INTERNATIONAL JOURNAL FOR PARASITOLOGY: DRUGS AND DRUG RESISTANCE

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AUTHOR INFORMATION PACK

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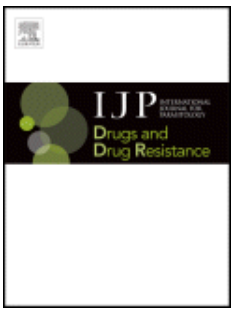

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AUDIENCE

Parasitologists, Zoologists, Entomologists, schools of tropical medicine.

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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. **AI631510**, **AI631511**, **AI632198**, and **BF223228**), a B-cell tumor from a chronic lymphatic leukemia (GenBank accession no. **BE675048**), and a T-cell lymphoma (GenBank accession no. **AA361117**)’ .

Additionally, any multiple alignments of nucleotide or protein data must be submitted to a recognised database and must also receive a unique accession number. The accession number can appear in the text in the relevant section of the Results, as: ’ Alignment files are available by anonymous FTP from FTP.EBI.AC.UK in directory/pub/databases/embl/align or via the EMBLALIGN database via SRS at http://srs.ebi.ac.uk; under accession(s)’ . The usual method for submitting alignments is by the World Wide Web to the European Bioinformatics Institute (via Webin-Align: http://www.ebi.ac.uk). Microarray data, in MIAME-compliant format, should be submitted to ArrayExpress (http://www.ebi.ac.uk/arrayexpress/) or GEO (http://www.ncbi.nlm.nih.gov/geo/). Accession identifiers relating to the data should be provided in the manuscript text.

Policy on bioinformatics papers. In silico analysis: The following guidelines apply to papers that exclusively use in silico analysis or rely heavily on this approach for analysis and conclusions. Such papers should address a significant biological issue or issues. Bioinformatic data should be supported by novel or published biological data. Work would typically use information from a number of databases and even from a number of parasite or host species and use a number of analytical methods. Types of ’ metaanalysis’ are encouraged either across a wide range of parasites or, say, at a number of points in a metabolic or signalling pathway or an immune cascade. In silico analysis may be especially suitable for review articles.

Guidelines for reporting of protein identifications using mass spectrometry

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 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 spectrum. The number of matched peaks, the number of unmatched peaks and the sequence coverage should also be reported along with all parameters and thresholds used to analyse the data. This includes mass accuracy, resolution, calibration methods, contaminant exclusions along with the scoring scheme used and measure of the false-positive rate.

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