GENERAL AND COMPARATIVE ENDOCRINOLOGY

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DESCRIPTION

General and Comparative Endocrinology publishes articles concerned with the many complexities of vertebrate and invertebrate endocrine systems at the sub-molecular, molecular, cellular and organismal levels of analysis. Although by no means comprehensive, submission of manuscripts in the following areas of endocrine science are encouraged:

• endocrine regulation and interactions in physiological processes ("systems" biology - reproduction, body fluid homeostasis, skeletal and calcium homeostasis; gastrointestinal function; integumentary function; neurophysiology; cardiovascular function etc);
• endocrine pharmacology;
• the role of gene expression in endocrine systems;
• behavioral endocrinology;
• developmental endocrinology;
• growth factors;
• endocrine- environmental interactions;
• immuno-endocrine interactions;
• neuroendocrinology, neuropeptides, neurotransmitters;
• hormonal receptors;
• molecular evolution of hormones and gene families.
• Comparative Molecular Analyses
  - Genomics
  - Proteomics
  - Transcriptomics
  - Metabolomics

Manuscripts that advance understanding within and between these broad disciplines are especially encouraged.

All articles published in General and Comparative Endocrinology will be immediately assigned to an issue upon acceptance, without having to wait in press. This will mean immediate publication for all authors, upon completion of post-acceptance publishing processes.

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INTRODUCTION

General and Comparative Endocrinology publishes articles concerned with the many complexities of vertebrate and invertebrate endocrine systems at the sub-molecular, molecular, cellular and organismal levels of analysis. Although by no means comprehensive, submission of manuscripts in the following areas of endocrine science are encouraged:

- endocrine regulation and interactions in physiological processes ("systems" biology - reproduction, body fluid homeostasis, skeletal and calcium homeostasis; gastrointestinal function; integumentary function; neurophysiology; cardiovascular function etc);
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- neuroendocrinology, neuropeptides, neurotransmitters;
- hormonal receptors;
- molecular evolution of hormones and gene families.

Comparative Molecular Analyses
- Genomics
- Proteomics
- Transcriptomics
- Metabolomics

Manuscripts that advance understanding within and between these broad disciplines are especially encouraged.

General and Comparative Endocrinology will consider for publication of research articles that address endocrinology in its widest sense, i.e. both among, and within, living organisms - vertebrate, invertebrate and plant - including their evolutionary antecedents. Original and novel information in acute, and in the longer term, evolutionary adaptive homeostasis are of especial interest to the journal.

The European Society for Comparative Endocrinology, North American Society for Comparative Endocrinology, The Division of Comparative Endocrinology of the Society for Integrative and Comparative Biology, the Asia and Oceania Society for Comparative Endocrinology and the Japan Society for Comparative Endocrinology are affiliated to General and Comparative Endocrinology.

Types of article

Regular article - Full-length original research papers, reporting novel findings in all endocrinology related fields.

Short Communications – these are articles that present a new technique, idea or concept and are typically 10 double spaced pages in length.

Communications in Comparative Molecular Analyses - these are original research manuscripts ranging from 10 to 24 double spaced pages which report studies deploying any kind of "omics" technologies, which are relevant to the endocrine literature (i.e., results of small to high throughput studies). Manuscripts can report the analysis of primary data or in silico analysis or meta-analysis of data deposited in databases and should frame the significance of the data in light of comparative endocrinology and endocrine function.

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*Article structure*

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Divide your article into clearly defined and numbered sections. Subsections should be numbered 1.1 (then 1.1.1, 1.1.2, ...), 1.2, etc. (the abstract is not included in section numbering). Use this numbering also for internal cross-referencing: do not just refer to 'the text'. Any subsection may be given a brief heading. Each heading should appear on its own separate line.

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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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Provide sufficient details to allow the work to be reproduced by an independent researcher. Methods that are already published should be summarized, and indicated by a reference. If quoting directly from a previously published method, use quotation marks and also cite the source. Any modifications to existing methods should also be described.

**Material and methods Guidelines for Immunohistochemistry & RTqPCR assays**

1. **Immunohistochemistry**

In the Methods section, for antibodies it is important to indicate the origin (eg. human, rat, fish) and sequence of the immunogen against which the animal was immunized. If using commercially generated antisera provide the name of company that made the antisera, the species that was immunized and whether the reagent is a monoclonal or polyclonal antibody. It is important to provide characterization information which can include Western blot analysis, radioimmunoassay or ELISA. Reference to previous publications is acceptable as long as the above characterizations have been performed in those publications. Controls may include pre-adsorption with the original antigen if the antigen is available and/or incubation with secondary antibody only. For analyses that involve transfected cells, the controls should include: incubation of the non-transfected cell line with primary and secondary antibody, and incubation of the transfected cells with secondary antibody only.

2. **What to look for when evaluating reviewers comments about real time quantitative PCR (RTqPCR) assays**

There is considerable debate and an ever growing literature about the "best way" to perform real time quantitative PCR (RTqPCR). One publication which gives extensive and helpful guidelines about RTqPCR is Nolan et al., 2006 Nature protocols 1; 1559 and if you are looking for formal guidelines and recommendations consult Clinical Chemistry (Bustin et al., 2009 55, 611). Some simple guidelines:

1. The Dnase treatment and protocol should be indicated.
2. The primers chosen for reverse transcription should be indicated.
3. The RTqPCR primers and probe sequence (if used), the amplicon size along with the mix and supplier should be indicated.
4. The sequence accession number should be provided.
5. Steps taken to optimize and validate RTqPCR assays should be indicated (eg. primer concentration, MgCl2 concentration, dNTP concentration, melt temperature) and melting curve dynamics and absence of primer dimers should be confirmed.
6. The complete RTqPCR thermocycle should be provided.
7. The specificity of the RTqPCR assay should have been established by sequencing the reaction product at least once.
8. The efficiency of the PCR reaction should be indicated (theoretically 100%), as should the method of validation (eg. cDNA or standard dilution curves).
9. The choice of gene(s) for normalization should be justified and they should be referred to as reference genes and not as housekeeping genes. The method of normalization should be provided.
Results
Results should be clear and concise.

Discussion
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Conclusions
The main conclusions of the study may be presented in a short Conclusions section, which may stand alone or form a subsection of a Discussion or Results and Discussion section.

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