



INTERNATIONAL JOURNAL FOR PARASITOLOGY: PARASITES AND WILDLIFE

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AUTHOR INFORMATION PACK

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DESCRIPTION

The *International Journal for Parasitology: Parasites and Wildlife (IJP-PAW)* publishes the results of original research on parasites of all wildlife, invertebrate and vertebrate. This includes free-ranging, wild populations, as well as captive wildlife, semi-domesticated species (e.g. reindeer) and farmed populations of recently domesticated or wild-captured species (e.g. cultured fishes). Articles on all aspects of wildlife parasitology are welcomed including taxonomy, biodiversity and distribution, ecology and epidemiology, population biology and host-parasite relationships. The impact of parasites on the health and conservation of wildlife is seen as an important area covered by the journal especially the potential role of environmental factors, for example climate. Also important to the journal is 'one health' and the nature of interactions between wildlife, people and domestic animals, including disease emergence and zoonoses.

The principal form of publication is the full-length article which contains substantial, original research. The journal also accepts brief reports that have similar subject scope as the full-length article, but do not merit a full-length publication. In addition, the journal commissions articles with emphasis on shorter, focused reviews of topical and emerging issues as well as strategically important subjects. The journal encourages critical comment and debate on matters of current controversy in the area of parasites and wildlife via "Current Opinions".

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INTRODUCTION

The *International Journal for Parasitology: Parasites and Wildlife (IJP:PAW)* publishes the results of original research on parasites of all wildlife, invertebrate and vertebrate. This includes free-ranging, wild populations, as well as captive wildlife, semi-domesticated species (e.g. reindeer) and farmed populations of recently domesticated or wild-captured species (e.g. cultured fishes). Articles on all aspects of wildlife parasitology are welcomed including taxonomy, biodiversity and distribution, ecology and epidemiology, population biology and host-parasite relationships. The impact of parasites on the health and conservation of wildlife is seen as an important area covered by the Journal especially the potential role of environmental factors, for example climate. Also important to the journal is 'one health' and the nature of interactions between wildlife, people and domestic animals, including disease emergence and zoonoses.

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Additional information

Submission of sequence data to databases

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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**)' .

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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 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.
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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