

# JUST RIGHT FOR GENOMICS

## ROOTED IN GENOMIC RESEARCH, DEVELOPED FOR THE FUTURE.

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.



More at [AATI-US.COM](http://AATI-US.COM)

# 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](http://thermofisher.com/ionS5)

**ThermoFisher**  
SCIENTIFIC

# Ultra-pure dNTPs at unbeatable prices

## 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



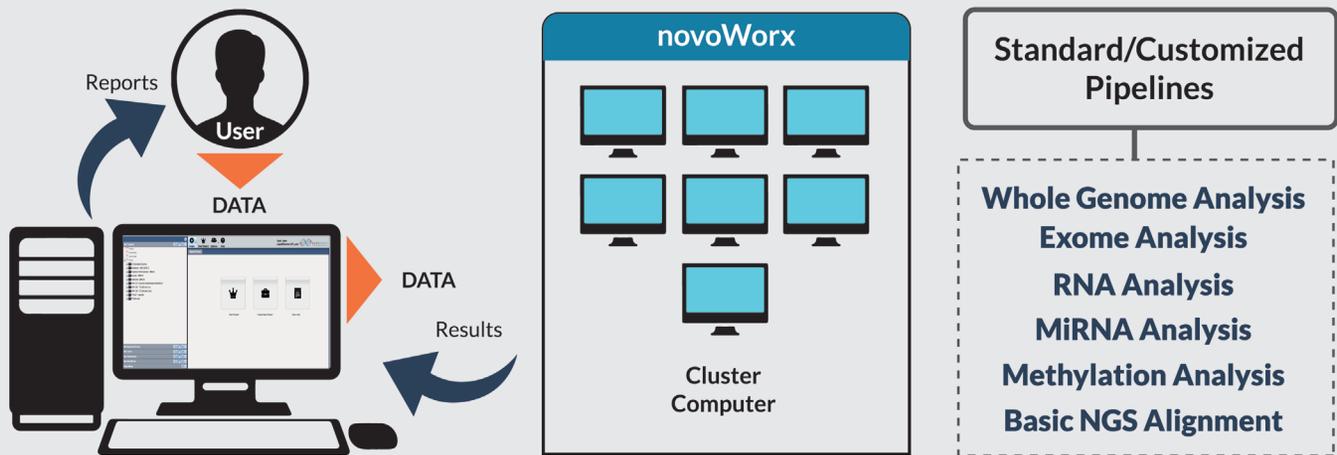
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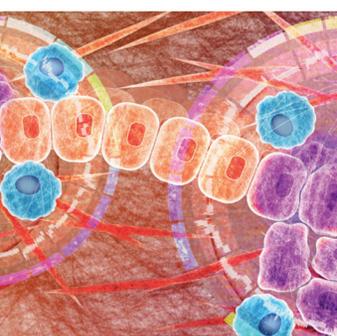
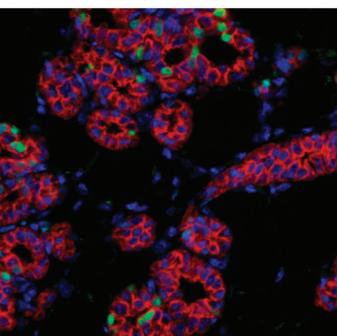
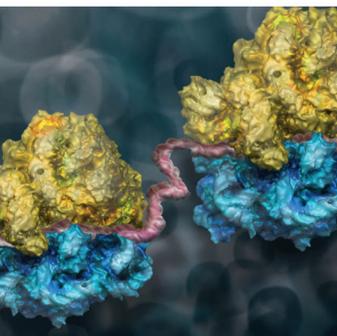
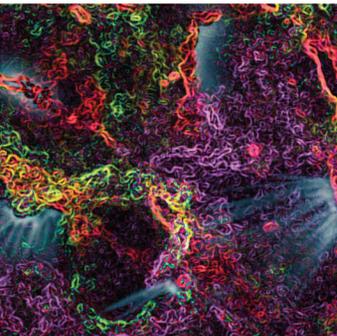
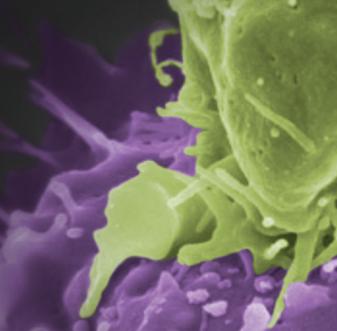


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# 2016-2017 SCIENTIFIC CONFERENCES

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

Learn more and register at  
[AACR.org/Calendar](http://AACR.org/Calendar)

**AACR** American Association  
for Cancer Research

FINDING CURES TOGETHER™



Echo® Acoustic LIQUID HANDLING  
for GENOMICS

## 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

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

For more information, visit [www.labcyte.com/sequencing](http://www.labcyte.com/sequencing).

