INTERNATIONAL JOURNAL FOR PARASITOLOGY: DRUGS AND DRUG RESISTANCE

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AUTHOR INFORMATION PACK

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DESCRIPTION

The International Journal for Parasitology – Drugs and Drug Resistance 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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In addition, the journal provides a medium for highlighting selected articles reporting highly significant original findings, as Editor's Choice Manuscripts. It also commissions articles with emphasis on shorter, focused Reviews of topical issues and strategically important subjects. The journal encourages critical comment and debate on matters of current controversy in the area of parasite drug resistance and anti-parasite drugs via "Current Opinions".

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The *International Journal for Parasitology: Drugs and Drug Resistance* 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. Because of its breadth of organism coverage, all contributions should include relevant information about the parasite of interest in order to be comprehensible to non-experts in the particular subject of the articles.

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Additional information

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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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