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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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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.
5. For large-scale experiments a false-positive determination should be reported. This may be the result of randomized database searches or other approaches.
6. Each protein identification should include the accession number, score generated by the search algorithm used, sequence coverage and the number of unique peptide sequences assigned in the protein identification.
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