\* Low-Cost, high-throughput sequencing of DNA assemblies using a highly multiplexed Nextera process. Shapland et al. ACS Synth. Biol., 2015

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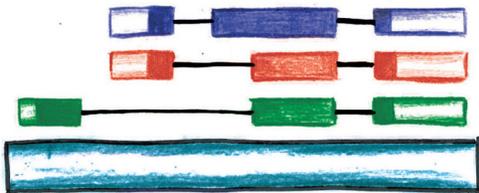


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# What if my RNA-Seq is wrong?



## 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.**



# 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](http://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](http://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](http://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](http://www.keystonesymposia.org/17J5) | [www.keystonesymposia.org/17J6](http://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](http://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

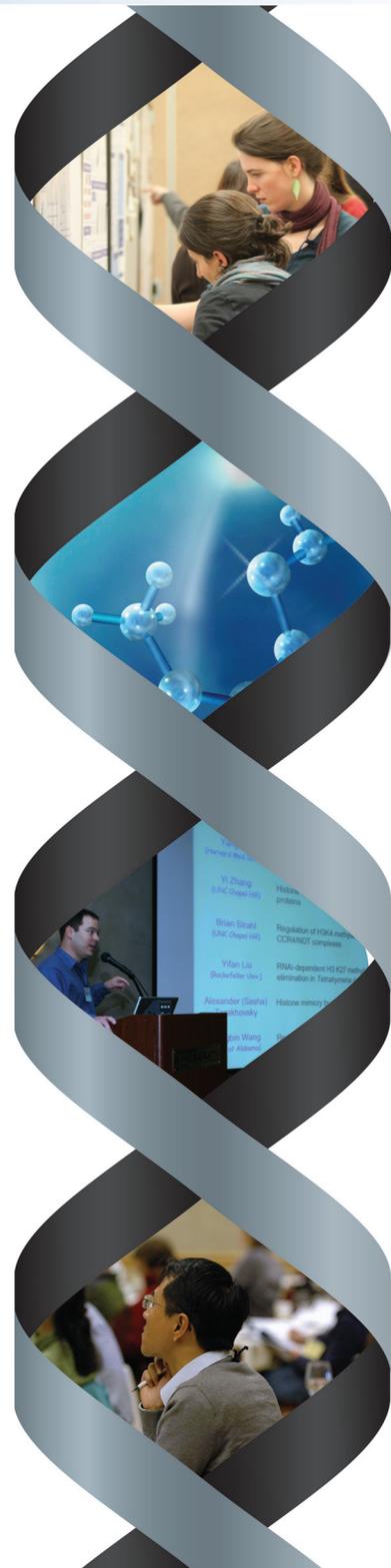
joint with **Molecular Mechanisms of Heart Development**

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

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

[www.keystonesymposia.org/17X8](http://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](http://www.keystonesymposia.org/genetics)

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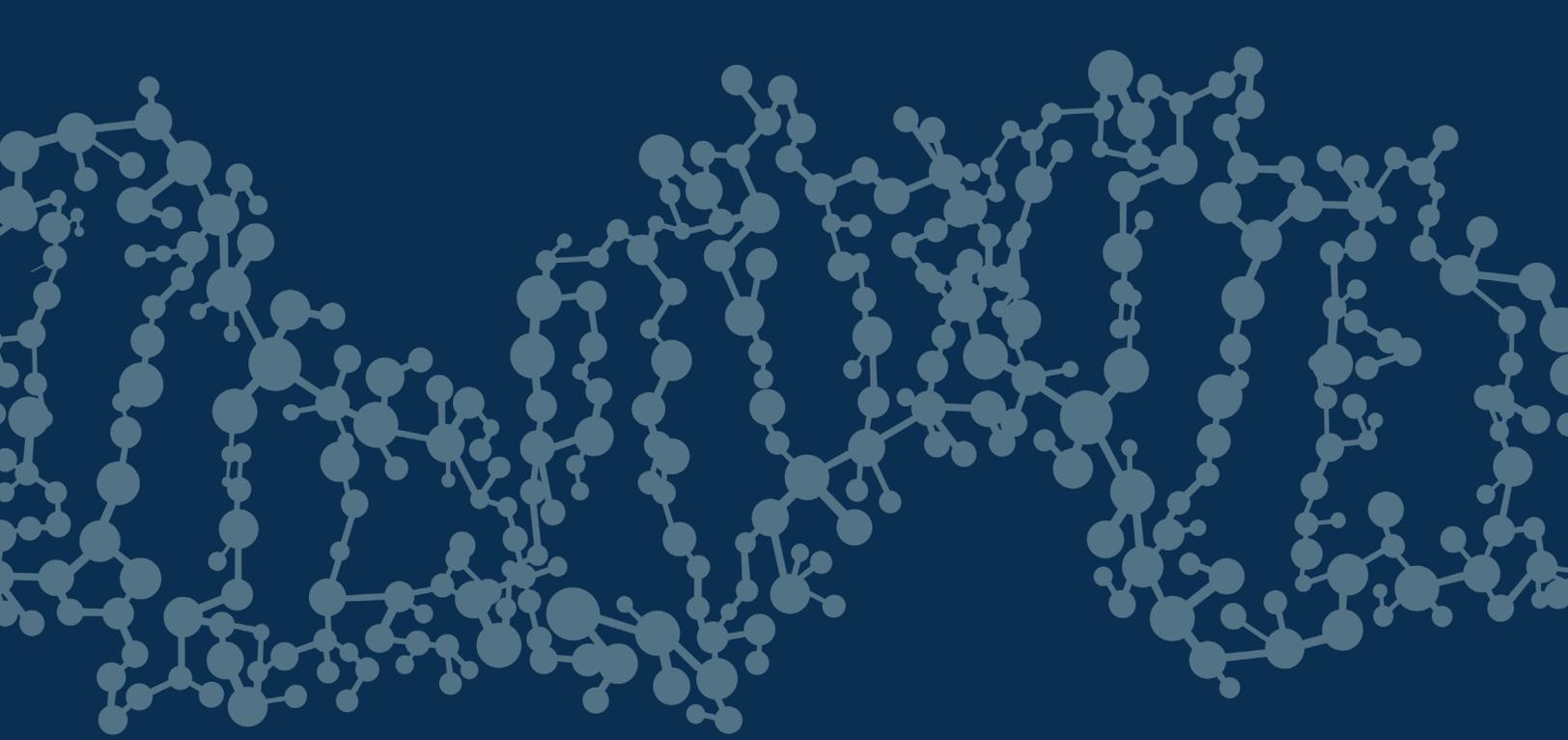
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23-17810-01



