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# Expand Your Epigenetics Discovery by Sequencing More of the Methylome

## Accel-NGS® Methyl-Seq Library Kit

- Simple 2-hour protocol
- DNA inputs from 100 pg to 100 ng
- Low bias library preparation
- Compatible with WGBS, RRBS,  
and other enrichment methods



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12/15, 15-0565

# 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



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## **Bulk M-MLV and RNasin at competitive prices**

◎ **M-MLV (H-) Reverse Transcriptase  
US\$1.5 per KU for more than 1,000 KU**

- H minus Moloney Murine Leukemia Virus (M-MLV) Reverse Transcriptase is a recombinant M-MLV reverse transcriptase. RNase H activity has been eliminated by a point mutation in the RNase H domain of M-MLV RTase, ensuring high yields.
- Deficient RNase H activity to reduce RNA template degradation during the first-strand cDNA synthesis.
- cDNA up to 12 kb.

◎ **RNasin (RNase inhibitor)  
US\$6.7 per KU for more than 100 KU**

RNasin is a ribonuclease inhibitor extracted from human placenta with a molecular weight 51 kDa. It inhibits the activity of RNase by specifically binding up to RNase with a non-covalent bond. RNasin, free of RNase or Nickase, can maintain its activity at pH from 5 to 8, and the highest one at pH7.8.

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# BD FACSseq™ Cell Sorter and BD™ Precise Assays

Gene expression assays for single cells



## NGS-ready samples for gene expression

Thousands of single cells, individually barcoded and indexed, now at the transcript level

The new BD FACSseq™ cell sorter selects thousands of individual cells, quickly discarding any dead/dying cells and then isolating them into PCR plates that contain preloaded BD™ Precise reagents for your customized targeted gene expression assays. A much simplified workflow prepares the samples for absolute and direct molecular counting of transcripts by next generation sequencing (NGS), while minimizing amplification bias that can potentially occur in these crucial steps.

The affordable BD FACSseq cell sorter combined with BD Precise assays lets you easily amp up your lab's productivity to help ensure that your high quality single cell samples are ready for gene expression assays. And, you can significantly increase data accuracy and throughput while controlling costs.

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# Time for change.

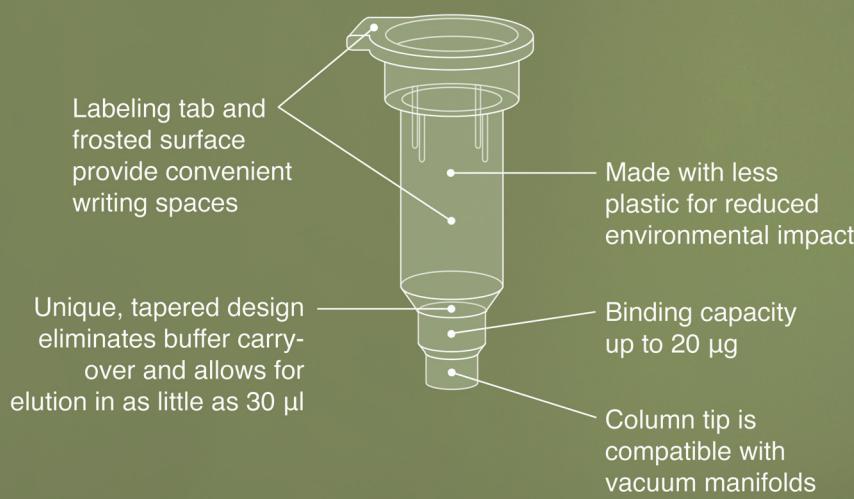
## Introducing Monarch<sup>™</sup> Nucleic Acid Purification Kits

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# Does your TCR profiling data tell the whole story?

