

Forefront of Gene Therapy Manufacturing

FROM BENCH TO BEDSIDE



AFFORDABLE

Providing low-cost, high-quality vectors for use in cells, small/large animal models and in the clinic. Scalable proprietary transfection process, providing the benefit of higher cost-effectiveness.



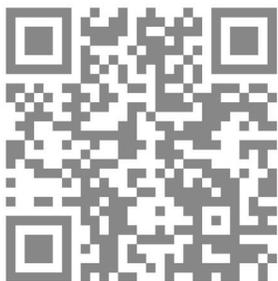
RESEARCH TOOLS

High Titer, High Purity. Rapid turn around times. Additional research tools include AAV Biosensors - GCaMP, RCaMP, CaMPARI, jRGECO1; ORF clones, ZIKA, viral controls.



PRE-CLINICAL/CLINICAL

Providing custom, on-demand virus for pre-clinical and clinical applications. Additional services: Master and Working cell banking, Aseptic filling, QC testing. Compliant with US FDA and EU EMA regulatory requirements.



Feature Viral Vector Application Note.

Discover the advantage of Vigene's viral-tools and technologies to help meet your basic, preclinical, and/or clinical application needs. Specializing in **AAV**, **Adenovirus** and **Lentivirus** gene delivery.

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APPLICATION NOTE

vigenebio.com/virus-manufacturing

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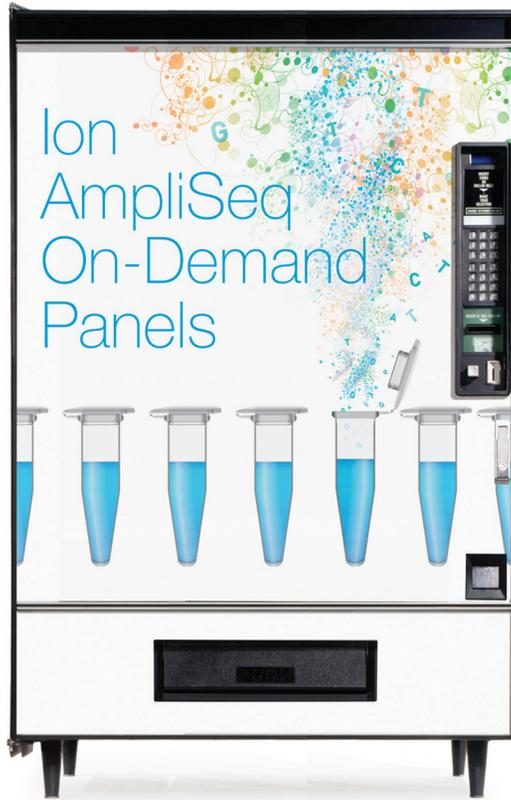
Compatible. No matter the sample.

A targeted sequencing solution that fits. Period. This revolutionary single-tube assay format is compatible with the most challenging and precious biological samples, including FFPE and cfDNA. Accel-Amplicon Custom NGS Panels generate highly multiplexed libraries for comprehensive coverage of critical hotspot SNVs, contiguous tiled regions in coding sequences, and intron-exon boundaries. And it is compatible with your existing Illumina® and Ion Torrent™ sequencing platforms.

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KN2.0 is the 2nd generation gene knockout kit with non-homology mediated efficiency and GFP puro selection. The vast majority of gene knockout is bi-allelic.

