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-clinincal and clinical applications. Additional services: Master and Working cell banking, Aseptic filling, QC testing. Compliant with US FDA and EU EMA regulatory requirements.

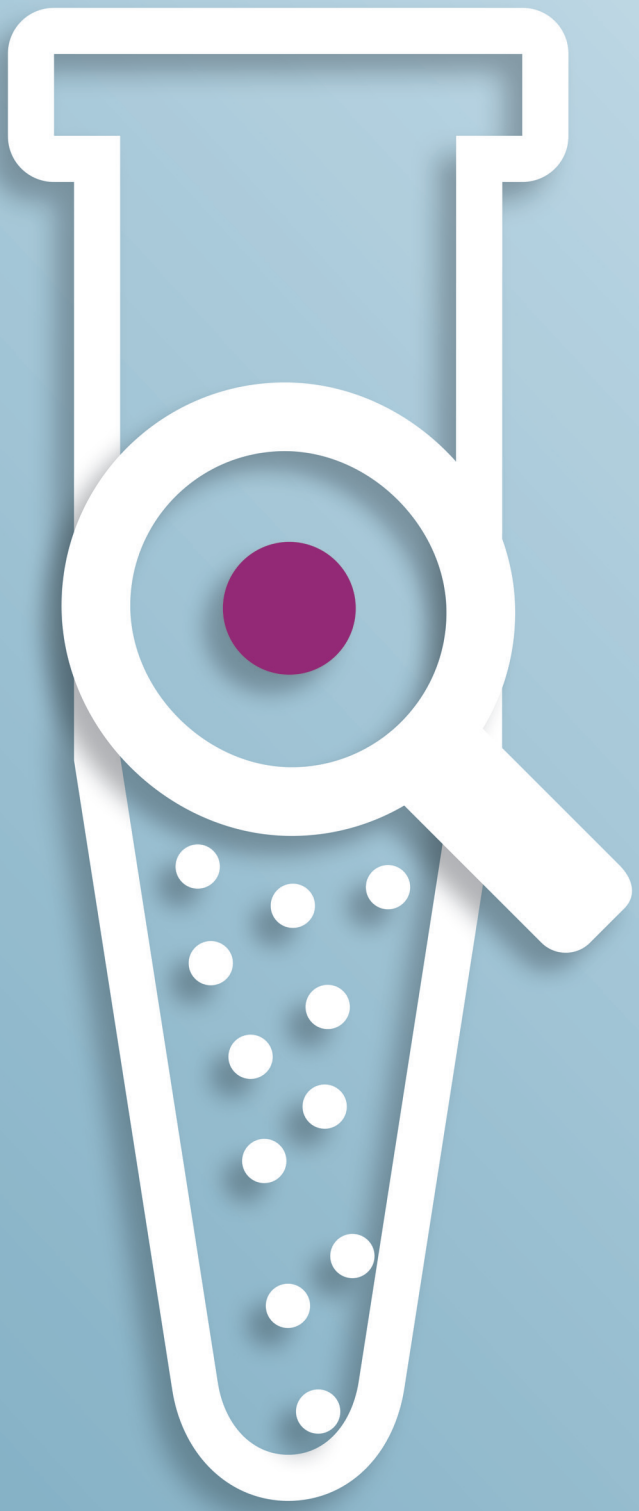
Feature Viral Vector Application Note.

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.

DOWNLOAD FREE APPLICATION NOTE **vigenebio.com/virus-manufacturing**

Vigene Biosciences
Excellence in Gene Delivery

1-800-485-5808
vigenegmp.com
vigenebio.com



More data. One reaction.

Totally on-target assay design. The most intelligent targeted sequencing assay design ever. With comprehensive coverage of critical hotspot SNVs, contiguous tiled regions in coding sequences, and intron-exon boundaries in a revolutionary fast, simple, single-tube workflow, characterization and screening of your targets of interest is finally within reach. And on-target.

Accel-Amplicon™ Custom NGS Panels

Swift BIOSCIENCES™

swiftbiosci.com

ion torrent

Gene panels on demand, how and when you want them

Ion AmpliSeq On-Demand Panels help you get more from targeted next-generation sequencing

- **Now more selection**—build custom panels from a growing catalog of **over 5,000 pretested genes** most relevant in inherited disease research*
- **Now more sizes**—order the exact quantity you need: 8, 24, 32, and 96 reactions per pack

With practical pack sizes that help lower up-front cost, and a powerful content selection engine that automates optimal gene selection, Ion AmpliSeq™ On-Demand Panels help you do targeted sequencing in your own lab, your own way.