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- **Diversity data for TCR $\alpha$  and/or TCR $\beta$ :** Analyze your choice of TCR subunits, either in the same experiment or separately.
- **High sensitivity and flexible sample inputs:** Detect low-abundance TCR clonotypes, starting from 10 ng–3  $\mu$ g of RNA obtained from peripheral blood, or from 50–10,000 purified T cells.
- **Illumina-ready sequencing libraries:** Incorporate Illumina adapter and index sequences in a ligation-independent manner, and multiplex up to 96 libraries in a single flow-cell lane.

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

<sup>1</sup> 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
- Exact 3' UTR tagging
- From 100 pg total RNA input including low quality RNA and FFPE samples
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4th Annual



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Earlybird Booking Deadline:

**June 27, 2016**

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- Systems Immunobiology
- Immunodiversity and Immune Repertoires
- Role of Common Variants in Disease
- Immunogenomics and Immunotherapy
- Genomics, Evolution and Host-Pathogen Interactions



## Keynote Speakers:



**Herbert "Skip" Virgin**  
Washington University  
School of Medicine, St. Louis, MO



**Alan Aderem**  
Center for Infectious  
Disease Research, Seattle, WA

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# Empowering Research Through Smart Solutions

The right tools for your bioinformatics analysis needs

## novoAlign

- The market's leading aligner for accurate and speedy multi-threaded sequence alignment.
- Powerful tool designed for mapping of short reads onto a reference genome.
- Now available on BaseSpace.

## novoSort

- The fastest multi-threaded sort/merge tools for BAM files.
- Sort and mark duplicates in a flash.

## novoLR package

- novoLRcleaver
- novoLRcorrector
- novoLRpolish
- Genome assembly prep using hybrid technology for mixed short reads and single molecule long reads.
- Long reads hybrid correction using in-house algorithms for read ranking and correction.
- Post-assembly sequence polishing.

## novoWorx

A on-site, integrative, customizable workbench that allows users to run an entire pipeline without using command lines interface. The platform mainly utilizes Novocraft's proprietary software; novoAlign for alignment and novoSort for sorting and SAM to BAM conversion. A combination of unique in-house softwares and open source modules to decipher your big data into meaningful results.

## novoClinic

A patient-centric NGS targeted sequence analysis platform that provides integrated sample tracking for quality control and compliance. The built-in customizable analysis pipeline and straight-forward data reporting system will ease the burden of data mining and interpretation, allowing clinicians to focus on diagnosis and treatment.



NOVOCRAFT TECHNOLOGIES SDN. BHD.

C-23A-05, 3 Two Square, Section 19, 46300 Petaling Jaya, Selangor, Malaysia

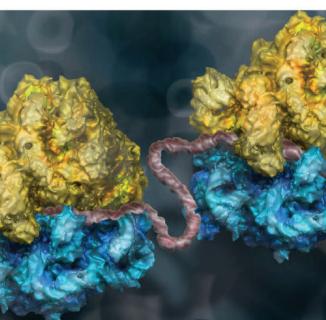
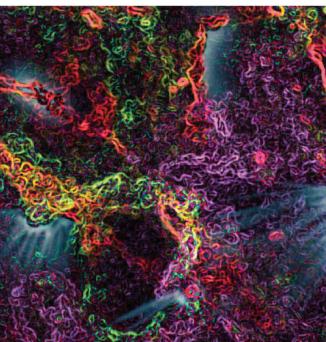
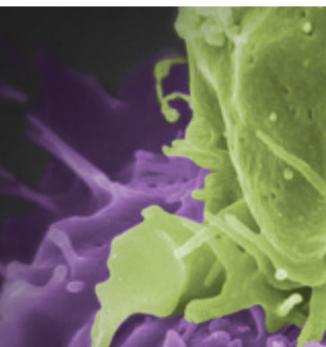
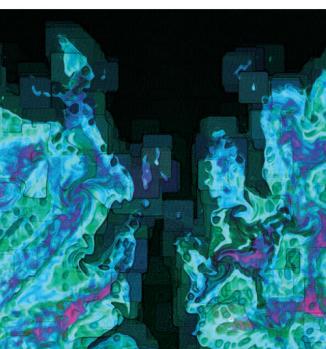
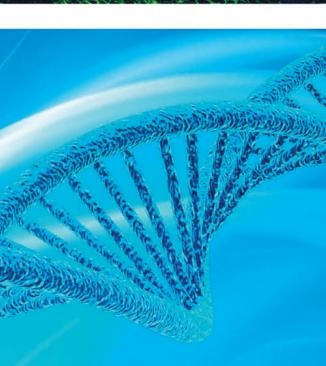
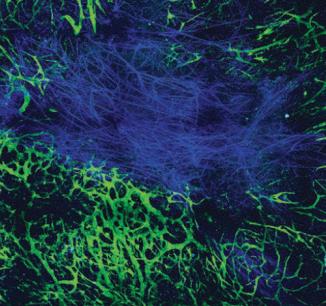
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# 2016 SCIENTIFIC CONFERENCES