- High Knockout Efficiency
- Non-homology Mediated
- GFP-puro Selection

Kit Components Include:

- 2 guide RNA vectors to ensure efficient cleavage
- Donor cassette: EF1a-GFP-P2A-Puro



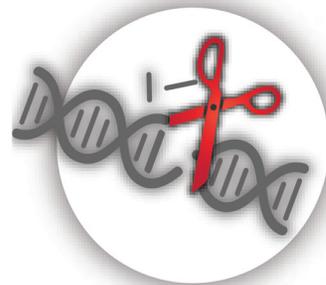
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Custom Oligonucleotides

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- ◆ Taqman probes
- ◆ Molecular beacon
- ◆ Oligo pool & microarray

Custom Peptide Synthesis

- ◆ Purities from desalt to 98%
- ◆ Acetylation/Amidation
- ◆ Phosphorylated peptides
- ◆ Fluorescein/Biotin labeled peptides
- ◆ Specialty peptides with unnatural amino acids
- ◆ Cyclic peptides
- ◆ KLH/BSA/OVA Conjugation
- ◆ Multiple Antigenic Peptides
- ◆ Peptide nucleic acid (PNA)



Programmable Nucleases

Purified, recombinant proteins for genome editing applications

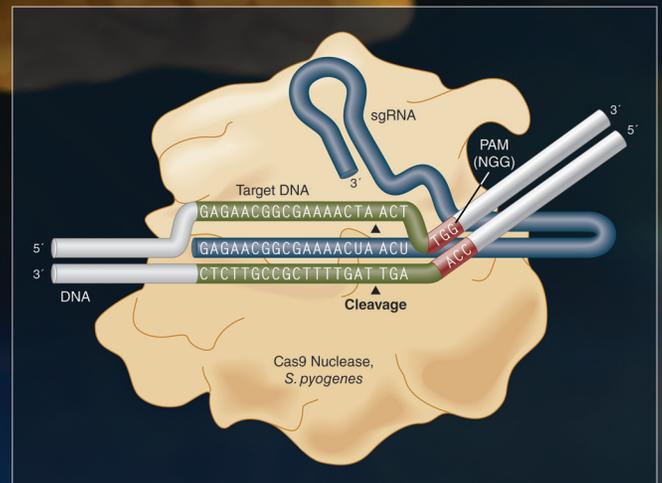
Cas nucleases, key proteins involved in CRISPR/Cas genome editing, are now available from New England Biolabs®. These Cas nucleases expand the portfolio of products from NEB® that support CRISPR workflows, including sgRNA cloning, transcription and HDR template construction.

Download our Genome Editing Brochure at www.neb.com/GenomeEditing

NOW AVAILABLE:

EnGen® Spy Cas9 Nickase, EnGen Spy dCas9 (SNAP-tag®) and EnGen Lba Cas12a (Cpf1)

Schematic representation of Cas9 Nuclease, *S. pyogenes* sequence recognition and DNA cleavage



Custom PNA Synthesis

PNA (Peptide Nucleic Acid) is an artificially synthesized polymer similar to DNA or RNA. The various purine and pyrimidine bases are linked to the backbone by methylene carbonyl bonds as in peptides. Since PNA contains no charged phosphate groups, the binding between PNA and DNA is stronger than that between DNA and DNA due to the lack of electrostatic repulsion. PNA is resistant to DNases and proteases, and is extremely stable in vivo as well as in vitro.

PNA Applications

- ◎ Sequence specific PCR blocker (PNA clamp)
- ◎ FISH probes for telomere, centromere, gene specific probes, infection test
- ◎ Anti-sense/ anti-microbial reagents
- ◎ miRNA inhibitors
- ◎ Double strand DNA invasion & capture
- ◎ Microarray probes



PNA Order

- ◎ The price of custom oligo is dependent on the length, amount and label
- ◎ HPLC and MALDI-TOF data will be provided
- ◎ Synthesis scales: 50 nmole, 100 nmole, and 200 nmole
- ◎ Purity: >90%, and >95%
- ◎ Turn-around: 2~3 weeks for the most cases





GO EXPONENTIAL

Accelerate the pace of discovery with the power of Linked-Reads

In a world of incremental improvements, true breakthroughs are born from massive leaps forward. The genomics community is not about shifting paradigms but shattering them. With Linked-Read sequencing data, we can achieve a comprehensive understanding of genomic variation. Power your next discovery with Chromium™ Solutions that uncover the genome and exome data you've been missing. Now, you can resolve ambiguous single nucleotide variants, obtain phasing and haplotype information, identify structural variants, and assemble genomes without breaking a sweat.

