

TRIzol[®] IN

Direct-zol[™] RNA Purification

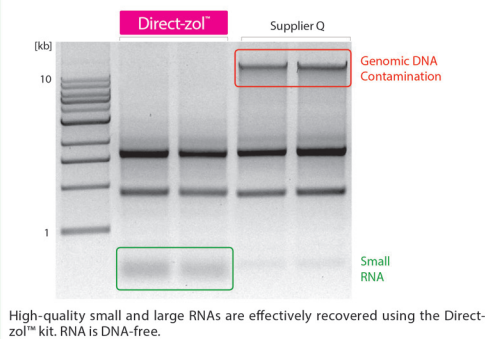
- ✓ No phase separation
- ✓ No precipitation
- ✓ No RNA loss



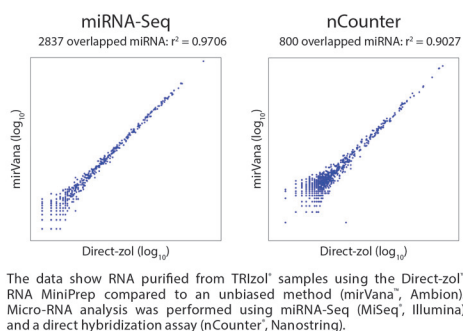
RNA OUT

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

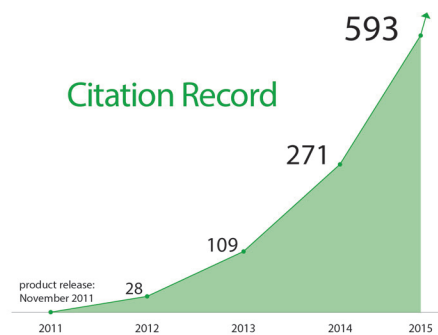
High-quality small & large RNA



Non-biased miRNA recovery



Highly cited



Learn more at

www.zymoresearch.com/direct-zol

Samples available at zymoresearch.com/direct-zol or call (949) 679-1190

Product	Cat. No.	Size
Direct-zol [™] RNA MiniPrep Plus	R2070, R2071* R2072, R2073*	50 Preps. (≤100 µg RNA) 200 Preps. (≤100 µg RNA)
Direct-zol [™] RNA MiniPrep	R2050, R2051* R2052, R2053*	50 Preps. (≤50 µg RNA) 200 Preps. (≤50 µg RNA)
Direct-zol [™] RNA MicroPrep	R2060, R2061* R2062, R2063*	50 Preps. (≤10 µg RNA) 200 Preps. (≤10 µg RNA)

96-well spin plate & MagBead formats also available

* = Supplied with TRI Reagent[®]

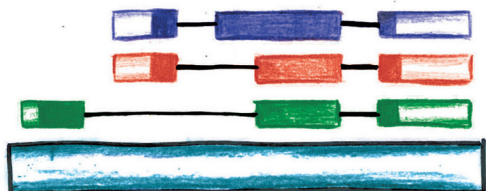


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What if my RNA-Seq is wrong?



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.



Break free from qPCR

Find gene targets faster



Validating gene targets with qPCR is often slow and costly due to lengthy primer design, experimental assay optimization, and sample processing time.

QuantiGene® Plex Assays validate gene targets faster:

