

# nature

Vol 437 | Issue no. 7058 | 22 September 2005

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## PUBLICATION POLICIES, AUTHOR GUIDELINES AND INFORMATION

This is a summary of Nature's guide to authors, publication policies and other author information, available in full on the web via our main author information page at [www.nature.com/nature/authors](http://www.nature.com/nature/authors).

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### SHORT VERSION OF GUIDE TO AUTHORS

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ARTICLES are original reports whose conclusions represent a substantial advance in understanding of an important problem and have immediate, far-reaching implications. They do not normally exceed 5 pages of Nature and have no more than 50 references. (One page of unadorned text is about 1,300 words.)

Articles have a summary for readers outside the discipline, separate from the main text and containing no references, of up to 150 words. The summary does not contain numbers, abbreviations, acronyms or measurements unless essential. It contains a brief account of the background and rationale of the work, followed by a statement of the main conclusions, introduced by the phrase 'Here we show' or its equivalent.

The Article itself typically has about 3,000 words of text, beginning with up to 500 words of referenced text expanding on the background to the work (some overlap with the summary is acceptable), followed by a concise, focused account of the findings, and ending with one or two short paragraphs of discussion. The text can contain a few short subheadings consisting of about 20 but no more than 40 characters (including spaces) each.

Figures are as small as possible: Articles typically have 5 or 6 figures. Legends and/or methods are additional to the main text. Methods sections are no more than 800 words long and ideally shorter; legends should not exceed 100 words each and start with a one-sentence title for the figure, followed by a brief explanation of the parts and symbols.

LETTERS TO NATURE are short reports of original research focused on an outstanding finding whose importance means that it will be of interest to scientists in other fields. They do not normally exceed 4 pages of Nature, and have no more than 30 references. They begin with a fully referenced paragraph of not more than 300 words, aimed at readers in other disciplines. This paragraph contains a summary of the background and rationale for the work, followed by a one-sentence statement of the main conclusions introduced by the phrase 'Here we show' or its equivalent, and ending with two to three sentences describing the implications in context.

The main text which follows is typically up to 1,500 words long. This text can, if the author requires, start with a further brief paragraph of introductory material, not repeating information in the summary paragraph. A description of the research then follows. Any discussion at the end of the text should be as succinct as possible.

Figures are as small as possible: Letters to Nature typically have 3 or 4 figures. Legends and/or methods are additional to the main text. Methods sections are no more than 800 words long and ideally shorter; legends should not exceed 100 words each and start with a one-sentence title for the figure, followed by a brief explanation of the parts and symbols.

FORMATS for figures, legends, tables, references, methods, supplementary (online only) information and other material are all explained in full at [www.nature.com/nature/authors](http://www.nature.com/nature/authors).

OTHER TYPES OF CONTRIBUTION to Nature that are considered for publication via online submission are Communications ARISING (which are scientific comments about peer-reviewed material previously published in Nature). See also [www.nature.com/nature/authors/gta/others.html](http://www.nature.com/nature/authors/gta/others.html) for: Reviews and Progress (pre-submission enquiries to [reviewsandsights@nature.com](mailto:reviewsandsights@nature.com)); Commentary (synopses and enquiries to [nature@nature.com](mailto:nature@nature.com)); and Correspondence (submit to [correspond@nature.com](mailto:correspond@nature.com)).

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## Spec for the Masses

### Mass spectrometry slams out results

Mass spectrometry combines proteomics and high-throughput strategies to identify components of complex protein samples and their posttranslational modifications, giving researchers important insight into the dynamic world of protein interactions.

#### MALDI-TOF

Mass spectrometry can be tedious, consuming laborious hours, making high-throughput screening difficult. In the next few months, Agilent Technologies will release new electrospray ionisation (ESI) time-of-flight (TOF) mass spectrometry (MS)-based products. These innovations will greatly increase lab productivity with 40 scans per second and scan cycle completion taking less than 1 second. The Agilent Multimode Source will allow researchers to use electro-spray and atmospheric pressure chemical ionisation simultaneously, eliminating the need for source exchange and sample rerun. For ESI-TOF MS applications, Agilent will combine its high-performance liquid chromatography chip with mass spectrometry to generate a microfluidics-based system that reduces leaks and dead volumes by eliminating half of the fittings.

Thermo Electron Corporation introduces the Finnigan™ LXQ™, a linear ion trap mass spectrometer for high-throughput analytical labs. The LXQ™ bases its technology on a patented ion trap technology that delivers fast cycle times and improved ion statistics, delivering increased sensitivity and high-quality MS spectra.

Researchers interested in protein biomarker discovery will benefit from Applied Biosystems/MDS SCIEX 4800 MALDI TOF/TOF™ Analyzer. The new system increases its sensitivity by ten-fold from previous versions with its TOF/TOF™

optics technology and a new OptiBeam™ on-axis laser that delivers more ions into the ion path. The enhanced QuanTIS™ ion allows researchers to identify precursor ions better, giving more accurate and easier-to-interpret results. With its proprietary ITRAQ™ and ICAT™ reagents, the 4800 MALDI TOF/TOF™ Analyzer allows researchers to calculate relative and absolute protein quantification with or without tagging chemistry. Included GPS Explorer™ database-based software supports automated analysis and filtering to achieve data of the highest relevance.

#### GC/MS

The bench-top Micromass® GCT Premier™ from Waters combines orthogonal acceleration TOF MS with GS that gives researchers a powerful new tool to characterize volatiles. Data generated provide highly conclusive quantitative and qualitative information for compound discovery and confirmation purposes. Researchers benefit from GCT Premier™'s high-throughput capacity and simplified data interpretation. Its dynamic range of up to four orders of magnitude gives increased resolution capacity to complex samples. A variety of ionisation options include electron impact ionisation (EI), chemical ionisation (CI), desorption chemical ionisation (DCI), field ionisation (FI), field desorption (FD) probe and solids probe.

