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Automating genomic discovery

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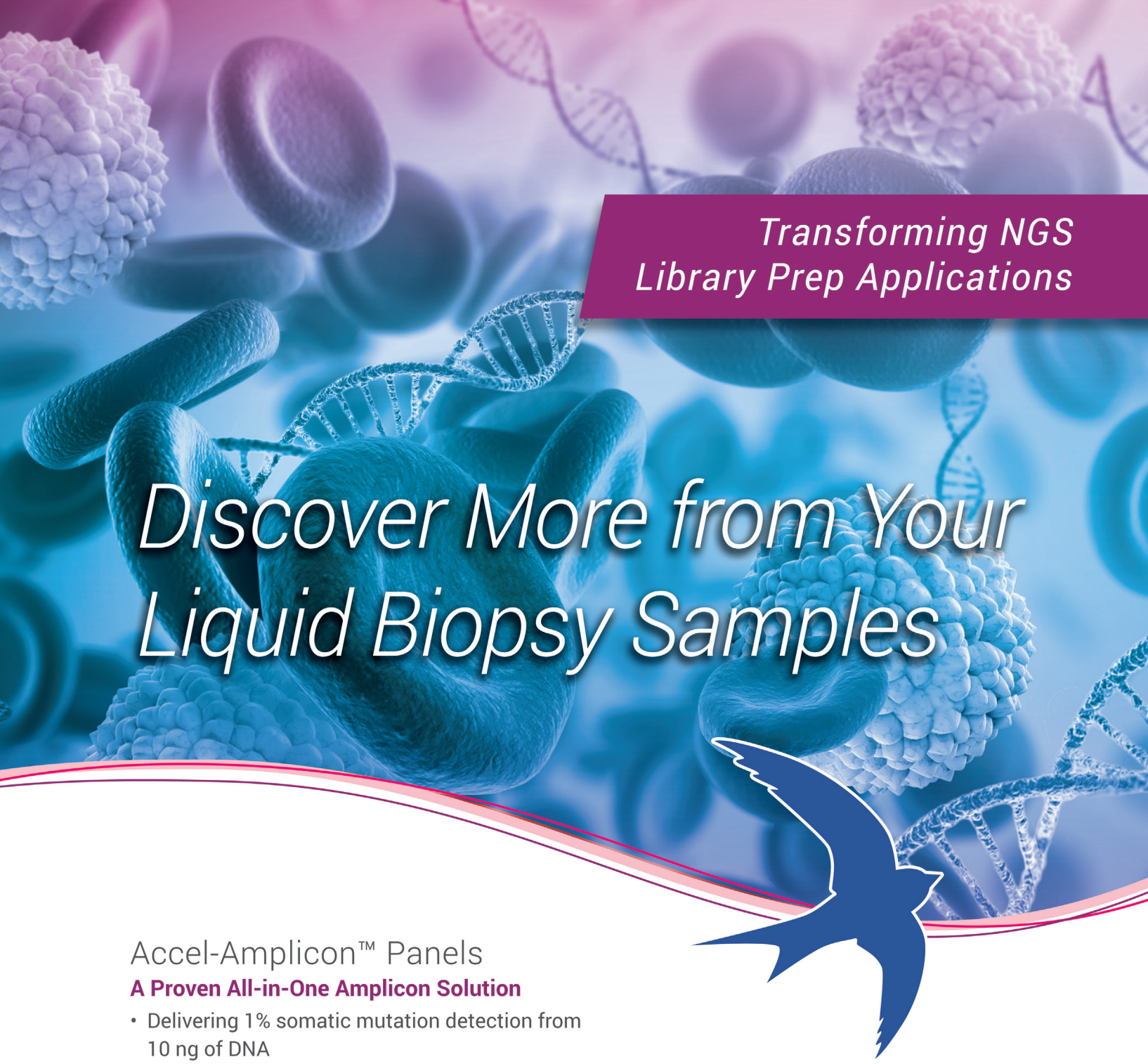

