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Qualify and quantify nucleic acids for ANY throughput.

Streamline sample analysis for ANY application.

**NGS QC - RNA QC - gDNA - SSRs**



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

## **Accel-NGS<sup>®</sup> 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

**Swift** 

**BIOSCIENCES<sup>™</sup>**

[www.swiftbiosci.com](http://www.swiftbiosci.com)

 **Accel-NGS<sup>®</sup>**

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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

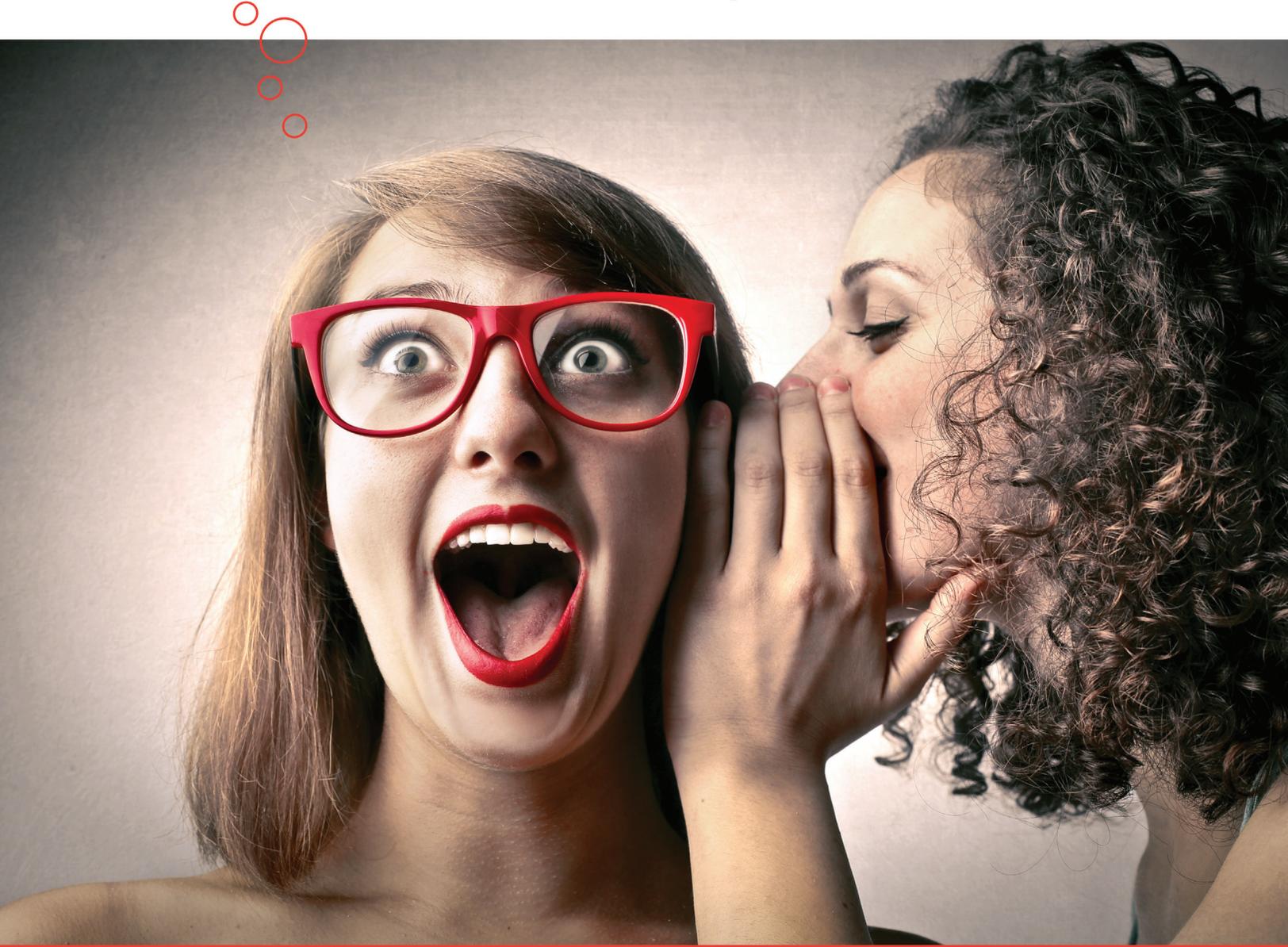
Fastest run time of any benchtop sequencer



Watch the Ion S5 System in action at  
[thermofisher.com/ionS5](http://thermofisher.com/ionS5)

**ThermoFisher**  
SCIENTIFIC

# An isothermal that really works?



Microfluidics, digital PCR and sequencing innovators the world over are enjoying DNA **amplification times as low as 7 minutes** without a thermocycler. You can too with isothermal enzymatic *recombinase polymerase amplification* (RPA) and your next big idea.

