

HUPO minimum information publication guidelines (HPG)

Version 1.0 – May 17th 2018

All original manuscripts submitted to proteomics journals that contain large-scale protein/peptide information produced by mass spectrometry are required to comply with the proteomics journal-established guidelines. Most of the non-proteomics journals in life sciences do not or partially require additional information to help authors make their papers acceptable for publication. The present HUPO minimum information publication guidelines (HPG) are intended to help both non-proteomics life sciences journals and authors to provide enough information to explain the experiments, to assess the reliability of the results and to support the results in a homogeneous compliant manner. The below publication guidelines are the minimum information suggested by HUPO and created by the HUPO publication committee based on the original Paris, Philadelphia and HPP data interpretation guidelines. The HPG guidelines are published on the HUPO website <https://hupo.org/page-1757217>.

HUPO Publications Guidelines Check List

For all items in the checklist, please provide either the page number (P) where the item has been described, or provide the explanation number (using blank space provided at bottom of checklist) for why the guideline item was not fulfilled.

1. Search parameters information to be included in the methods section:

	Y	N/A	Page
Program and Methods used to create the peak list			
Critical search parameters (including the mass over charge (m/z) and the charge (z) of the precursor ion, precursor and fragment mass tolerance, cleavage rules used, allowance for number of missed cleavages, fixed and variable modifications, excluded contaminants)			
Search engine (including name and version)			
Sequence database/Spectral library			
Number of protein entries in sequence database			
For large-scale experiments, please provide the methods to calculate false positive rates at PSM, peptide and protein levels			
For reporting on post-translational modifications, please describe the program and methods used to discover the modification			
Program and Methods for protein inference and protein group(s) when needed			

2. Protein/Peptide identification information to be included in the results and supplemental data section:

Submit all MS data to a repository (preferably ProteomeExchange) in its complete form, and provide the corresponding identifier(s) (e.g. PXD)

Peptide sequence and modification localization

Peptide and modification scores

Measures of certainty (e.g. FDR, p-values)

Score value for accepting single MS/MS spectra

For each protein identified, provide accession number, number of identified peptides and sequence coverage

Y N/A Page

Y	N/A	Page

3. Protein/Peptide quantification information to be included in the methods and results sections:

Description of the number of technical and biological replicates and how sample size was calculated

Description of how MS data was processed to get quantification data

Estimates of certainty (tests, FDR, p-values)

Y N/A Page

Y	N/A	Page