

TRIZOL IN

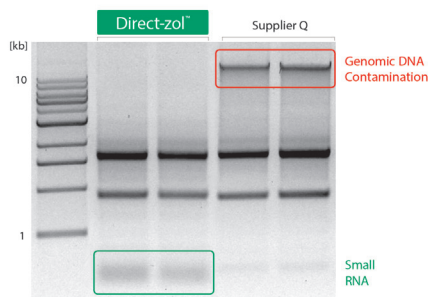
- ✓ No phase separation
- ✓ No precipitation
- ✓ No RNA loss



RNA OUT

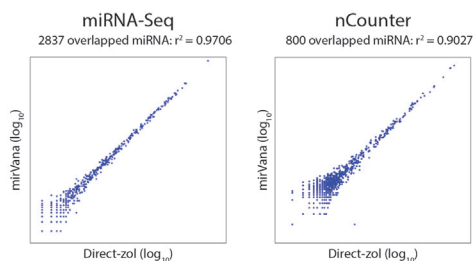
7 minutes from TRIZOL® to RNA:
Mix sample in TRIZOL®, TRI Reagent®, or similar.
Add ethanol & load into the Zymo-Spin™ column.
Patented technology

High-quality small & large RNA



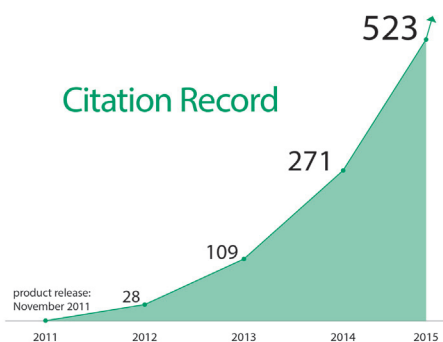
High-quality small and large RNAs are effectively recovered using the Direct-zol™ kit. RNA is DNA-free.

Non-biased miRNA recovery



The data show RNA purified from TRIZOL samples using the Direct-zol™ RNA MiniPrep compared to an unbiased method (mirVana®, Ambion). Micro-RNA analysis was performed using miRNA-Seq (MiSeq®, Illumina) and a direct hybridization assay (nCounter®, Nanostring).

Highly cited



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

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

96-well spin plate & MagBead formats also available

* = Supplied with TRI Reagent®

Extraordinary variation of floral organs in *Phalaenopsis* orchid is due to differential expression of multiple genes in sepal, petal, and labellum.¹

¹ Hsiao, Y. et al. *Gene*. 518, 91-100 (2013).

Differential gene expression creates beauty

Differential gene expression plays a significant role in development of many species including orchids.

Phalaenopsis orchids are important species for development and evolutionary studies. Moreover, they are well recognized for their exceptional beauty. The flowers have several organs (i.e. sepal, petal, and labellum), which are significantly different, however together compose conspicuous and harmonious look (view photo). The unique shape of these flower organs is a result of differential expression of multiple genes involved in their development.

Lexogen is focusing on development of accurate and affordable tools for transcriptome analysis with RNA-Seq. QuantSeq is a dedicated kit for expression profiling. It is an easy protocol for producing highly strand-specific next generation sequencing libraries from the 3' end of polyadenylated RNA. Only one fragment per transcript is produced, directly linking the number of mapping reads to the gene expression values. Restricted length saves sequencing space and allows for high level of multiplexing, enabling cost-efficient and fast RNA-Seq experiment.



Expression Profiling RNA-Seq Library Prep Kit

- Gene expression analysis
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- From 100 pg total RNA input including low quality RNA and FFPE samples
- Cost-effective sequencing of up to 96 samples / lane
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Validating gene targets with qPCR is often slow and costly due to lengthy primer design, experimental assay optimization, and sample processing time.

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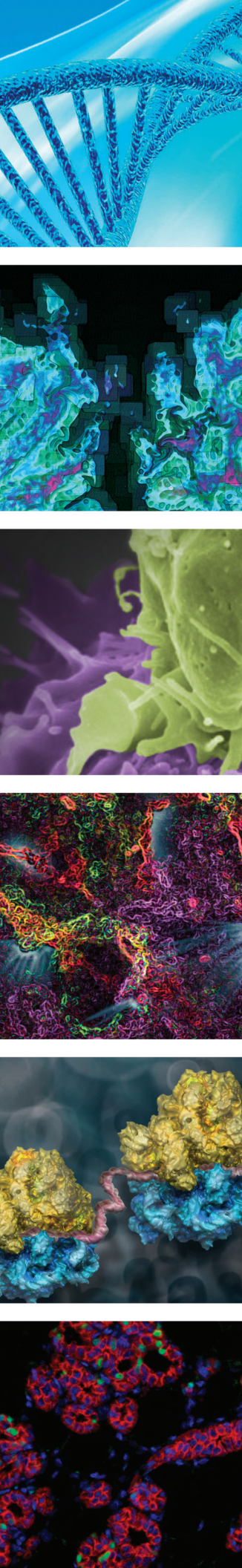
- No RNA purification or reverse transcription is required
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2016-2017 SCIENTIFIC CONFERENCES

