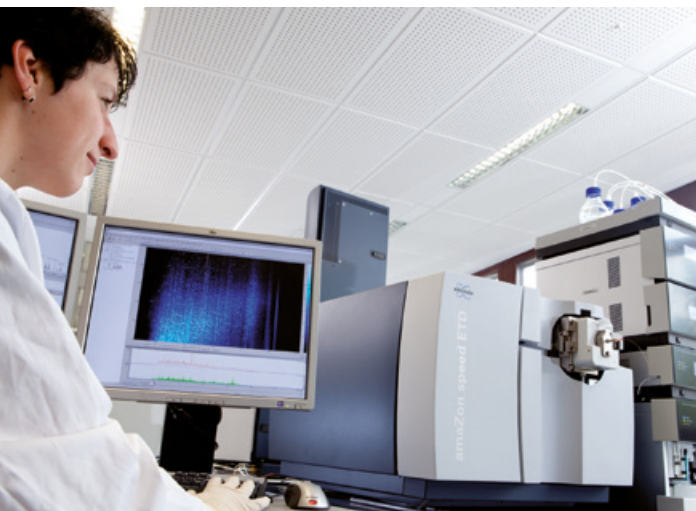




amaZon speed

- Ion Trap Performance Beyond Imagination

amaZon – Turning Speed into Solutions

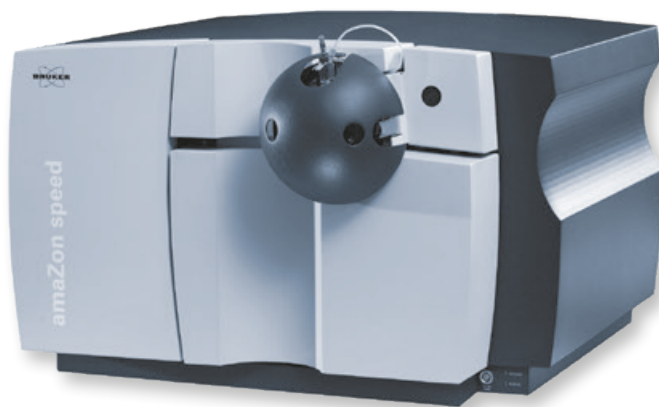


The amaZon speed ion trap series sets new analytical standards for proteomics and small molecule applications.

Design improvements to a well proven platform, offer dramatically enhanced speed, mass resolution, MS/MS efficiency and reproducible quantitation, delivering unsurpassed performance.

Unmatched ion trap performance through innovation

- Greatly increased MS/MS duty cycle for more productive data acquisition
- Further improved resolution on a market-leading system with an unrivalled value of 30,000 in full scan
- Highest ion trap mass accuracy through proprietary RF generator design
- Unrivalled ETD performance: most sensitive, robust and reliable technology
- Leading dual ion funnel technology for unparalleled sensitivity
- Zero Delay Alternating™ for polarity switching with 20 Hz MS acquisition speed
- New SMART isolation and fragmentation



● Accelerate your Success

Speed for proteomics

- Bottom-up proteomics identifying more low abundant proteins
- Outstanding ETP/PTR applications for full PTM analysis
- Top-down sequencing (TDS) for highest protein sequence coverage

