New Guidelines for Clinical Proteomics Manuscripts

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Several years ago, the editors of MCP[1], concerned with the widely varying standards in articles reporting large scale protein identifications, undertook the task of drafting and adopting guidelines for manuscripts that laid out what it felt (and strengthened by considerable advice and comments received from numerous experts in the field) were the minimum set of requirements for reporting and analyzing this type of data (1). The purpose was to raise awareness to the fact that if articles were severely flawed by incorrect or incomplete information, the field of proteomics was bound to suffer a major loss of credibility. Most importantly, opportunities to use the enormous potential of the underlying technology to make major strides in biomedical research would be lost. Since the adoption of the original guidelines for reporting protein identification data in 2005 (1), the journal has made a serious effort to enforce them (not, it must be said, without a fair amount of trial and tribulation for both editors and authors) and compliance has steadily improved. However, since their introduction, we have, admittedly, not attempted to assess their impact either on the content of MCP or on the field of proteomics in general. Rather, we are satisfied that this was an appropriate, and necessary, step and we do note that others share our concerns and in general are quite supportive of our efforts.

We have now initiated a similar approach that targets an emerging and highly important area of proteomics, namely, that dealing with clinically relevant research. Clinical proteomics has, and continues to, emphasize translational applications and is perceived to be the most "relevant" discipline to foster the translation of basic discoveries into clinical applications for the benefit of the patient (2). Unfortunately, clinical proteomics is beginning to suffer from the same over-hyping that dominated proteomics at the time MCP was introduced (~2001) (3–5), and that has left the field struggling to live up to unrealistic claims and promises (6). As a case in point, a major focus of the efforts of clinical proteomic researchers has been the identification and validation of biomarkers and targets. This has proven to be far more difficult than originally anticipated and as a result, it has generated something of a field day for the naysayers and pessimists, who are often quite vociferous in their denouncements. Those with a somewhat longer view of things likely find this amusing as they accept as true that little of lasting value is achieved in whirlwind approaches and are content to thoughtfully build the technology and the knowledge-base knowing that in due course real dividends will be achieved in the form of new and improved diagnostics, therapeutics, and prophylactics. The editorial staff of MCP shares this view.

With the above considerations in mind, the journal has now prepared guidelines for authors that deal specifically with the reporting of studies based on clinically relevant material. As it was the case in developing the guidelines for peptide/protein identification, our aim was to ensure that the reports published in MCP are accurate and appropriately documented and thereby will help to bring the potential power of proteomics to productively bear on clinical applications. The underlying issues have been well discussed by Mischak *et al.* (7) who already provided a cogent case for developing community standards. Of course, the issues that had to be addressed in developing guidelines for clinically relevant manuscripts are more complex than those associated with the peptide/protein identification problem, and therefore presented a much greater challenge. The guidelines for protein identification largely dealt with a single technology, mass spectrometry, but that was not the case here. Nonetheless, the approach used to generate the protein identification guidelines, *i.e.* bringing together a group of stakeholders for a 2-day meeting to prepare a working draft, followed by a period of public scrutiny and comment, and then a final editing to produce the finished document, seemed an appropriate way to proceed. Accordingly, some two dozen individuals (identified on the MCP web site) met in Copenhagen, Denmark on April 24–25 of this year where presentations that outlined the issues were given and then a draft document was prepared. This draft was posted on the MCP web site and widely circulated for input from the community at large. The responses received were used to generate the final version, which is now posted (www.mcponline.org) and has been incorporated into our Instructions to Authors. We, and the other members of the journal editorial staff, are indebted to this group for their many efforts and contributions that made the development of these guidelines possible.

The guidelines deal with a broad spectrum of issues, and of course, only a fraction may apply to any given manuscript. In recognition of this, the guidelines contain both required and recommended information. Most of the required information deals with ethical issues, sample collection and handling, or data that is necessary in order to allow peer evaluation and/or experimental repetition. For the next several months it is our

[1] The abbreviation used is: MCP, Molecular and Cellular Proteomics.

intention to use these guidelines as a mean of familiarizing both authors and reviewers with its use, but we expect to begin rigorous compliance checks, as we do now with protein identification manuscripts, after the first of the year.

We have also appointed a panel of experts to help monitor compliance with the guidelines and, among other activities, provide input and potential changes. As with the peptide/protein identification document, we recognize that the field is changing quite rapidly, and portions of these guidelines may require modifications in the future. We will depend on our Clinical Proteomics Advisory Committee (CPAC) for this advice. We also expect this group to provide ideas for new initiatives, including special issues for the journal, and to monitor the field in general. The Committee is composed of Nils Brünner (Royal Veterinary & Agricultural Hospital, Copenhagen, Denmark), Robert E. Gerszten (Massachusetts General Hospital, USA), Darren Hodgson (AstraZeneca, UK), Elise C. Kohn (NCI, USA), David F. Ransohoff (UNC, USA), and Peter H. Riegman (Erasmus Medical Center, Rotterdam, Netherlands), and many of these people had a hand in preparing these guidelines. The Chair and Deputy Chair of the Committee are Julio E. Celis and Steven A. Carr, respectively. Individuals who wish to contact the journal on matters to do with this aspect of proteomics should feel free to contact them.

In adopting these guidelines, we once again hope that the community at large will respond positively, recognizing that we are instituting them in a genuine attempt to achieve greater uniformity and reliability in the proteomics literature.

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