BRUKER

autoflex®

the high-throughput

MALDI-TOF

BRUKER DALTONICS®

Enabling Life Science Tools Based on Mass Spectrometry™

"The new challenges of the post-genomic era lie before us: recognizing genomic variability, reading the proteomes of hundreds of cell types and their variability, and exploring the function or malfunctions of millions of proteins."

Meet the challenges of the post-genomic era

We now can read the human genome. We have learned, in principle, how genes "translate" into proteins by the genetic code. But there are millions of "pre-translational modifications (the mutations), of "translational modifications" (the slicing variants), and of "posttranslational modifications" like glycosylation, phosphorylation, cross-linkings and many others. A major challenge!

Reading the human genome was a tool-driven effort: without the development of fast sequencers we could not have celebrated this success. Reading the mutations, the proteomes, the modifications will be another tooldriven effort - and mass spectrometry will play a dominant role.

Demands on the instrumentation for this task are high: automated, high sample throughput mass spectrometers are required, higher mass ranges, and more accurate mass determinations.

With instruments like the autoflex, designed for tens of thousands of MALDI samples per day, Bruker Daltonics will help you meet the challenges of the post-genomic era.

autoflex – trained to be top

The autoflex MALDI-TOF MS is the first MALDI-TOF system thoroughly designed for High Sample Throughput in Genomics and Proteomics.

What does that mean?

Automation

Ultra-fast, automated analysis of thousands of samples, carried out with the high data quality known from the Daltonics FLEX series of MALDI-TOF systems.

Flexibility

Modularity: another characteristic of a Daltonics system. The linear autoflex, tailored for SNP genotyping, can be upgraded with reflector and AutoPSD accessory to make it a powerful protein analysis tool.

Reliability

All system components have been carefully designed and tested for maximum life and minimum wear.

PERFORMANCE

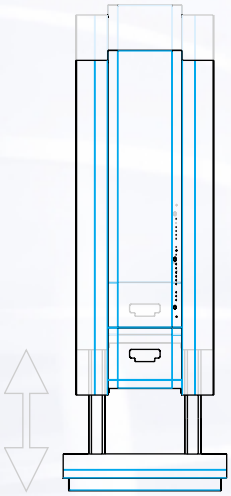
autoflex: a quantum leap in MALDI-TOF automation and sample throughput

The autoflex won the iF Product Design Award 2001 of the German Industrie Forum Design for its “uncompromising symbiosis of high-tech and ergonomics”.

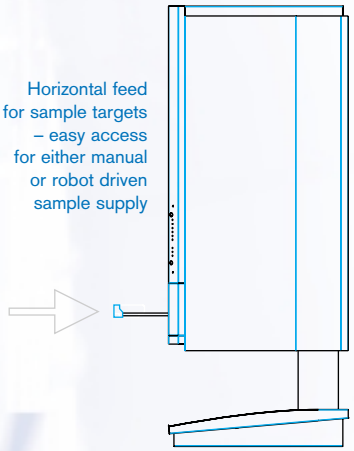
Flexibility by Design

- Small footprint – saves expensive lab space
- Horizontal, height adjustable probe inlet – adaptable to any process line
- Linear TOF configuration can be upgraded with reflector and PSD equipment

The reflectron increases mass spectrometric resolution



The autoflex adapts to any operating height your lab facilities require



Horizontal feed for sample targets – easy access for either manual or robot driven sample supply

Flexibility in Use: flexControl™

flexControl is Bruker Daltonics' new, universal MALDI-TOF software platform for quick and easy instrument control. The GUI is highly intuitive and provides quick drag-and-drop of information, as well as context-sensitive menus.

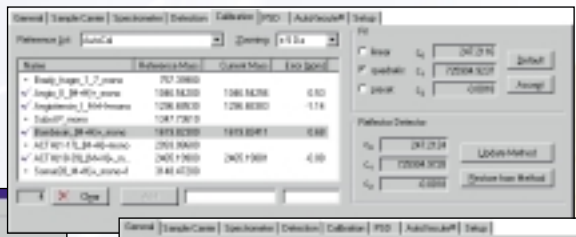
flexControl features Bruker Daltonics' proven AutoXecute module for intelligent on-the-fly optimization of acquisition parameters.

AutoXecute methods are pre-selectable and can even cover on-line post-processing, e.g. protein database search.