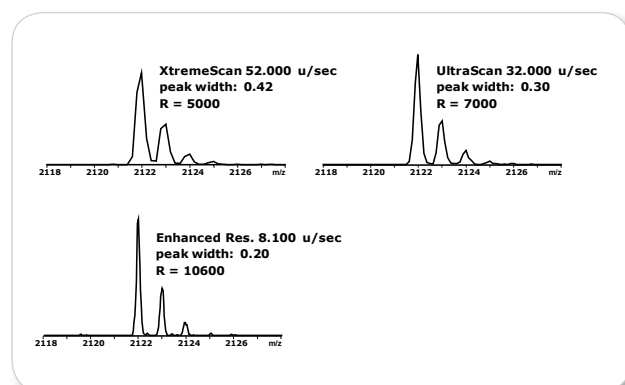
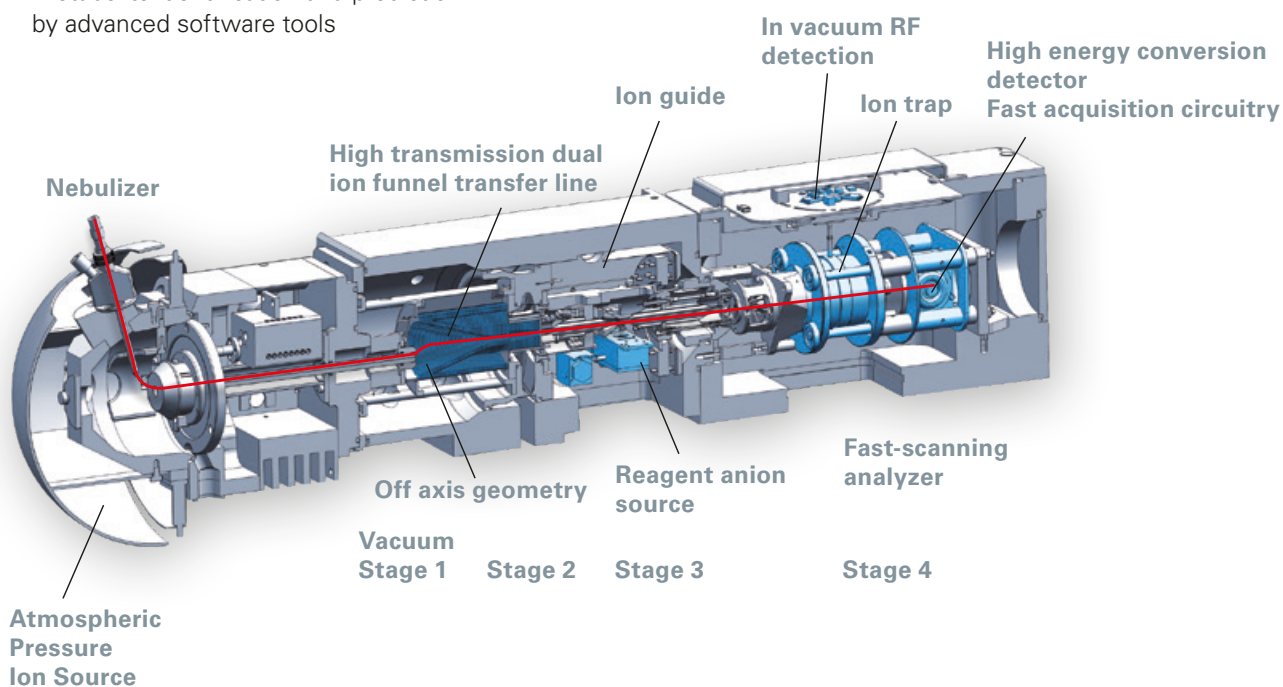
Flexibility for general chemistry

- Walk-up OpenAccess push-button software
- Fast MSⁿ library search solutions

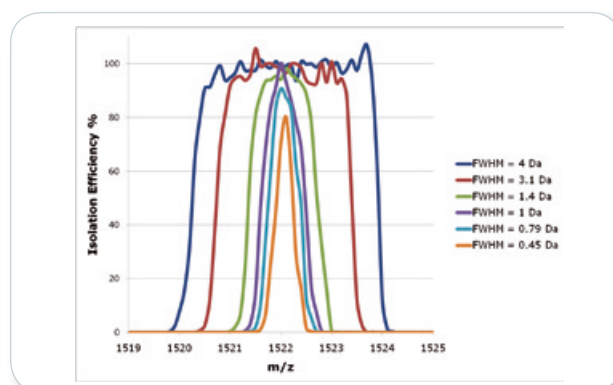
Most flexible API sources including the new CaptiveSpray™ for proteomics, APCI, and DIP for solid samples

Speed for drug research

- Drug quantification by UHPLC driven LC-MS methods
- Metabolite identification and prediction by advanced software tools



Different scan rates and respective resolution. Even in the fastest XtremeScan a peak width well below 0.5 u can be achieved opening up the capability to resolve 2+ ions.



New fast isolation of 1522 m/z ion with isotopic isolation showing no compromise in efficiency. Ions with a peak width of 0.45 Da are isolated with 80 % efficiency.

Translating Speed into Proteomic Information

Bottom-up analysis with a maximum number of identified proteins

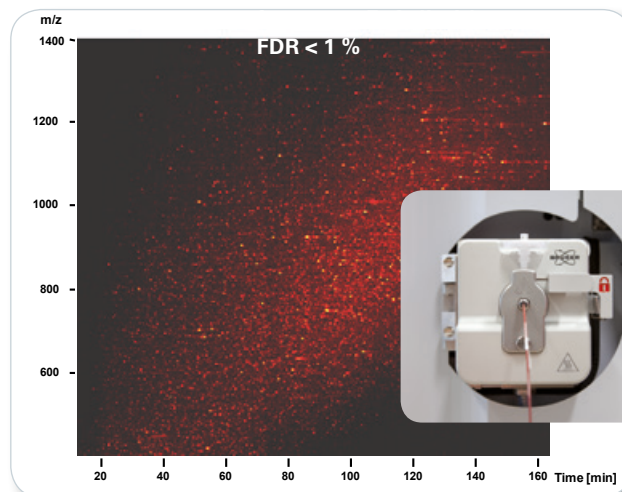
The complexity of the proteome still challenges analytical technologies. The high dynamic range and complexity due to posttranslational modifications require maximum speed and sensitivity to capture as many peptides as possible. The amaZon speed ion trap sets new standards in protein identification due to its enhanced MS/MS speed, new faster isolation and SMART fragmentation. This results in the identification of > 1200 unambiguously identified proteins in a single LC-MS/MS run from 1 µg *E. coli* digest.

