

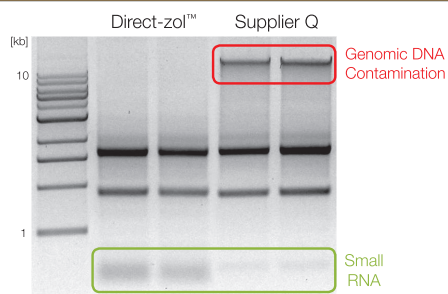
TRIzol[®] in, RNA out

Direct-zol[™] RNA Purification



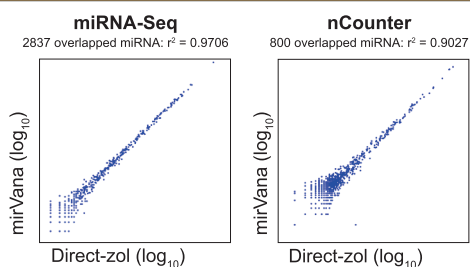
Short protocol: Mix sample in TRIzol[®], TRI Reagent[®], and similar with ethanol, load into the Clean-Spin[™] column, wash & elute RNA

High-quality small & large RNA



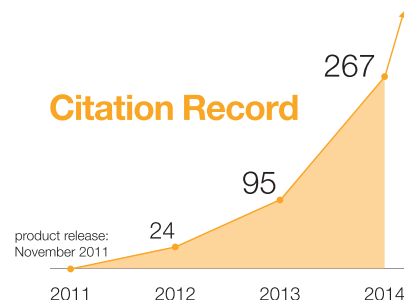
High-quality small and large RNAs are effectively recovered using the Direct-zol[™] kit. RNA is DNA-free.

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



RNA Purification
Made Simple[™]

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

Product	Cat. No.	Size
Direct-zol [™] RNA MiniPrep	R2050, R2051* R2052, R2053*	50 Preps. 200 Preps.
Direct-zol [™] -96 RNA	R2054, R2055* R2056, R2057*	2 x 96 Preps. 4 x 96 Preps.
Direct-zol [™] -96 MagBead RNA	R2100, R2101* R2102, R2103* R2104, R2105*	2 x 96 Preps. 4 x 96 Preps. 8 x 96 Preps.

* = Supplied with TRI Reagent[®]

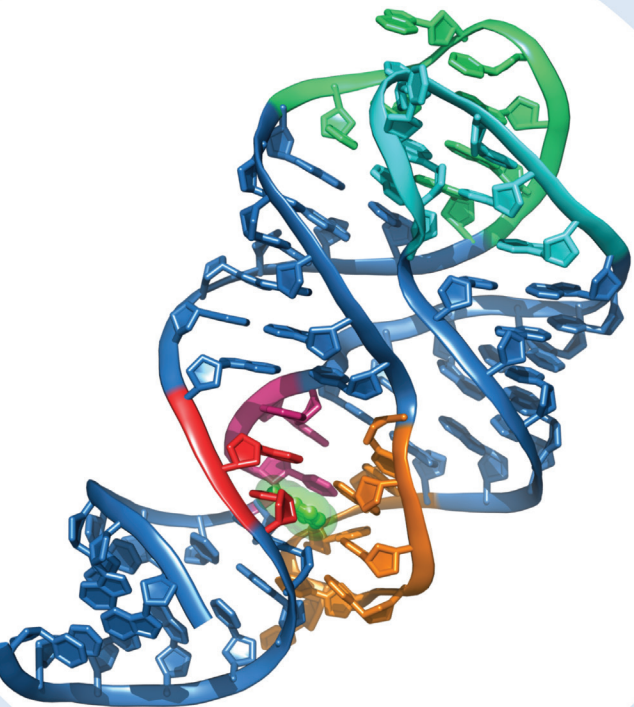
TRIzol[®] and TRI Reagent[®] are registered trademarks of Molecular Research Center, Inc.

