Box 1 Contents snapshot for MIAPE-CE

The full MIAPE-CE document is divided into two parts: an introduction, providing background and an overview of the content, and the full list of items to be reported. The MIAPE-CE guidelines themselves are subdivided as follows:

1. General features: the overall type and aim of the experiment.
2. Sample details and method-specific sample preparation.
3. Equipment used, in terms of the instrumentation, software and capillary; with a description of type and manufacturer along with any subsequent modifications.
4. Run process: the steps followed in each experiment and all the parameters that are associated with this. For example, capillary and sample temperatures, auxiliary data channels, time of data collection, step name/purpose, step length/order, pressures, voltages, geometries, flush solution and electrolyte compositions.
5. Detection: type, wavelengths/mass range, data collection rate, whether direct or indirect and detector calibration requirements.
6. Electropherogram data processing.

Capillary electrophoresis comprises a broad family of techniques, for all of which the subtleties of operation are the key to obtaining robust and reliable results. Therefore, it is necessary to specify that a significant degree of descriptive detail be captured, for the equipment deployed, its manner of use, the sample analyzed and the data processing performed. The MIAPE-CE guidelines provide a checklist of the information that should be provided when describing a capillary electrophoresis experiment (**Supplementary Table 1**). Providing the information requested by MIAPE-CE enables improved corroboration of results by enhancing the comparability of data, whether they are to be submitted to a public repository or reported in a scientific publication (e.g., in a 'materials and methods' section). MIAPE-CE does not specify the format in which to transfer data, or the structure of any repository or document. Nor does it require a description of the preparation of the sample (excepting directl assay-related preparation) or the 'fate' of the analyzed sample beyond the process of detection. Items falling outside the scope of this module may be captured in complementary modules.

These guidelines will evolve as circumstances dictate. The most recent version of MIAPE-CE is now available (http://www.psidev.info/miape/ce/) and the content is replicated here as supplementary information (**Supplementary Table 1**). To contribute or to track progress to remain 'MIAPE compliant', browse the HUPO-PSI website (http://www.psidev.info/miape/).

Note: Supplementary information is available on the Nature Biotechnology website.

COMPETING FINANCIAL INTERESTS
The authors declare no competing financial interests.

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1. Taylor, C.F. *et al. Nat. Biotechnol.* **25**, 887–893 (2007).
2. Taylor, C.F. *et al. Nat. Biotechnol.* **26**, 860–861 (2008).
3. Binz, P.-A. *et al. Nat. Biotechnol.* **26**, 862 (2008).
4. Gibson, F. *et al. Nat. Biotechnol.* **26**, 863–864 (2008).

Guidelines for reporting the use of gel image informatics in proteomics

To the Editor:

We present the gel informatics module (MIAPE-GI) of the minimum information about a proteomics experiment (MIAPE) guidelines[1]. MIAPE-GI—a component of the MIAPE documentation system developed by the Human Proteome Organisation's Proteomics Standards Initiative (HUPO-PSI; http://www.psidev.info/)—results from a coordinated effort by practitioners of gel informatics and representatives of appropriate software vendors, in consultation with the wider proteomics community. Previous MIAPE modules for mass spectrometry and gel electrophoresis have already been described in *Nature Biotechnology*[1–3].

The MIAPE-GI guidelines cover the processing of images derived from two-dimensional gel electrophoresis to detect and quantify features, for example, relating to distinct proteins. The guidelines describe the relationships between (sets of) features on different images established through analyses or known to exist prior to the experiment (such as standards), and the stable location at which data have been deposited (**Box 1**). These guidelines were developed with a view to supporting the sharing of best practice, validation of results, discovery of results and sharing of experimental data sets. For a full discussion of the principles underlying this specification, please refer to the MIAPE 'Principles' document[1].

For MIAPE modules to work well together, their scope must be tightly constrained. Therefore, the MIAPE-GI guidelines do not cover the preparation and running of a gel, nor do they cover image capture; those areas are the province of the MIAPE gel electrophoresis document (MIAPE-GE[4]). Items outside the scope of this module may be addressed in later

Box 1 Contents snapshot for MIAPE-GI

The full MIAPE-GI document is divided into two parts: an introduction providing background and overview of the content and a full list of the items to be reported. The guidelines have been designed to cope with different types of workflows, as performed by particular software packages. As such, a number of items are optional if they refer to a specific procedure not employed by the software used. The MIAPE-GI guidelines themselves are subdivided as follows:

- General features describing the type of electrophoresis performed, the source images for analysis and the analysis software used.
- The gel analysis design with respect to replicates, groupings and standards used.
- Image preparation steps before bioinformatics analysis, such as scaling, resizing or crops.
- Image processing, such as image alignment, performed by bioinformatics software.
- Data extraction, including feature detection, feature matching and feature quantification (if performed).
- Data analyses performed, for example, extracting features with significant differential expression.
- Results of data analysis, including feature locations, matches and relative quantities where appropriate.

versions or by complementary modules, such as MIAPE-GE, which can be obtained from the MIAPE web page (http://www.psidev.info/miape/). As is the case for all MIAPE modules, this specification does not recommend a particular format in which to transfer data nor the structure of any related repository or document.

These guidelines will evolve as circumstance dictates. The most recent version of MIAPE-GI is available from the HUPO-PSI website and the content is replicated here in **Supplementary Table 1**. To contribute or to track progress to remain 'MIAPE compliant', browse the HUPO-PSI website (http://www.psidev.info/miape/).

Note: Supplementary information is available on the Nature Biotechnology website.

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The 20-year environmental safety record of GM trees

To the Editor:

In a commentary last May, Strauss *et al.*[1] pointed out that opposition to genetically modified (GM) organisms has recently intensified on GM trees and that recommendations of the Conference of the Parties (COP) to the Convention on Biological Diversity (CBD) have encouraged regulatory impediments to undertaking field research. We concur with Strauss *et al.* that the CBD appears to be increasingly targeted by activist groups whose opinions are in stark contrast to the scientific consensus and indeed the opinions of most respected scientific and environmental organizations worldwide. Strauss *et al.* call for more science-based (case-by-case) evaluation of the value and environmental safety of GM trees, which requires field trials. However, the regulatory impediments being erected by governments around the world, with full corroboration of the COP, are making such testing so costly and Byzantine, it is now almost impossible to undertake field trials on GM trees in most countries. Here we summarize the key published evidence relating to the main environmental concerns surrounding the release of GM trees (**Box 1**). On the basis of our findings, we urge the COP to consider the opportunity costs for environmental and social benefits, and not just risks, in its deliberations of field trials and releases.

A very large amount of performance and safety data related to GM crops and trees has now been gathered since field trials were first initiated in 1988 (ref. 2). Our search in publicly accessible databases worldwide