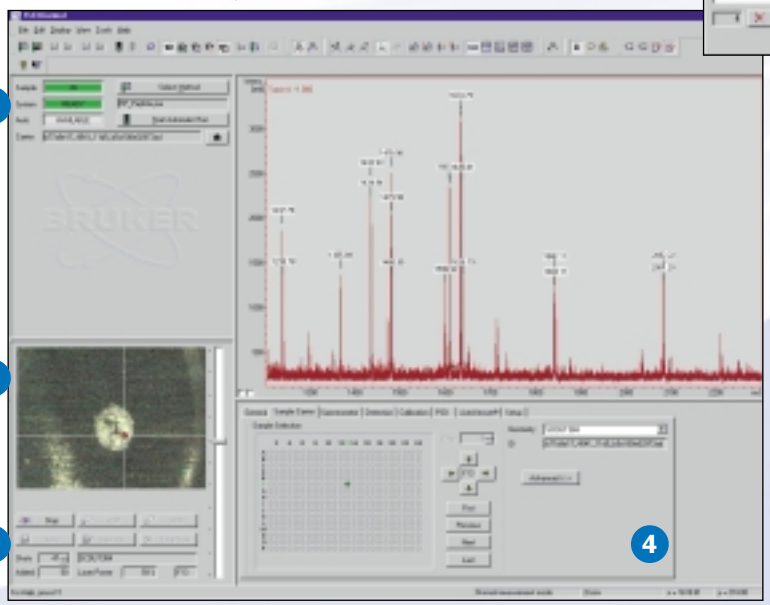
Seamless Integration

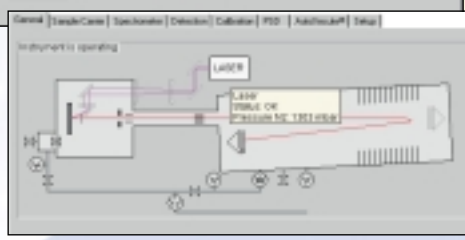
flexControl networks with the Daltonics Proteomics (mapControl™/biotools™/MASCOT™) and Genomics (genotools™) software suites.

The "Calibration" tab allows for quick calibration setup



flexControl gives straight access to all relevant instrument parameters





The "General" tab allows to check the system status, including all basic operating parameters

1 Online Function Control (OFC)

2 Video optics: spots can be manually selected via mouse click!

3 Acquisition Control

4 Acquisition Parameter Control

As a real high-throughput system, the autoflex features maximum reliability of all system components for many millions of analyses.

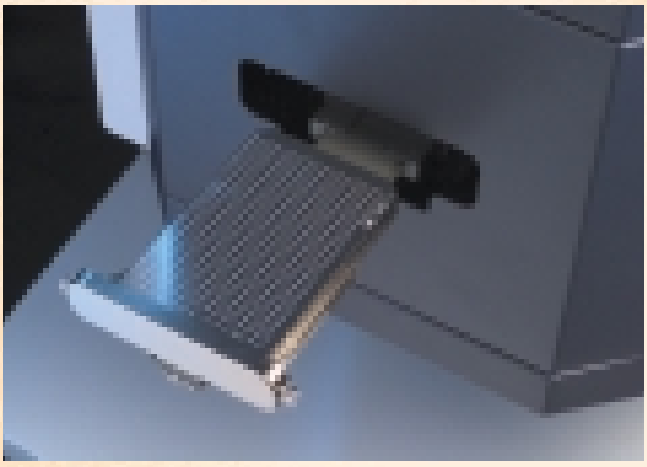
Automated Sample Handling

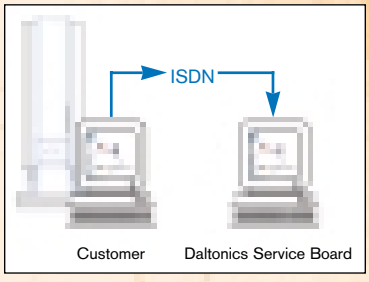
- Safe, automated microtiter plate handling by the Twister

Optimized MALDI Process

- Low-friction xy-table for many tens of millions of speedy “stop and go” operations
- A laser which can provide over 100 million shots without service
- Highly reproducible positioning of the sample spots using our patented AnchorChip technology, which overcomes the need for “spot-hunting”.

The sample tray:
easy-to-handle sample supply





Remote service via ISDN point to point links

Extended Self Diagnostic and Service Capabilities

- Automated self diagnosis routines
- Remote service capability via safe ISDN point-to-point link

Maximum up-time

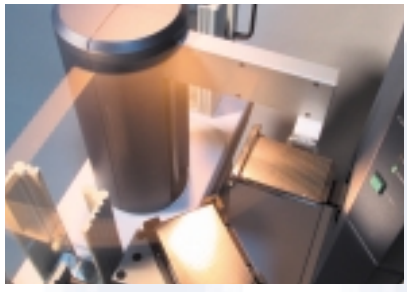
The built-in remote service capability allows the Bruker Daltonics help desk to access the customer’s system and do on-line trouble-shooting. Often problems can be solved in this way. In case that hardware faults are localized on-line, the service engineer can take along the spare needed part with him.

automation

Full Microtiterplate Compatibility

The microtiterplate format of the scoutMTP MALDI targets guarantees for optimum workflow in the lab without compatibility problems.