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

## **Engineering and Physical Sciences in Oncology**

Conference Co-Chairpersons: Joan Brugge, Rakesh Jain, and Robert Langer  
June 25-28, 2016 • Boston, MA

## **Fifth JCA-AACR Special Joint Conference on the Latest Advances in Hematological Cancer Research: From Basic Science to Therapeutics**

Conference Co-Chairpersons: Jonathan D. Licht, Ross L. Levine, Catriona Jamieson, Takuro Nakamura, Issay Kitabayashi, and Shigeru Chiba  
July 13-15, 2016 • Urayasu, Japan

## **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

## **AACR International Conference on Translational Cancer Medicine**

Conference Co-Chairpersons: Carlos L. Arteaga, and Carlos Gil M. Ferreira  
October 13-15, 2016 • São Paulo, Brazil

## **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

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



American Association  
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# EMBL 2016

## Conferences

18 - 20 MAY | EMBL Conference

**BioMalPar XII:**

**Biology and Pathology of the Malaria Parasite**

G. Christophides, F. Osier, A. Scholzen, T. Voss | EMBL Heidelberg, Germany

3 - 5 JUN | EMBL Conference

**Hematopoietic Stem Cells: From the Embryo to the Aging Organism**

K. Kiss, C. Lançrin, C. Lo Celso, C. Robin | EMBL Heidelberg, Germany

12 - 15 JUN | EMBL Conference

**CTLS 2016 - Core Technologies for Life Science**

P. England, R. Pepperkok, S. Shorte | EMBL Heidelberg, Germany

26 - 29 JUN | EMBO | EMBL Symposium  
**Innate Immunity in Host-Pathogen Interactions**

Z. Chen, W-D. Hardt, N. Pariente, F. Randow | EMBL Heidelberg, Germany

5 - 7 JUL | EMBL Conference  
**Lifelong Learning in the Biomedical Sciences**

M. Hardman, C. Janko, C. Johnson | EMBL Heidelberg, Germany

24 - 26 JUL | EMBL Conference

**Microfluidics 2016**

C. Merten, S. Quake | EMBL Heidelberg, Germany

27 - 30 AUG | EMBL Conference  
**Transcription and Chromatin**

D. Duboule, E. Furlong, A. Shilatifard, M. Timmers | EMBL Heidelberg, Germany

31 AUG - 3 SEP | EMBO Conference

**Chemical Biology 2016**

M. Köhn, J. Overington, C. Schultz | EMBL Heidelberg, Germany

7 - 10 SEP | EMBO | EMBL Symposium  
**Actin in Action: From Molecules to Cellular Functions**