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

EORTC-NCI-EMA-AACR International Conference on Innovation and Biomarkers in Cancer Drug Development

Conference Co-Chairpersons:
Denis A. Lacombe and John W. Martens
September 8-9, 2016 • Brussels, Belgium

11th Biennial Ovarian Cancer Research Symposium

Conference Co-Chairpersons: *Deborah K. Armstrong, Martin M. Matzuk, Gordon B. Mills, and Saul E. Rivkin*
September 12-13, 2016 • Seattle, WA
Co-presented with the Rivkin Center for Ovarian Cancer

Colorectal Cancer: From Initiation to Outcomes

Conference Co-Chairpersons: *Ernest T. Hawk, Steven H. Itzkowitz, Kenneth W. Kinzler, and Johanna W. Lampe*
September 17-20, 2016 • Tampa, FL

Ninth AACR Conference on The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved

Conference Co-Chairpersons: *Rick A. Kittles, Folakemi T. Odedina, Jeffrey N. Weitzel, and Jun J. Yang*
September 25-28, 2016 • Fort Lauderdale, FL

CRI-CIMT-EATI-AACR Second International Cancer Immunotherapy Conference: Translating Science into Survival

Conference Co-Chairpersons: *James P. Allison, Philip D. Greenberg, Christoph Huber, and Guido Kroemer*
September 25-28, 2016 • New York, NY

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. Coditz, 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

Learn more and register at
AACR.org/Calendar

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for Cancer Research

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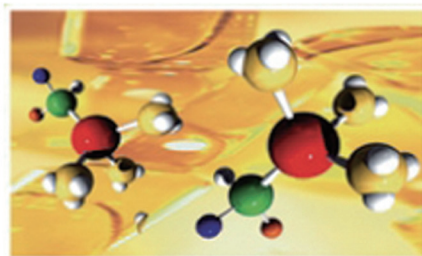
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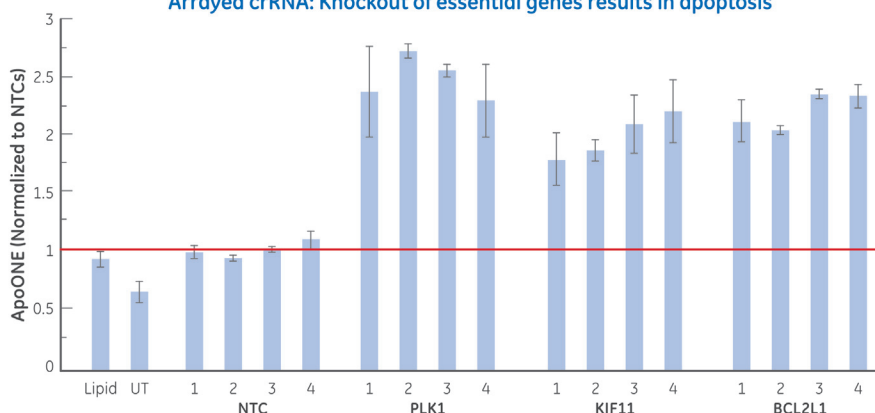
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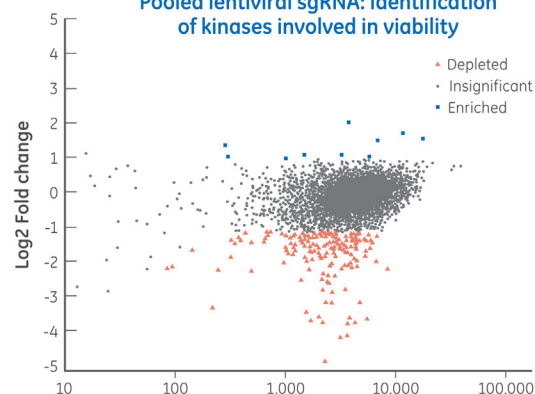
Edit-R crRNA Libraries | Edit-R Pooled Lentiviral sgRNA Libraries

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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involved in biological networks and pathways, including disease states.

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