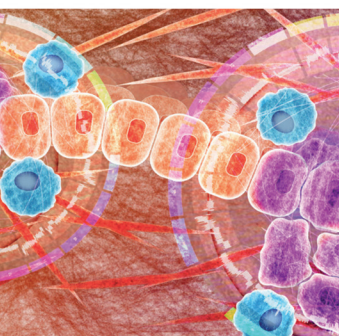
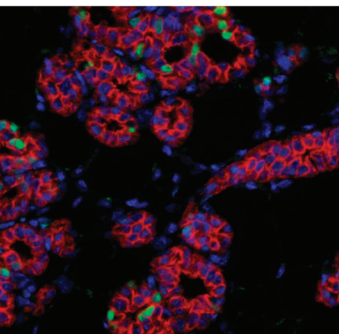
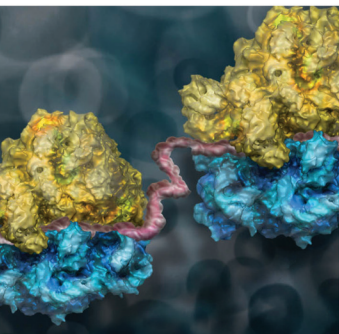
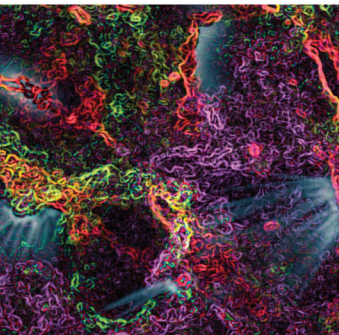
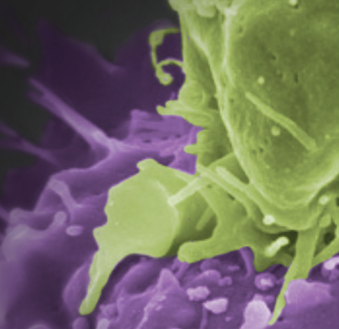
- No RNA purification or reverse transcription is required
- Multiplex panels of up to 80 genes are functionally validated
- One QuantiGene Plex® plate provides as much information as 20 qPCR plates

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2016-2017 SCIENTIFIC CONFERENCES

Presenting the most significant research on cancer etiology, prevention, diagnosis, and treatment

Tumor Immunology and Immunotherapy

*Conference Co-Chairpersons: James P. Allison,
Pamela S. Ohashi, Antoni Ribas,
and Ton Schumacher*
October 20-23, 2016 • Boston, MA

Translational Control of Cancer: A New Frontier in Cancer Biology and Therapy

*Conference Co-Chairpersons:
Jennifer A. Doudna, Frank McCormick,
Davide Ruggero, and Nahum Sonenberg*
October 27-30, 2016 • San Francisco, CA

DNA Repair: Tumor Development and Therapeutic Response

*Conference Co-Chairpersons: Robert G. Bristow,
Maria Jasin, and Theodore S. Lawrence*
November 2-5, 2016 • Montreal, Quebec, Canada

New Horizons in Cancer Research: Delivering Cures Through Cancer Science

*Conference Co-Chairpersons:
José Baselga and Scott A. Armstrong*
November 2-5, 2016 • Shanghai, P.R. China

Improving Cancer Risk Prediction for Prevention and Early Detection

*Conference Co-Chairpersons: Graham A. Colditz,
Susan M. Gapstur, Kenneth R. Muir,
and Mark E. Sherman*
November 16-19, 2016 • Orlando, FL

EORTC-NCI-AACR Molecular Targets and Cancer Therapeutics Symposium

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

San Antonio Breast Cancer Symposium

*Symposium 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

*Conference 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

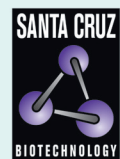
*Conference Co-Chairpersons:
Peter A. Jones and Frank McCormick*
January 18-22, 2017 • Cape Town, South Africa

AACR Annual Meeting 2017

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

AACR International Conference on Translational Cancer Medicine

*Conference Co-chairpersons:
Carlos L. Arteaga and Carlos Gil M. Ferreira*
May 4-6, 2017 • São Paulo, Brazil



