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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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Unlock the Power of FFPE Samples with Exome Sequencing from 25 ng DNA

Accel-NGS® 2S Hyb DNA Library Kit
Enabling Targeted Sequencing of Limiting Samples

- Increased library complexity
- 5' and 3' repair steps for damaged samples
- No adapter titrations required
- Compatible with all hybridization panels



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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

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Agarose for Molecular Biology

Besta™ LE Agarose, Multi-purpose

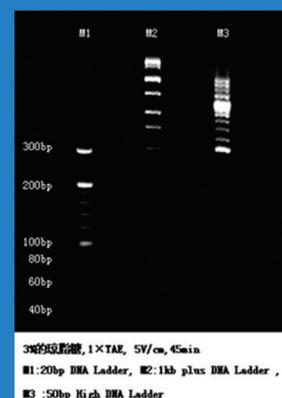
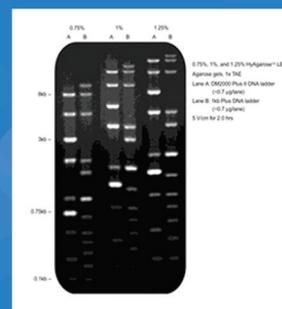
Besta™ LE Agarose is a low EEO, multi-purpose, standard melting point agarose that yields high resolution sharp DNA bands with high clarity and low background. Its optimized gel strength enhances ease of gel processing and handling.

Besta™ LM Agarose

Besta™ LM Agarose is a Low Melting and gelling point agarose producing gels with great sieving properties and higher clarity when compared with standard agarose. Besta™ LM Agarose is ideal for in-gel manipulations which can be performed without prior extraction of the DNA from the gel slice.

Besta™ HR Agarose

Besta™ HR Agarose is a PCR grade, intermediate melting point agarose that efficiently separates small DNA fragments between 20 and 800 bp in length and yields ultra-high resolution with high clarity and low background. It is suitable for the analysis of AFLP's (Amplified Fragment Length Polymorphisms), STR's (Short Tandem Repeats) and tetra-nucleotide repeats.



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.

Find out how at
bdbiosciences.com/go/facsseq

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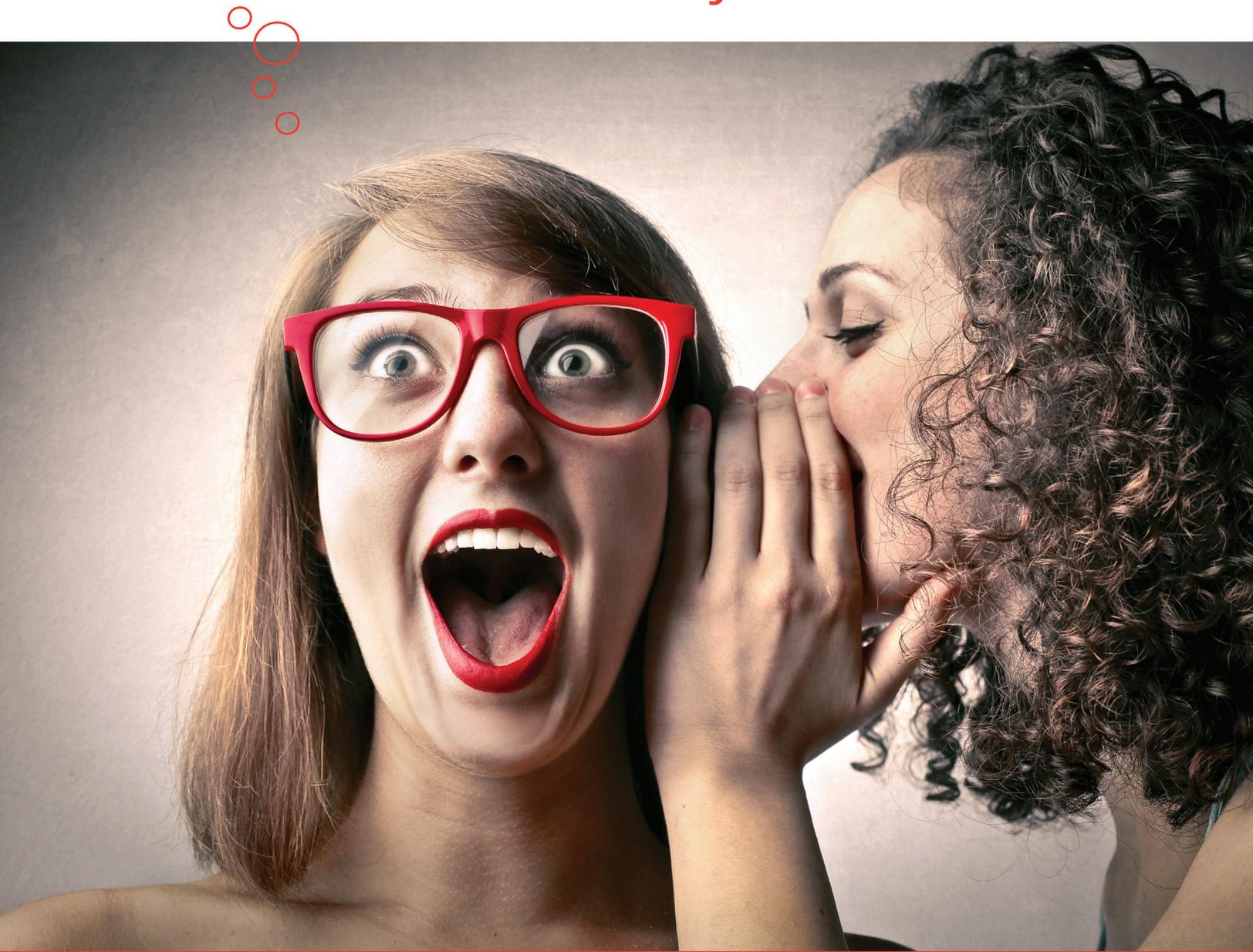
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Extraordinary variation of floral organs in *Phalaenopsis* orchid is due to differential expression of multiple genes in sepal, petal, and labellum.¹

