Register Today!

Tenth Annual

Functional Genomics Screening Strategies

September 24 - 25, 2013

Part One: Utilizing RNA Interference (RNAi) Screens to Explore Drug Targets and Cellular Pathways

Session Topics:

- Where and How to Apply siRNA and shRNA Screens
- Exploring Diverse Applications
- Combining Use of RNAi and Other Technologies

September 25 - 26, 2013

Part Two: Exploring Novel Screening Platforms and Cellular Models for Next-Generation Screens

Session Topics:

- Synergistic Use of RNAi and Chemical Genomics Screens
- Use of 3D Cell Cultures for Functional Screening
- *In Vivo* RNAi Screening
- Stem Cell and Long Non-Coding RNA (lncRNA)-Based Screens

PART OF

11th Annual Discovery on TARGET

DiscoveryOnTarget.com

September 24 - 26, 2013

Westin Boston Waterfront
Boston, MA

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PLENARY KEYNOTE SPEAKERS

Towards a Patient-Based Drug Discovery

Stuart L. Schreiber, Ph.D., Director, Chemical Biology, Founding Member, Broad Institute of Harvard and MIT; Howard Hughes Medical Institute Investigator; Morris Loeb Professor of Chemistry and Chemical Biology, Harvard University

Enteroendocrine Drug Discovery for Treatment of Metabolic Diseases

Paul L. Feldman, Ph.D., Senior Vice President, GlaxoSmithKline

FEATURED PANELS:

PANEL DISCUSSION: Advanced RNAi Screening: Strengths, Caveats and Pitfalls at Reaching the 14-Year Milestone

Moderator: Christophe Echeverri, Ph.D., CEO & CSO, Cenix BioScience USA, Inc.

TECHNOLOGY PANEL: Tools for Next-Generation Functional Genomics Screens

Moderator: Christophe Echeverri, Ph.D., CEO & CSO, Cenix BioScience USA, Inc.

Organized by
CHI Cambridge Healthtech Institute

About the Functional Genomics Screening Event:

In the screening world there is definitely no one-size-fits-all and no dearth of options to choose from in terms of assay platforms, protocols, cells or reagents. So how do you decide which screening strategy will work best for you? Can different screening techniques be utilized in tandem or be staggered to better validate results and overcome inherent shortcomings? Which type of screen will provide information that is most accurate and physiologically relevant to your biological query? Cambridge Healthtech Institute's tenth annual conference on Functional Genomics Screening Strategies will cover the latest in the use of RNA interference (RNAi) screens, combination (RNAi and small molecule) screens, chemical genomics and phenotypic screens, for identifying and validating new drug targets and exploring unknown cellular pathways. The first half of the conference will focus on the design and use of RNAi screens, while the second half will explore the use of chemical genomics and long non-coding RNA (LncRNA) screens and the transition into advanced cellular models such as, 3D cell cultures and stem cells that will launch the next-generation of functional screens. Screening experts from pharma/biotech as well as from academic and government labs will share their experiences leveraging the utility of such diverse screening platforms and models for a wide range of applications.

Plenary Keynote Speakers

Towards a Patient-Based Drug Discovery

Stuart L. Schreiber, Ph.D., Director, Chemical Biology, Founding Member, Broad Institute of Harvard and MIT; Howard Hughes Medical Institute Investigator; Morris Loeb Professor of Chemistry and Chemical Biology, Harvard University

Enteroendocrine Drug Discovery for Treatment of Metabolic Diseases

Paul L. Feldman, Ph.D., Senior Vice President, GlaxoSmithKline

Recommended Short Courses*

MONDAY, SEPTEMBER 23 | 3:30 – 6:30 PM

SC6: Setting Up Effective RNAi Screens: Getting From Design to Data

Instructors:
Caroline Shamu, Ph.D., Director, ICCB-Longwood Screening Facility, Harvard Medical School
Eugen Buehler, Ph.D., Group Leader, Informatics, National Center for Advancing Translational Sciences, National Institutes of Health
John Doench, Ph.D., Research Scientist, Broad Institute of Harvard and MIT
Scott Martin, Ph.D., Team Leader, RNAi Screening, NIH Chemical Genomics Center, NIH Center for Translational Therapeutics, National Institutes for Health

