Molecular & Cellular Proteomics
electronic submission

Important Information for MCP Authors

All original manuscripts submitted to MCP that contain protein and post-translational modification identifications determined by mass spectrometry must be in compliance with our established guidelines for this type of data. Any required supplemental data, up to 100 mb, may be submitted along with the manuscript. If supplemental files are larger than this limit, authors must contact the editors before submitting their manuscript. Manuscripts containing identification data will be initially checked to ensure they comply with the guidelines and will be returned to authors, without further review, if found to be seriously deficient. **This does not constitute a review of the manuscript as the compliance checkers ONLY determine if the article conforms to the guidelines, i.e. contains the requisite information.** They do not judge the quality of the data or evaluate the scientific suitability of the manuscript. The actual review of the manuscript is only initiated after the compliance issues have been resolved. Manuscripts, which pass the compliance check, may be found not to be appropriate for publication, for other reasons. Manuscripts that are found to be non-compliant after two evaluations will not be considered further.

To aid authors in preparing their manuscripts, the check list of the items that must be included is given below. Authors are encouraged to print out this document and use it to ascertain that the complete set of required information has been included. Click here to open a power point tutorial that explains each point on the list, and why it has been included. Authors submitting this type of data for the first time are particularly encouraged to use both the checklist and tutorial.

Check list for Publication of Peptide & Protein Identification Data in MCP:

The following information should be included in the ***Experimental*** section:

1. Information on MS/MS database search

Name of peaklist-generating software and release version (number or date) given	yes	na PAGE 8
Parameters used – default vs altered - given	yes	na PAGE 8
Name of the search engine and release version (number or date) provided	yes	na PAGE 8
Search parameters included:		
enzyme specificity considered	yes	na PAGE 8
# of missed cleavages permitted	yes	na PAGE 8
fixed modification(s) (including residue specificity)	yes	na PAGE 8
variable modifications (including residue specificity)	yes	na PAGE 8
mass tolerance for precursor ions	yes	na PAGE 8
mass tolerance for fragment ions	yes	na PAGE 8
name of database searched and release version/date	yes	na PAGE 8
species restriction and justification for searching only a subset of a database	yes	na
number of protein entries in the database *actually* searched	yes	na PAGE 8
Cut-off score/expectation value for accepting *individual* MS/MS spectra provided	yes	na (SUPPLEMENT TABLE 1 (PAGE 9)
Justification of the threshold employed provided	yes	(na)

For large datasets
estimation of false positive rate provided and information how this was calculated listed. yes na PAGE 9

If post-translational modifications are reported
software/method used to evaluate site assignment given yes na

2. Peptide Mass Fingerprint Data

Name of software used for peak-picking and its release version given yes na

Parameters and thresholds used for peak-picking; e.g. intensity or S/N threshold, resolution, means of calibrating each spectrum, list of excluded contaminant ions and justification given yes na

Acceptance criteria provided yes na

3. Protein Appears in databases under different names and accession numbers

If peptides match to multiple members of a protein family, criteria used for selecting which one to report; i.e. how was the redundancy eliminated/handled, provided(This is an issue for *all* protein databases). yes na PAGE 8

How isoforms/individual members of a protein family were unambiguously identified provided yes na

4. Quantitative Studies

How the quantitation was performed (number of peaks, peak intensity, peak area, XIC) provided yes na PAGE 9

Minimum thresholds required for data to be used for quantitation given yes na PAGE 9

Justification of removal of outlier datapoints given. yes na PAGES 10-12

Explanation of statistics used to assess accuracy and significance of measurements provided. yes na PAGES 10-12 PAGES 13-15

Indication of how biological and analytical reproducibility was addressed by experimental design provided yes na PAGES 10-12 PAGES 13-15

Should be included in the ***Results*** section

5. For each protein identified the following should be reported in a table:

accession number yes na

number of *unique* (in terms of amino acid sequence) peptides identified yes na PAGE 9 (Supplement Table 1)

% sequence coverage identified from MS/MS data or a list of sequences identified yes na

6. In addition for single-peptide-based protein identifications or post-translationally modified peptides: – *report in a single Table the following*

sequence identified	yes	na
the precursor m/z and charge observed	yes	na
score/E-value for this peptide	yes	na
+ MS/MS spectrum appropriately labeled should be included – masses detected as well as fragment assignments	yes	na

PAGE 9 (Supplement Table 2) (Spectra.zip) file supporting data

7. In addition for Peptide Mass Fingerprint Data

Number of masses matched given	yes	na
Number of masses not matched given	yes	na
% sequence coverage provided	yes	na
Criteria for acceptance supplied	yes	na
+ MS spectrum appropriately labeled should be included – masses detected as well as peptide assignments	yes	na

8. For quantitation data:

Number of peptides used for protein quantitation measurement given	yes	na
Protein quantitation measurement and accuracy (e.g. mean and standard deviation) provided	yes	na

PAGE 10 PAGE 13-15 PAGE 16 (Supplement Table 3)