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
- Exact 3' UTR tagging
- From 100 pg total RNA input including low quality RNA and FFPE samples
- Cost-effective sequencing of up to 96 samples / lane
- Ready-to-sequence libraries in 4.5 hours
- Illumina™ and Ion Torrent™ compatible
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- 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

+603 7960 0541

office@novocraft.com

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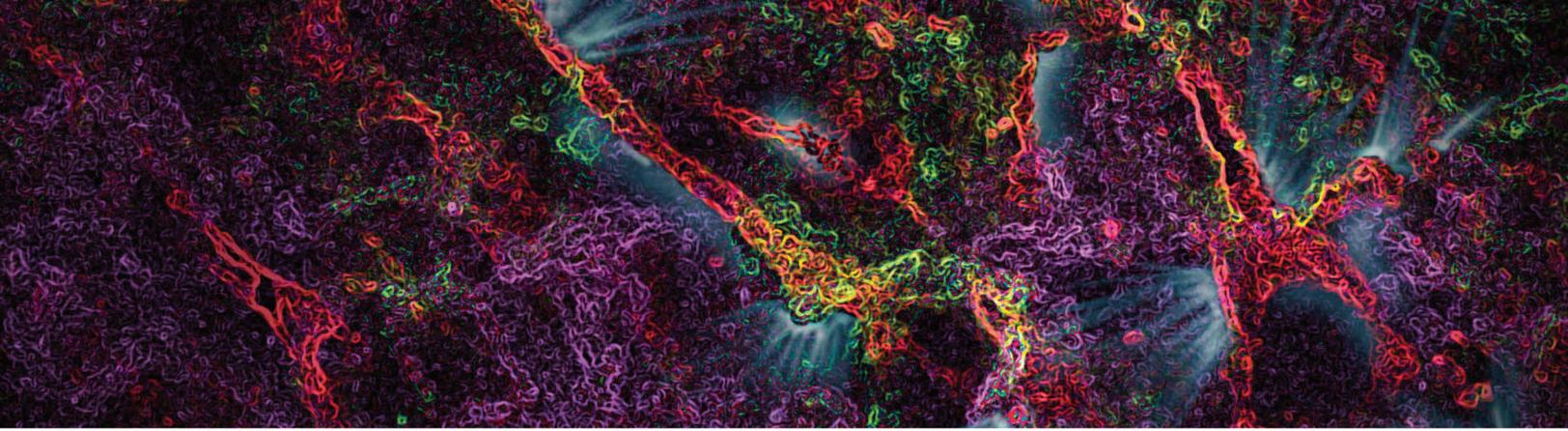
**University of Illinois College of Medicine
Cancer Biology and Pharmacology
Assistant/Associate Professor – Tenure-Track**

The Department of Cancer Biology and Pharmacology of the University of Illinois College of Medicine at Peoria (UICOMP) has recently expanded its faculty and cancer research scope to include new areas of investigation in Cancer Microbiomics, Cancer Immunology and Immunotherapy, and Cancer Metabolism. We are now inviting applications for a tenure-track Assistant or Associate Professor level position in Cancer Computational –OMICs and Systems Biology. Early and mid-career investigators with a solid training in computer science and in cancer research, with a strong track record of scholarly productivity, an uncompromised commitment to a culture that is conducive to collaborative interdisciplinary research, and a genuine interest in contributing to the educational mission of the medical school are highly encouraged to apply. The selected candidate will be expected to develop a vibrant and highly interactive systems biology and computational –OMICs cancer research program that will not only provide support for big data analysis, but also will pursue development of innovative methodologies for integrative –OMICs systems-based research. In addition, the selected candidate will be expected to aggressively seek federal funding, and to teach our medical students.