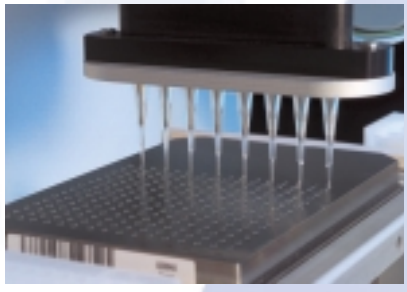
The Twister Microplate Handler automatically processes up to 80 scoutMTP targets, each carrying up to 1536 samples. Sample targets can be identified via barcode and transponder.



The twister smoothly interfaces sample preparation in the biochemical lab with the mass spectrometer.

The key to high productivity

The patented AnchorChip coating of the scout MTP targets provides highest sensitivity from smallest sample amounts. Highly reproducible positioning of the sample spots using AnchorChips shortens analysis times considerably.



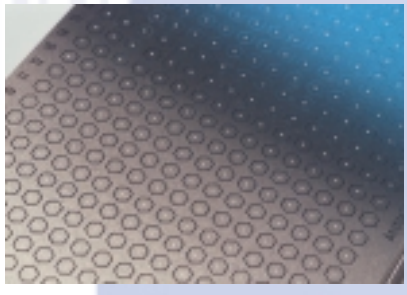
The microtiter plate format of the scout MTP™ MALDI targets guarantees for optimum workflow in the biochemical lab without compatibility problems

1995 – 26 samples

1998 – 384 samples

1999 – 1,536 samples

2000 – 30,000 samples



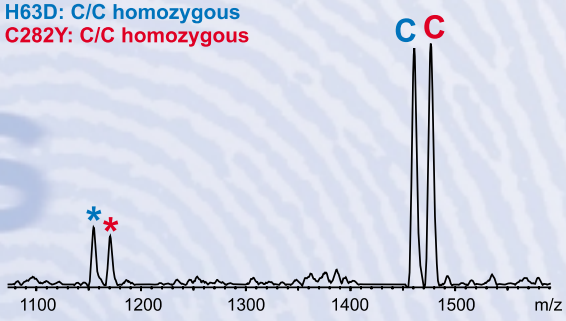
High sample throughput

Through the last decade, we have trained our FLEX MALDI TOF systems to process a growing number of samples automatically.

Result list in ASCII format

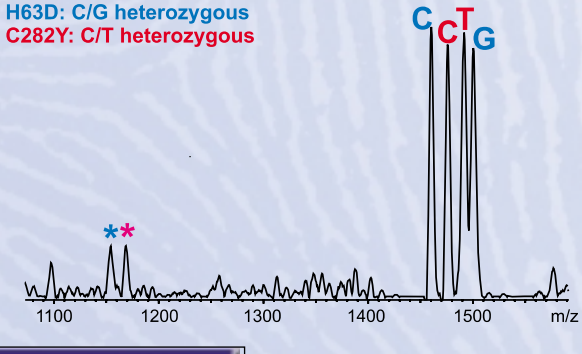
Automated SNP Genotyping

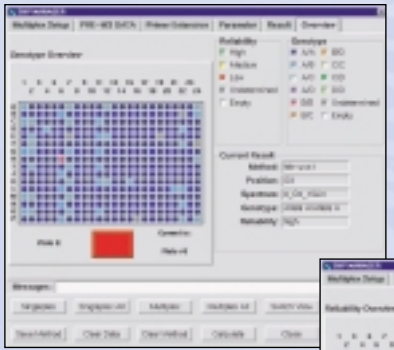
With its high reliability and sample throughput, MALDI-TOF MS is the method of choice for SNP genotyping. The autoflex allows for automated genotyping on an industrial scale within a few seconds per sample.



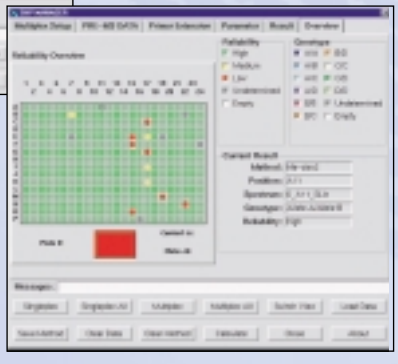
Duplex genotyping assay for H63D and C282Y in the HFE gene

The necessary data quality is already achieved in the linear TOF configuration. An intelligent acquisition routine judges the data quality on-the-fly and, if necessary, optimizes the acquisition parameters. The genotools™ software assigns the genotypes and displays the results in an MTP viewer format.





