

Corrections and Clarifications

The ScienceScope item "NIH biodiversity grants could benefit shamans" (10 Dec., p. 1635) should have mentioned that the International Cooperative Biodiversity Groups (ICBG) Program is a collaboration between the National Institutes of Health, the National Science Foundation, and the Agency for International Development.

Marcia Barinaga's News & Comment article "New test catches drug-resistant TB in the spotlight" (7 May, p. 750) did not mention that the idea of using reporter phages as indicators of bacterial growth was first suggested in a 1987 publication by Shimon Ulitzur and Jonathan Kuhn of the Israel Institute of Technology. What was technically new in the publication discussed in Barinaga's article was the engineering of mycobacteria phages as vectors to carry the firefly luciferase gene into mycobacteria, which include the bacteria that cause tuberculosis.

In the report "Lack of acidification in *Mycobacterium* phagosomes produced by exclusion of the vesicular proton-ATPase" by S. Sturgill-Koszycki *et al.* (4 Feb., p. 678), figure 3 (p. 679) was incorrectly printed. The correct figure appears below.

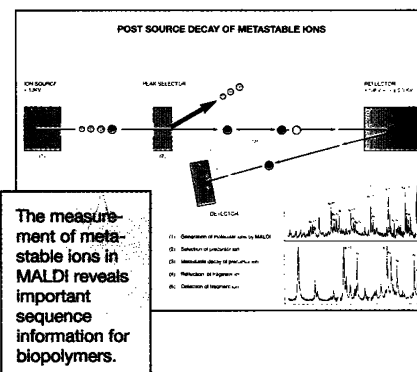


The Research News article "Boning up: Newly isolated proteins heal bad breaks" by Joseph Alper (21 Jan., p. 324) incorrectly attributed the rescue of dpp-minus *Drosophila* by human bone morphogenic protein (BMP) to the laboratory of Michael Hoffmann. That work was published by the laboratory of William Gelbart at Harvard [R. W. Padgett, J. M. Wozney, W. M. Gelbart, *Proc. Natl. Acad. Sci. U.S.A.* **90**, 2905 (1993)]. The work from Hoffmann's laboratory that pertains to the issue of the functional conservation of BMPs during evolution reported that the *Drosophila* proteins dpp and 60A that are similar in sequence to the human BMPs are effective in stimulating bone formation in the rat. This work was done in collaboration with T. Kuber Sampath at Creative BioMolecules [T. K. Sampath, K. E. Rashka, J.-S. Doctor, R. F. Tucker, F. M. Hoffmann, *Proc. Natl. Acad. Sci. U.S.A.* **90**, 6004 (1993)].

Opinion

Matrix Assisted Laser Desorption/Ionization (MALDI) has brought remarkable improvements to the analysis of biomolecules. Time-of-Flight mass spectrometers using MALDI show extraordinary sensitivity and good mass accuracy for molecules otherwise intractable to mass spectrometry.

Maldi has primarily been used to determine molecular weights. However, it has recently been applied to gain structural information about sensitive biomolecules. Some glycoproteins for example show extensive metastable decay of the molecular ion. Comparing the mass spectrum in the linear time of flight mode with the spectrum in the reflector mode reveals the mass of an oligosaccharide moiety being lost. Remarkably, this can be achieved even with fragments of around 1000 Dalton lost from a glycoprotein with molecular mass of 80 000 Dalton.



The VISION 2000 system has been designed to be easily adapted to new applications. This has enabled Finnigan MAT to immediately make available a system that can cover these new applications by operating in different modes depending on the type of analysis required.

The Post Source Decay (PSD) of metastable ions created under MALDI conditions reveals important biopolymer sequence information. The VISION 2000 can be switched from reflector mode to PSD mode under full data system control, leaving all necessary voltage changes in the system transparent to the user. Sequencing of a peptide in PSD mode becomes an easy task.

**Finnigan
MAT**

The OPINION column features technical tips & preliminary information relating to instruments designed & built at Finnigan MAT GmbH, Bremen, Germany.

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