# LEAD NATIONAL-SCALE GENOMICS PROJECTS

We are scientists, engineers, communicators, and data lovers.  
We are musicians, homebrewers, yogis, cyclists, and chess players.

Our team is passionate about how genomics and technology can impact and improve human health. And, as part of an innovative startup building the most advanced cloud computing platform for biomedical data analysis - that impact is huge.

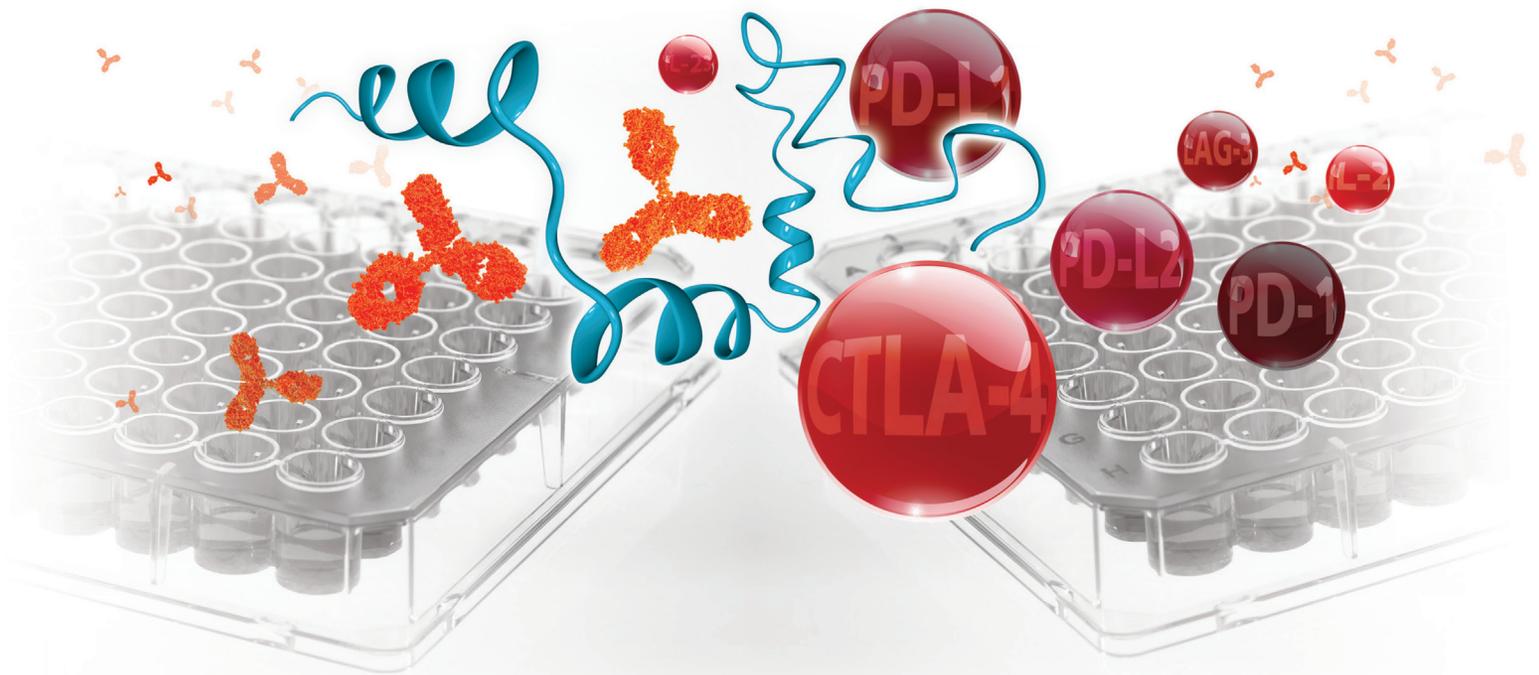
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