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• Telephone and fax numbers
• Keywords
• All figure captions
• All tables (including title, description, footnotes)
Further considerations:
• Manuscript has been "spellchecked" and "grammar-checked"
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• All references mentioned in the Reference list are cited in the text, and vice versa
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Additional information

Submission of sequence data to databases

Novel nucleotide or protein sequence data must be deposited in the GenBank™, EMBL or DDBJ databases and an accession number obtained before the paper can be accepted for publication. Submission to any one of the collaborating databanks is sufficient to ensure entry in all. The accession number should be included as a footnote on the title page of the manuscript: 'Note: Nucleotide sequence data reported in this paper are available in the GenBank™, EMBL and DDBJ databases under the accession number(s)'. If requested the database will withhold release of data until publication. The usual method for submitting sequence data is by the World Wide Web to either GenBank (via BankIt: http://www.ncbi.nlm.nih.gov/BankIt/), EMBL (via WebIn: http://www.ebi.ac.uk/subs/allsubs.html) or to DDBJ (via SAKURA: http://sakura.ddbj.nig.ac.jp/). Special types of submissions, such as genomes, bulk submissions, segmented sets, and population/phylogenetic/mutation studies, can be more easily prepared with the Sequin programme (available from the above Web sites). Authors are encouraged by the databases to update their entries as the need arises.

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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.
2. The program, and version number, of the program used for database searching. Parameters used for searching should be specified, including, but not limited to, precursor-ion mass tolerance, fragment-ion mass tolerance, modifications allowed for, missed cleavages and enzymes used in protein cleavage.
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.
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.
7. Single peptide identifications should include an annotated MS/MS spectrum showing fragment assignments together with the peptide sequence, precursor mass, charge and error.
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