Do targeted sequencing your way at **ampliseq.com**

Learn more at **thermofisher.com/ampliseqondemand**

ThermoFisher SCIENTIFIC

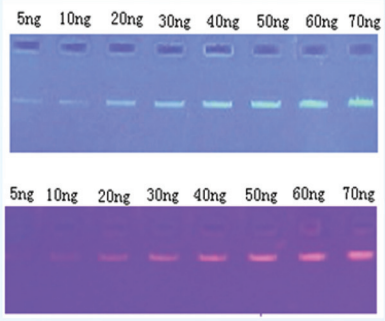
SBS Genetech Co., Ltd.

GoodView™ Nucleic Acid Stain

——An alternative to EB

GoodView™ is a new nucleic acid stain, an alternative to the traditional ethidium bromide (EB) stain for detecting nucleic acid in agarose gels. It emits green fluorescence when bound to DNA or RNA. This new stain has two fluorescence excitation maxima when bound to nucleic acid, one centered at 268 nm and another at 294 nm. In addition, it has one visible excitation at 491 nm. The Fluorescence emission of GoodView™ bound to DNA is centered at 530 nm.

Comparative sensitivity test of GV and EB



Sensitivity test result of GV at UV 300nm.

Sensitivity test result of EB at UV 300nm.

The result of electrophoresis demonstrates GV is almost as sensitive as EB.

The Test Report from Institute for Environmental Health and Related Product Safety of Chinese Center for Disease Control and Prevention concludes that:

- Acute Oral Toxicity Test: GoodView™ Nucleic Acid Stain belongs to nontoxic.
- Mouse Marrow Chromophilous Erythrocyte Micronucleus Test: Negative. There is no significant difference in the incidence of micronuclei between test and control groups.
- Ames Test: Negative. No mutagenicity was observed.
- In Vitro Mammalian Cell Chromosome Aberration Test: Negative. No increasing aberration rate was observed.

The test report is available upon request.

Beijing SBS Genetech Co. , Ltd.
Fax: +86-10-82784290
Email: order@sbsbio.com Website: www.sbsbio.com

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.

Biology is challenging. Research is a race. Get there faster.
Learn more at **go.10xgenomics.com/linked-reads**

10x GENOMICS®

arbor biosciences

Experts in Targeted Sequencing

INTRODUCING
v4 Chemistry & Streptavidin Beads Included in Kit

myBaits®

TARGETED SEQUENCING KITS

- Complimentary Probe Design Service
- Compatible with Any NGS Library Prep
- Predesigned Kits for Immediate Shipment
- Custom Kits for Unique Organisms

myReads®

NGS SERVICES FOR TARGETED SEQUENCING

- Experimental Design Services
- Project Management by Dedicated Scientists
- Best-in-Class Library Preparation and Enrichment
- Sequencing on Illumina® and PacBio®

ArborBiosci.com | info@arborbiosci.com | +1 734-998-0751 | *Follow us on Twitter:* @ArborBio

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.

Echo acoustic liquid handling allows...

- 100-fold reduction of library prep reaction volumes
- 30-fold reduction of sample pooling turnaround time
- 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*

LABCYTE™
The Future of Science is Sound

@LabcyteInc
info-us@labcyte.com

Challenges with structural variant detection?

...How about from FFPE?

Dovetail's technologies are redefining structural variation.

Learn more at **dovetailgenomics.com/gr/**

It's a new transfection reagent, not just another one

Helix-IN™
DNA Transfection Reagent

OZ Biosciences revolutionizes polymer-based transfection with the design of a novel patented **C**ationic **H**ydroxylated **A**mphiphilic **M**ulti-block **P**olymer (*CHAMP™* Technology).

Helix-IN™ reagent, biocompatible & biodegradable, opens up new possibilities for addressing issues of classical transfection technologies.

