

New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins

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Molecular & Cellular Proteomics is pleased to announce new guidelines and requirements for papers describing the development and application of targeted *mass spectrometry measurements of peptides, modified peptides and proteins* (PDF). These guidelines will be implemented for papers submitted starting June, 2017.

Over the past several years, representatives from academia, clinical laboratories, and pharma, who are active developers and users of targeted mass spectrometry methods and analysis tools for quantification of peptides and proteins in complex biological or clinical samples, have worked together to develop a set of guidelines and requirements for

authors who want to publish targeted proteomics papers. Our goals were to define what information authors must provide regarding how such analyses were performed and the resulting data analyzed to ensure that reviewers and readers have the ability to independently establish that the measurements being reported using targeted MS methods are reliable—*i.e.* that they specifically identify and quantify the analytes targeted in a sample—and that the measurements are reproducible. The guidelines and requirements for authors that have been developed grew out of an NCI-sponsored meeting and subsequent publication describing a tiered, fit-for-purpose approach to targeted assay development in mass spectrometry-based proteomics (1). We have also incorporated numerous helpful and important suggestions from the community obtained during the 4-month-long public commentary period.

The need for establishing guidelines for targeted MS measurements parallels the situation in discovery proteomics prior to 2004 when similar issues relating to lack of ability to ascertain reliability of published results prompted the journal *Molecular & Cellular Proteomics* to develop and adopt the first set of guidelines for publication of peptide and protein identification data using mass spectrometry (2). These guidelines, which have been repeatedly revised and updated over the past several years (3–5), have been embraced in whole or in part by other journals. The goal now, as it was then, is to try

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to ensure that reliable and reproducible high quality data and results are entering the proteomics literature. We have endeavored to avoid making these guidelines overly prescriptive and intend to be flexible so as to allow for new technologies and approaches that will inevitably arise. We also intend to regularly revisit and revise the guidelines as

needed, as we have done for our other documents for author guidance.

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