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Direct-zol[™] RNA Purification

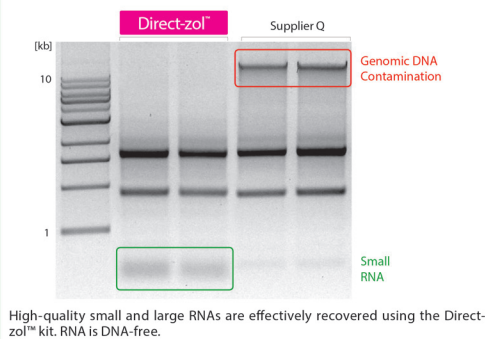
- ✓ No phase separation
- ✓ No precipitation
- ✓ No RNA loss



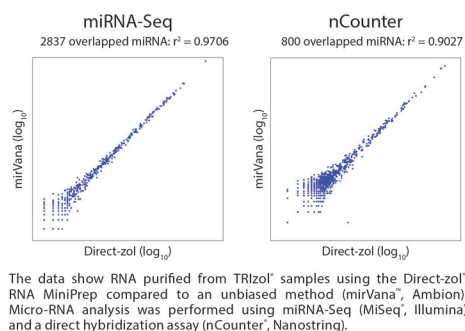
RNA OUT

7 minutes from TRIzol[®] to RNA:
Mix sample in TRIzol[®], TRI Reagent[®], or similar.
Add ethanol & load into the Zymo-Spin[™] column.
Patented technology

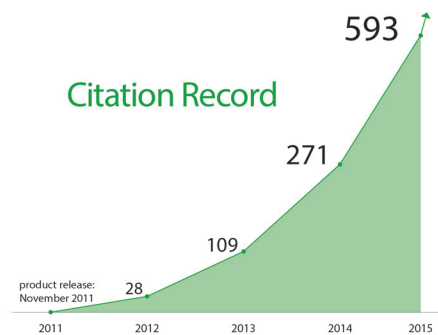
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Non-biased miRNA recovery



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Product	Cat. No.	Size
Direct-zol [™] RNA MiniPrep Plus	R2070, R2071* R2072, R2073*	50 Preps. (≤100 µg RNA) 200 Preps. (≤100 µg RNA)
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* = Supplied with TRI Reagent[®]

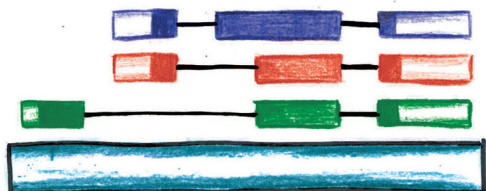


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What if my RNA-Seq is wrong?



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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miR-ID[®] and miR-Direct[®] miRNA/isomiR assays **for sensitive and specific quantification**

Superior isomiR discrimination

	miR-ID [®] assays			
	0/0	0/+1	-1/0	-1/+1
0/0 (mature)	100%	0.09%	1.72%	0.00%
0/+1 isomiR	0.09%	100%	0.20%	0.17%
-1/0 isomiR	0.75%	0.72%	100%	0.00%
-1/+1 isomiR	0.01%	0.05%	0.13%	100%

	AT assay
0/0	100%
0/+1 isomiR	37.89%
-1/0 isomiR	8.89%
-1/+1 isomiR	21.53%

Cross-discrimination assays using a synthetic reference miRNA and its isomiRs by miR-ID[®] (top) and the leading competitor's advanced technology (AT, bottom). -1, 0, +1 symbolize addition, no change, or deletion of single nucleotides with respect to the parent miRNA at the 5' or 3' ends.

miR-ID[®]

- ❖ Superior single nucleotide polymorphism discrimination at any position
- ❖ 5'- and 3'- isomiR quantification
- ❖ Uncompromised sensitivity
- ❖ Multiplexing capabilities
- ❖ Distinguishes 3' end modifications (2'-OMe/2'-OH)

Superior isoform discrimination

	miR-ID [®] assays		AT assays	
	miR-19a	miR-19b	miR-19a	miR-19b
miR-19a	100%	0.23%	100%	4.98%
miR-19b	1.43%	100%	3.11%	100%

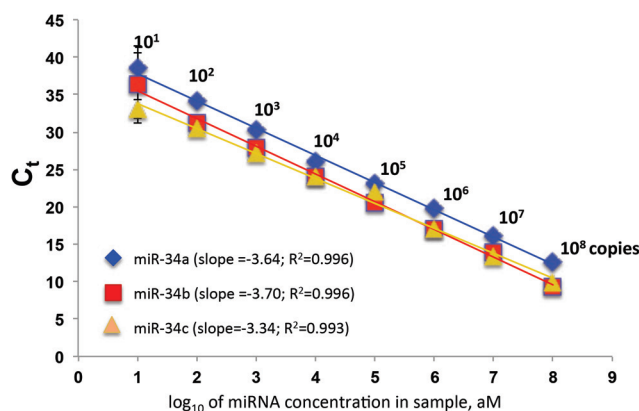
hsa-miR-19a-3p UGUGCAAUUCUUGCAAAACUGA
hsa-miR-19b-3p UGUGCAAUUCUUGCAAAACUGA

miRNA isoform discrimination by miR-ID[®] (left) and leading competitor's advanced technology (AGS, right).