*Transforming NGS Library Prep Applications*

# *Discover More from Your Liquid Biopsy Samples*

## Accel-Amplicon™ Panels

**A Proven All-in-One Amplicon Solution**

- Delivering 1% somatic mutation detection from 10 ng of DNA
- Simple single-tube, 2-hour workflow

## Accel-NGS® 2S Hyb DNA Library Kit

**Highest Library Diversity, Lowest Inputs**

- Enabling whole exome sequencing from 25 ng of DNA
- Compatible with all hybridization enrichment panels

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ion torrent

# The S is for Simplicity


## The new Ion S5™ System. Targeted sequencing has never been simpler.

Simple library prep tools, cartridge-based reagents and automated data analysis have reduced DNA-to-data hands-on time to less than 45 minutes. So you'll spend less time doing routine molecular biology, and more time informing time-sensitive decisions.

**Ion AmpliSeq™ technology**
As little as 1 ng low-quality DNA sample input for library prep

**Cartridge-based reagents**
Less than 15 minutes of sequencing setup time

**2.5 to 4 hours of run time**
Fastest run time of any benchtop sequencer

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**thermofisher.com/ionS5**

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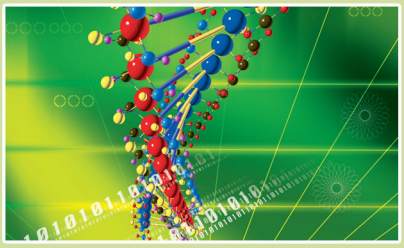
# Gene Synthesis Services

## As low as... US$0.27 per bp

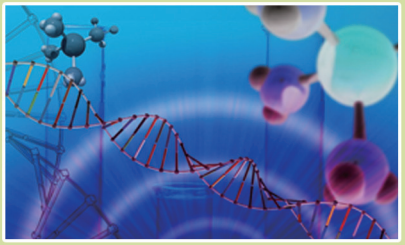
Give me sequences, and return you genes:

| | | |
|---|---|---|
| Up to 300 bp | $80 per gene | 1-2 weeks |
| 300 bp to 1,000 bp | $0.27 per bp | 1-2 weeks |
| 1,001 bp to 2,000 bp | $0.30 per bp | ~ 2 weeks |
| 2,001 bp to 3,000 bp | $0.35 per bp | 2-3 weeks |
| Larger than 3,000 bp | inquiry | inquiry |



◎ Fully cloned and 100% sequence verified.
◎ Free codon optimization

Genes with challenging features such as complex secondary structure, repetitive sequences (direct or indirect), high(>80%) or low (<20%) GC content, or long polypurine/polypyrimidine runs can be synthesized with our unique proprietary technology. Please contact us for a quote.