B. Baum, J. Faix, P. Lenart, D. Mullins, F. Nedelec, C. Sykes | EMBL Heidelberg, Germany

14 - 17 SEP | EMBL-Wellcome Genome

**Campus Conference Proteomics in Cell Biology and Disease Mechanisms**

A.-C. Gavin, A. Lamond, M. Mann | EMBL Heidelberg, Germany

25 - 27 SEP | EMBL-Wellcome Genome

**Campus Conference Big Data in Biology and Health**

E. Birney, B. Grossman, J. Korbel, C. Relton | EMBL Heidelberg, Germany

5 - 8 OCT | EMBO | EMBL Symposium

**The Complex Life of mRNA**

A. Ephrussi, N. Sonenberg, J. Steitz, D. Tollervey | EMBL Heidelberg, Germany

12 - 15 OCT | EMBO | EMBL Symposium  
**Organoids: Modelling Organ Development and Disease in 3D Culture**

M. Bissell, J. Knoblich, E. Schnapp | EMBL Heidelberg, Germany

19 - 23 OCT | EMBO Conference  
**Experimental Approaches to Evolution and Ecology Using Yeast and Other Model Systems**

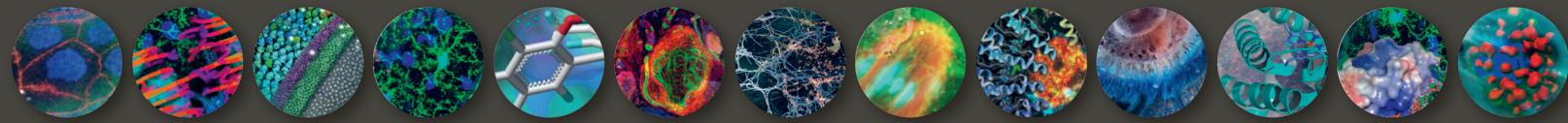
J. Berman, M. Dunham, J. Leu, L. Steinmetz | EMBL Heidelberg, Germany

12 - 15 NOV | EMBO Conference  
**From Functional Genomics to Systems Biology**

E. Furlong, F.C.P. Holstege, N. Rajewsky, M. Walhout | EMBL Heidelberg, Germany

20 - 23 NOV | EMBO Conference  
**Molecular Machines: Integrative Structural and Molecular Biology**