The Power to Question

CRISPR Plasmids

KNOCKOUT & ACTIVATION

CRISPR/Cas9
Knockout Plasmids

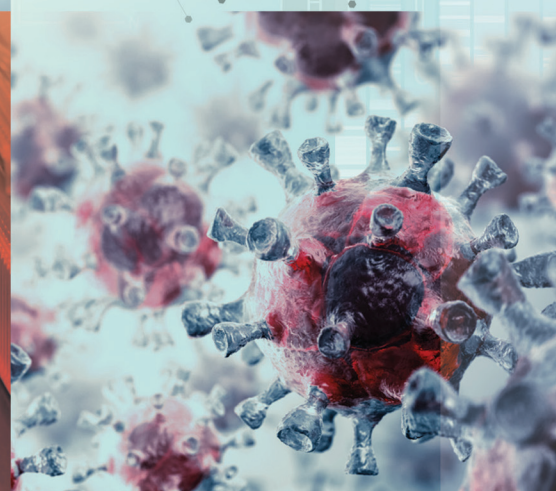
Homology Directed
Repair Plasmids

Double Nickase
Knockout Plasmids

CRISPR/dCas9
Activation Plasmids

Lentiviral Activation
Particles

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With years of experience profiling microRNAs in liquid biopsies, our team of biofluid experts know how to ensure top quality microRNA sequencing data with >80 % mappable reads – even from clinical serum/plasma samples.

Starting from RNA isolation, we use automated workflows and high-throughput robotic pipetting stations for maximum reproducibility. Our strict Standard Operating Procedures are optimized specifically for biofluid samples. Rigorous QC at every stage of the analysis ensures reliable results and complete peace of mind.

Take the fast track to biomarker discovery.

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Biofluid microRNA sequencing services
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Announcing Keystone Symposia's 2016–2017 RNA Conferences

Precision Genome Engineering

Scientific Organizers: J. Keith Joung, Emmanuelle Charpentier and Olivier Danos

January 8–12, 2017 | Breckenridge, Colorado | USA

www.keystonesymposia.org/17A2

Deadlines: Scholarship/Discounted Abstract – Sep 13, 2016; Abstract – Oct 6, 2016; Discounted Registration – Nov 9, 2016

Omics Strategies to Study the Proteome

Scientific Organizers: Alan Saghatelian, Chuan He and Ileana M. Cristea

January 29–February 2, 2017 | Breckenridge, Colorado | USA

www.keystonesymposia.org/17A8

Deadlines: Scholarship/Discounted Abstract – Sep 28, 2016; Abstract – Oct 27, 2016; Discounted Registration – Nov 29, 2016

Epigenetics and Human Disease: Progress from Mechanisms to Therapeutics

Scientific Organizers: Johnathan R. Whetstone, Jessica K. Tyler and Rabinder K. Prinjha

January 29–February 2, 2017 | Seattle, Washington | USA

www.keystonesymposia.org/17A9

Deadlines: Scholarship/Discounted Abstract – Sep 29, 2016; Abstract – Oct 27, 2016; Discounted Registration – Nov 30, 2016

Noncoding RNAs from Disease to Targeted Therapeutics

Scientific Organizers: Kevin V. Morris, Archa Fox and Paloma Hoban Giangrande

joint with **Protein-RNA Interactions: Scale, Mechanisms, Structure and Function of Coding and Noncoding RNPs**

Scientific Organizers: Gene W. Yeo, Jernej Ule, Karla Neugebauer and Melissa J. Moore

February 5–9, 2017 | Banff, Alberta | Canada

www.keystonesymposia.org/17J5 | www.keystonesymposia.org/17J6

Deadlines: Scholarship/Discounted Abstract – Oct 5, 2016; Abstract – Nov 2, 2016; Discounted Registration – Dec 6, 2016

mRNA Processing and Human Disease

Scientific Organizers: James L. Manley, Siddhartha Mukherjee and Gideon Dreyfuss

March 5–8, 2017 | Taos, New Mexico | USA

www.keystonesymposia.org/17C3

Deadlines: Scholarship/Discounted Abstract – Nov 2, 2016; Abstract – Dec 6, 2016; Discounted Registration – Jan 10, 2017

RNA-Based Approaches in Cardiovascular Disease

Scientific Organizers: Thomas Thum and Roger J. Hajjar

joint with **Molecular Mechanisms of Heart Development**

Scientific Organizers: Benoit G. Bruneau, Brian L. Black and Margaret E. Buckingham

March 26–30, 2017 | Keystone, Colorado | USA

www.keystonesymposia.org/17X8

Deadlines: Scholarship/Discounted Abstract – Nov 30, 2016; Abstract – Jan 11, 2017; Discounted Registration – Jan 26, 2017



Submit an abstract to participate fully in the conference via a poster presentation and possible selection for a short talk. Scholarships are available for graduate students and postdoctoral fellows. For full program, speaker, abstract and scholarship details, visit www.keystonesymposia.org/genetics

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Stability

All of our dNTPs are very stable – we guarantee 100% stability for 2 years from the date of purchase.

