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BOOK REVIEW

Young Min Kwon, Steven C. Ricke: High throughput next generation sequencing, methods and applications. Methods in molecular biology

Humana Press, 733

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I like books! And despite my best attempts it took me a long time to like this one. Like Robert Louis Stevenson's Jeckyll and Hyde, the book has dual personalities. Early on there are three chapters describing protocols for the Helioscope. These chapters contain considerable repetition and are a little pointless as there are only one or two Institutes in the world that operate this platform. Likewise there are several similar chapters on microbial diversity and 454 sequencing that again are very repetitious. I wish I had a sum of money for every time I had read that only a very small fraction of the planet's microbial community can be cultured. A couple of chapters just describe the use of particular kits and are little more than a repeat of the manufacturer's protocols.

However, there are definitely some highlights that will make this book of use to both NGS Newbies and experienced practitioners. For example

Chapter 2 describes a method for WGA of uncultured bacterium and seems well balanced mentioning the known problems with this approach.
Chapter 5 provides protocols for preparing next gen sequencing libraries of bacterial small RNAs.
Chapter 9 describes how to do amplicon sequencing on the 454 platform.
Chapter 15 describes how to sequence from and determine the position of transposon insertions, a valuable technique for identifying essential genes for particular growth conditions.
Chapter 16 gives details of two approaches for determination of DNA methylation patterns.
Chapter 17 reviews the Nextera NGS library preparation approach.
Chapter 18 describes how to make Illumina sequencing libraries without PCR and so avoid amplification bias.
Chapter 19 describes a method for target selection using hairpin selector probes.
Chapter 20 provides information on how to multiplex up to 96 libraries in a single Illumina lane.

Overall then it is worthwhile but it is not a Sambrook and Russell (or Maniatis of old) that you turn to time and time again. Nor is it what it says on the cover. There are huge areas of NGS methods and applications missing. Whilst there are three chapters dedicated to Helicos sequencing there are no applications for SOLiD. Nor are there any general RNA seq or ChIP seq chapters. Also missing are protocols for preparation of mate pair libraries.

However, whilst it is often said that books are not useful as they are out of date as soon as they are published this is not the case here and many readers will find this a very useful book.

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