Patent Pending

Tel: (949) 679-1190

www.zymoresearch.com/direct-zol

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- Total RNA
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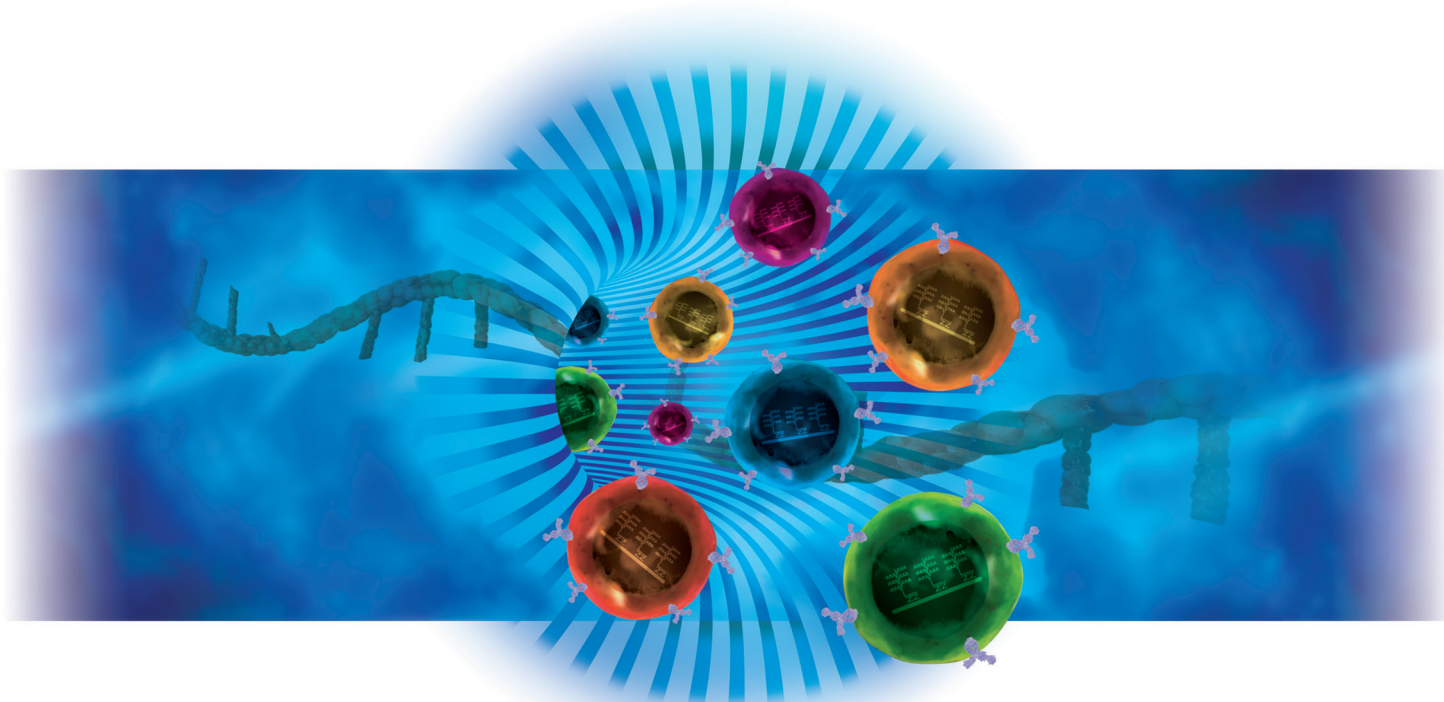
Magnetic Poly (A)⁺ RNA isolation kit