Preserve Viability, Reduce Cellular Stress & Experience High Efficiency

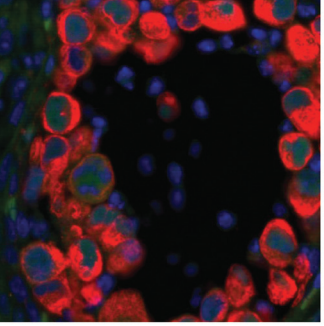
REQUEST FREE SAMPLE

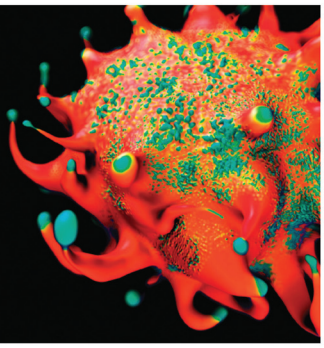
Limited-time offer - use code JDV

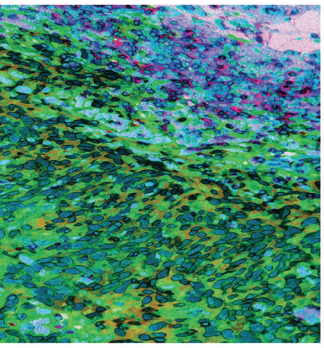
contact@ozbiosciences.com

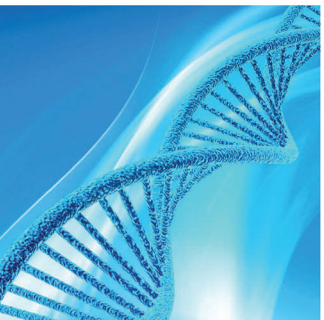
OZBIOSCIENCES
The art of delivery systems


SYNTHEGO
High Efficiency Chemically Modified Synthetic sgRNA for CRISPR
Essential for CRISPR Editing in Primary, Stem Cells, Therapeutic Applications and Challenging Cell Lines.
synthego.com/cshl









2018 SCIENTIFIC CONFERENCES

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

Cancer Dormancy and Residual Disease
Conference Cochairs: Julio A. Aguirre-Ghiso, Ann F. Chambers, Cyrus M. Ghajar, Christoph A. Klein, and Dorothy A. Sipkins
June 19-22, 2018 | Montreal, QC, Canada

Inaugural AACR International Meeting on Advances in Malignant Lymphoma: Maximizing the Basic-Translational Interface for Clinical Application
Scientific Committee Chair: Ari M. Melnick
June 22-26, 2018 | Boston, MA

Sixth JCA-AACR Special Joint Conference on the Latest Advances in Lung Cancer Research: From Basic Science to Therapeutics
Organizing Committee: Hiroyuki Mano, Seiji Yano, Hiroyoshi Nishikawa, Alice T. Shaw, Roy S. Herbst, and Charles M. Rudin
July 10-12, 2018 | Kyoto, Japan

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
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: Systems Biology and Physical Sciences in Oncology
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: Laura Fejerman, Scarlett Lin Gomez, Augusto C. Ochoa, Brian M. Rivers, and Ivis Sampayo
November 2-5, 2018 | New Orleans, LA

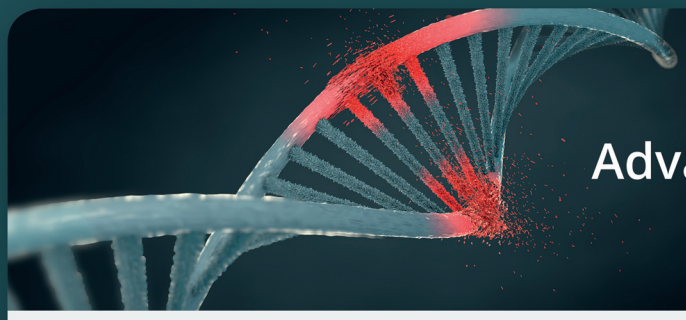
EORTC-NCI-AACR Molecular Targets and Cancer Therapeutics Symposium
Scientific Committee Cochairs: Charles Swanton, James L. Gulley, and Antoni Ribas
November 13-16, 2018 | Dublin, Ireland

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

Learn more and register at
AACR.org/Calendar

AACR American Association for Cancer Research®
FINDING CURES TOGETHER®



2nd Annual

Advances in Transgenic Technology

USA Congress

Taking place over 10 - 11 May at the Hyatt Regency Boston, the congress and co-located events will bring together over 250 delegates to discuss the latest developments and trends in transgenic technology and genome editing. Alongside innovative case studies of translational applications using animal models such as rats, fish, pigs and cattle, there is a dedicated stream on the challenges of improving in-vivo CRISPR genome editing.