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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.

Echo acoustic liquid handling allows...

- ▶ 100-fold reduction of library prep reaction volumes
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- ▶ Increased sample throughput
- ▶ 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	0.06 - 2.0 ng
DNA volume (Rxn)	25 µL	200 nL
Library prep volume (Rxn)	25 µL	300 nL
Total volume	50 µL	0.5 µL
Reactions per kit	96	9600
Cost per reaction	\$72.91	\$0.73

For more information, visit 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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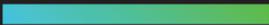
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Introducing



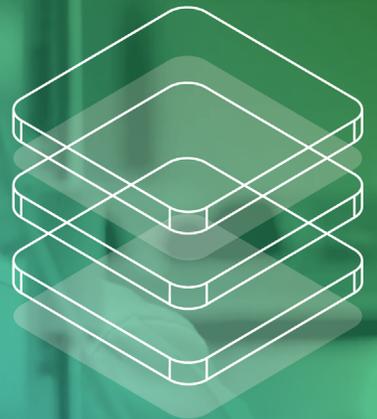
Engineered Cells



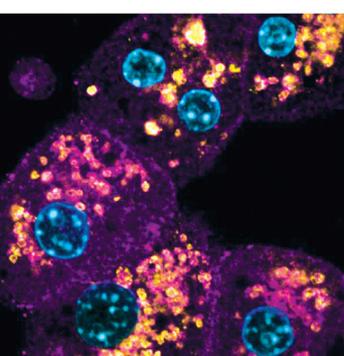
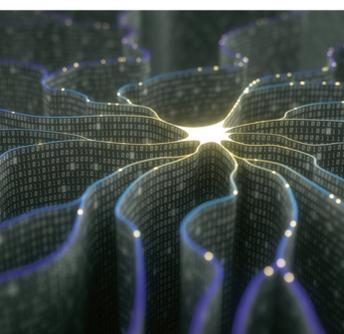
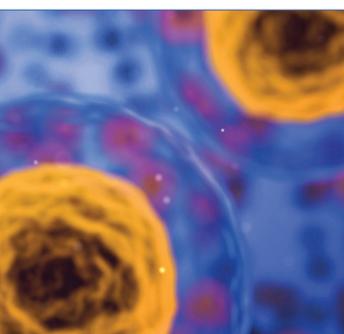
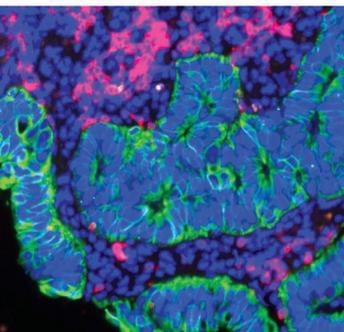
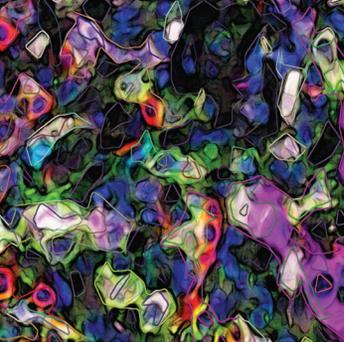
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2018 SCIENTIFIC CONFERENCES

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

12th Biennial Ovarian Cancer Research Symposium

Conference Cochairs: Frances R. Balkwill, Mary L. (Nora) Disis, Pamela S. Ohashi, and Elizabeth M. Swisher
September 13-15, 2018 | Seattle, WA

Pancreatic Cancer: Advances in Science and Clinical Care

Conference Cochairs: Ronald M. Evans, Manuel Hidalgo, Steven D. Leach, Gloria M. Petersen, and Brian M. Wolpin
September 21-24, 2018 | Boston, MA

