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## Preface

The *Xenopus* system had a long and prominent history during the twentieth century as an accessible model system for studying vertebrate biology. Many discoveries in biochemistry, cell biology, and in particular in developmental biology have their roots in experimental investigation using *Xenopus*. Among the inherent advantages of the *Xenopus* model are the ease with which large numbers of eggs can be collected; the large size of those eggs and the embryos that develop from them after fertilization; a consistent fate map; the external development of these embryos and the speed with which the conserved vertebrate body plan is organized. The large cells in the early embryos were ideal for addressing cell biological questions but also allowed early embryonic patterning of the vertebrate embryo and the fate map to be unraveled. Many fundamental processes in vertebrate development were first discovered in *Xenopus* in areas such as axial development, mesoderm induction, neural patterning, and more recently organogenesis and regeneration, to name but a few. The absence of well-developed genetics has often been cited as the one disadvantage of the *Xenopus laevis* model system compared to mouse or zebrafish for instance, but as this volume shows very clearly this criticism has been thoroughly put to rest.

This volume of Methods in Molecular Biology on *Xenopus* comes at a crucial juncture for our model system. The recent publication of the draft genome for *Xenopus tropicalis* marks an important milestone. It reveals that the *Xenopus* genome is in itself an ideal model for vertebrate genomes since it manifests conserved vertebrate genomic organization and therefore reinforces the uniquely advantageous phylogenetic position of *Xenopus* as a general vertebrate model. The genome and the embrace of genomic approaches enabled by *X. tropicalis* as an experimental model have invigorated the entire *Xenopus* field, not just those working with *X. tropicalis*. This volume seeks to focus on these new approaches. *X. tropicalis* offers tractable genetics that will complement the traditional strengths of *Xenopus* as a model system, as do the powerful transgenics methods pioneered in *Xenopus*. The genome and new deep sequencing approaches open up a new chapter in the analysis of gene expression on a whole transcriptome level and of protein expression and interaction on a proteome level; here in particular the traditional advantages of the *Xenopus* model system synergize very directly with the new information technology available to enable completely novel approaches. However, this impact is also felt in new methodology to image these expressed transcripts and proteins in embryos and in cells, particularly with sophisticated fluorescence microscopy; and of course in new systems approaches and applications for stem cell technology and regeneration. As a consequence, the computer and online databases will become as much a tool for *Xenopus* researchers in the future as the micropipette, the injection needle, and the dissection scalpel have been for many years.

The new approaches inspired by the *X. tropicalis* genome combined with the unique experimental advantages of *X. laevis* and their distinctive phylogenetic position make them unique model systems for vertebrate embryonic development in the twenty-first century. The protocols in this volume written by the leading experts in each method provide a tool-kit that will enable every laboratory to maximize the power of this extraordinary experimental system.

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Xenopus Protocols

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