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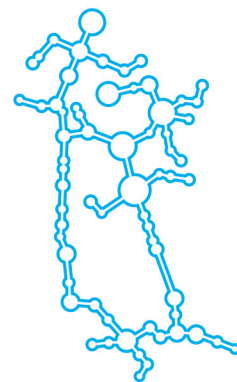
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Our scientists work in state-of-the-art facilities following strict Standard Operating Procedures. We use automated workflows and high-throughput robotic pipetting stations for maximum reproducibility. Rigorous QC at every stage of the analysis ensures reliable results.

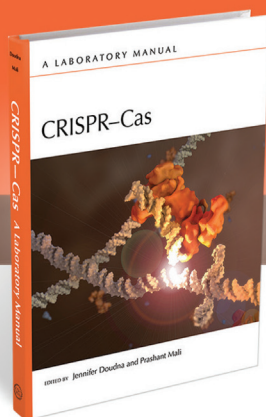
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CRISPR-Cas

A Laboratory Manual



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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ISBN 978-1-621821-31-1

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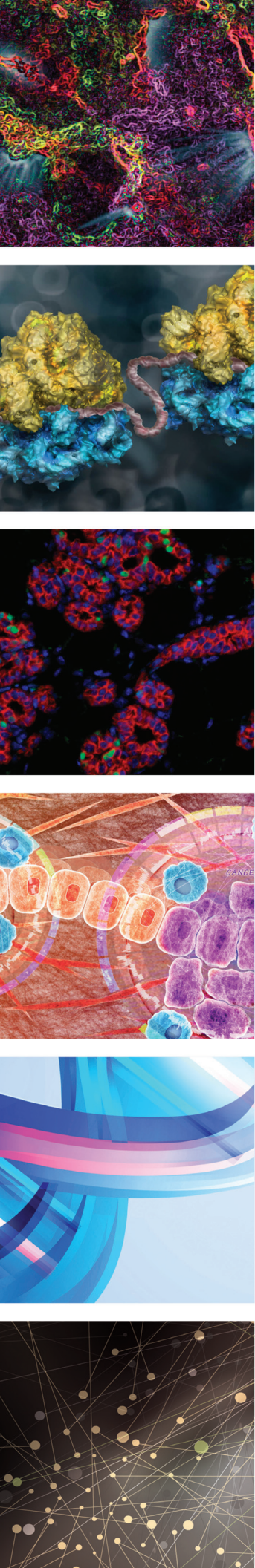
Custom Oligonucleotides

- ◆ Regular oligos
- ◆ Long oligos
- ◆ Phosphorothioated oligos (S-Oligos)
- ◆ Modified oligos
- ◆ Fluorescent oligos
- ◆ Taqman probes
- ◆ Molecular beacon
- ◆ Oligo pool & microarray

Custom Peptide Synthesis

- ◆ Purities from desalt to 98%
- ◆ Acetylation/Amidation
- ◆ Phosphorylated peptides
- ◆ Fluorescein/Biotin labeled peptides
- ◆ Specialty peptides with unnatural amino acids
- ◆ Cyclic peptides
- ◆ KLH/BSA/OVA Conjugation
- ◆ Multiple Antigenic Peptides
- ◆ Peptide nucleic acid (PNA)





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Co-Chairpersons: Robert G. Bristow, Maria Jasin, and Theodore S. Lawrence
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Co-Chairpersons: José Baselga and Scott A. Armstrong
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EORTC-NCI-AACR Molecular Targets and Cancer Therapeutics Symposium

Co-Chairpersons: Jean-Charles Soria, Lee J. Helman, and Levi A. Garraway
November 29-December 2, 2016
Munich, Germany

San Antonio Breast Cancer Symposium Presented by CTRC-AACR-BCM

Co-Directors: Carlos L. Arteaga, Virginia G. Kaklamani, and C. Kent Osborne
December 6-10, 2016 • San Antonio, TX

Precision Medicine Series: Opportunities and Challenges of Exploiting Synthetic Lethality in Cancer

Co-Chairpersons: René Bernards, William C. Hahn, and Louis M. Staudt
January 4-7, 2017 • San Diego, CA

AACR International Conference on New Frontiers in Cancer Research

Co-Chairpersons: Peter A. Jones and Frank McCormick
January 18-22, 2017 • Cape Town, South Africa