UICOMP is one of the regional campuses of the University of Illinois College of Medicine, and is part of a 900-bed hospital district containing two major hospital systems as well as the medical school. UICOMP's educational programs include 150 medical students and 240 residents/fellows in 20 different post-graduate programs. This regional campus has made cancer one of its main focus areas of basic and translational science investigation, which is widely supported by the community, clinical and corporate partners. A new 24,000 square foot Cancer Research building provides exceptional laboratory space, state-of-the art research equipment, and core facilities.

The successful candidate will have a Ph.D., M.D., or M.D./Ph.D. in computer engineering, computer science, or basic research in a field of health science, with at least 3 years of postdoctoral training in cancer research, bioinformatics, or systems biology, and a solid record of scholarly productivity, as evidenced by peer-reviewed publications, fellowship and grant awards, and participation in national and international meetings

For fullest consideration, please respond by June 6th, 2016. Applicants should submit a cover letter, NIH style biosketch, the names and contact information of three references, summary of research contributions, a research plan and statement of research interests, and teaching goals. To apply, click on the following link: <https://jobs.uic.edu/job-board/job-details?jobID=63884>. The University of Illinois is an Affirmative Action/Equal Opportunity employer. Minorities, women, veterans, and individuals with disabilities are encouraged to apply. The University of Illinois may conduct background checks on all job candidates upon acceptance of a contingent offer. Background checks will be performed in compliance with the Fair Credit Reporting Act.



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Register and Save By: Friday, September 9, 2016

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ABOUT THIS CONFERENCE

A hallmark of this AACR immunology series is the integration of several sub-disciplines of cancer immunology and immunotherapy, with a broad focus on strategies to harness the immune system for the treatment and prevention of different cancers. Leaders in the field will present their latest work and provide critical updates on our deepening understanding of the immune response towards cancer. This Special Conference will also provide a unique opportunity for the authors of highly rated abstracts to present their work to an audience of researchers from around the world. Ample time will be provided for the stimulating discussions that are necessary to further the scientific and translational goals of the field. As the sixth in the series, this conference will continue to provide a forum for the effective exchange of ideas between basic cancer immunologists, non-immunologists, and clinical oncologists—from academia to industry.



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for Cancer Research

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4th Annual



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Abstract Deadline:

July 15, 2016

Earlybird Booking Deadline:

June 27, 2016

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The Immunogenomics 2016 conference explores the application of genomic technologies to better understand the immune system. This innovative research promises to revolutionize the way we view, diagnose and treat disease and the way we cultivate good health.

This interdisciplinary and international program will feature invited talks on the following topics:

- Microbiome
- Single Cell Approaches, New Technologies and Bioinformatics
- Epigenomics of Immune Cells
- 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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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

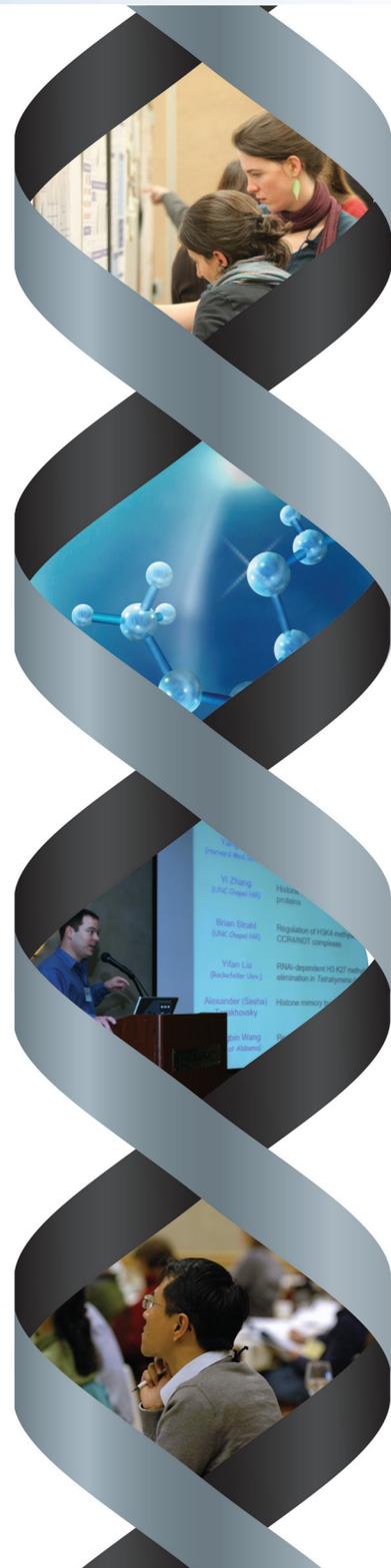
joint with **Molecular Mechanisms of Heart Development**

