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By simultaneously quantifying and qualifying nucleic acid samples in parallel, the Fragment Analyzer™ is transforming sample prep analysis for the world’s leading genomic research institutions. Automate genomic QC for an array of applications, including total and degraded RNA isolations, genomic DNA extractions and NGS library preparations—giving you better results in less time, with less effort.

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PCR-Free NGS Libraries from 10 ng of Circulating, Cell-Free DNA

Accel-NGS® 2S PCR-Free DNA Library Kit

*Highest Library Diversity, Lowest Inputs*

- PCR-free libraries from 10 ng cfDNA and 100 ng high molecular weight DNA
- Exceptional coverage of AT-/GC-rich sequences
- Tremendously efficient adapter technology

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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

Watch the Ion S5 System in action at thermofisher.com/ionS5

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**Description**
dNTPs contain dATP, dCTP, dGTP and dTTP (monosodium salts) at a concentration of 10mM or 100mM each in sterile deionized water at pH7.5, whose purity is up to 99.5% (HPLC). It is free of RNase and DNase, and suitable for any molecular biology application that requires pure deoxynucleotides, such as PCR, DNA sequencing, cDNA synthesis and nick translation.

**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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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. Heilman, 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

Learn more and register at AACR.org/Calendar
Reduce Library Prep Costs

100-Fold

Echo Liquid Handlers enable library preparation in low microliter volumes for a range of sequencing methods. Dramatically reduce reagent costs, conserve samples, and eliminate steps — all while improving library quality.

Customer data* show that the use of Echo Acoustic Liquid Handling allows for...

- 100-fold reduction of library prep reaction volumes
- Increased sample throughput time
- Automation of workflow to easily prepare thousands of samples
- Improved accuracy of results

Comparison of Liquid Handling Methods

<table>
<thead>
<tr>
<th></th>
<th>Manual Pipetting</th>
<th>Echo® Liquid Handler</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amount of DNA</td>
<td>50 ng</td>
<td>0.06 – 2.0 ng</td>
</tr>
<tr>
<td>DNA volume (Rxn)</td>
<td>25 µL</td>
<td>200 nL</td>
</tr>
<tr>
<td>Library prep volume (Rxn)</td>
<td>25 µL</td>
<td>300 nL</td>
</tr>
<tr>
<td>Total volume</td>
<td>50 µL</td>
<td>0.5 µL</td>
</tr>
<tr>
<td>Reactions per kit</td>
<td>96</td>
<td>9600</td>
</tr>
<tr>
<td>Cost per reaction</td>
<td>$72.91</td>
<td>$0.73</td>
</tr>
</tbody>
</table>

For more information, visit www.labcyte.com/sequencing.

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 miRNA 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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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

**Omens 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  

**Epigenetics and Human Disease: Progress from Mechanisms to Therapeutics**  
Scientific Organizers: Johnathan R. Whetstine, Jessica K. Tyler and Rabinder K. Prinjha  
January 29–February 2, 2017 | Seattle, Washington | USA  
www.keystonesymposia.org/17A9  

**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 RNP**s  
Scientific Organizers: Gene W. Yeo, Jernej Ule, Karla Neugebauer and Melissa J. Moore  
February 5–9, 2017 | Banff, Alberta | Canada  

**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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