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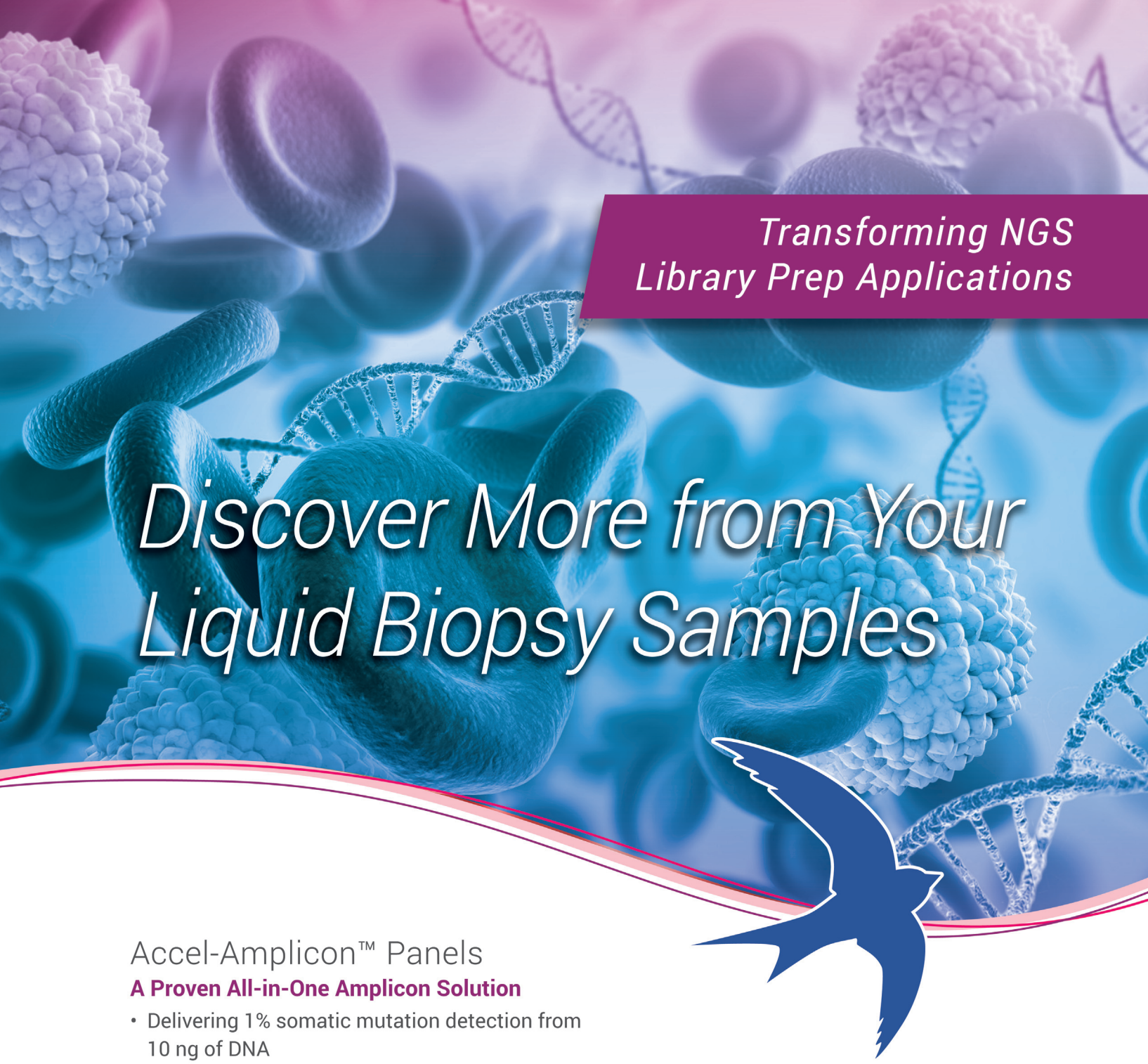