UNMISSABLE PRESENTATIONS FROM

Genome Project Write: Highly Multiplexed – 20 To 400,000 Changes

GEORGE CHURCH

Professor of Genetics, Health Sciences and Technology, Wyss Institute at Harvard University

Biomedical Applications of Genome Editing in Large Animals

PERRY HACKETT

Professor, Department of Genetics, Cell Biology, and Development, University of Minnesota

How to Improve Efficiency of CRISPR in Creating Mouse Models

GHASSAN YEHIA

Scientific Director, Genome Editing Core Facility, Rutgers Cancer Institute of New Jersey

WHY ATTEND THIS CONGRESS?

- **Gain an in-depth industry perspective** on translational applications using animal models
- **Evaluate the challenges** of regulating specificity in in-vivo CRISPR genome editing
- **Benefit from dedicated networking opportunities** to engage in scientific discussion
- **Learn more about transgenic models** of disease and therapeutic applications
- **Hear case studies** on transgenic models of oncology, cardiovascular disease and metabolic disorders
- **Discuss the future** of transgenic technologies including large animal transgenic models
- **Access over 45 talks** at the co-located Genome Editing USA Congress and Synthetic Biology USA Congress

Download the agenda at: www.genomeeditingusa-congress.com/request-prices-agenda-transgenic-usa/

REGISTER FOR OUR COMPLIMENARY WEBINAR

Latest CRISPR Genome Editing and Therapeutic Applications of Mouse and Rat Models

Presented by CHENGYU LIU, Core Director, Transgenic Core, National Heart, Lung, and Blood Institute and SHANRONG ZHAO, Director, Computational Biology and Bioinformatics, Pfizer

- Comparison of CRIPSR/Cas9 with competing technologies
- Large scale analyses of on-target mutations generated by microinjecting Cas9 mRNA & sgRNAs
- Concerns about off-target mutations in mice created by CRISPR/Cas9
- Introduction to ZSF1 model, a model of human type 2 diabetes
- Identification of disease progressive markers from RNA-seq
- Scientific Insights gained from computational analysis of alternative splicing

Register your interest online at: www.genomeeditingusa-congress.com/2018-free-webinar-recordings/

For further information

Contact Danielle at d.dalby@oxfordglobal.co.uk or visit www.genomeeditingusa-congress.com

OXFORD GLOBAL CONFERENCES

CAGE

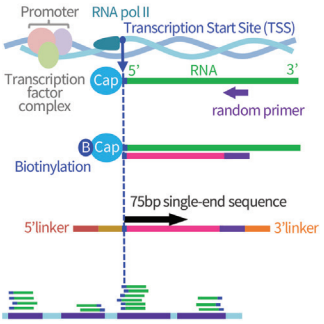
5’-RNA sequence service/kit

New approach for genome-wide promoter identification and gene expression profiling

A unique transcriptome analysis which quantify all RNA Polymerase II transcripts

Cap Analysis of Gene Expression (CAGE) utilizes “cap-trapping” technology to capture the 5’ cap of all RNA polymerase II transcripts. Through high volume parallel sequencing of cDNA corresponding to 5’-end of RNA and analysis of the sequenced tags, Transcription Start Sites (TSS) and transcript amount are inferred on a genome-wide scale (Fig. 1).

CAGE allows transcriptional network analysis and transcriptome characterization.



1. cDNA synthesis using random primers
2. Biotinylation of 5’ cap of RNA and trapping by streptavidin
3. Strand specific RNA library preparation and sequencing
4. Map all the reads on the reference genome and count reads for each gene

Figure 1. Overview of CAGE.

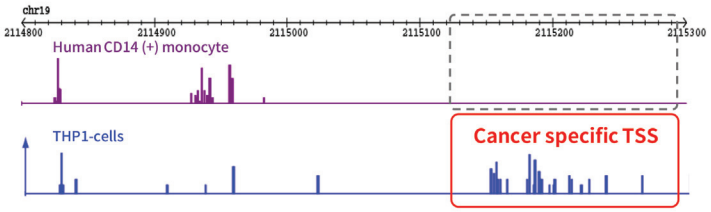


Figure 2. CAGE expression pattern of a histone H3 methyltransferase gene of human CD14(+) monocytes (above) and THP-1 leukemia monocytic cells (below). CAGE detects TSS variants of mRNAs/ncRNAs, which vary in expression level and pattern depending on the type of cancer cells, diseased/normal organs. TSS variants are valuable candidate of biomarkers even in the case that there are no difference at the transcript level.