J. Briggs, T. Carlomagno, G. Kleywegt, D. Panne, D. Svergun | EMBL Heidelberg, Germany



## Courses

4 - 5 JUL, 28 - 29 NOV | EMBL Courses

**NGS: Whole Genome Sequencing Library Preparation**

V. Benes, J. Dreyer-Lamm, A. Heim | EMBL Heidelberg, Germany

11 - 15 JUL, 21 - 25 NOV | EMBL Courses

**NGS: Enrichment Based Targeted Resequencing**

V. Benes, J. Dreyer-Lamm, A. Heim | EMBL Heidelberg, Germany

11 - 15 JUL | EMBL Course

**Quantitative Proteomics**

J. Krieger, M. Savitski | EMBL Heidelberg, Germany

25 - 30 JUL | EMBL Course

**Super-Resolution Microscopy**

M. Lampe, R. Pepperkok, J. Schröder, U. Schwarz | EMBL Heidelberg, Germany

28 AUG - 5 SEP | EMBO Practical Course

**Cryo-Electron Microscopy and 3DImage Processing**

J. Briggs, B. Boettcher, L. Passmore, C. Sachse, H. Stahlberg | EMBL Heidelberg, Germany

29 AUG - 2 SEP | EMBL Course

**Chromatin Signatures During Differentiation**

J. Dreyer-Lamm, P. Grandi, K.-M. Noh | EMBL Heidelberg, Germany

12 - 14 SEP | EMBL-EBI Course

**Metagenomics Bioinformatics**

H. Denise, L. Emery, A. Mitchell | EMBL-EBI Hinxton, UK

12 - 20 SEP | EMBO Practical Course

**Protein Expression, Purification and Characterization**

C. Loew, R. Meijers, A. Parret | EMBL Hamburg, Germany

19 - 23 SEP | EMBL-EBI Course

**Structural Bioinformatics**

T. Hancock, G. Kleywegt, C. Orengo | EMBL-EBI Hinxton, UK

19 - 24 SEP | EMBL Course

**Extracellular Vesicles: from Biology to Biomedical Applications**

J. Dreyer-Lamm, A. Hendrix, E. Nolte-'t Hoen | EMBL Heidelberg, Germany

3 - 6 OCT | EMBL-EBI Course

**Introduction to Next Generation Sequencing**

T. Hancock, J. Randall, M. Rossello | EMBL-EBI Hinxton, UK

4 - 7 OCT | EMBL Courses

**Whole Transcriptome**

**Data Analysis**

V. Benes, R. Calogero | EMBL Heidelberg, Germany

17 - 24 OCT | EMBO Practical Course

**Solution Scattering from Biological Macromolecules**

A. Kihney, D. Svergun | EMBL Hamburg, Germany

17 - 23 OCT | EMBO Practical Course

**High-Throughput Microscopy for Systems Biology**

J. Ellenberg, D.W. Gerlich, B. Neumann, R. Pepperkok | EMBL Heidelberg, Germany

7 - 11 NOV | EMBL-EBI-Wellcome Genome

**Campus Course Resources for Computational**

**Drug Discovery**

T. Hancock | EMBL-EBI Hinxton, UK

9 - 10 NOV | EMBL Course

**Microinjection into Adherent Cells**

J. Dreyer-Lamm, S. Stobrawa | EMBL Heidelberg, Germany

28 NOV - 2 DEC | EMBL-EBI Course

**Biological Interpretation of Next Generation Sequencing**

G. Rustici | EMBL-EBI, Hinxton UK

4 - 9 DEC | EMBL-EBI-Wellcome Genome

**Campus Course Proteomics Bioinformatics**

L. Emery | EMBL-EBI, Hinxton UK

7 - 11 DEC | EMBL Course

**Microbial Communities: Modelling Meets Experiments**

R. Mahadevan, K. Patil, K. Sasaki | EMBL Heidelberg, Germany

For full event listing please visit our website

[www.embl.org/events](http://www.embl.org/events)



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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](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. Whetstine, 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)

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## 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