Features

- Ultra-pure: >99% by HPLC
- Reliable, consistent results
- Available both as ready-to-use mix and a set

Applications

- PCR and qPCR
- cDNA synthesis
- Primer extension
- DNA sequencing
- DNA labeling
- Mutagenesis

Quality control

- Purity assay (HPLC) >99%
- Free of pyrophosphate, DNA and RNA
- DNase, RNase and nickase free
- Tested for PCR, qPCR and RT-PCR



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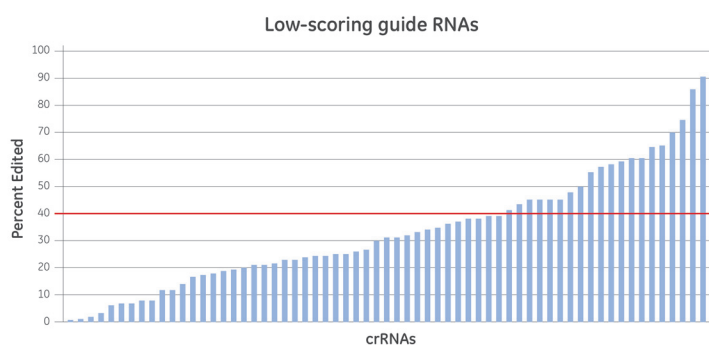
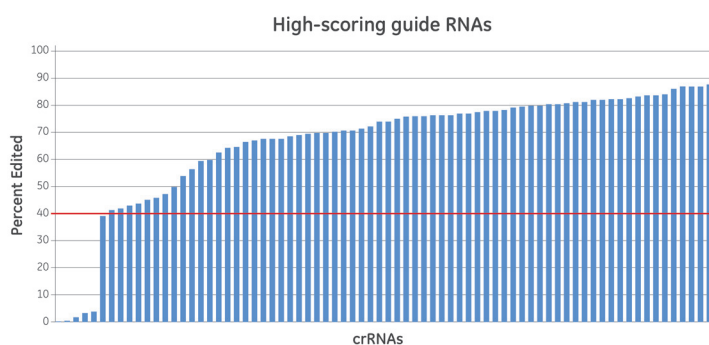
CRISPR

Dharmacon reagents help you move forward. Faster.

Simplify your gene editing workflow with the Dharmacon™ Edit-R™ CRISPR-Cas9 platform. Custom or predesigned ready-to-use DNA and synthetic RNA leverage a validated algorithm to select highly functional, specific targets for gene knockout – enabling you to quickly assess multiple target sites per gene across one or hundreds of genes.

CRISPR Guide RNAs | CRISPR Screening Libraries | Cas9 Nucleases

crRNAs that have high functionality scores show high editing efficiency



HEK293T-CAG-Cas9 cells were transfected with either high-scoring or low-scoring crRNAs (50 nM crRNA:tracrRNA) using DharmaFECT 1 transfection reagent (0.25 μ L/well) in 96-well format. Gene editing efficiencies were determined using next-generation sequencing. 93% of the top 10 high-scoring crRNAs targeting ten different genes have > 40% indel formation and only 33% of the 10 lowest scoring designs have > 40% indel formation.



Targeting the Pathways of Human DiseaseSM with microRNA Therapeutics

A single microRNA can target and regulate up to hundreds of genes.

These genes are in turn integrally

involved in biological networks and pathways, including disease states.

Targeting pathways of human disease with microRNA-based drugs

represents a potentially powerful therapeutic approach.



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