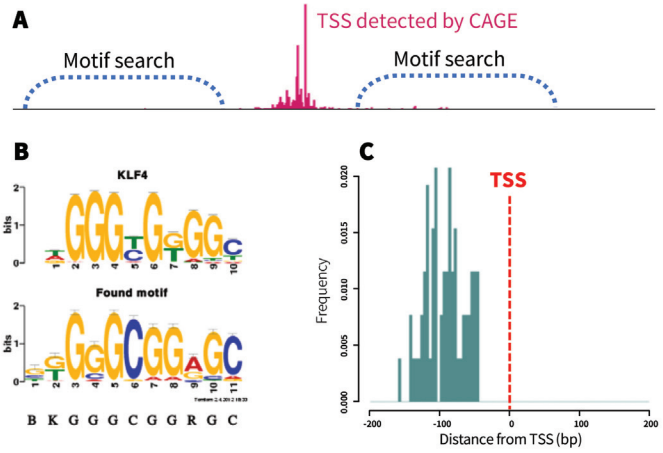


Figure 3. Exploration of transcription factor binding motifs based on TSS. **(A)** With CAGE, you can perform a genome-wide motif search around precise TSS positions which have different expression profiles depending on case and control. **(B)** Kruppel-like factor 4 (KLF4)-like binding motif discovered by a motif search based on CAGE and **(C)** distance distribution of motifs from TSS. In addition to a similar sequence, the positioning of the motif relative to TSS (100bp upstream of TSS) strongly suggests that KLF4 is involved in transcription of the motif because the motif position is consistent with the reported transcription pattern of KLF4.

Ordering information

CAGE library preparation & analysis services	
Library preparation [2]	500 USD/sample
Sequencing, andBioinformatics analysis	250 USD/sample each

CAGE library preparation Kit	
8 samples (Cat. 52003-8)	2,000 USD
48 samples (Cat. 52003-48)	10,000 USD

Representative papers using CAGE

1. Yoshida E, et al. *Sci. Rep.* 2017 Oct 26;7:14160.
2. Hon CC, et al. *Nature.* 2017 Mar 9;543(7644):199-204.
3. Arner E, et al. *Science.* 2015 Feb 27;347(6225):1010-4.
4. Dieterich LC, et al. *Cell Rep.* 2015 Nov 17;13(7):149
5. Fort A, et al. *Nat. Genet.* 2014 Jun 28;46:558-566.
6. Andersson R, et al. *Nature.* 2014 Mar 27;507(7493):455-61

Find out more at https://cage-seq.com/
contact@dnaform.jp

DNAFORM
Precision gene technologies

horizon
INSPIRED CELL SOLUTIONS

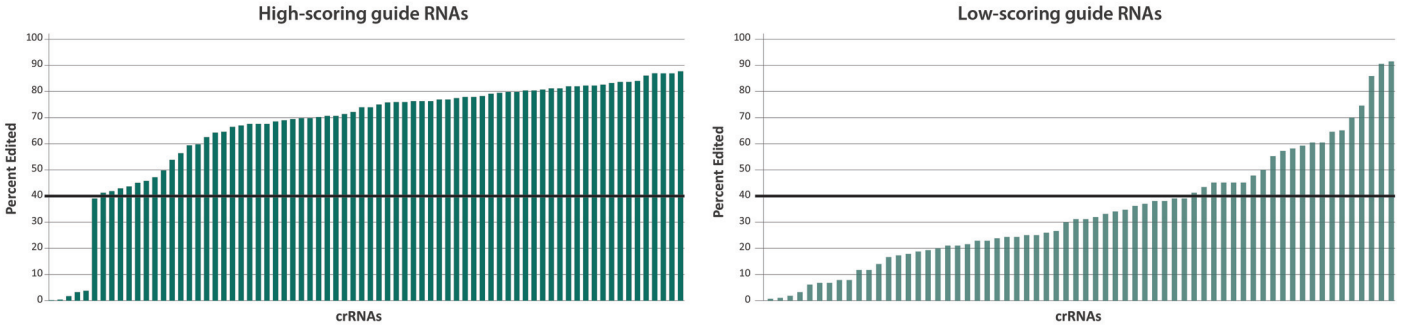
Dharmacon™ CRISPR reagents help you move forward. Faster.

Simplify your gene editing workflow with the Dharmacon™ Edit-R™ CRISPR-Cas9 platform. Custom or predesigned ready-to-use lentiviral and synthetic guide RNAs 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 µL/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.

dharmacon.com/CRISPR