Initial Guidelines for Manuscripts Employing Data-independent Acquisition Mass Spectrometry for Proteomic Analysis

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Proteomic research began largely as an approach for characterizing sample compositions, but most contemporary studies involve a quantitative aspect. Quantification enables comparing sample classes (*e.g.* healthy *versus* disease) to uncover markers of dysregulation, or comparing protein pull-down experiments to mock pull-downs to determine specific interaction partners. For small-scale comparisons, isotopic labeling, whether introduced metabolically or chemically, is very effective and allows comparison of multiple samples mixed together. However, for comparing a larger number of samples (a dozen or more), label-free strategies are often the most practical option. Reproducible and accurate quantification of a large number of protein and peptide analytes across a large panel of samples remains a singular goal of the proteomics field in general.

Data-independent acquisition mass spectrometry (DIA-MS) is a set of strategies that aim to provide comprehensive coverage and quantification of components in complex peptide mixtures. DIA-MS was developed to circumvent the issues of irreproducible selection of analytes for fragmentation analysis associated with data-dependent acquisition (DDA) and limited analyte coverage (typically *m/z* range, most commonly broken down into a series of isolated wide *m/z* range windows (1–5). It has seen considerable growth in the last couple of years as instrumentation that can produce high mass accuracy fragmentation spectra at rates in excess of 10 Hz has become widely available. In parallel to development of acquisition methodologies, new analysis software has also emerged to interpret the resulting data.

Molecular and Cellular Proteomics has led the proteomics field in establishing rules for minimum information needed to be provided in submitted manuscripts to evaluate results from different analysis strategies, producing guidelines for authors performing data-dependent MSMS analysis (6), targeted proteomics (7), glycomics/glycoproteomics (8), and clinical proteomic studies (9). These guidelines have in general elevated the standard of published results.

Of late, the journal has published several DIA-MS studies, and it has become evident that even though DIA-MS strategies are still rapidly evolving, a first set of guidelines is required to advise authors on information that should be included in such manuscripts. Hence, in June 2018, the journal organized a meeting of leading researchers in the DIA-MS field in San Diego, CA, to formulate a mutually agreeable set of rules to cover current and anticipated analysis strategies. Representatives from key DIA method, software, and instrument development groups ensured broad community participation. The full list of attendees is provided at the bottom.

The guidelines produced from this meeting were opened to a two-month period of public comment, and the final version is now published (http://www.mcponline.org/page/DIA-guidelines) along with this issue of the journal. A companion checklist has also been constructed to assist authors in meeting these guidelines. The journal intends to start implementing these guidelines for relevant manuscripts on March 1.

As DIA-MS methods are still developing, it is anticipated that these guidelines will need to evolve over time to encompass new approaches, but having a first set of guidelines in place will provide a framework for ensuring that results published using these approaches are accountable.

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