Excellent dynamic range

The UPS-2 standard is a mixture of 48 proteins spanning a concentration range of 6 decades in total. The amaZon speed allows protein identifications over 5 concentration levels in a single run.

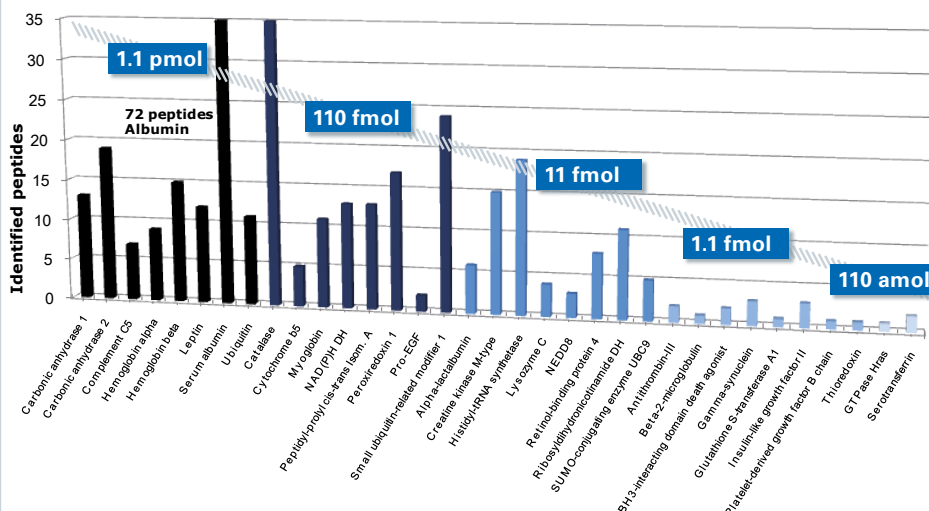
Productivity, robustness and high sequence coverage by CaptiveSpray™

The amaZon speed is equipped with the high-transmission, robust CaptiveSpray source for highest performance and reproducibility in Bottom-up studies.

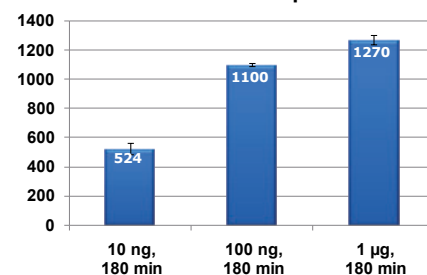


Survey view of an *E. coli* digest (1 µg) separated by a nano UHPLC using a 25 cm column and a 3 h LC gradient. MS detection was performed using the amaZon speed ETD system equipped with a CaptiveSpray ion source.