Second AACR International Conference on Translational Cancer Medicine

Conference Cochairs: Carlos L. Arteaga, Carlos Gil M. Ferreira, and Gabriel A. Rabinovich
September 27-29, 2018 | São Paulo, Brazil

Intestinal Stem Cells and Colon Cancer: Biology to Therapy

Conference Cochairs: Anil K. Rustgi, Johanna Bendell, Hans Clevers, Christina Curtis, and Owen Sansom
September 27-30, 2018 | Washington, DC

Metabolism and Cancer

Conference Cochairs: Ralph J. Deberardinis, Tak W. Mak, Joshua D. Rabinowitz, and M. Celeste Simon
September 28-October 1, 2018 | New York, NY

Fourth CRI-CIMT-EATI-AACR International Cancer Immunotherapy Conference: Translating Science into Survival

Conference Cochairs: Nina Bhardwaj, Christoph Huber, Elizabeth M. Jaffee, and Guido Kroemer
September 30-October 3, 2018 | New York, NY

EACR-AACR-ISCR Conference: The Cutting Edge of Contemporary Cancer Research

Conference Cochairs: Richard M. Marais, Eli Pikarsky, and Robert A. Weinberg
October 9-11, 2018 | Jerusalem, Israel

30th Anniversary AACR Special Conference Convergence: Artificial Intelligence, Big Data and Prediction in Cancer

Conference Cochairs: Phillip A. Sharp and William C. Hahn
October 14-17, 2018 | Newport, RI

11th AACR Conference on The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved

Conference Cochairs: Ivis Febus-Sampayo, Laura Fejerman, Scarlett Lin Gomez, Augusto C. Ochoa, and Brian M. Rivers
November 2-5, 2018 | New Orleans, LA

EORTC-NCI-AACR Molecular Targets and Cancer Therapeutics Symposium

Scientific Committee Cochairs: Charles Swanton, James L. Gulley, and Antoni Ribas
November 13-16, 2018 | Dublin, Ireland

AACR-KCA Joint Conference on Precision Medicine in Solid Tumors

Program Committee Cochairs: Tae-You Kim and Charles L. Sawyers
November 15-17, 2018 | Seoul, South Korea

Tumor Immunology and Immunotherapy

Conference Cochairs: James P. Allison, Lisa M. Coussens, Ira Mellman, and Drew M. Pardoll
November 27-30, 2018 | Miami Beach, FL

Innovation and Biomarkers in Cancer Drug Development: A Joint Meeting Presented By EORTC, NCI, EMA, and AACR

Organizing Committee Chair: Denis A. Lacombe
November 29-30, 2018 | Brussels, Belgium

Targeting PI3K/mTOR Signaling

Conference Cochairs: Lewis C. Cantley, David M. Sabatini, and Jean J. Zhao
November 30-December 3, 2018 | Boston, MA

Learn more and register at
AACR.org/Calendar

AACR American Association
for Cancer Research®

FINDING CURES TOGETHER®

EMBL 2019 PREVIEW

Courses and Conferences

JANUARY

- 14 – 18 Jan • EMBL Course
Advanced Training with Oxford Nanopore Technologies
- 21 – 25 Jan • EMBL Course
Bioinformatics for Discovery
- 29 – 31 Jan • EMBL Course
Data Carpentry

FEBRUARY

- 3 – 8 Feb • EMBL Course
Analysis and Integration of Transcriptome and Proteome Data
- 4 – 8 Feb • EMBL Course
Metabolomics Bioinformatics for Life Scientists
- 6 – 8 Feb • EMBL Industry Workshop
Cryo-EM in Industry and Academia
- 11 – 15 Feb • EMBL Course
Introduction to Multiomics Data Integration
- 26 – 28 Feb • EMBL Course
Bioinformatics Resources for Protein Biology