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

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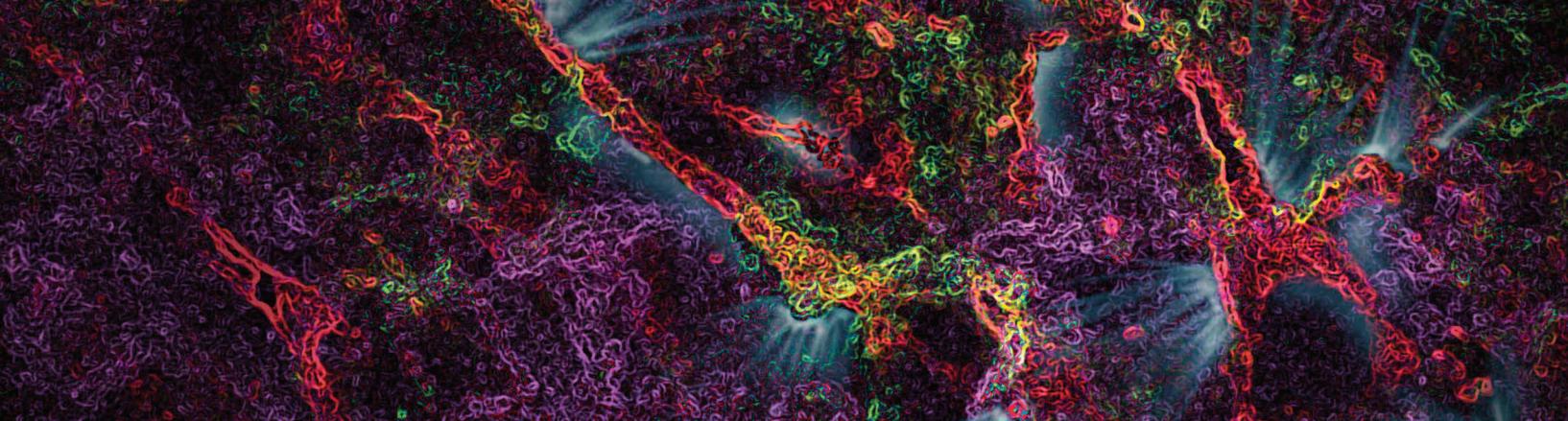
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