CATALOG #: **10760013-1**

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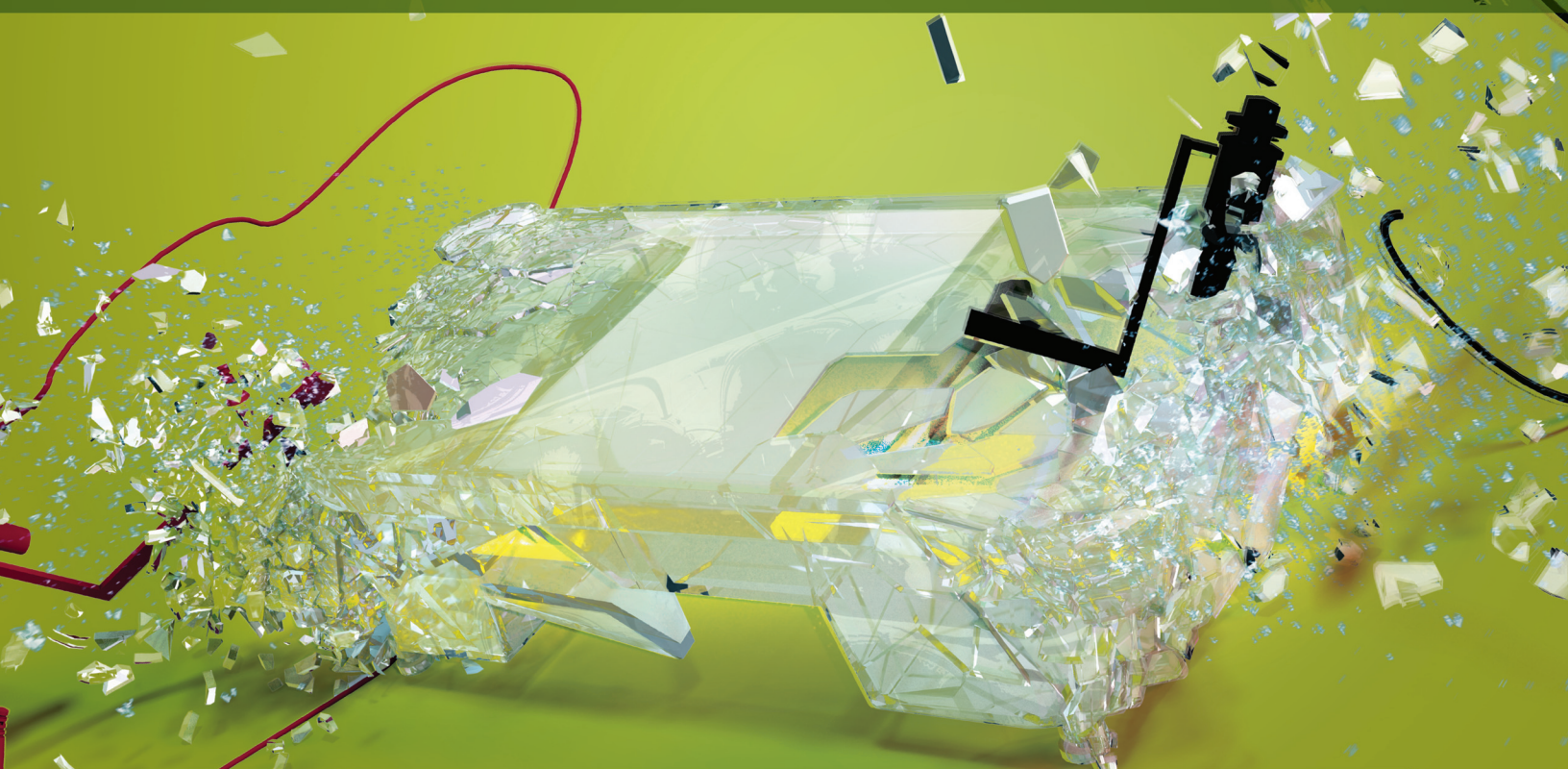
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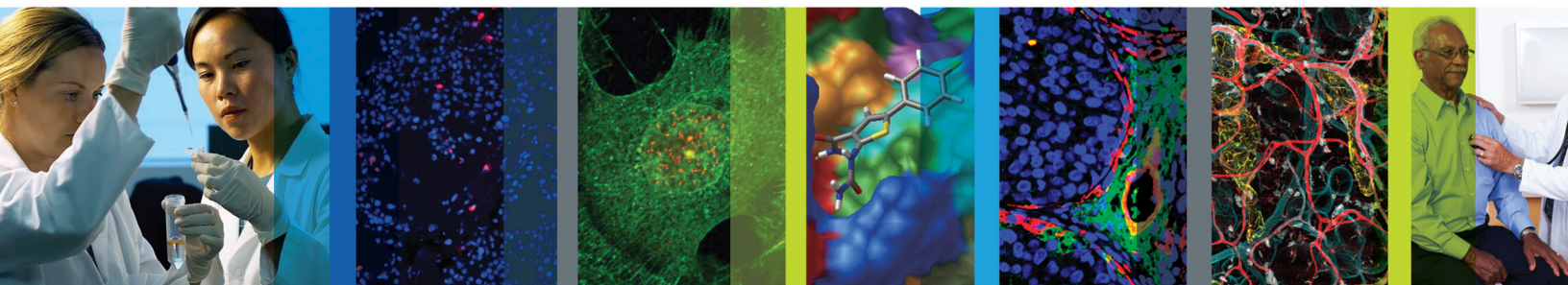


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American Association
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ANNUAL MEETING

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Join Keystone Symposia
for the 2015 conference on:

MicroRNAs and Noncoding RNAs in Cancer

June 7–12, 2015
Keystone Resort
Keystone, Colorado, USA

Scientific Organizers: Frank J. Slack, Manel Esteller and Lin He

This meeting focuses on the exciting biology of microRNAs and noncoding RNAs in controlling developmental and cancer processes like cell proliferation, differentiation, cell cycle, apoptosis and metastasis, as well as the latest efforts to harness the power of these RNAs as agents in the fight against cancer. In addition, this meeting brings together the best researchers working in small RNAs and cancer in one place for critical discussions that should advance the field and accelerate the benchside-to-bedside use of this technology. It will also provide a stimulating environment in which students, postdocs and junior investigators can present and discuss their research in the company of the best minds in the field.