MARCH

- 4 – 8 Mar • EMBL Course
Single-Cell Immunology
- 7 – 9 Mar • EMBL–Wellcome Genome Campus Conference
Proteomics in Cell Biology and Disease Mechanisms
- 11 – 15 Mar • EMBL Course
Target Engagement in Biology and Drug Discovery
- 13 – 15 Mar • EMBO Workshop
Visualizing Biological Data (VIZBI 2019)
- 17 – 20 Mar • EMBO | EMBL Symposium
Synthetic Morphogenesis: From Gene Circuits to Tissue Architecture
- 17 – 22 Mar • EMBL Course
Genome Engineering: CRISPR/Cas
- 19 – 20 Mar • EMBL Course
Exploring Human Genetic Variation
- 25 – 29 Mar • EMBL Course
Optogenetics: From Design to Cell Signalling to Tissue Morphogenesis
- 25 – 29 Mar • EMBL Course
Introduction to Metabolomics Analysis
- 27 – 28 Mar • EMBL Course
Transgenic Animals - Micromanipulation Techniques
- 31 Mar – 3 Apr • EMBO | EMBL Symposium
Reconstructing the Human Past - Using Ancient and Modern Genomics
- 31 Mar – 5 Apr • EMBL Course
Techniques for Mammary Gland Research

APRIL

- 1 – 5 Apr • EMBL Course
Statistical Methods in Bioinformatics with R/Bioconductor
- 1 – 5 Apr • EMBL Course
Introduction to Next Generation Sequencing
- 7 – 12 Apr • EMBO Practical Course
High-Accuracy CLEM: Applications at Room Temperature and *in Cryo*
- 8 – 12 Apr • EMBL Course
Advanced RNA-Seq Analysis
- 10 – 13 Apr • EMBO | EMBL Symposium
Probing Neural Dynamics with Behavioural Genetics

MAY

- 1 – 4 May • EMBO Workshop
Chromatin and Epigenetics
- 2 – 4 May • EMBL Course
Techniques for Studying Iron in Health and Disease
- 5 – 10 May • EMBL Conference
8th Congress of the International Biolron Society
- 5 – 10 May • EMBL Course
Quantitative Proteomics: Strategies and Tools to Probe Biology
- 12 – 18 May • EMBL Course
Single-Cell Omics
- 13 – 17 May • EMBL Course
Fundamentals of Widefield and Confocal Microscopy and Imaging
- 13 – 17 May • EMBL Course
Networks and Pathways
- 13 – 24 May • EMBL Course
Computational Molecular Evolution
- 15 – 18 May • EMBO | EMBL Symposium
The Identity and Evolution of Cell Types
- 19 – 24 May • EMBL Course
Advanced Fluorescence Imaging Techniques
- 28 – 30 May • EMBL Conference
BioMalPar XV: Biology and Pathology of the Malaria Parasite

JUNE

- 2 – 8 Jun • EMBL Course
Extracellular Vesicles: From Biology to Biomedical Applications
- 3 – 4 Jun • EMBL Conference
Biological Solutions for the Global CO₂ Challenge
- 3 – 7 Jun • EMBL Course
Whole Transcriptome Data Analysis
- 4 – 6 Jun • EMBL Course
Managing a Bioinformatics Core Facility
- 4 – 6 Jun • EMBL Course
Bioinformatics for Principal Investigators
- 10 – 14 Jun • EMBL Course
Metagenomics Bioinformatics
- 12 – 19 Jun • EMBL Course
Microbial Metagenomics: A 360° Approach
- 17 – 21 Jun • EMBL Course
Cancer Genomics
- 24 – 28 Jun • EMBL Course
Summer School in Bioinformatics
- 30 Jun – 5 Jul • EMBL Course
Proteomics Bioinformatics

JULY

- 1 – 5 Jul • EMBL Course
Shift Your DNA and RNA Sequencing Library Preparation into Hyper-Drive
- 2 – 4 Jul • EMBL Course
Micromanipulation in Zebrafish & Medaka: From Transgenesis to CRISPR
- 3 – 6 Jul • EMBO | EMBL Symposium
Mechanical Forces in Development
- 7 – 12 Jul • EMBL Course
Super-Resolution Microscopy
- 7 – 12 Jul • EMBL Course
***In Silico* Systems Biology**
- 9 – 12 Jul • EMBO | EMBL Symposium
New Approaches and Concepts in Microbiology
- 15 – 19 Jul • EMBL Course
Bioinformatics Resources for Immunologists
- 29 Jul – 2 Aug • EMBL Course
Hands-On Flow Cytometry - Learning by Doing!

