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ISSN: 1874-7787

### DESCRIPTION

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The journal publishes papers on all functional and evolutionary aspects of **genes, chromatin, chromosomes** and (meta)**genomes** of **marine** (and freshwater) **organisms**. It deals with new genome-enabled insights into the broader framework of environmental science. Topics within the scope of this journal include:

- Population **genomics** and ecology
- Evolutionary and developmental genomics
- Comparative genomics
- Metagenomics
- Environmental genomics
- Systems biology

More specific topics include: geographic and phylogenomic characterization of aquatic organisms, metabolic capacities and pathways of organisms and communities, biogeochemical cycles, genomics and integrative approaches applied to microbial ecology including (meta)transcriptomics and (meta)proteomics, tracking of infectious diseases, environmental stress, global climate change and ecosystem modelling.

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### AUDIENCE

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Marine and freshwater biologists and ecologists, molecular biologists, geneticists, biotechnologists, oceanographers and modellers.

### IMPACT FACTOR

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## ABSTRACTING AND INDEXING

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Elsevier BIOBASE  
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Zoological Record  
Abstracts of Mycology  
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**M. S. Clark**, British Antarctic Survey, Cambridge, UK

RESEARCH INTERESTS: Transcriptome response in Antarctic marine invertebrates and vertebrates. Physiological adaptations in cold-adapted marine organisms. Heat-shock response. Environmental genomics of Antarctic organisms. Molecular analyses of marine organisms. "Omics" technologies in environmental science

**J.M. Cock**, UMR CNRS 7139, Roscoff, France

RESEARCH INTERESTS: Genetic regulation and development of brown algae. Life cycle regulation. Sex determination. Algal genomics

**N. Dubilier**, Max Planck Institute (MPI) for Marine Mikrobiologie, Bremen, Germany

RESEARCH INTERESTS: Symbionts in marine invertebrates. Transfer of energy from the geosphere to the biosphere at hydrothermal vents and cold seeps. Ecology of chemosynthetic environments. Microbial ecology

**A. Falciatore**, CNRS-UPMC UMR 7238, Paris, France

RESEARCH INTERESTS: Diatom functional genomics. Diatom photoreceptors, signaling pathways and function. Genome expression and light response regulation

**J.M.O Fernandes**, Bodø University College, Bodø, Norway

RESEARCH INTERESTS: Genetic networks controlling growth in teleosts. Fish epigenetics. Role of microRNAs (miRNAs) in animal ontogenesis. Muscle development. Antimicrobial peptides. Transcriptomics, with focus on differential miRNA expression.

**J.A. Gilbert**, Argonne National Laboratory, Argonne, Illinois, USA

RESEARCH INTERESTS: Microbial communities: temporal and biogeographic structure. Bioprospecting. Metagenomics. Metatranscriptomics. Bioinformatics, Microbial Ecology. Microbial metabolic dynamics

**W.R. Hess**, Albert-Ludwigs-Universität Freiburg, Freiburg, Germany

RESEARCH INTERESTS: Marine microbiology and functional genomics in bacteria. Transcription and RNA processing. Nuclear, mitochondrial and plastid gene expression in cyanobacteria. Systems biology approaches and methods

**G. Procaccini**, Stazione Zoologica Anton Dohrn, Napoli, Italy

RESEARCH INTERESTS: Functioning of pelagic and benthic systems at organismal, community and ecosystem levels. Genetics and genomics of sea grass. Molecular systematics and population genetics

**J. Raes**, Vrije Universiteit Brussel (VUB), Brussels, Belgium

RESEARCH INTERESTS: Computational approaches for large-scale, next-generation sequencing projects. Bioinformatics. Human microbiome. Ecological communities. Metagenomics, metatranscriptomics and meta-metabolomics. Molecular eco-systems biology

**F. Raible**, University of Vienna, Vienna, Austria

RESEARCH INTERESTS: Metazoan evolution. Evolution of hormones and neurosecretory brain centers in Bilateria. Regulation of reproductive cycles. Regeneration. Biology of marine annelids.

**J.K. Sky Yu**, Academia Sinica, Nankang, Taipei, Taiwan

RESEARCH INTERESTS: Biology of cephalochordate amphioxus. Evolutionary transition from invertebrates to vertebrates. EST resources and genome sequencing data. Expression patterns of developmental genes and functional analysis of signaling pathways. Evolutionary origin of vertebrate body plan

**F. Volckaert**, KU Leuven, Leuven, Belgium

RESEARCH INTERESTS: Evolution at higher trophic levels. Phylogenetics, phylogenomics, population genetics, evolutionary & ecological functional genomics and metagenomics of fishes and their parasites. Connectivity and demography based on genotype, phenotype, micro-chemistry and modelling. Fisheries, aquaculture and conservation genetics

## GUIDE FOR AUTHORS

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## INTRODUCTION

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### Data Articles:

This section will consider high quality and standardized reports describing results of all aspects of genome-scale analysis (microarray and next-generation sequencing) in all types of marine (and freshwater) organisms. The genomic data/results will function as points of record for the new data generation methods.

**ALL DATA ARTICLES WILL BE PRE-SCREENED AT THE EDITORIAL LEVEL TO EVALUATE THE PERCEIVED GENERAL INTEREST OF THESE ARTICLES AND ASSESS THEIR POTENTIAL SUITABILITY FOR THE JOURNAL BEFORE BEING SENT OUT FOR DETAILED REVIEW.**

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Article layout for Data Articles:

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2. Introduction, providing the rationale to choose the strain or habitat for genome/transcriptome or metagenome/metatranscriptome sequencing and if the species/study is part of a project, if yes provide information on the project.
3. Data description, with phenotypic (if available), physiological and biochemical key features following the MIxS mandatory information of the MIxS checklist and environmental packages. This information should be provided in a Table.

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If your article includes any Videos and/or other Supplementary material, this should be included in your initial submission for peer review purposes.

Divide the article into clearly defined sections.

The format of Data Articles is:

- \* Maximum length of 2500 words (including abstract and legend to figures, excluding references)
- \* Maximum 25 references
- \* 3 figures/tables maximum

Article layout for Data Articles:

1. Abstract
2. Introduction, providing the rationale to choose the strain or habitat for genome/transcriptome or metagenome/metatranscriptome sequencing and if the species/study is part of a project, if yes provide information on the project.
3. Data description, with phenotypic (if available), physiological and biochemical key features following the MIxS mandatory information of the MIxS checklist and environmental packages. This information should be provided in a Table.

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A Theory section should extend, not repeat, the background to the article already dealt with in the Introduction and lay the foundation for further work. In contrast, a Calculation section represents a practical development from a theoretical basis.

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