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## Preface

Conventional gene targeting is widely used to generate knockout mice. However, the conventional method depends on a rare event, spontaneous homologous recombination. This makes it impossible to produce gene-targeted mice directly from fertilized eggs, which in any case are limited in numbers for use in experiments. Consequently, for conventional gene targeting, embryonic stem cells (ESCs) are used instead of eggs because the former can be easily propagated. However, because generation of germline-competent ESCs is extremely difficult, conventional gene targeting is only possible for mice and rats, for which ESCs are available. This problem was solved by the advent of genome editing technologies, which enable specific cleavage of targeted loci, frequently followed by non-homologous end joining (NHEJ) or homology-directed repair (HDR). NHEJ results in a small deletion or insertion at the target locus, whereas HDR can yield a knock-in at the target locus if a donor DNA is provided. There are three genome editing technologies: zinc-finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and the clustered regularly interspaced short palindromic repeat (CRISPR)/Cas9 system.

*Genome Editing in Animals: Methods and Protocols* aims to collect protocols that can be used for the generation of knockout animals. The first three chapters introduce basic protocols for three genome editing technologies that can be applied to all animals. Chapter 4 introduces target design tools that can also be used in all animals. Starting in Chapter 5, specific protocols for each animal are provided: mouse (Chapters 5–8), rat (Chapter 9), rabbit (Chapter 10), pig (Chapter 11), monkey (Chapter 12), chicken (Chapter 13), zebra fish (Chapter 14), medaka (Chapter 15), *Xenopus* (Chapter 16), silkworm (Chapter 17), cricket (Chapter 18), sea squirt (Chapter 19), and *C. elegans* (Chapter 20).

I thank all of the authors for their outstanding contributions to this volume. On behalf of all of us, I hope that our effort to make these methods accessible will prove useful to genome editing aficionados around the world.

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Genome Editing in Animals

Methods and Protocols

Hatada, I. (Ed.)

2017, XI, 256 p. 67 illus., 45 illus. in color., Hardcover

ISBN: 978-1-4939-7127-5

A product of Humana Press