Result overview for 379 samples



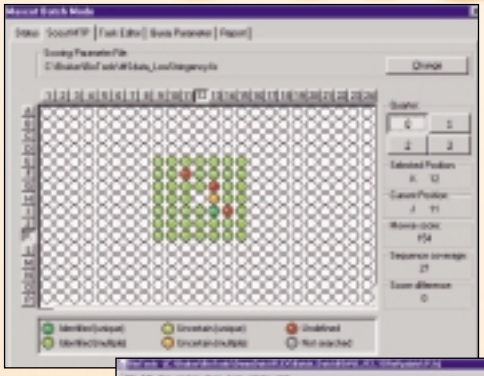
Quality control of the results

Automated Protein Identification

Mass spectrometry is the key technology for unlocking the proteome. And in current mass-spectrometric based proteomics strategies, MALDI-TOF MS is the initial screening step – thus the speed and reliability of your MALDI-TOF system will decide on your high throughput success in protein identification!

Go Proteineering!

The autoflex is part of the *PROTEINEER*™ suite – the most advanced hardware and software platform for protein identification and characterization.

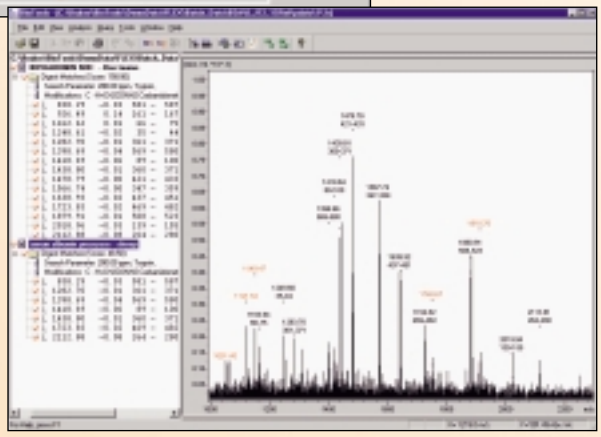


Protein identification as batch process: the biotools software automatically classifies the quality of the search result for each sample spot and displays a color coded result overview.

Screening analysis - MALDI-TOF Peptide Mapping

The tryptic digest of a protein delivers peptides with masses of about 800 to 4,000 Da – the so-called "peptide map", which is the basis for mass spectrometry-based protein identification. MALDI-TOF analysis of the digest and subsequent protein database search leads to a result list of proposed proteins.

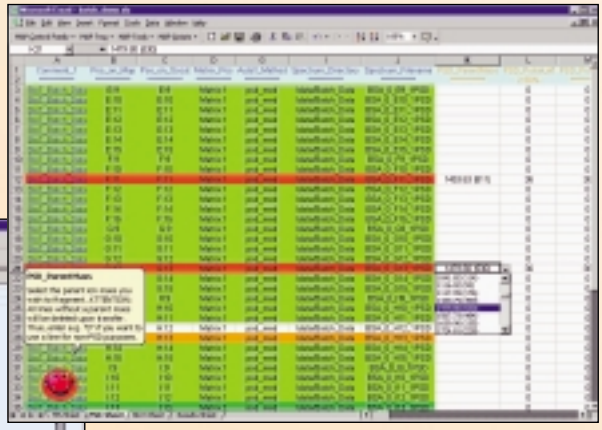
The *PROTEINEER* suite supports this identification procedure as batch process. A central excel sheet contains all sample-specific parameters and controls all steps from sample preparation and MALDI-TOF analysis through to data interpretation.



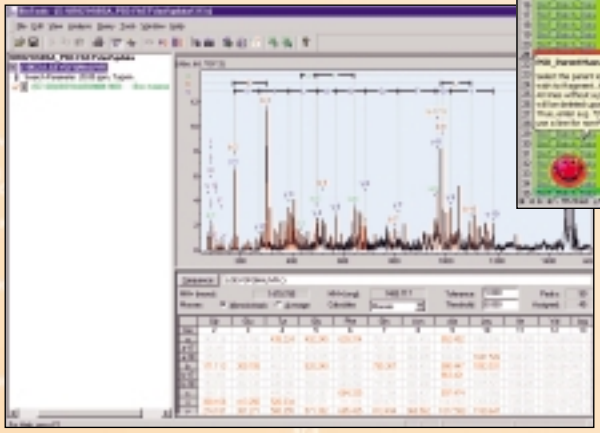
High quality (most important: sensitivity) of MALDI-TOF data is crucial for high success rates in Protein ID. Here: 300 amol BSA digest.

MS/MS Fragment Analysis - AutoPSD

In the case of a questionnable result from the digest, additional MS/MS (PSD) data can be collected from the same prepared sample. The new AutoPSD function facilitates the automated processing of this second analysis stage.



The parent masses for PSD fragmentation are selected in the central Excel sheet.



biotools automatically annotates the sequence resulting from the search to the PSD spectrum. Thus the quality of the assignment is immediately visualized.

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