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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.

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Novocraft-Technologies-Sdn-Bhd

# Does your TCR profiling data tell the whole story?

IMMUNE PROFILING WITH NEXT-GEN SEQUENCING

## Introducing the SMARTer<sup>®</sup> Human TCR a/b Profiling Kit



### Sequence entire TCR variable regions with high sensitivity

By employing a 5' RACE-based approach that draws upon our proven SMART<sup>®</sup> technology, the SMARTer Human TCR a/b Profiling Kit provides a powerful and elegant solution for high-throughput analysis of TCR repertoire diversity on Illumina<sup>®</sup> sequencing platforms.

Benefits of the SMARTer approach:

- **Full-length V(D)J sequence information:** Obtain full-length sequences for variable regions of TCR mRNA transcripts.
- **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.

Learn more by visiting  
[www.clontech.com/SMARTer-Human-TCR](http://www.clontech.com/SMARTer-Human-TCR)  
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# Binuclease® 50ku \$58.00

## Binuclease® (For the Digestion of DNA and RNA)

Binuclease is a genetically engineered endonuclease from *Serratia marcescens*. The enzyme is produced and purified from eukaryotic yeast cells, without contamination of endotoxin from prokaryotic cells. Functionally, this promiscuous nuclease digests all forms of DNA and RNA, including single stranded, double stranded, linear, circular and supercoiled DNA and RNA. The enzyme cleaves the phosphodiester bond of nucleic acids, producing 5' monophosphate terminated oligonucleotides 2-5 bases in length. The Binuclease is not a sequence dependent nuclease, capable of cleaving the phosphodiester bond at all positions among a nucleic acid chain. This promiscuous endonuclease is applied for removing nucleic acids in biological products. In the industry of vaccine, protein and saccharides pharmaceuticals, this endonuclease is widely used to get rid of nucleic acids, reducing the nucleic acid contaminant in the vaccines and protein products. This promiscuous nuclease is the ideal choice for viscosity reduction of cell lysate and cell culture clarification.

# Mutant Proteinase K 100mg \$17.00

## Mutant Proteinase K

The application of this Mutant Proteinase K is similar with wild type Proteinase K. But this mutant one has higher specific activity and more stable at room temperature. It is a non-specific serine proteinase with broad substrates. It is active over the pH range from 4 to 12. It can be used at any situation to digest native and denatured proteins. For instance, it is used for isolating mRNA or genomic DNA from different tissues and modifying glycoprotein for structure studies. Mutant Proteinase K is active with SDS, urea and EDTA and active between 15°C and 75°C.

Beijing SBS Genetech Co. Ltd.

Fax: +86-10-82784290

Email: [order@sbsbio.com](mailto:order@sbsbio.com) Website: [www.sbsbio.com](http://www.sbsbio.com)

During the passage from the shore to marine life penguins acquire a tremendous capability of survival in cold waters and experience corresponding morphological alterations. These are results of gene expression changes.<sup>1</sup>



<sup>1</sup> Teulier, L. et al. Proc Biol Sci. 279, 2464–2472 (2012).

## The difference comes from changes in gene expression

Gene expression profile changes play significant role in life cycles of many organisms including penguins.

An essential life step for penguins is a passage from shore to marine life, a step towards nutrition independence. Penguins acquire exceptional capability to survive in cold water and morphological alterations happen. At the time of departure to sea, the thick down of juveniles is replaced by waterproof feathers (view photo). These differences come from changes in gene expression profile.

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 generation of highly strand-specific NGS 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.



