

# Reporting Protein Identification Data

THE NEXT GENERATION OF GUIDELINES

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In June 2004, in response to a growing concern among both editors and reviewers, we published a set of instructions to authors, developed in house by a committee chaired by Steve Carr, which spelled out criteria for reporting protein identifications determined by mass spectrometry. The overall response from the community at large to this effort was quite favorable, and we were encouraged to expand on this document by soliciting broader input from a larger group of stakeholders with the view of fashioning a universal set of guidelines that might be useful, in general, for publishers of journals reporting this type of data. Accordingly, with support from the American Society for Biochemistry and Molecular Biology (ASBMB) and the organizational skills of Mike Baldwin, including important input from Steve Carr, Ruedi Aebersold, and Al Burlingame, a two-day workshop was held in mid-May 2005 in the Maison de la Chimie in Paris, France, that was attended by 30 (of the ~60 invited) scientists, engineers, bioinformaticians, and editors/publishers representing academia, research/government institutes, and the private sector (see below). This group reflected an excellent cross-section of individuals involved in the development of mass spectrometry and its proteomic applications. The attendees spent a day presenting/discussing the issues,<sup>1</sup> and then, using the Carr guidelines as a point of departure, divided into four subgroups, with each working through a section. The four rewritten (or, in some cases, new) sections were resynthesized into a single document and were then subjected to further post-meeting editing. In mid-July the draft document was released and broadly disseminated for public comment, suggestions, and criticism. In October, these were collated and returned to the original Paris groups for further editing. The final document was assembled in late January/early February 2006. In mid-February, the final guidelines were aired and discussed at an open forum at the Association of Biomolecular Resource Facilities (ABRF) meeting in Long Beach, CA. They have been subsequently sent to the editors of journals interested in this type of data.

The guidelines are now posted on the MCP website (<http://www.mcponline.org>) and have been officially adopted by the journal as the instructions to authors for papers in this area. They eventually will be shifted to that part of the journal, but we felt initially that it was appropriate to make them as visible as possible. At the same time that the Paris guidelines were

being developed, MCP incorporated a mechanism for evaluating papers for their compliance with the guidelines (initially the Carr guidelines but now those developed in Paris) that inserts an independent evaluation in the review process. A simplified outline of the guidelines in the form of a checklist is used and will be returned to authors by the Associate Editor that documents any areas of deficiency. The checklist will also be sent to the reviewers, along with the submitted materials to facilitate the review and to make compliance with the guidelines more consistent. Additional comments also may be added to help clarify the problems detected. This assessment is not considered to be a review, and unless the deficiencies are deemed to be so great by the Associate Editor, after receiving the checker's report, that in the Associate Editor's opinion the manuscript cannot be appropriately reviewed until the deficiencies are corrected, they will be returned along with the usual reviewer critiques, and the compliance issues can be dealt with at the time any other corrections/changes are made.

Our initial experiences with this independent evaluation have been quite favorable, and we feel that it is already having the desired effect of bringing papers reporting protein identifications into a more consistent form. However, the main goal of these efforts was to address the problem of misidentifications and secure the integrity of the scientific literature. To this end we naturally hope that authors, reviewers and editors alike will find these guidelines useful and worthy of serious consideration. We also appreciate that science is a dynamic process and that today's guidelines can become tomorrow's burdens. Therefore, we will be watchful for advances in technology that make any part of these guidelines obsolete and will welcome suggestions and comments that will aid us in keeping them current.

We would also like to thank the many people who contributed freely of their time to make this goal a reality. We particularly thank Alexey Nesvizhskii, Robert Chalkley, and Karl Clauser for their help in preparing the original Carr document, to Mike Baldwin and all the participants at the Paris meeting, and to the ASBMB for their financial and intellectual support.

#### LIST OF PARTICIPANTS IN THE PARIS MEETING

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Rolf Apweiler, European Bioinformatics Institute  
Kathy Aschheim, Nature Biotechnology  
David Baker, University of Washington  
Ronald Beavis, Beavis Informatics, Ltd.

<sup>1</sup> Powerpoint files of these presentations can be found on the MCP website at <http://www.mcponline.org>.

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