SEPTEMBER

- 1 – 6 Sep • EMBL Course
Chromatin Signatures During Differentiation: Integrated Omics Approaches to Neuronal Development
- 4 – 7 Sep • EMBL Conference
Protein Synthesis and Translational Control
- 8 – 17 Sep • EMBO Practical Course
Current Methods in Cell Biology
- 11 – 13 Sep • EMBO | EMBL Symposium
Multionics to Mechanisms - Challenges in Data Integration
- 14 – 22 Sep • EMBO Practical Course
Synthetic Biology in Action: Bridging Natural/Non-Natural
- 16 – 20 Sep • EMBL Course
Structural Bioinformatics
- 22 – 25 Sep • EMBO Workshop
Creating is Understanding: Synthetic Biology Masters Complexity
- 23 – 27 Sep • EMBL Course
Introduction to Next Generation Sequencing
- 23 – 28 Sep • EMBL Course
Liquid Biopsies
- 29 Sep – 2 Oct • EMBO | EMBL Symposium
Systems Genetics: From Genomes to Complex Traits
- 30 Sep – 4 Oct • EMBL Course
Whole Transcriptome Data Analysis

OCTOBER

- 7 – 9 Oct • EMBL Conference (Hamburg)
Tools for Structural Biology of Membrane Proteins
- 8 – 10 Oct • EMBL Course
Exploring Biological Sequences
- 9 – 12 Oct • EMBO | EMBL Symposium
Seeing is Believing – Imaging the Molecular Processes of Life
- 16 – 18 Oct • EMBL Course
Computing Skills For Reproducible Research: Software Carpentry
- 16 – 19 Oct • EMBO | EMBL Symposium
The Non-Coding Genome
- 21 – 25 Oct • EMBL Course
Analysis of High-Throughput Sequencing Data
- 24 – 25 Oct • EMBL Science and Society Conference
Science as Storytelling: From Facts to Fictions
- 29 – 30 Oct • EMBL Course
Micromanipulation into Adherent Cells

NOVEMBER

- 3 – 8 Nov • EMBL Course
Humanized Mice in Biomedical Research: Challenges and Innovations
- 4 – 7 Nov • EMBL Conference
Cancer Genomics
- 11 – 15 Nov • EMBO Practical Course
The Fundamentals of High-End Cell Sorting
- 14 – 16 Nov • EMBL Conference
Precision Health: Molecular Basis, Technology and Digital Health
- 17 – 22 Nov • EMBL Course
Circular RNAs
- 20 – 23 Nov • EMBO | EMBL Symposium
Metabolism Meets Epigenetics
- 28 – 30 Nov • EMBL Conference
21st EMBL PhD Symposium

DECEMBER

- 1 – 7 Dec • EMBL Course
Measuring Translational Dynamics by Ribosomal Profiling
- 8 – 10 Dec • EMBL–Wellcome Genome Campus Conference
Target Validation Using Genomics and Informatics

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ASSOCIATE PARTNERS:

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CONFERENCES are held at the EMBL Advanced Training Centre Heidelberg, Germany (unless indicated otherwise)

COURSE LOCATIONS: Heidelberg | Hinxton

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EMBL



30th Anniversary AACR Special Conference

CONVERGENCE: ARTIFICIAL INTELLIGENCE, BIG DATA AND PREDICTION IN CANCER

October 14-17, 2018 | Newport Marriott | Newport, RI

Register Online or Onsite!