WEDNESDAY, SEPTEMBER 25 | 6:45 – 9:30 PM

Dinner will be provided

SC9: Setting Up Effective Functional Screens Using 3D Cell Cultures

Instructors:
Geoffrey A. Bartholomeusz, Ph.D., Assistant Professor and Director, siRNA Core Facility, Department of Experimental Therapeutics, Division of Cancer Medicine, The University of Texas MD Anderson Cancer Center
Lesley Matthews, Ph.D., Research Scientist, Biomolecular Screening and Profiling/Probe Development Group, National Center for Advancing Translational Sciences, NIH
Additional Instructors to be Announced

**Separate Registration Required for Short Courses*

Conference-at-a-Glance

Mon. Sept. 23	**Pre-Conference Short Courses*** SC6: Setting Up Effective RNAi Screens					
Tues. Sept. 24	Targeting Epigenetic Readers	Targeting Histone Methyltransferases	GPCR-Based Drug Discovery	Functional Genomics Screening Strategies – Part 1	Novel Strategies for Kinase Inhibitors	Antibodies Against Membrane Protein Targets – Part 1
Wed.AM Sept. 25	Targeting Epigenetic Readers	Targeting Histone Methyltransferases	GPCR-Based Drug Discovery	Functional Genomics Screening Strategies – Part 1	Novel Strategies for Kinase Inhibitors	Antibodies Against Membrane Protein Targets– Part 1
Wed. PM Sept. 25	Next-Generation Histone Deacetylase Inhibitors	Targeting Histone Demethylases	GPCR-Targeted Therapeutic	Functional Genomics Screening Strategies – Part 2	Cardio-Metabolic Drug Targets	Antibodies Against Membrane Protein Targets– Part 2
6:45 - 9:30 PM	**Conference Short Courses*** SC9: Setting Up Effective Functional Screens Using 3D Cell Cultures					
Thurs. Sept. 26	Next- Generation Histone Deacetylase Inhibitors	Targeting Histone Demethylases	GPCR-Targeted Therapeutics	Functional Genomics Screening Strategies – Part 2	Cardio-Metabolic Drug Targets	Antibodies Against Membrane Protein Targets– Part 2

**Separate Registration Required.*

Present a poster and save $50!

Cambridge Healthtech Institute encourages attendees to gain further exposure by presenting their work in the poster sessions. To secure a poster board and inclusion in the conference materials, your abstract must be submitted, approved and your registration paid in full by August 16, 2013. Please see registration page for details.

Reasons you should present your research poster at this conference:

- Your poster will be exposed to our international delegation
- Receive $50 off your registration
- Your poster abstract will be published in our conference materials
- Your research will be seen by leaders from top pharmaceutical, biotech, academic and government institutes

"In one day I wrote more notes than in full week-long conferences. Truly the state-of-the-art science at CHI!"

Assistant Professor, U. of Connecticut

MEDIA PARTNERS

Functional Genomics Screening Strategies

Part One: Utilizing RNA Interference (RNAi) Screens to Explore Drug Targets and Cellular Pathways

» SUGGESTED EVENT PACKAGE

September 23: Setting Up Effective RNAi Screens: Getting From Design to Data **Short Course 6**

September 24-25: Functional Genomics Screening Strategies **Conference Part One**

September 25: Setting Up Effective Functional Screens Using 3D Cell Cultures **Dinner Short Course 9**

September 25-26: Functional Genomics Screening Strategies **Conference Part Two**

TUESDAY, SEPTEMBER 24

7:00 am Registration and Morning Coffee

WHERE AND HOW TO APPLY siRNA AND shRNA SCREENS

8:10 Chairperson's Opening Remarks

8:15 Comparative Analysis of Arrayed RNAi Screening Performance of siRNA versus shRNA at Genome-Scale