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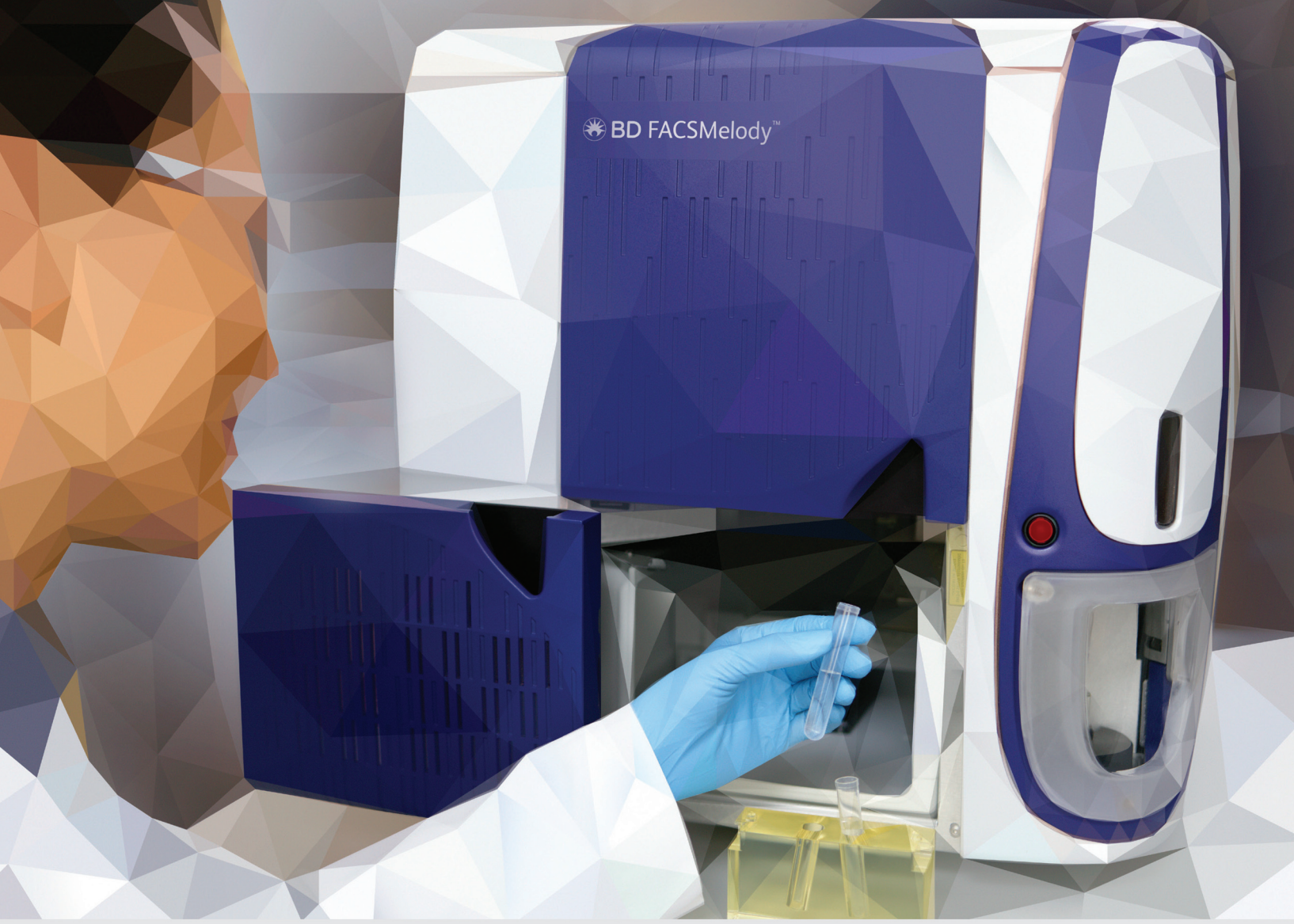


# THE DIFFERENCE OF ONE SIMPLE SORT

**ONE RESEARCHER, ONE SORTER, ONE CELL, MANY DISCOVERIES.** BD is dedicated to developing easy-to-use cell sorting technologies that simplify accurate and reliable flow cytometry. The **BD FACSMelody™** cell sorter introduces a powerful combination of high performance, reproducible results and automated ease of use from a brand whose integrated flow cytometry portfolio and rigorous standards you can trust. BD FACSMelody is an affordable cell sorter that requires minimal training making it an ideal solution to advance your research. Its software guides the operator through every step, with a system sort readiness of less than 17 minutes for optimal timeliness. Designed to improve efficiency and throughput, it comes with the full suite of BD service and support to help you maximize your investment. Learn more about the one cell sorter that is easy to learn, to use and to maintain. Discover the difference one company can make. **Discover the new BD.**

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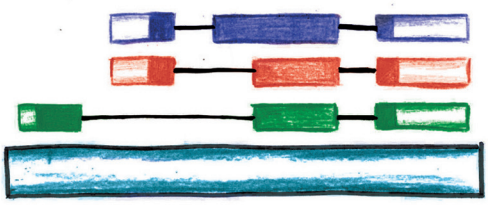

# What if my RNA-Seq is wrong?

## Only with SIRVs can you be confident.

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.

