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DESCRIPTION

The Journal provides a medium for the rapid publication of both full-length articles and short communications on novel and innovative aspects of **biotechnology**. The Journal will accept papers ranging from genetic or molecular biological positions to those covering biochemical, chemical or bioprocess engineering aspects as well as computer application of new software concepts, provided that in each case the material is directly relevant to **biotechnological systems**. Papers presenting information of a multidisciplinary nature that would not be suitable for publication in a journal devoted to a single discipline, are particularly welcome. The following areas are covered in the Journal:

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INTRODUCTION

Journal of Biotechnology provides a medium for the rapid publication of both full-length articles and short communications on novel and innovative aspects of biotechnology. The Journal will accept papers ranging from genetic or molecular biological positions to those covering biochemical, chemical or bioprocess engineering aspects as well as computer application of new software concepts, provided that in each case the material is directly relevant to biotechnological systems. **Papers presenting information of a multidisciplinary nature that would not be suitable for publication in a journal devoted to a single discipline, are particularly welcome.** The following areas are covered in the Journal:

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- * Medical Biotechnology
- * Agro- and Food Biotechnology
- * Genomics and Bioinformatics

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(4) **Short Genome Communications With Relevance to Biotechnology**

High-throughput DNA sequencing is a widely used technology, which has been used to generate tens of thousands of complete and partial genomic sequences thus far. It is now possible to rapidly generate complete genomic sequences, especially up to a size of 100 megabase pairs to determine the sequence of species and strains with relevance to Biotechnology.

Journal of Biotechnology has a specific section for publications related to novel and innovative Genome projects, called Short Genome Communications. With the recent advances in DNA Sequencing and Genome Annotation technologies, the requirements for publication in this section are shifting. While initially, papers were accepted to a section called Genome Announcements without peer review, all submissions to the Short Genome Communications section are now subjected to the regular peer review process at Journal of Biotechnology.

Submissions without relevance to Biotechnology, submissions lacking novelty, as well as submissions without experimental backup of the claims with regards to the biotechnological relevance do not fall within the scope of the Short Genome Communications section and will be rejected outright. Also, submissions dealing with incomplete genomes (=partial genome sequences) will no longer be accepted for publication in Journal of Biotechnology. This applies to genomic sequences of all sizes, including for example fungal genomes. It is of course still possible to include data from partial sequencing experiments in other sections of Journal of Biotechnology as back-up evidence. Relevance to Biotechnology does not include submissions dealing with sequences from pathogenic strains (human, animal, plant), which were sequenced for medical reasons, or strains used for nutritional purposes (nutraceuticals etc.).

Successful submissions to the Short Genome Communications section therefore include: (a) a complete sequence of an organism or strain with novel biotechnological aspects (it is no longer sufficient to simply confirm the presence of an already known gene cluster in another strain); (b) experimental data to demonstrate that the biotechnological function, or improvement of a biotechnological process via alterations of the genomic sequence is indeed active in the strain (it is for

example not sufficient to assume that the function might be active based on database comparisons only) and (c) a GenBank accession number under which the sequence can be accessed by the general public. Comparative work and a discussion of the improvements of a biotechnological process using the new sequence information is strongly encouraged.

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