Methods in ENZYMOLOGY

Volume 497

Synthetic Biology, Part A

Methods for Part/Device Characterization and Chassis Engineering

Edited by

Christopher Voigt

VOLUME FOUR HUNDRED AND NINETY-SEVEN

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METHODS IN ENZYMOLOGY

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CHRISTOPHER VOIGT
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PREFACE

This is the first volume of a two-part series in *Methods in Enzymology* on tools and techniques used in synthetic biology. Synthetic biology is an engineering discipline that seeks to construct living systems that do not exist in nature. The field refers to the process by which genetic systems are designed and constructed, as opposed to any particular application. Along these lines, these volumes are organized into two areas. Volume I focuses on the assay techniques and design principles underlying the characterization of genetic parts, their combination into devices and programs, and their integration into various hosts. Volume II focuses on computational tools and biophysical models to aid in the design and organization of genetic programs and modern methods to synthesize and assemble the associated DNA.

The chapters in Volume I have been organized to reflect the hierarchy from simple genetic parts to complete systems in complex hosts. Genetic parts are units of DNA that encode a simple function, such as a promoter- or ribosome-binding site. The first set of chapters focus on new methods to rapidly construct and characterize such parts. This includes methods to rapidly assay transcription (e.g., ChIP-seq) and translational processes, and the application of directed evolution to design promoter libraries. The next set of chapters deal with the design principles for assembling parts into various devices. These devices can encode genetic circuits that function analogously to their electronic counterparts (e.g., logic gates, oscillators, pulse generators). The biochemistry that underlies these circuits varies, and examples are included that rely on proteins and RNA.

Devices often encode complex, dynamic functions, making their characterization a challenge. To this end, a variety of advanced techniques are described, including the application of microscopy and microfluidics to measure the dynamics of single cells. The characterization of a circuit requires its perturbation. Typically, this has been accomplished through the addition (or removal) of an inducer such as IPTG. This process is slow and inaccurate and relies on a transcriptional process. New methods in "optogenetics" allow the perturbation of signaling networks using light. This allows rapid (millisecond) activation and deactivation of a pathway.

The design of metabolic devices is also included. Several chapters are focused on projects that have been designed as teaching modules in undergraduate labs, including a banana-scented bacterium and bacterial photography/edge detection.

The most common host organism in synthetic biology for prokaryotes is *Escherichia coli* and for eukaryotes is *Saccharomyces cerevisiae*. This is due to the

availability of simple methods for genetic manipulation. In the natural world, there are innumerable organisms with useful functions and applications. Much progress has been made in establishing genetic tools for model organisms. To this end, chapters have been included that focus on photosynthetic organisms (*Rhodobacter* and *Cyanobacteria*), organisms relevant for fuel/chemical/pharmaceutical production (*Streptomyces* and *Desulphovibrio*), plants, and mammalian viruses.

CHRISTOPHER VOIGT

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