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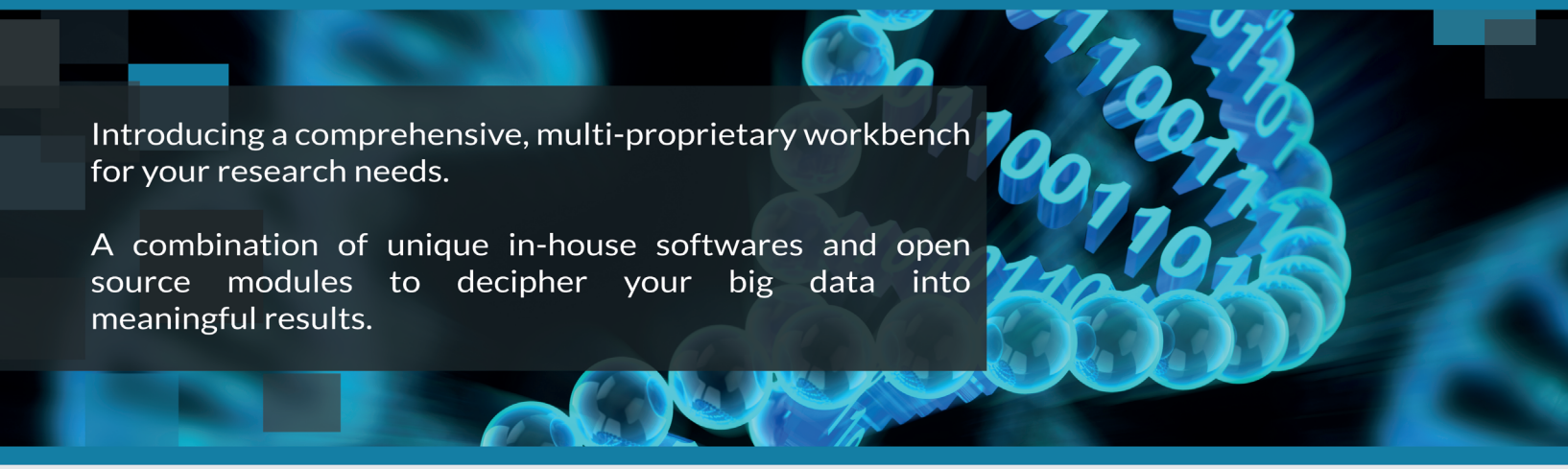

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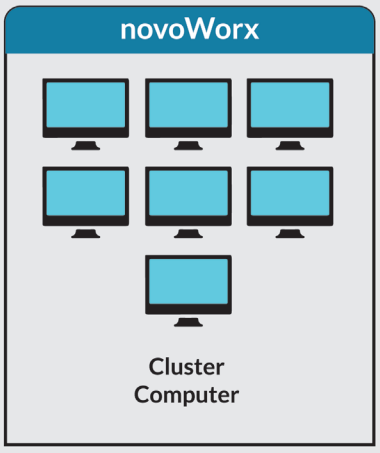

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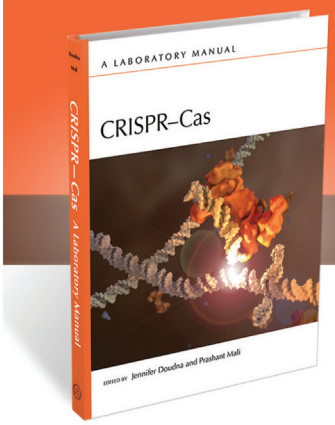

CRISPR-Cas

A Laboratory Manual

CSH PRESS

The essential guide to CRISPR-Cas

Edited by Jennifer Doudna, *University of California, Berkeley;*
Prashant Mali, *University of California, San Diego*

The development of CRISPR–Cas technology is revolutionizing biology. Based on machinery bacteria use to target foreign nucleic acids, these powerful techniques allow investigators to edit nucleic acids and modulate gene expression more rapidly and accurately than ever before.

Featuring contributions from leading figures in the CRISPR–Cas field, this laboratory manual presents a state-of-the-art guide to the technology. It includes step-by-step protocols for applying CRISPR–Cas-based techniques in various systems, including yeast, zebrafish, *Drosophila,* mice, and cultured cells (e.g., human pluripotent stem cells). The contributors cover web-based tools and approaches for designing guide RNAs that precisely target genes of interest, methods for preparing and delivering CRISPR–Cas reagents into cells, and ways to screen for cells that harbor the desired genetic changes. Strategies for optimizing CRISPR–Cas in each system—especially for minimizing off-target effects—are also provided.

Authors also describe other applications of the CRISPR–Cas system, including its use for regulating genome activation and repression, and discuss the development of next-generation CRISPR–Cas tools. The book is thus an essential laboratory resource for all cell, molecular, and developmental biologists, as well as biochemists, geneticists, and all who seek to expand their biotechnology toolkits.