**QUANT  
SEQ**<sup>™</sup>  
Sequencing that counts

### 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<sup>™</sup> and Ion Torrent<sup>™</sup> compatible
- Reduced data analysis time
- Custom solutions available

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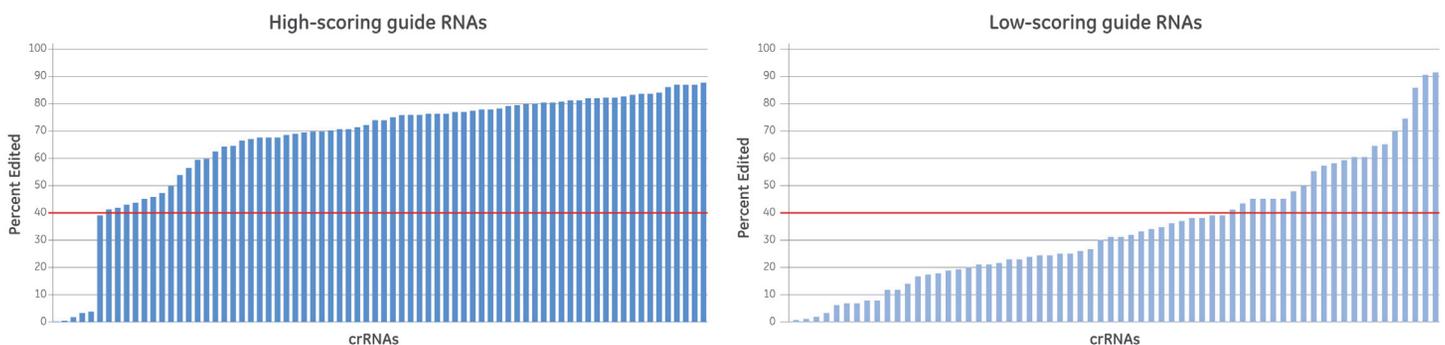
# CRISPR

## Dharmacon reagents help you move forward. Faster.

Simplify your gene editing workflow with the Dharmacon™ Edit-R™ CRISPR-Cas9 platform. Custom or predesigned ready-to-use DNA and synthetic RNA leverage a validated algorithm to select highly functional, specific targets for gene knockout – enabling you to quickly assess multiple target sites per gene across one or hundreds of genes.

CRISPR Guide RNAs | CRISPR Screening Libraries | Cas9 Nucleases

### crRNAs that have high functionality scores show high editing efficiency



HEK293T-CAG-Cas9 cells were transfected with either high-scoring or low-scoring crRNAs (50 nM crRNA:tracrRNA) using DharmaFECT 1 transfection reagent (0.25  $\mu$ L/well) in 96-well format. Gene editing efficiencies were determined using next-generation sequencing. 93% of the top 10 high-scoring crRNAs targeting ten different genes have > 40% indel formation and only 33% of the 10 lowest scoring designs have > 40% indel formation.



# BD FACSseq™ Cell Sorter and BD™ Precise Assays

Gene expression assays for single cells



Helping all people  
live healthy lives

## NGS-ready samples for gene expression

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



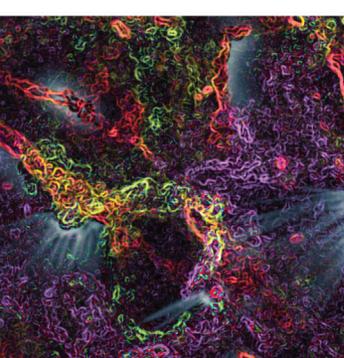
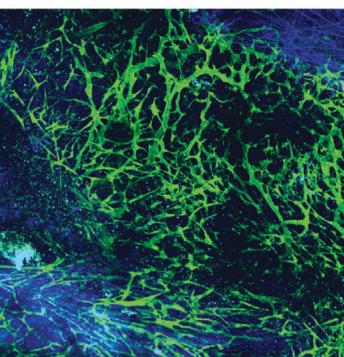
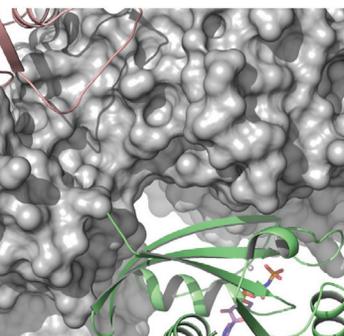
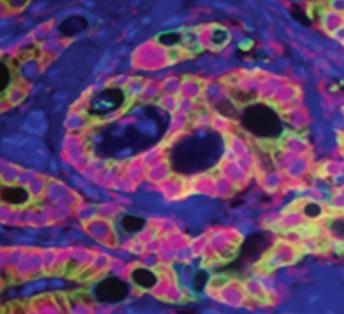
The new BD FACSseq™ cell sorter selects thousands of individual cells, quickly discarding any dead/dying cells and then isolating them into PCR plates that contain preloaded BD™ Precise reagents for your customized targeted gene expression assays. A much simplified workflow prepares the samples for absolute 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](http://bdbiosciences.com/go/facsseq)

