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DESCRIPTION

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

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

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RESEARCH INTERESTS: genome evolution, comparative and population genomics, RADseq analysis, computational biology and algorithm development.

C-H. C. Cheng, University of Illinois at Urbana-Champaign, Urbana, Illinois, USA
RESEARCH INTERESTS: Evolutionary cold adaptation and cold specialization of Arctic and Antarctic fishes. Genome and transcriptome evolution in the cold. Evolvability of polar species to changing climate. Molecular and environmental physiology.

**M. S. Clark**, British Antarctic Survey, Cambridge, England, UK

Transcriptome response in Antarctic marine invertebrates and vertebrates; Physiological adaptations in cold-adapted marine organisms; Heat-shock response; Environmental genomics of Antarctic adapted 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 Microbiology, 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. Falcicatore**, CNRS-UPMC UMR 7238, Paris, France


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


**J.A. Gilbert**, University of Chicago, Chicago, Illinois, USA

Microbial communities: temporal and biogeographic structure; Bioprospecting. Metagenomics; Metatranscriptomics; Bioinformatics; Microbial Ecology; Microbial metabolic dynamics

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


**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


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


**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

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
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INTRODUCTION

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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.

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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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* Maximum length of 2500 words (including abstract and legend to figures, excluding references)
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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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State the objectives of the work and provide an adequate background, avoiding a detailed literature survey or a summary of the results.

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Vitae
Submit a short (maximum 100 words) biography of each author. Please provide this in an editable format (e.g. Word), not in PDF format.

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