Hakim Djaballah, Ph.D., Director, HTS Core Facility, Molecular Pharmacology and Chemistry Program, Memorial Sloan Kettering Cancer Center

We utilized the two most popular RNAi technologies (siRNA duplex and shRNA hairpin) in order to perform a head-to-head comparison of both performance and hit nomination output. Using a previously developed EGFP-based high content biosensor cell based assay, we first executed on a siRNA screen against the Ambion Silencer Select V4.0 library nominating 1,273 candidates, followed by a second shRNA screen against the TRC1 library nominating 497 candidates. I will present our findings and discuss some likely reasons for the observed differential outcomes.

8:45 Swimming in the Deep End – Sources Leading to a False Sense of Security in RNAi Screen Data

Scott Martin, Ph.D., Team Leader, RNAi Screening, NIH Chemical Genomics Center, NIH Center for Translational Therapeutics, National Institutes for Health

There has been a growing skepticism surrounding RNAi data and the validity of hits arising from large-scale RNAi screens. Much of this comes from a lack of agreement between screens conducted in similar biological systems and difficulty in validating published screen hits. In light of these realities, we must rethink some widely held beliefs about screening and validation strategies. These issues and relevant data will be discussed.

9:15 Rebuilding the RNAi Screen

Eugen Buehler, Ph.D., Group Leader, Informatics, National Center for Advancing Translational Sciences, National Institutes of Health

Recent work has demonstrated the prevalence of false positives in RNAi screen results and the role of seed-based off-target effects in causing them. We will detail our efforts to implement a screening pipeline that accounts for and leverages seed based effects, from library design all the way to follow-up experiments.

9:45 Grand Opening Coffee Break in the Exhibit Hall with Poster Viewing

10:45 RNAi Screening: Strategies, Examples and Outcomes

David Root, Ph.D., Director, RNAi Platform and Project Leader, The RNAi Consortium, The Broad Institute of MIT and Harvard

11:15 Rapid RNAi-based *In Vivo* Screening in Mice

Daniel Schramek, PhD, Emerald Foundation Young Investigator, Human Frontier of Science Postdoctoral Fellow, Howard Hughes Medical Institute HHMI, Laboratory of Mammalian Cell Biology and Development, Rockefeller University

11:45 PANEL DISCUSSION: Advanced RNAi Screening: Strengths, Caveats and Pitfalls at Reaching the 14-Year Milestone

Moderator: Christophe Echeverri, Ph.D., CEO & CSO, Cenix BioScience USA, Inc.

Panelists:

Caroline Shamu, Ph.D., Director, ICCB-Longwood Screening Facility, Harvard Medical School

David Root, Ph.D., Director, RNAi Platform and Project Leader, The Broad Institute

Hakim Djaballah, Ph.D., Director, HTS Core Facility, Memorial Sloan Kettering Cancer Center

Scott Martin, Ph.D., Team Leader, RNAi Screening, NIH Chemical Genomics Center

12:45 pm Luncheon Presentation: Screening with MISSION® miRNA inhibitors and Pooled shRNA Libraries

Sponsored by SIGMA Life Science

Shawn L. Shafer, Ph.D., Market Segment Manager, Functional Genomics, Sigma® Life Science

Sigma develops innovative microRNA and RNAi tool. Sigma recently partnered with Drs. Iba and Haraguchi at the University of Tokyo to develop a new class of miRNA inhibitors designed using a proprietary algorithm based upon the Tough Decoy (TuD) design. As a member of The RNAi Consortium (TRC), Sigma uses

the largest, most validated shRNA library available to create our lentiviral shRNA pools and also offers deep sequencing services for deconvolution of pooled shRNA screens.