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# 2016 SCIENTIFIC CONFERENCES

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

## **Pancreatic Cancer: Advances in Science and Clinical Care**

*Conference Co-Chairpersons: Manuel Hidalgo, Christine Iacobuzio-Donahue, and Robert H. Vonderheide*  
May 12-15, 2016  
Orlando, FL

## **AACR Precision Medicine Series: Targeting the Vulnerabilities of Cancer**

*Conference Co-Chairpersons: Stephen W. Fesik, Jeffrey E. Settleman, and Paul Workman*  
May 16-19, 2016  
Miami, FL

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

*Conference Co-Chairpersons: Rakesh Jain, Robert Langer, and Joan Brugge*  
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: Takuro Nakamura, Issay Kitabayashi, Shigeru Chiba, Jonathan D. Licht, Ross L. Levine, and Catriona Jamieson*  
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

## **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

## **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

## **EORTC-NCI-AACR Molecular Targets and Cancer Therapeutics Symposium**

November 29-December 2, 2016  
Munich, Germany

## **San Antonio Breast Cancer Symposium**

*Conference Co-Directors: Carlos L. Arteaga, Virginia G. Kaklamani, and C. Kent Osborne*  
December 6-10, 2016  
San Antonio, TX

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

**AACR** American Association  
for Cancer Research

FINDING CURES TOGETHER<sup>SM</sup>



Join Keystone Symposia  
for the conference on:

# Understanding the Function of Human Genome Variation

May 31–June 4, 2016

Uppsala Konsert & Kongress | Uppsala | Sweden

Scientific Organizers:

Kerstin Lindblad-Toh and Xavier Estivill

*One of the most complex problems in medical and evolutionary genomics is interpreting the function of the millions of variants the genome contains, most being rare and private to each individual or with consequences constrained to specific cells or tissues. The functional consequences of variation in coding regions are well established, but the majority of genetic variation resides in the noncoding portion of the human genome. The goal of this meeting is to bring together experts that may address important questions such as the function of noncoding variation, the connection between selection and disease, the diverse action of variants in different physiological and pathological scenarios, who develop and apply novel tools to connect genotype and phenotype both in disease and in an evolutionary context. By combining the diverse knowledge of many aspects of genomic analysis, we hope to bring out critical discussion and novel approaches to understanding human genome variation of crucial importance for the individualized genome analysis that precision medicine proposes. We are now entering the age of precision medicine with the capacity to analyze the genome of every subject, evaluating the functional consequences of variability and its interaction with the environment at different time-points in life.*

Session Topics:

- Pleiotropy and Epistasis of Variants Involved in Disease
- Finding the Causative Variant(s)
- Connection between Selection and Disease
- Defining the Functional Elements in the Human Genome
- Human History, Migration and Evolution
- Selection and Population Genetics
- Complex Disease and Genetic Variation
- Structural Variation

## CONFIRMED SPEAKERS

(as of March 11, 2016):

Jessica Alföldi  
Cynthia M. Beall  
Gill Bejerano  
Jada BennTorres  
Barak Alon Cohen  
Evan E. Eichler  
Xavier Estivill  
Michel A. J. Georges  
Ed Green  
William J. Greenleaf  
Iiris Hovatta  
Elinor Karlsson  
Tuuli Lappalainen  
Ben Lehner  
Nuria Lopez-Bigas  
Tomas Marques-Bonet  
Svante Pääbo  
Len Pennacchio  
Joseph K. Pickrell  
Luis Quintana-Murci  
Heidi Rehm  
Jonathan Sebat  
Michael Snyder  
Nicole Soranzo  
Sarah A. Tishkoff  
Peter M. Visscher\*  
Cisca Wijmenga

\*Keynote Speaker

Organized in collaboration with:

*Knut och Alice  
Wallenbergs  
Stiftelse*

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To view the full program, please visit  
[www.keystonesymposia.org/16K1](http://www.keystonesymposia.org/16K1).