2016, 192 pages, illustrated (20 color, 4 B&W), index

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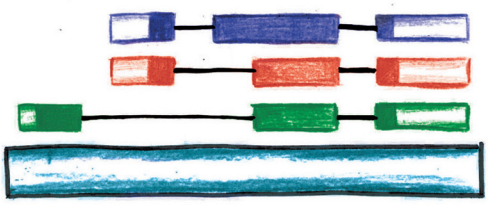

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Spike-in controls are essential in RNA-Seq experiments to assess workflow and platform properties. However, external RNA controls existing to date are generally mono-exonic and non-variant, significantly limiting their ability to reflect the true nature of eukaryotic transcriptomes. These are characterized by extensive splicing, alternative and antisense transcription, overlapping genes, and rare events like the formation of fusion genes. The performance of RNA preparation, library generation, sequencing, and bioinformatics algorithms can furthermore not be assessed adequately without known transcript spike-in controls of representative complexity.

To address this gap, Lexogen has conceived Spike-In RNA Variants (SIRVs) for the quantification of mRNA isoforms in Next Generation Sequencing. The accuracy of mapping, isoform assembly and quantification can be assessed, making isoform-quantification based experiments comparable.

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- **Validation of the RNA-Seq pipeline.**
- **Quantification of differential expression on the transcript level.**

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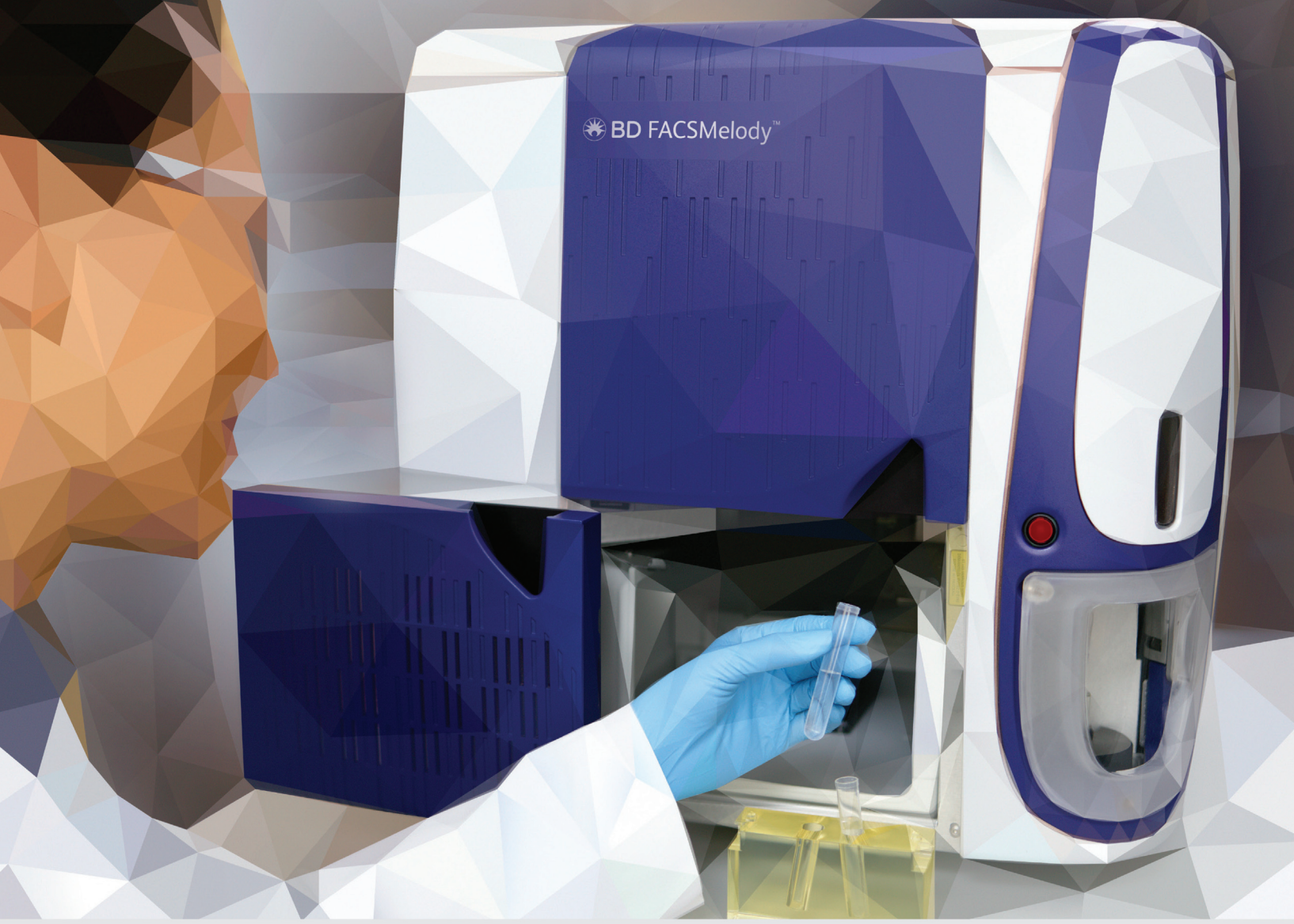

