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## Preface

Homing endonucleases are site-specific DNA endonucleases that primarily function as mobile genetic elements, promoting their spread by recombination-based pathways. Homing endonucleases are easily distinguished from other site-specific DNA endonucleases by their lengthy recognition sequences (~14–40 bp) and by their tolerance to nucleotide substitutions within their recognition sites. The biotechnological potential of homing endonucleases as rare-cutting endonucleases was recognized soon after their discovery. Detailed structural, biochemical, and bioinformatic studies on homing endonuclease–DNA interactions has led to the realization that the specificity of homing endonucleases, especially the LALIGDADG family members, can be reprogrammed to target desired sequences. Engineering of designer homing endonucleases has set the stage for genome editing of complex eukaryotic genomes, with a broad range of potential applications including targeted gene knockouts in model organisms and gene therapy in humans. This volume is aimed at providing molecular biologists with a comprehensive resource to identify and characterize homing endonucleases from genomic sequence, to deduce the biological basis of binding and cleavage specificity, as well as to provide protocols to redesign endonuclease target specificity for genome-editing applications.

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Homing Endonucleases

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