EXPLORING DIVERSE APPLICATIONS

2:15 Chairperson's Opening Remarks

2:20 Target Identification and Validation of Novel Ion Channels in Cancer

Alex Gaither, Ph.D., Senior Research Investigator, Developmental and Molecular Pathways, Novartis Institutes for Biomedical Research

The calcium-activated chloride channel anoctamin 1 (ANO1) is located within the 11q13 amplicon. RNAi mediated knockdown of ANO1 in breast and head and neck cancer cell lines inhibited proliferation, induced apoptosis, and reduced tumor growth in xenografts. RNAi knockdown or pharmacological inhibition of its chloride-channel activity reduced EGF receptor (EGFR) and calmodulin-dependent protein kinase II (CAMKII) signaling, which attenuated AKT, SRC, and ERK activation. Our results highlight the involvement of the ANO1 chloride channel in tumor progression and provide insights into oncogenic signaling in human cancers.

2:50 Cell-Based Functional Profiling of Lipid-Traits and Cardiovascular Disease

Heiko Runz, M.D., Group Leader, Institute of Human Genetics, University of Heidelberg and Group Leader, Molecular Medicine Partnership Unit (MMPU), University of Heidelberg/EMBL

Analyzing the genomes of large cohorts has identified numerous genes and genetic variants associated with common and rare human disorders. However, albeit a basis for therapy development, the mechanisms how genetic variation contributes to disease typically remain elusive. We demonstrate how systematic gene knockdown and over-expression approaches in cells may help us to understand how factors identified through profiling the genomes of thousands of individuals relate to altered blood lipid levels and the risk for cardiovascular disease.

3:20 Pooled RNAi Genetic Screening to Identify Functional Genes and Novel Drug Targets

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Paul Diehl, Ph.D., Director, Business Development, Cellecta, Inc.

Pooled lentiviral-based shRNA expression libraries enable simultaneous screening of thousands of transcripts to identify those driving specific cellular responses. This approach has proven highly efficient, flexible, and cost-effective when integrated with quantitative next generation sequencing which accurately measures changes in hairpin representation present in populations of transduced cells. This presentation will present results from both "drop-out" screens to identify genes essential for cell viability and positive-selection "rescue" screens to identify genes blocking a lethal response.

3:50 Refreshment Break in the Exhibit Hall with Poster Viewing

4:30 Cell-Based Small Molecule and siRNA Screen to Identify Targets for Retinal Neuroprotection

Donald J. Zack, M.D., Ph.D., Professor, Departments of Ophthalmology, Molecular Biology and Genetics, and Neuroscience, Johns Hopkins University School of Medicine

Death of retinal ganglion cells (RGCs) and photoreceptors is responsible for the visual loss caused by glaucoma and retinal degeneration, respectively. We have developed a High Content Screening approach utilizing cultures of primary retinal neurons to identify neuroprotective molecules and genes. Through this HCS screen, we have identified a number of protein kinase inhibitors as being potent promoters of RGC survival, have identified the MAP3K12 pathway as being important for RGC survival, and shown that inhibition of MAP3K12 is neuroprotective *in vivo* following optic nerve injury.

5:00 Deep Coverage shRNA Screens for Epigenetics Target Discovery

Gregory Hoffman, Ph.D., Investigator II, Novartis Institutes for Biomedical Research

5:30 Interactive Breakout Discussion Groups

6:30 Welcome Reception in the Exhibit Hall with Poster Viewing

7:30 Close of Day

WEDNESDAY, SEPTEMBER 25

7:30 am Registration and Morning Coffee

COMBINING USE OF RNAi AND OTHER TECHNOLOGIES

8:00 Chairperson's Opening Remarks

8:05 RNAi Screening to Enable Translational R&D For Oncology and Immuno-Oncology Target Discovery

Namjin Chung, Ph.D., Senior Research Investigator, Applied Genomics, Bristol Myers Squibb Co.

8:35 siRNA Screening and RNA-seq for Identification of Targets for the Treatment of Alzheimer's Disease

Paul Kassner, Ph.D., Director, Research, Amgen, Inc.