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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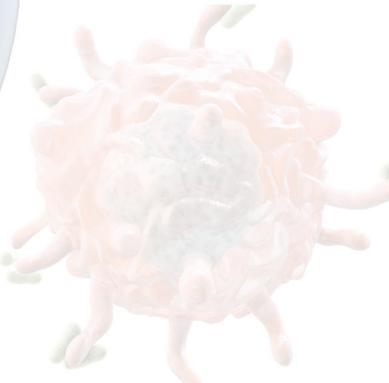
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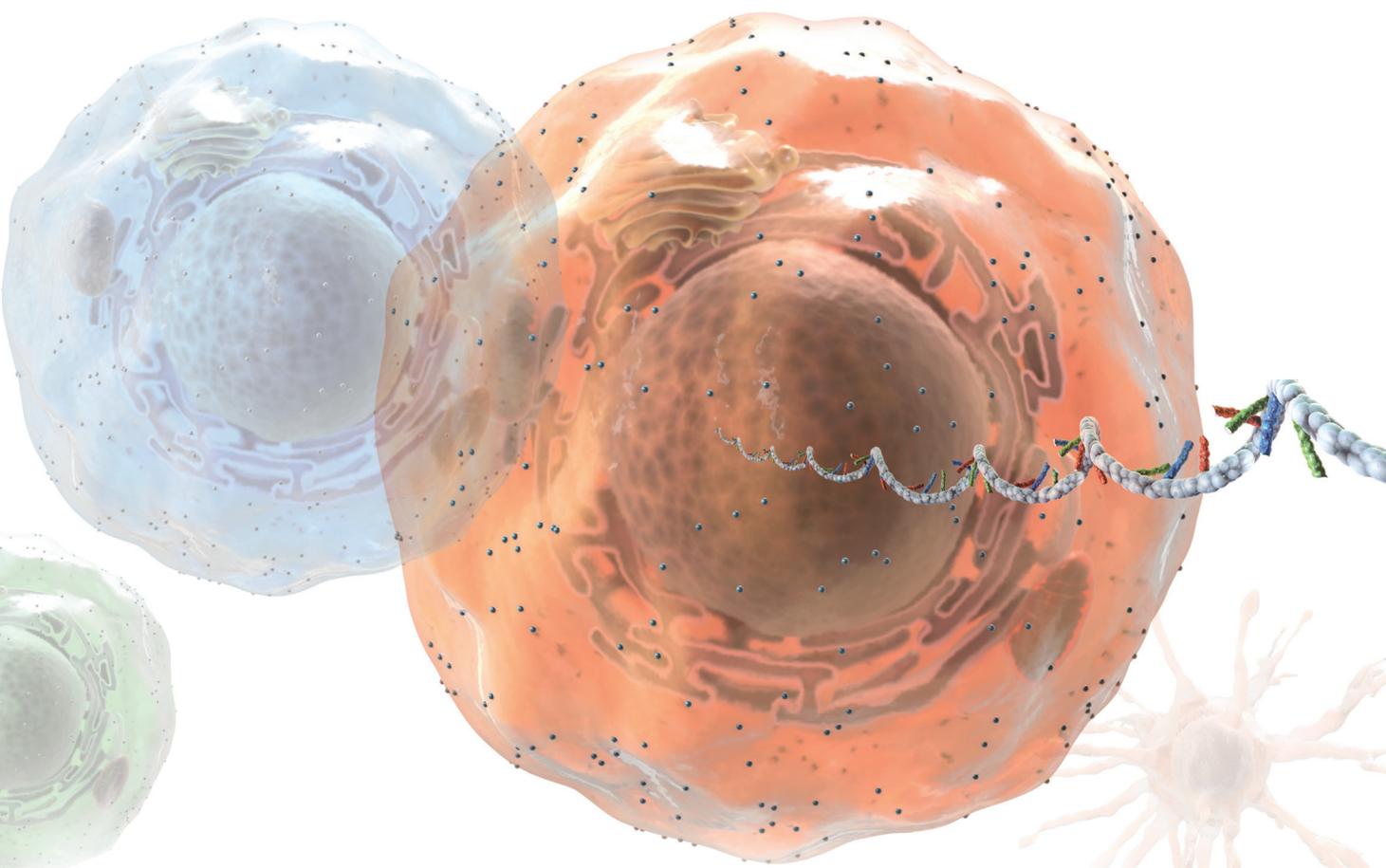
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