ID over 5 levels of protein concentration - UPS-2 standard



Number of identified proteins



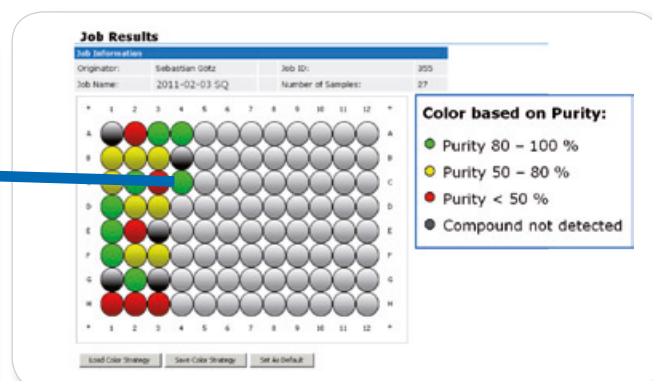
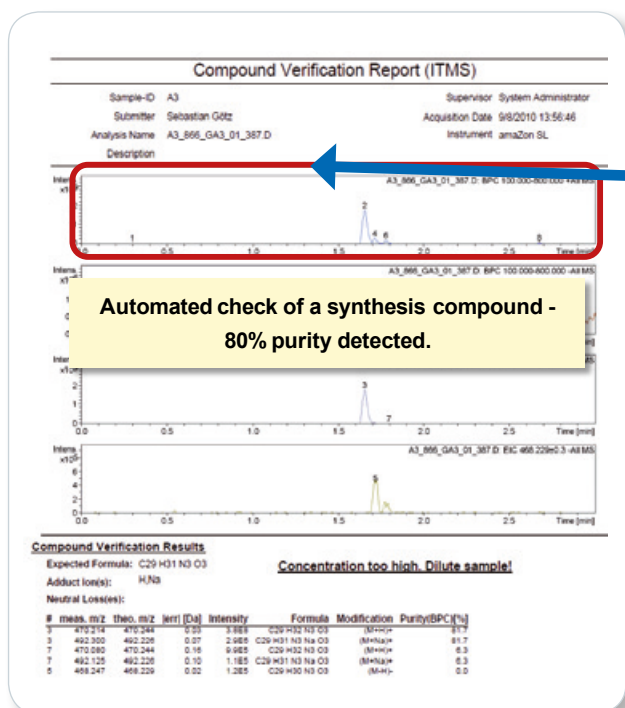
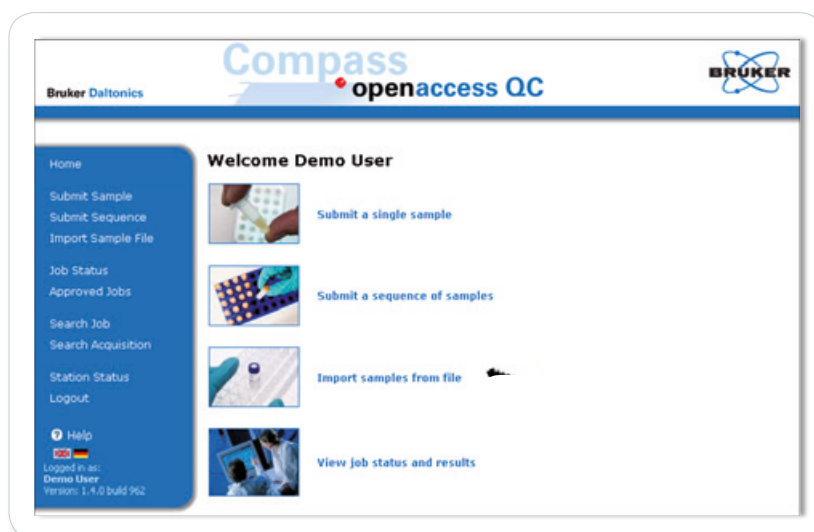
Number of identified proteins from *E. coli* digests (average of three technical replicates for different protein loadings).

● OpenAccess

Walk-up solutions for a multi-user environment

The Compass OpenAccess OA/QC software allows users with little to no training to generate valuable LC-MS/MS data on the fly. This is a web-based client server system with push-button solutions i.e. for quality control (QC),

recombinant protein MW verification and automatic library searches. The intuitive workflow-oriented GUI in combination with the flexibility and speed of the amaZon is an ideal solution for multi-user industrial or teaching labs.



Compass OpenAccess guides the user through all necessary steps to acquire high-quality data in an intuitive, automated workflow. Results, for purity checks of synthetic compounds, are visualized in MTP formats. PDF reports with all needed data information are provided in a customized fashion and sent automatically after sample analysis by email.

Technical Specifications

Technology driven solutions

- SmartFrag™ for reproducible MS/MS spectra generation and confident library searches
- Zero Delay Alternating™ polarity for up to 20 Hz MS acquisition speed supporting UHPLC applications
- Dual ion funnel for maximum sensitivity over a broad m/z range
- Patented SmartICC™ for optimal ion storage
- SMART isolation and SMART fragmentation
- Panorama fragmentation (PAN) enabling CID fragmentation without 1/3 cutoff

MS/MS modes

- Data-dependent auto MSⁿ
- Preferred mass lists for automated feedback experiments from MetaboliteTools and ProteinScape
- Scheduled precursor lists supporting MS², MS³ in positive and negative mode
- Neutral loss scans for analysis of target compounds and posttranslational modifications (by ETD)
- Multiple reaction monitoring (MRM) for quantification
- Manual MSⁿ up to MS¹¹ in all scan modes for structural elucidation
- Highly efficient and sensitive ETD/PTR capabilities for PTM detection and Top-down proteomics

Source options

- ESI, APCI, APPI
- DIP source for direct analysis of solids and liquids
- CaptiveSpray nanoBooster: robust and reliable plug-and-play nano/cap ESI source for flow rates from 50-5000 nl/min
- Smart CE-MS coupling with grounded spray needle

Software solutions

- ProteinScape including GlycoQuest glycan DB search engine
- RapiDeNovo for de-novo sequencing of proteins
- MetaboliteTools for metabolite prediction and identification
- ProfileAnalysis for statistical comparison of metabolite and proteomic profiles
- Compass OpenAccess client server based system for walk-up users
- Compass Security Pack for work in regulated environments
- ACD/MS Manager for structural interpretation and classification

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