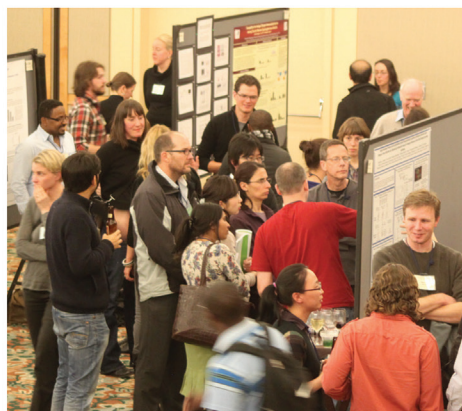
Session Topics:

- Small RNAs in Development
- MicroRNAs in Development
- MicroRNAs in Animal Development
- MicroRNAs and Cancer I, II & III
- Noncoding RNA in Development and Physiology
- Long ncRNAs and Cancer
- Workshop 1: miRNA Biogenesis/ Turnover/Mechanism
- Workshop 2: Industry Applications
- Workshop 3: Breaking News

CONFIRMED SPEAKERS (as of January 21, 2015):

Irene Bozzoni
George A. Calin
Carlo M. Croce*
George Q. Daley
Manel Esteller
Elsa R. Flores
Richard I. Gregory
Helge Großhans
Mitchell Guttman
Lin He
Eva M. Hernando
Eran Hornstein
Leanne Jones
Joshua T. Mendell
Silvia Monticelli
Kevin V. Morris
Pier Paolo Pandolfi
Amy E. Pasquinelli
John L. Rinn
Michael G. Rosenfeld
Anita G. Seto
Frank J. Slack
David L. Spector
Joan A. Steitz*
Markus Stoffel
Sohail F. Tavazoie
Andrea Ventura
Xiao-Fan Wang
Anton Wutz

*Keynote speaker



Abstract Deadline: March 5, 2015
Discounted Registration Deadline: April 7, 2015

To see the full program and for additional details,
visit www.keystonesymposia.org/15E5.

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Sequence Exosome RNAs

Exosomes are 60 - 150 nm membrane signaling vesicles secreted by most cell types in vivo and in vitro. Exosomes are found in blood, urine, amniotic fluid, malignant ascite fluids and contain distinct subsets of microRNAs, mRNAs, lncRNAs and other ncRNAs. The identity and abundance of these RNAs has been shown to be a valuable approach to discover sequence signatures for the diagnosis and prognosis of disease. SBI's Exo-NGS service provides the exosome researcher with a comprehensive, expert service to isolate and identify exosome-associated RNA biomarkers.

Compare exo-RNA sequence profiles across patient samples.

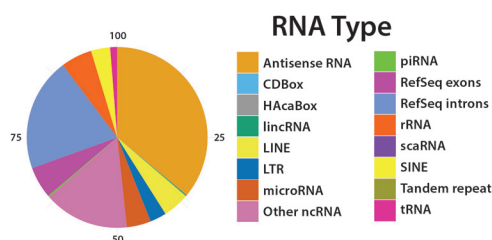
Building Exosome RNA NGS Libraries

- ▶ Exosomes isolated from samples
- ▶ Exo-RNAs purified with chromatography
- ▶ Illumina bar-codes added and amplified
- ▶ Library size-selection and PAGE purification
- ▶ High sensitivity library QC with Bioanalyzer
- ▶ Multiplexed NGS runs performed

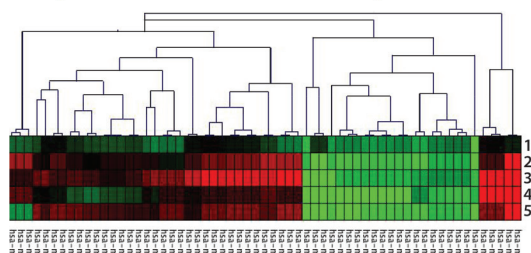
Primary Data Deliverables

- Raw sequencing reads in FASTA format
- Sequencing read quality values
- Analyzed Data – Small RNA Workflow
- Relative abundance of each RNA type
- Table of counts of mature microRNAs
- Publication-ready figures generated

RNA Type Charts



Expression Heatmaps



Custom Genome Browser with Your Data



- ▶ Sequencing data uploaded
- ▶ Access to public databases
- ▶ Analyze with accepted analytics
- ▶ Visualize your data automatically
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