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The following information should be provided for protein or peptide identifications using mass spectrometry:

1. The program, and version number, used to create peak lists and the parameters used in the creation of the list.
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3. The name and version number of the sequence database used in searches. If a custom-made database is used then complete information on the origin of the sequences and database size should be disclosed. Given the dependence of scoring on database size, the use of a small database, or one excluding contaminants, should be justified.
4. A short description of the methods used to interpret the significance of search results, including any statistical analysis, confidence thresholds and other values specific to judging the certainty of the identification.
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