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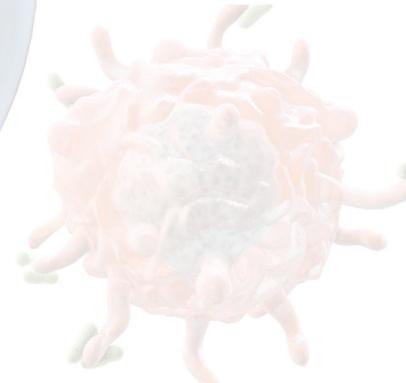
All The Cancer Genome Atlas data and more than \$1,000,000 in funding is available to support your compute and data storage on the system.



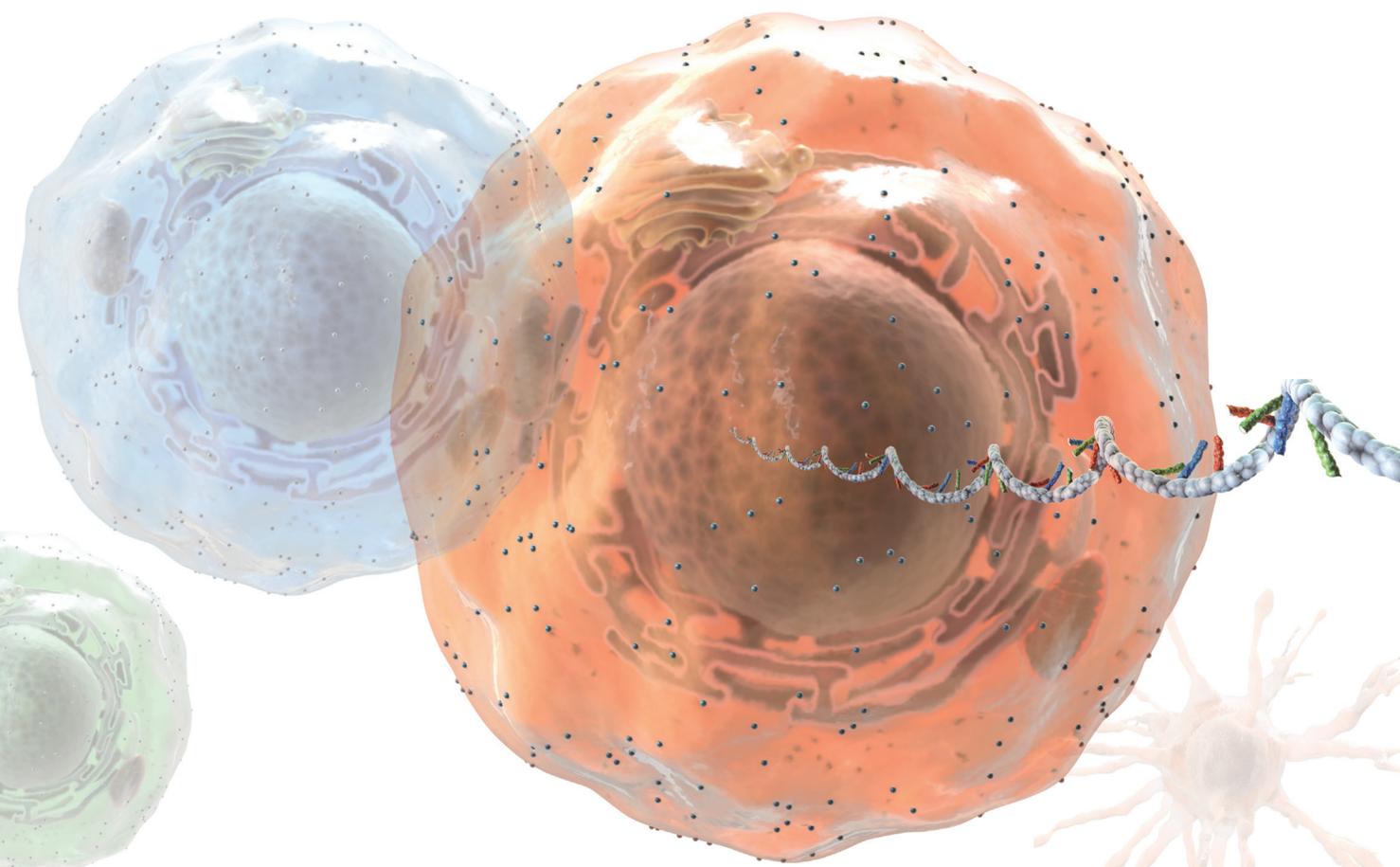
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