Rapid Alarm and Identification Devices (RAID) use state-of-the-art IMS (ion mobility) technology in detecting chemical warfare agents. The RAID instruments are hand-held, portable and mounted chemical warfare agent, and toxic chemical compound detectors with automatic alarm functions. These detectors can be operated in the field, on vehicles or ships, and in buildings. A mounted version, the RAID-S, is designed for long-term operation as a trace gas detector in buildings, and may be used as a detector for high-volume air conditioning and heating systems.

The RAPID is a long-distance detection system for chemical defense, security, disaster management, and pollution control. RAPID is based on infrared technology and has the ability to scan the horizon automatically. It can remotely identify most known chemical warfare agents, as well as many important toxic industrial chemicals, over distances of several kilometers. This rugged detector may be mounted on several platforms, including a tripod, and can even detect while in motion.

The Mobile Mass Spectrometer (MM1) for reconnaissance vehicles is an extremely rugged and field proven GC/MS system for chemical warfare agent detection. The MM1 is the key component in NBC reconnaissance vehicles for, among others, the United States, Great Britain, Germany, Saudi Arabia, and South Korea. The MM1 played a critical role in Operation Desert Storm.

The SVG 2 represents the new generation of nuclear radiation detectors. The SVG 2 is a hand-held, hardened microprocessor controlled radiation detector, based on state-of-the-art semiconductor technology. It is equipped with integrated sensors for gamma and neutron radiation detection, an external personal dosimeter, and an external a/b-g probe. A broad range for g-dose rate is covered.



RAID-S



SVG 2



RAPID



CBMS



RAID-M

# Create the Future

Throughout 2001, Bruker Daltonics' message was, "It's a whole New World, together we can do anything." That was a simple yet bold statement, and it reflects our vision for the company: **We have entered the post-genomic era, and things are forever changed. Our mass spectrometers, in the hands of our customers, have enormous potential.** This *enormous potential* in proteomics, genomics, drug discovery, or any of Bruker Daltonics' core disciplines is our key to the future.

We at Bruker Daltonics understand our role in this new era. We provide the solutions, the *enabling life science tools based on mass spectrometry™*, to help our customers achieve their goals. We are dedicated to life science mass spectrometry, and are determined to continue as a leader in providing the most powerful state-of-the-art instrumentation, automation, bioinformatics software, and consumables.

What's next? More tools, more answers...and then more questions, as the cycle repeats itself. The process continues as we strive to learn more about our world, and how to make it a healthier and safer place. So, it's logical that our message for 2002 reads, "Create the future... together we can do anything." In this new world of opportunities, challenges, and discovery, we have the power to contribute significantly to the future. Using our instrumentation and technologies, our customers are making people's lives healthier every day. Our ABCDE products also play a critical role in making the world not only a healthier place, but a safer one as well.





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