### SIRVs (Spike-in RNA Variant Control Mixes)

- **69 artificial transcript variants representing alternative splicing, promoter and poly(A) site usage, overlapping genes, and antisense transcription.**
- **Validation of the RNA-Seq pipeline.**
- **Quantification of differential expression on the transcript level.**


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Enabling complete transcriptome sequencing

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novoWORX

# Introducing novoWorx™, a Genome Data Management and Analytics platform

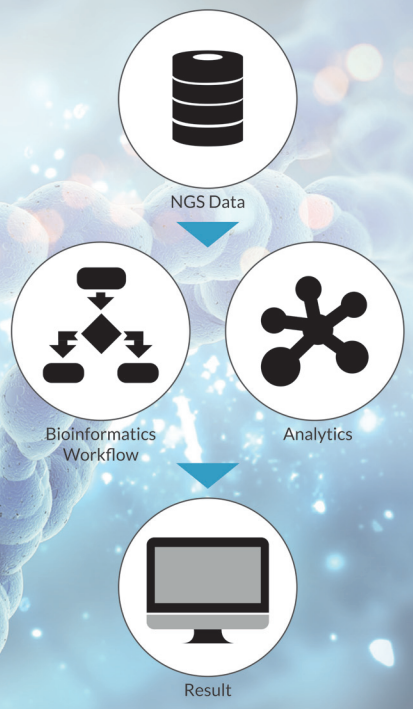
A comprehensive multi proprietary platform to accelerate your research by using sophisticated, fully automated solutions powered by the latest technologies.

## Why novoWorx™?

- The only commercially available tool to offer embedded novoAlign™ and novoSort™ programs for high-throughput bioinformatics analysis.
- A modular system for delivering canned genomics pipelines.
- Process large datasets consisting of multiple samples without programming knowledge.
- Generates all the outputs in standard formats required for downstream/tertiary analysis by other systems.

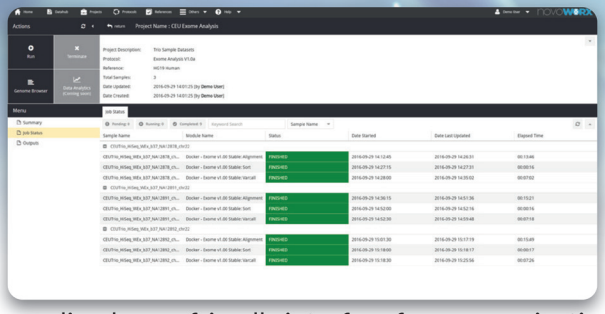
## Features

- Web-enabled and secure interface with access control.
- Drag and drop files into the interface.
- Supports multiple samples run from a single click, no coding required to loop through large sample collection sets.
- Integrated genome browser.
- Cluster-aware (SGE support) and monitor all running, pending and completed jobs.
- Result file downloads.
- Browse all files as reactive tables and figures.




*Information on pipelines and analytics tools are available on the website.*

**CONTACT US FOR A DEMO TODAY!**



Streamlined, user-friendly interface for easy navigation

Ready to use downloadable results

| Requirement | Minimum | Recommended |
|---|---|---|
| CPU | Dual Core 1.8 GHZ | Octa Core 3.2 GHZ |
| Memory | 4 GB DDR2 | 16 GB DDR3 |
| Storage space | 5 GB for installation media<br>15 GB post installation*<br>100 GB free space** | 5 GB for installation media<br>15 GB post installation*<br>100 GB free space** |
| Network | 500Kb/s download speed | 1 Mb/s download speed |
| Virtual Machine Environment | Any Virtual Machine Environment capable of importing OVA files | Oracle VirtualBox (recommended) or VMware |

**only takes into account the OVA installation media.*
***post installation file size.*

| | Files | Size |
|---|---|---|
| novoWorx™ (Required) | novoWorx Databases | 2 GB |
| | HG19 Reference files | 18 GB |

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# Reduce DNA Assembly and QC Costs
# 100-Fold

Echo® Liquid Handlers use acoustic energy to transfer DNA oligos and reagents, allowing the reduction of DNA assembly and NGS library preparation reaction volumes. Dramatically reduce reagent costs, save samples, and eliminate steps – all while improving the quality and throughput of synthetic genes.