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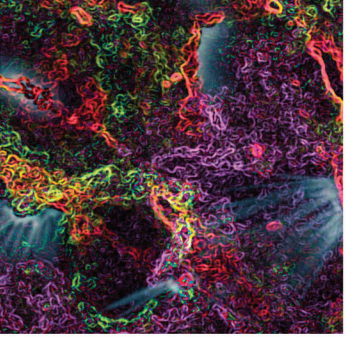

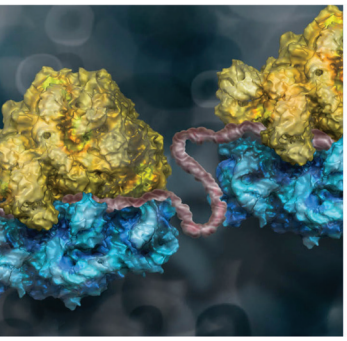

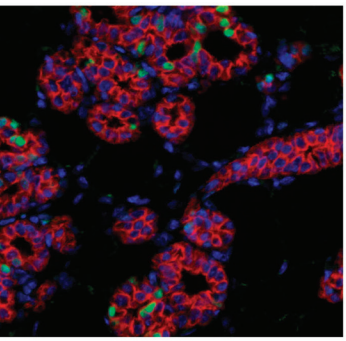

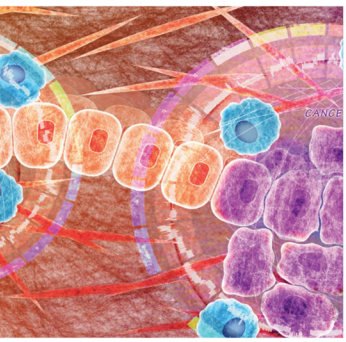

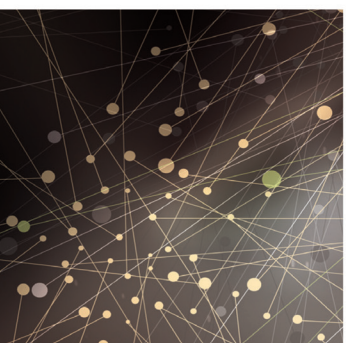

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DNA Repair: Tumor Development and Therapeutic Response
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Co-Chairpersons: José Baselga and Scott A. Armstrong
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November 16-19, 2016 • Orlando, FL

EORTC-NCI-AACR Molecular Targets and Cancer Therapeutics Symposium
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Munich, Germany

San Antonio Breast Cancer Symposium
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Precision Medicine Series: Opportunities and Challenges of Exploiting Synthetic Lethality in Cancer
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January 4-7, 2017 • San Diego, CA

AACR International Conference on New Frontiers in Cancer Research
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AACR Annual Meeting 2017
Program Committee Chairperson: Kornelia Polyak
April 1-5, 2017 • Washington, DC

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Chairperson: Jeffrey N. Myers
Co-Chairpersons: Jennifer Rubin Grandis, J. Silvio Gutkind, Quynh-Thu Le
April 23-25, 2017 • San Diego, CA

AACR International Conference on Translational Cancer Medicine
Co-Chairpersons: Carlos L. Arteaga and Carlos Gil M. Ferreira
May 4-6, 2017 • São Paulo, Brazil

International Conference on Malignant Lymphoma (ICML)
Co-Chairpersons: James O. Armitage, Martin F. Fey, and Emanuele Zucca
Hosting Chairperson: Franco Cavalli
June 14-17, 2017 • Lugano, Switzerland

EACR-AACR-SIC Special Conference 2017: The Challenges of Optimizing Immuno and Targeted Therapies: From Cancer Biology to the Clinic
Co-Chairpersons: Anton J.M. Berns, Nancy E. Davidson, and Silvia Giordano
June 24-27, 2017 • Florence, Italy

Advances in Modeling Cancer in Mice: Technology, Biology, and Beyond
Co-Chairpersons: Cory Abate-Shen, Kevin M. Haigis, Katerina A. Politi, and Julien Sage
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Learn more and register at
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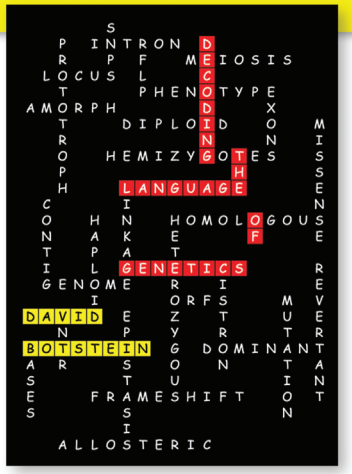
Decoding the Language of Genetics