CONFERENCE COCHAIRS



Phillip A. Sharp

David H. Koch Institute for Integrative Cancer Research at MIT, Cambridge, MA



William C. Hahn

Dana-Farber Cancer Institute, Boston, MA

ABOUT THIS CONFERENCE

Information technologies have transformed many aspects of society, but to date they have had a modest impact on diagnosis, prevention, or treatment of cancer. One of the first points of intersection of information technologies on advancing the understanding and control of cancer is the ability to predict the development, progression, and malignancy of the disease in both populations and individuals. New, transformative technologies are emerging that collect large sets of high-resolution data at levels of single molecules, single cells, specific tissues, organisms, and populations.

Extracting insights from these big data sets requires development of new methods in information technologies and machine learning and new concepts. It is this interface of cancer biology, computation, and clinical oncology that will most likely produce the future breakthroughs in control of cancer. This AACR Special Conference will cover the state of the art in understanding the disease of cancer from incident to early diagnosis, prevention, and treatment, with an emphasis on approaches that use big data and new computational methods such as machine learning.

Learn more and register at
AACR.org/AIBDP18

#AACR30SC18



American Association
for Cancer Research®

FINDING CURES TOGETHER®

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VENUE: LUISENSTR. 58/59
POSTER RECEPTION: HANNOVERSCHE STR. 28

11TH **BERLIN LATE
SUMMER MEETING**
OCTOBER 25 - 27, 2018
COMPUTATIONAL AND EXPERIMENTAL
MOLECULAR BIOLOGY MEET

CONFIRMED SPEAKERS

Ido Amit
Weizmann Institute of Science, Rehovot, Israel

Hans Clevers
Hubrecht Institute, Utrecht, the Netherlands

Patrick Cramer
MPI for Biophysical Chemistry, Göttingen, Germany

Claude Desplan
NYU Biology, New York, USA

Amanda Fisher
MRC LMS, London, UK

Eileen Furlong
EMBL, Heidelberg, Germany

Edith Heard
Institut Curie, Paris, France

Jürgen Knoblich
IMBA, Vienna, Austria

Ruth Lehmann
NYU School of Medicine, New York, USA

Mike Levine
Princeton University, Princeton, USA

Peter Lichter
DKFZ, Heidelberg, Germany

Christiane Nüsslein-Volhard
MPI for Developmental Biology, Tübingen, Germany

Lior Pachter
Caltech, Pasadena, USA

Bing Ren
UCSD School of Medicine, San Diego, USA

Phil Sharp
MIT, Cambridge, USA

Charles Swanton
The Francis Crick Institute, London, UK

SCIENTIFIC COMMITTEE

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CONTACT

Irena Perko Radulovic
irena.perkoradulovic@mdc-berlin.de
+49 30 9406 3034

Verena Maier
verena.maier@mdc-berlin.de
+49 30 9406 3076

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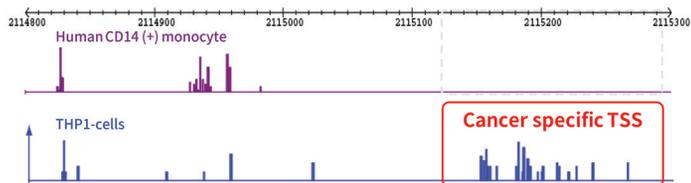




Promoter / Enhancer Annotation in the NGS era

Cap Analysis of Gene Expression (CAGE) is a new NGS library preparation method using “cap-trapping” technology which enables you to detect precise **transcription start site (TSS)** of RNA pol II transcripts including **mRNAs**, **lincRNAs** and **enhancer RNAs** and to quantify their expression accurately.