**100-fold reduction of Gibson or Golden Gate assembly reaction volumes**

**100-fold reduction of NGS library preparation volumes**

**Increased assembly and QC throughput**

**Automation to easily process thousands of assemblies**

## COMPARISON OF LIQUID HANDLING METHODS

| | Manual Pipetting | Echo® Liquid Handler |
|---|---|---|
| Amount of DNA | 50 ng | **0.06 – 2.0 ng** |
| DNA volume (Rxn) | 25 µL | **200 nL** |
| Library prep volume (Rxn) | 25 µL | **300 nL** |
| Total volume | 50 µL | **0.5 µL** |
| Reactions per kit | 96 | **9600** |
| Cost per reaction | $72.91 | **$0.73** |

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WASHINGTON, DC

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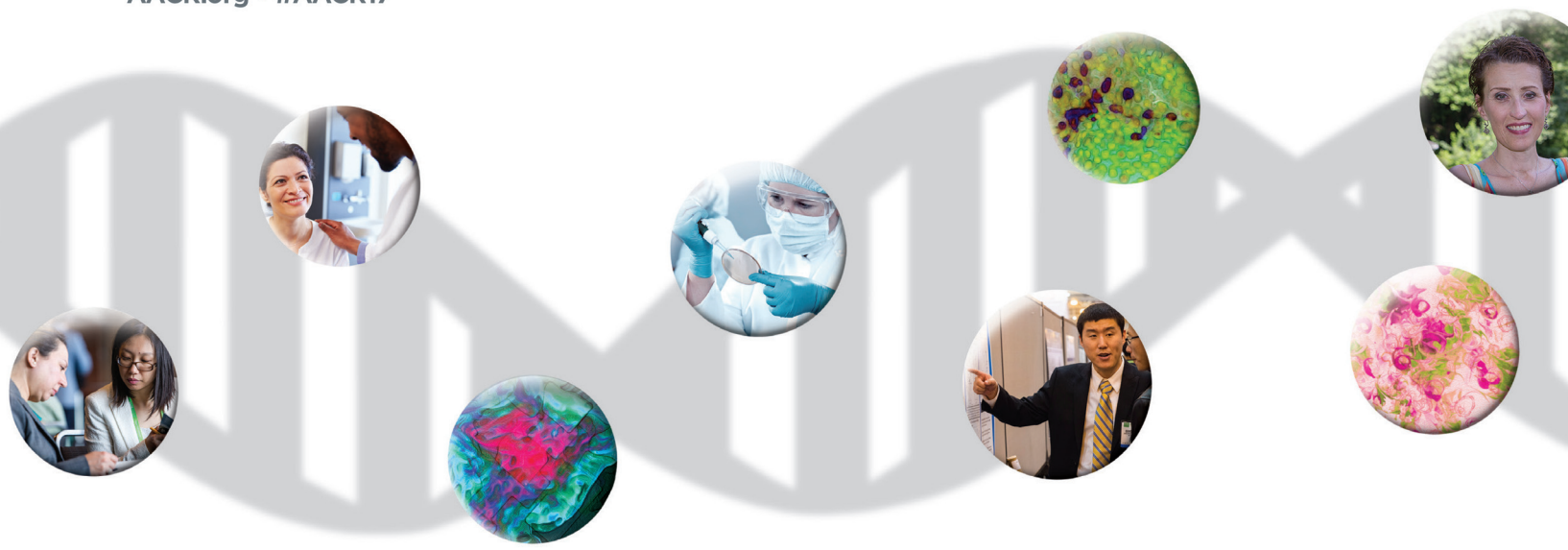
**April 1-5, 2017 • Walter E. Washington Convention Center • Washington, DC**

**AACR.org • #AACR17**



# Join us in Washington, DC

## for the latest innovative and inspiring cancer research from around the world... the AACR Annual Meeting 2017!

You won't want to miss this five-day, comprehensive program offering world-class opportunities to learn, collaborate, and share not only the progress made in cancer research, but also the promise of what is to come. This new era of cancer discovery is unprecedented with respect to rapidly emerging cancer science and new and effective molecularly targeted therapies.