By David Botstein, Lewis-Sigler Institute for Integrative Genomics

In this book, the distinguished geneticist David Botstein offers help and advice to scientists and physicians daunted by the arcane technical terms that flourish in his discipline. The science of gene function has a vocabulary of specialized, sometimes confusing terms to explain how traits and diseases are inherited, how genes are organized and regulated in the genome, and how the genetic code is read and translated by cells. These terms are often a barrier to full understanding of the underlying concepts. Yet, as more and more individuals learn about their genomes, the information these sequences contain cannot be understood or explained without reference to the basic ideas of genetics. Botstein draws on his long experience as a teacher and pioneering scientist to explain and illuminate what many genetic terms mean and how they entered common usage.

2015, 240 pages, illustrated (30 4C, 10 B&W), index
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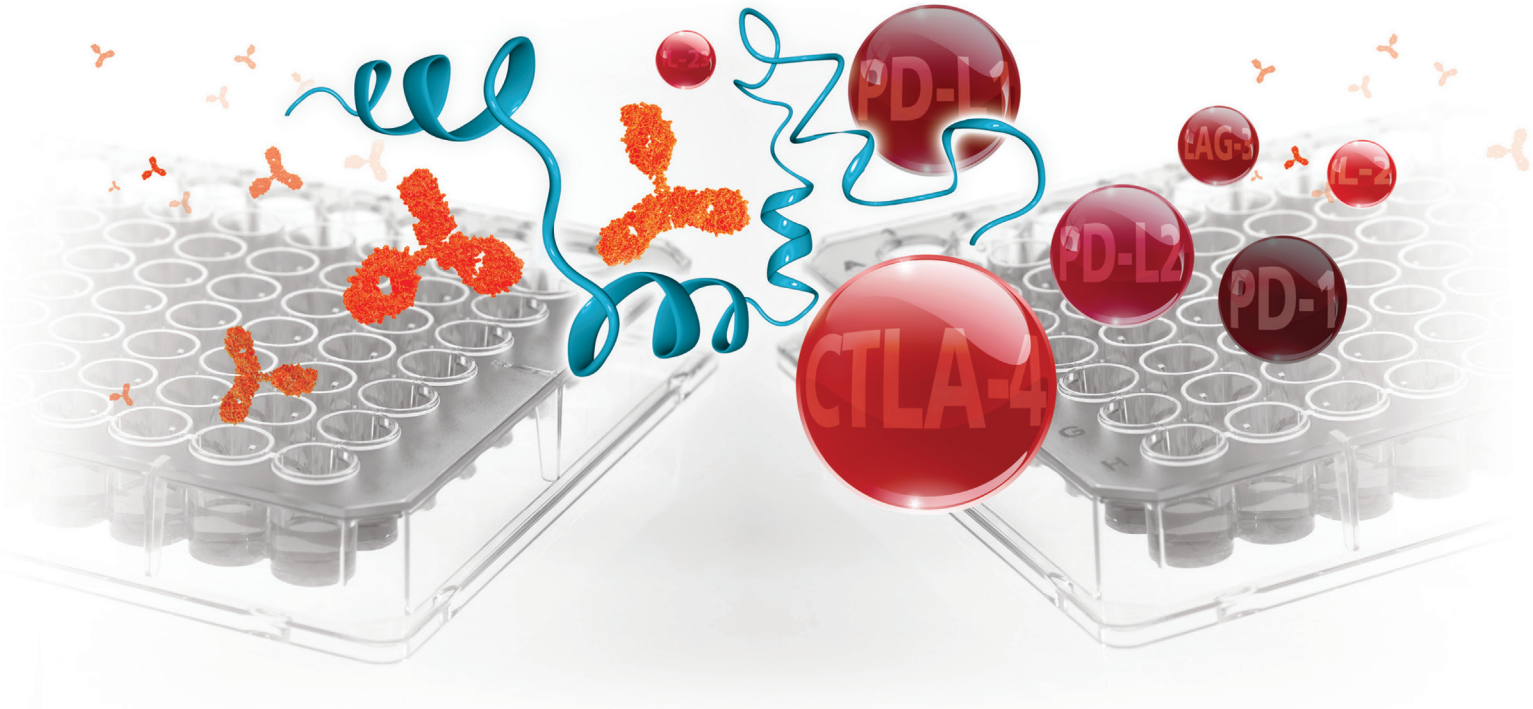

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