

AUTHOR'S STYLE GUIDE FOR PREPARING MANUSCRIPTS FOR SUBMISSION TO
ANTONIE VAN LEEUWENHOEK DESCRIBING NEW MICROBIAL TAXA

Your manuscript must follow the advice given in our **Instructions for Authors** at:
<http://www.springer.com/life+sciences/microbiology/journal/10482>

Additionally, Descriptions of New Microbial Taxa are subject to specific guidelines and formatting requirements which can be found in the accompanying pdf at
<http://www.springer.com/life+sciences/microbiology/journal/10482>

Notably, an explanation of what makes the novel taxon of general interest (beyond it simply being a previously undescribed taxon) is given appropriate emphasis in the text.

It is expected that descriptions of novel Archaeal and Bacterial taxa will include data from genome sequence analyses. In addition, we expect manuscripts containing genome data to present an analysis of genomic features of interest (beyond basic metrics such as G+C content, ANI and dDDH).

We recommend that descriptions of novel Archaeal and Bacterial taxa are accompanied by an entry in the Digital Protologue Database (DPD) and include a TaxonNumber (similar to current policy regarding deposition of information on novel fungal taxa in MycoBank). The DPD is available at <http://imedea.uib-csic.es/dprotologue/>

Please consider all of the following when preparing and submitting your manuscript:

- Certificates confirming deposition of the novel type strain in two different culture collections are included with the submission. If the novel type strain has been deposited in MTCC, confirmation of deposit in a third culture collection is required.
- Relevant DNA sequence(s) (e.g. barcoding; 16S rRNA gene sequences e.t.c.) have been deposited in Genbank and the accession number(s) provided. If the sequence has been deposited but is not yet freely available then it should be provided as a supplementary file.
- *Antonie van Leeuwenhoek* uses European spellings (e.g. 'characterised' not 'characterized', 'analysed' not 'analyzed', 'hydrolysed' not 'hydrolyzed' etc.)
- Remember that throughout the text you are describing living biological material (stored in laboratories and culture collections) and so the strict past tense is not always appropriate. For example:

"Strain X was catalase positive" is incorrect and should be phrased as "Strain X was found to be catalase positive"

"Strain X was Gram-negative" is incorrect and should be phrased as "Strain X was observed to be Gram-negative"

"Phylogenetic analysis showed strain X was a member of the genus Y" is incorrect and should be phrased as "Phylogenetic analysis showed strain X is a member of the genus Y".

- An exception is wet lab DNA:DNA hybridisation data – since these experimental results are 'one off' determinations, then these values, as **mean \pm SD** of a minimum of triplicates, should be reported in the past tense.
- Avoid absolutes such as "phylogenetic analysis revealed the **closest relative** of strain X is Z^T" as, in the future, a more closely related taxon may be described; a better wording is "phylogenetic analysis revealed strain X to be **closely related to** Z^T".

- Values in text and tables **must not** exaggerate the accuracy of the methods used. Rarely can values given to 2 or more decimal places be justified. For example, % composition in a cellular fatty acid profile should only be given to 1 decimal place (e.g. 12.3%). Likewise values for DNA G+C content determined experimentally (rather than from genome sequence data).
- Cellular components (notably polar lipids and fatty acids) that are cannot be precisely identified should be described as 'unidentified' (**not** 'unknown' – as they are reported in your work they must be 'known').
- The protologue of a species description based on a single strain should not contain data on antibiotic susceptibility as this is a potentially variable characteristic which can be greatly affected by the presence or absence of mobile genetic elements. Where antibiotic susceptibilities may still be relevant data the results can simply be stated in the main text.
- The protologue of a species description based on a single strain should not include long lists of data on substrate utilisation and enzyme activities (e.g. from commercial tests galleries such as API or Biolog) as this is a potentially variable characteristic. Such findings may still be relevant data and so should be stated in the main text or included as a Table.
- Specific percentages for the profiles of components such as fatty acids or quinones are **not given** in the protologue (as these may vary with growth conditions).
- **ALL** binomial microbial species names should be given in full at first usage and thereafter the genus name abbreviated (e.g. *Escherichia coli*, then *E. coli*). Where abbreviations may cause confusion, choose an appropriate 3 letter abbreviation. A guide to some recommended 3 letter abbreviations is given at LPSN: <http://www.bacterio.net/-abbreviations.html>).