Excelling in linearity and stability, the DELTA V series from Thermo offers gas isotope ratio mass spectrometry in a

mass spectrometry - product focus



Shimadzu Triple Detector SolidSpec-3700 Series UV-VIS-NIR Spectrophotometer

compact design and guarantees low noise emission. The DELTA V Advantage and the DELTA V Plus comes with a large selection of sample preparation systems, giving scientists complete specific solutions for a wide range of food and beverage, agricultural, forensic, pharmaceutical and medical research applications.

**LC/MS**

As a cost-effective solution whose applications range from the pharmaceutical to environmental fields, the **LCMS-2010EV Liquid Chromatograph/Mass Spectrometer** is available from Shimadzu. The LCMS-2010EV includes sensitivity-enhancing features such as a new metal electrospray probe, revised ion optics for enhanced transmission, expanded microprobe compatibility for ESI and an improved ion source design. The LCMS-2010EV's speed is also enhanced as its ESI can operate with flow rates as high as 2 mL/minute without flow splitting and its scanning electronics support 6000 amu/second. Included software allows researchers to collect data simultaneously with up to 64 different experiment combinations monitored within each analysis. Shimadzu's new product line also includes the **SolidSpec-3700 Series UV-VIS-NIR spectrophotometer** and the **Prominence HPLC** system for chromatography.

**Thermo Electron Corporation** brings a clear alternative to hybrid TOF systems by combining its Orbitrap™ patented electrostatic trap with its Finnigan™ ETQ linear ion trap. The result, the **ETQ Orbitrap™**, achieves outstanding mass accuracy, resolution and sensitivity in detecting and identifying compounds in complex mixtures. It features sub-femtomole sensitivity, no needed internal calibration and ease of use. Up to three MS scans can be performed per second with a wide dynamic range and the mass MS spectrum is typically recorded at a 60,000 resolution. Automated data acquisition and mass analysis can be coupled with rapid LC/MS analysis.

By reducing wasted time between scans, the new **LC/MSD Trap XCT Ultra** from **Agilent Technologies** can complete 3X the cycles at the same nominal scan speed. Its



Ultraflex II MALDI-TOF/TOF from Bruker Daltonics

powerful new processor can increase the identity of peptides from proteolytically digested proteins by 60 to 80 percent. Its traps can be equipped with ESI, APCI, APPI, and PDF-MALDI ion sources stretching analytical capacity from small molecules to proteins. To provide budget and performance flexibility to labs, Agilent offers a wide range of LC/MSD Trap based equipment, from the basic LC/MSD Trap VL to the Ultra.

**Triple Quadrupole**

For researchers who use the power of triple quadrupole-based mass spectrometry, the **Finnigan TSQ Quantum** series from **Thermo Electron Corporation** features new Heated Electrospray Ionization probes (H-ESI). Thermo offers four versions, each designed with specific needs. Discovery MAX is an ultra compact high-performance tool built for around-the-clock productivity without compromising sensitivity or precision. Its rugged design includes a patented analyser system, high efficiency ion transfer optics and a robust ion source. The Ultra EMR offers a range of up to 3000 Daltons, allowing high resolution of biopolymers such as peptides, polysaccharides and oligonucleotides. The Ultra features a novel ion source with interchangeable ESI and APCI probes with enhanced ion transmission. Finally, the Ultra AM has routine accurate mass measurement on the chromatographic timescale accurate to within ±5 ppm.

**Accessory Technologies**

Proteomic research includes not only global identification of proteins, but also their important post-translational modifications. **Bruker Daltonics Inc.** now gives researchers the power to investigate these modifications by introducing the **Electron Transfer Dissociation (ETD)** module for its high-capacity ion trap mass spectrometer, the **HCTUltra™**. From phosphorylation to glycosylation, ETD's unique peptide and protein fragmentation technique preserves these biologically unique and important alterations. With the **PhosphoScan™** mode of the HCTUltra, the ETD module offers researchers single-run experiments specifically for phosphorylation.

**"The use of protein biomarkers has the potential to radically change drug discovery and development over the next decade."**

*-Catherine M. Barak, President Applied Biosystems*

As new isotope labeling technologies emerge, analytical software needs to remain flexible. With this in mind, **Bruker** developed **ProteinScape-IC 1.1**, an LC-MS/MS-based quantitative proteomic solution and **ProteinScape 1.3**, a bioinformatic meta-search engine, both of which support even user-defined isotopic labels. **ProteinScape-IC 1.1** provides quantitative assessments of complex protein mixtures and supports the demand of increased protein fraction numbers. **ProteinScape 1.3** provides researchers a powerful data validation tool by integrating all major search engines, reducing the need for manual validation. The **ProteinScape** software suite extends workflow support using **Bruker Daltonics' Ultraflex II MALDI-TOF/TOF** and **HCTUltra** ion trap mass spectrometers.

**Dynal** has just released a new product in its proteomic preparation range, **Dynabeads® RPC 18**. Together with the recently launched **Dynabeads® WCX** and **Dynabeads® RPC Protein**, these products offer an alternative to chromatography columns, spin columns and pipette tips sample preparation technologies. Based on reversed phase chromatography (RPC) or weak cation exchange (WCX), these beads can fractionate mixed protein and peptide samples quickly and easily for downstream analysis such as mass spectrometry.

- Companies mentioned in this product focus:**
- Agilent Technologies: [www.agilent.com](http://www.agilent.com)
  - Applied Biosystems: [www.appliedbiosystems.com](http://www.appliedbiosystems.com)
  - Bruker Daltonics Inc.: [www.bdal.com](http://www.bdal.com)
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