- **Accurate promoter annotation** — reliable estimation of promoter positions and their activities based on precise TSS information
- **Estimation of transcription factor binding sites** — search transcription factor binding motif around TSS which have different expression profiles among samples
- **Detection of active enhancers** — identify active enhancers by detection of bidirectional enhancer RNAs
- **Development of new biomarkers** — TSS variants are valuable candidate of biomarkers even in the case that there are no difference at the gene expression level
- **Accurate quantification of gene expression** — PCR-free library preparation process without fragmentation allow for more reliable quantification of gene expression than RNA-seq



CAGE expression pattern of a histone H3 methyltransferase gene of human CD14(+) monocytes and THP-1 leukemia monocytic cells.

CAGE library preparation & analysis services

Library preparation for Illumina sequencers	500 USD/sample
Sequencing (Illumina HiSeq/ NextSeq)	250 USD/sample
Bioinformatics analysis	250 USD/sample

CAGE library preparation kit

8 samples (Cat. 52003-8)	2,000 USD
48 samples (Cat. 52003-48)	10,000 USD

More than 250 papers using CAGE have been published!
Learn more at cage-seq.com

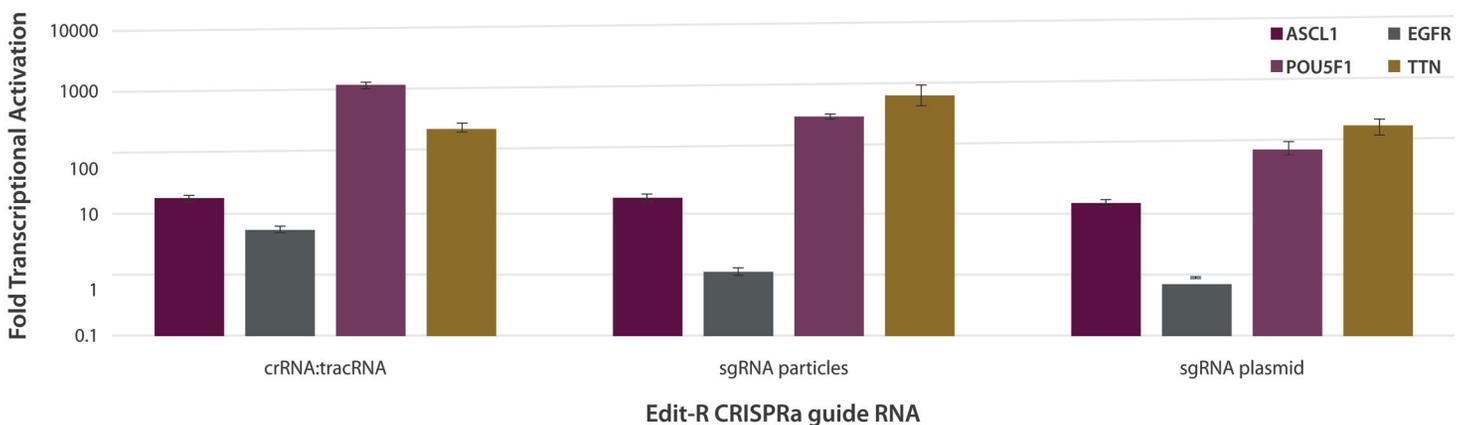


Powerful next-generation gene activation with Edit-R™ CRISPRa reagents

Increase target gene expression in your cell lines with Dharmacon Edit-R CRISPR activation (CRISPRa) reagents. From one gene up to the whole human genome, our reagents make gain-of-function studies easy and efficient.

Synthetic crRNA | Lentiviral sgRNA | Arrayed libraries

All Edit-R CRISPRa guide RNA formats provide effective target gene activation



U2OS cells stably expressing integrated Edit-R dCas9-VPR were treated with three formats of Edit-R CRISPRa guide RNAs: synthetic crRNA:tracrRNA, lentiviral sgRNA particles, or sgRNA plasmid, each targeting ASCL1, EGFR, POU5F1, or TTN genes. Relative gene expression was calculated using qRT-PCR.