The best and brightest researchers in the world will attend this meeting that covers every aspect of cancer – from molecular biology, clinical studies, epidemiology, and prevention to survivorship. And you'll want to be among them.

**Submit your abstract by THURSDAY, NOVEMBER 17.**

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**We look forward to seeing you in Washington, DC!**

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AACR
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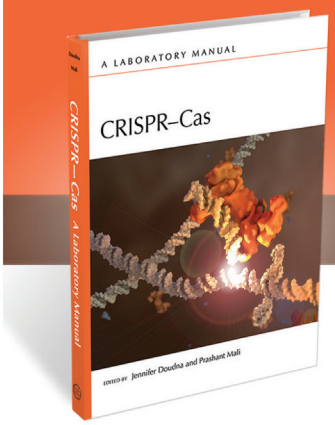


# CRISPR-Cas

## 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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## Contents



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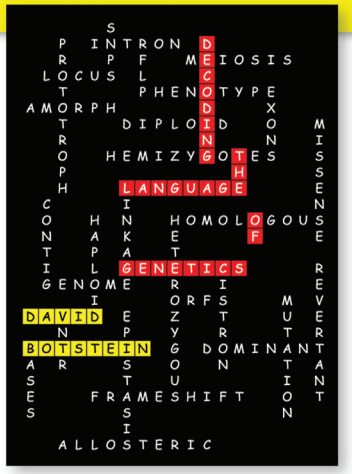
# Decoding the Language of Genetics




*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.

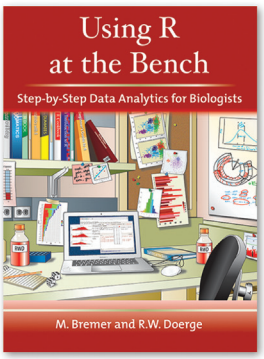
**2015, 240 pages, illustrated (30 4C, 10 B&W), index**
**Hardcover $79**
**ISBN 978-1-621820-92-5**

## Contents

# Using R at the Bench

## Step-by-Step Data Analytics for Biologists

By Martina Bremer, *Department of Mathematics, San Jose State University, California*;
Rebecca W. Doerge, *Departments of Statistics and Agronomy, Purdue University, Indiana*




*Using R at the Bench: Step-by-Step Data Analytics for Biologists* is a convenient bench-side handbook for biologists, designed as a handy reference guide for elementary and intermediate statistical analyses using the free/public software package known as "R." The expectations for biologists to have a more complete understanding of statistics are growing rapidly. New technologies and new areas of science, such as microarrays, next-generation sequencing, and proteomics, have dramatically increased the need for quantitative reasoning among biologists when designing experiments and interpreting results. Even the most routine informatics tools rely on statistical assumptions and methods that need to be appreciated if the scientific results are to be correct, understood, and exploited fully.

While the original *Statistics at the Bench* is still available for sale and has all examples in Excel, this new book uses the same text and examples in R. There is a new chapter that introduces the basics of R (where to download, getting people connected to it, and some basic commands and resources). There is also a new chapter that explains how to analyze Next Generation Sequencing data using R (specifically, RNA-seq). R has many functions for these analyses and *Using R at the Bench: Step-by-Step Data Analytics for Biologists* is an excellent resource for those biologists who want to learn R. This book is an essential handbook for working scientists providing a simple refresher for those who have forgotten what they once knew, and an overview for those wishing to use more quantitative reasoning in their research. Statistical methods, as well as guidelines for the interpretation of results, are explained using simple examples. Throughout the book, examples are accompanied by detailed R commands for easy reference.