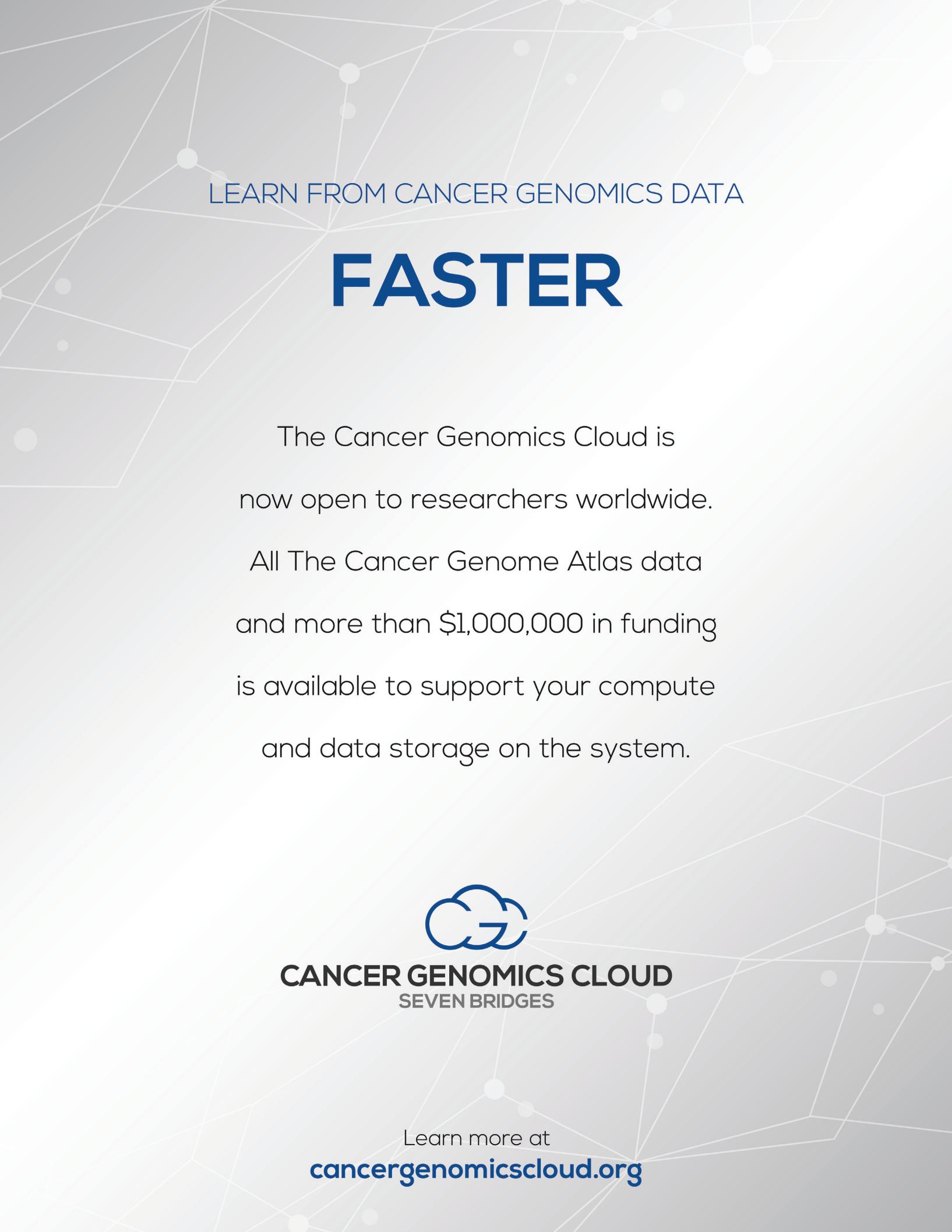
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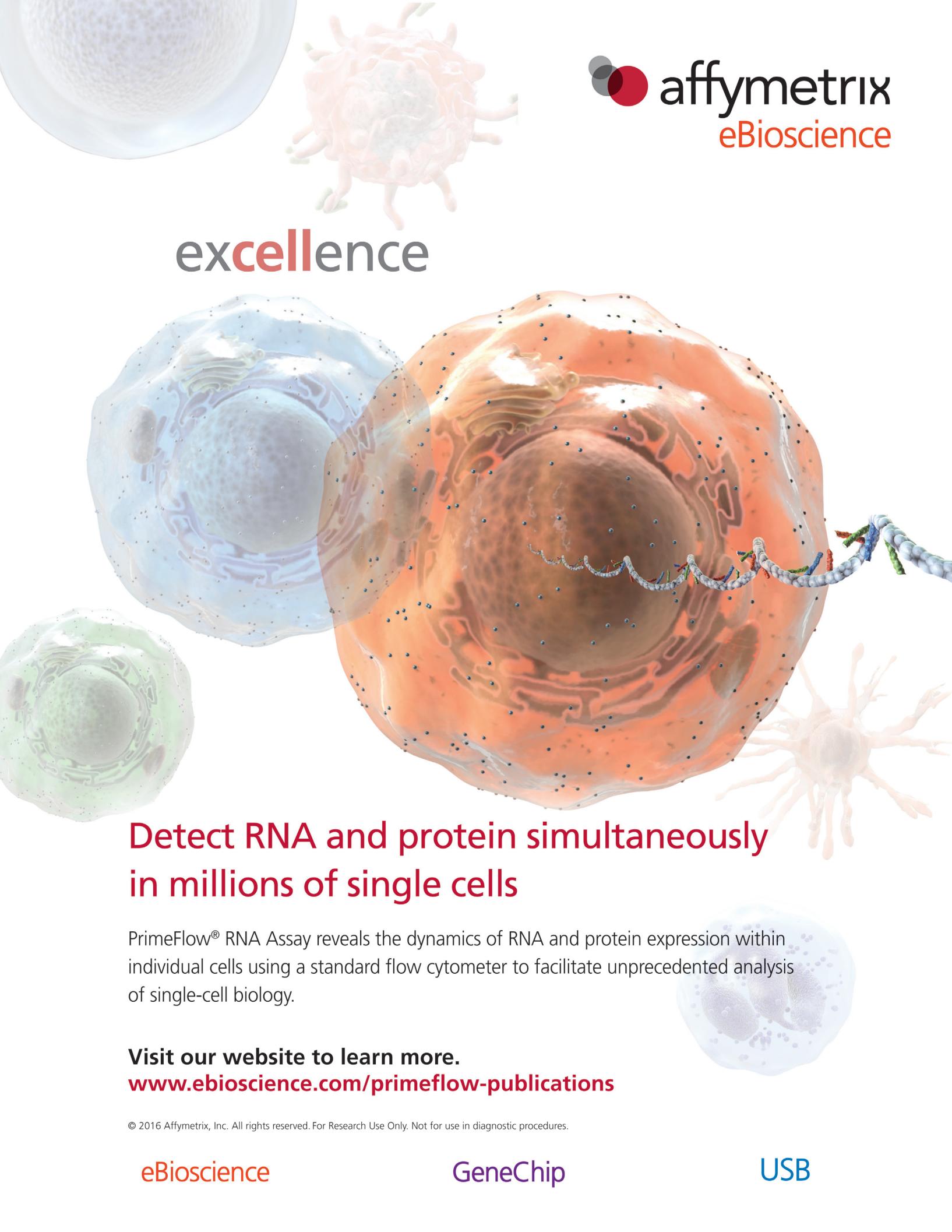
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