DESCRIPTION

The International Journal for Parasitology – Drugs and Drug Resistance is one of a series of specialist, open access journals launched by the International Journal for Parasitology. It publishes the results of original research in the area of anti-parasite drug identification, development and evaluation, and parasite drug resistance. The journal also covers research into natural products as anti-parasitic agents, and bioactive parasite products. Studies can be aimed at unicellular or multicellular parasites of human or veterinary importance.

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INTRODUCTION

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• E-mail address
• Full postal address
• Telephone and fax numbers
• Keywords
• All figure captions
• All tables (including title, description, footnotes)
Further considerations
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• References are in the correct format for this journal
• 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.

**GenBank/DNA sequence linking.** In order for automatic links to be made between papers and GenBank, authors should type the accession number in bold, underlined text. Letters in the accession number should always be capitalised. (See the example). When published they will appear in normal type.

Example: ′ GenBank accession nos. \textbf{AI631510}, \textbf{AI631511}, \textbf{AI632198}, and \textbf{BF223228}, a B-cell tumor from a chronic lymphatic leukemia (GenBank accession no. \textbf{BE675048}), and a T-cell lymphoma (GenBank accession no. \textbf{AA361117})′.

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

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 use 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.

8. Identifications arising from peptide mass fingerprinting should include an annotated mass
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