**2015, 200 pages, illustrated (36 2C, 52 B&W), index**
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**ISBN 978-1-621821-12-0**

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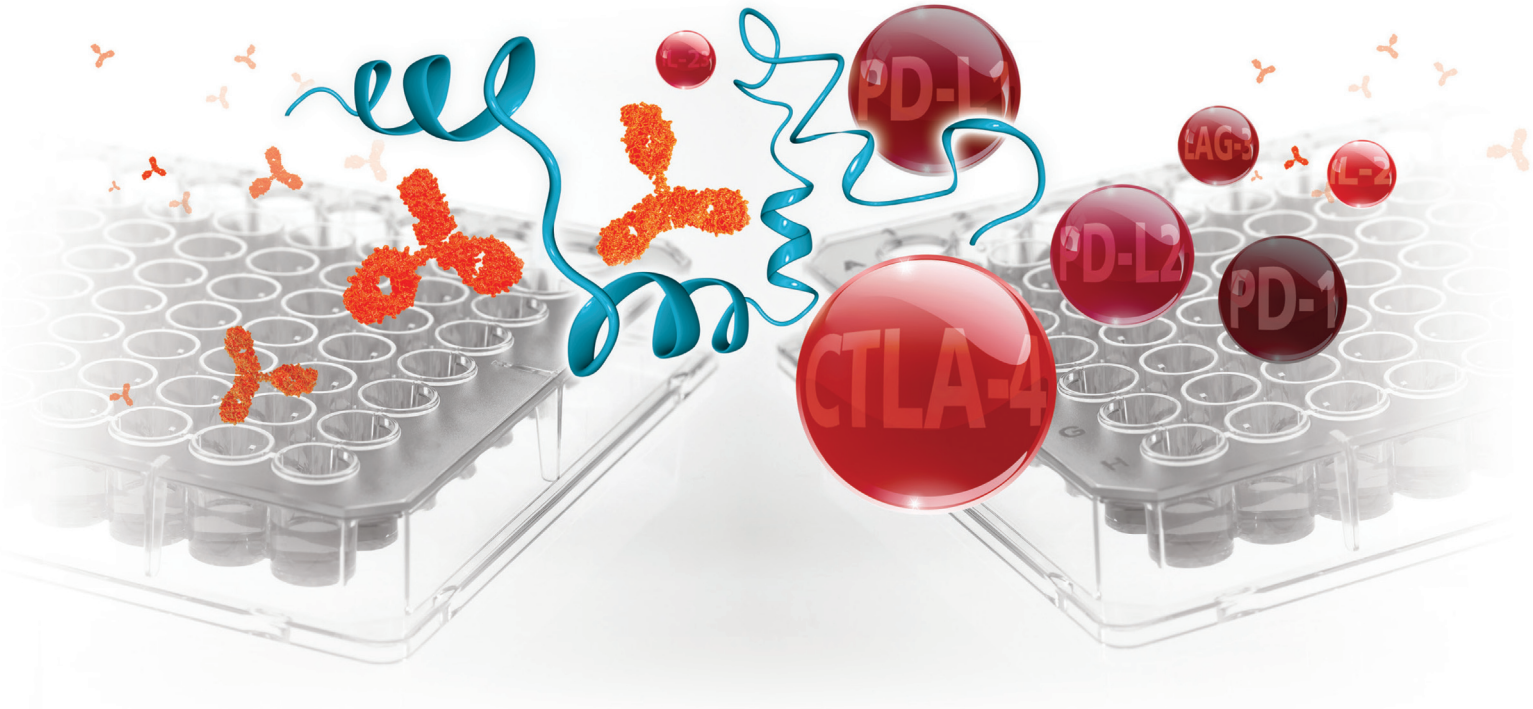


Immune checkpoints have come to the forefront of cancer therapies as a powerful and promising strategy to stimulate anti-tumor T cell activity. Affymetrix provides a wide range of products for immune-oncology research for the quantification of these important checkpoint proteins. ProcartaPlex® Human Immuno-oncology Checkpoint Panel enables simultaneous quantification of 14 checkpoint modulators. Speed, sensitivity, and specificity make Platinum ELISA the method of choice for biomarker evaluation.

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