AACR Annual Meeting 2017

Program Committee Chairperson: Kornelia Polyak
April 1-5, 2017 • Washington, DC

AACR-AHNS Head and Neck Cancer Conference: Optimizing Survival and Quality of Life Through Basic, Clinical, and Translational Research

Chairperson: Jeffrey N. Myers
Co-Chairpersons: Jennifer Rubin Grandis, J. Silvio Gutkind, Quynh-Thu Le
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AACR International Conference on Translational Cancer Medicine

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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
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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
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Co-Chairpersons: Cory Abate-Shen, Kevin M. Haigis, Katerina A. Politi, and Julien Sage
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The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved

Co-Chairpersons to be announced
September 25-28, 2017 • Atlanta, GA

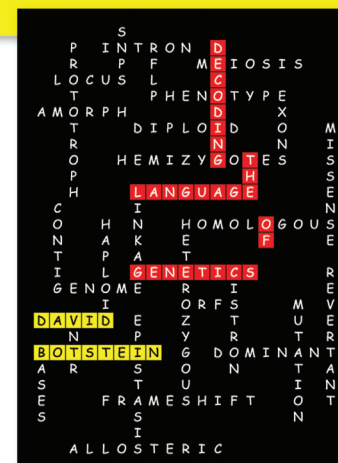
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Decoding the Language of Genetics

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

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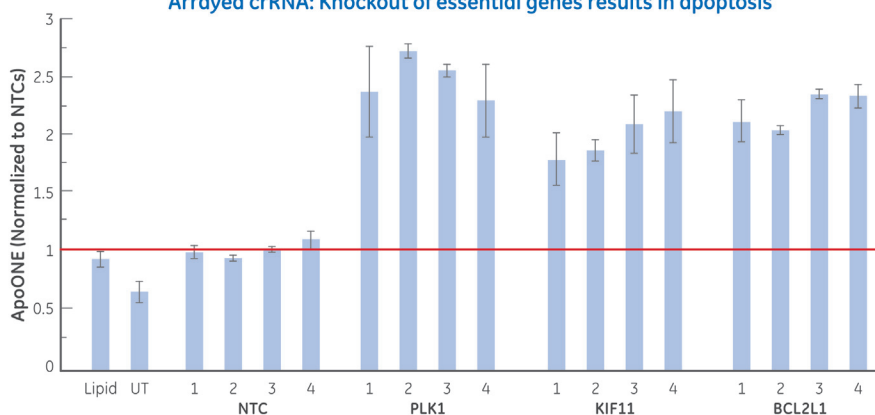
CRISPR

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Rapidly assess multiple target sites per gene across hundreds or thousands of genes with Dharmacon™ Edit-R™ CRISPR-Cas9 screening libraries. Our arrayed synthetic crRNA and pooled lentiviral sgRNA collections leverage our powerful CRISPR RNA design algorithm to deliver high functionality and superior specificity – for high-confidence, loss-of-function screens.

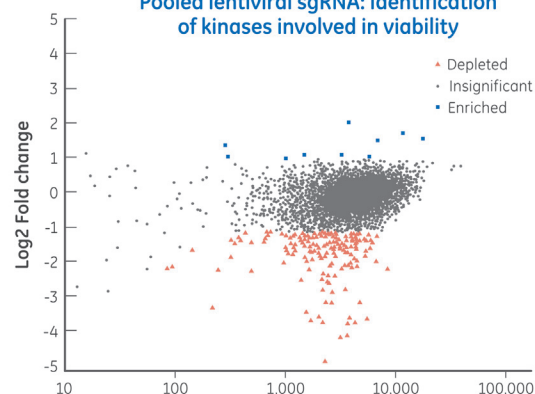
Edit-R crRNA Libraries | Edit-R Pooled Lentiviral sgRNA Libraries

Arrayed crRNA: Knockout of essential genes results in apoptosis



U2OS-(Ubi)EGFP-Cas9 stable cell seeded at 10,000 cells/well in 96-well format were transfected the following day with four different crRNA:tracrRNA complexes at 25 nM concentration targeting PLK1, KIF11 or BCL2L1 or four non-targeting crRNA controls (NTC). Wells transfected with lipid alone (Lipid) or left untreated (UT) were also included as controls. The effects on apoptosis were assayed using Casp3/9 homogeneous assay (ApoONE, Promega) at 48 hours post-transfection. Data normalized to average of NTC (non-targeting) crRNA controls.

Pooled lentiviral sgRNA: Identification of kinases involved in viability



Hits are identified by how strongly and significantly the experimental constructs are depleted at T1 compared to the constructs in the reference sample (T0). ≥ 1.5 -fold depletion [≤ 0.05 padj] value



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