9:05 Fusing RNAi Screening and Gene Expression Analyses to Reveal Pathway Responses

Alexander Bishop, Ph.D., Assistant Professor, Department of Cellular and Structural Biology, University of Texas Health Science Center at San Antonio

RNAi screening and gene expression analyses both provide global insight into the genes involved in a biological process of interest. However, both platforms have drawbacks, false-positive/negative results with RNAi screening and secondary expression changes irrelevant to the primary biological response. Fusion of RNAi and gene expression data results in no significant

overlap on a gene level. Here we demonstrate that these platforms can be fused when combined on a pathway level.

9:35 From High-Throughput Screens to Biomedical Knowledge

Frank Buchholz, PhD, Professor, Medical Systems Biology, University Hospital and Medical Faculty Carl Gustav Carus, Technical University Dresden

We are using endoribonuclease prepared (esi)RNA-mediated RNAi screens and and combine them with large-scale protein-tagging (TransgeneOmics) to investigate stem cell and cancer relevant processes to obtain a more comprehensive picture of cellular transformation. Examples of our work to interrogate tumor-relevant processes in stem cells and cancer cells will be presented.

10:05 Coffee Break in the Exhibit Hall with Poster Viewing

10:50 Use of Functional Genomics to Identify Patients at High Risk for Recurrence of Hepatitis C Following Liver Transplantation

Robert Carithers, M.D., Professor of Medicine, Director, Liver Care Line and Medical Director of the Liver Transplant Program, University of Washington Medical Center

Cirrhosis from hepatitis C is the most common indication for liver transplantation. Rapidly progressive fibrosis leads to cirrhosis in 15% of transplant recipients within 5 years. Using functional genomics we have been able to identify high risk patients at 3 months post OLT. This is a unique application of functional genomics to an important clinical problem.

11:20 TECHNOLOGY PANEL: Tools for Next-Generation Functional Genomics Screens

Moderator: Christophe Echeverri, Ph.D., CEO & CSO, Cenix BioScience USA, Inc.
Panelists:
Paul Diehl, Ph.D., Director, Business Development, Cellecta, Inc.
Prem K. Premsrirut, Ph.D., President & CEO, Mirimus, Inc.
Louise Baskin, Senior Product Manager, Marketing, ThermoFisher Scientific
Shawn L. Shafer, Ph.D., Market Segment Manager, Functional Genomics, Sigma® Life Science

11:50 Lunch on Your Own

1:40 pm PLENARY KEYNOTE PRESENTATIONS:

Towards a Patient-Based Drug Discovery

Stuart L. Schreiber, Ph.D., Director, Chemical Biology and Founding Member, Broad Institute of Harvard and MIT; Howard Hughes Medical Institute Investigator; Morris Loeb Professor of Chemistry and Chemical Biology, Harvard University

Small-molecule drugs were originally discovered using compound based drug discovery: opportunistic discovery of a biologically active compound, often a natural product (e.g., penicillin) followed by a search for a disease that might be treated with the compound. This remains a common approach to modern drug discovery (e.g., rapamycin and analogs for use as antifungal agents; immune suppression agents; anticancer agents; possibly others in the future). The advent of recombinant DNA accelerated a second approach – target-based drug discovery – where the therapeutic target is selected and subjected to methods that yield candidate drugs (mechanism-based design; structure-based design; screening). But this approach has its shortcomings – 97% of drug candidates that enter into clinical investigation eventually fail, many due to unanticipated toxicity and many others due to a lack of efficacy despite successful modulation of the target. Selecting therapeutic targets based on information derived from surrogates of patients has proved challenging. Advances in human biology, including human genetics and physiology, and in small-molecule science, including chemistry and chemical biology, are now accelerating a third approach – patient-based drug discovery. This lecture will present examples that aim to use: 1) information from heritable or somatic human genetics in human disease; for example, in Crohn's Disease and cancer, 2 advances in diversity-oriented synthetic chemistry and chemical biology to accelerate the discovery of safe and effective small-molecule therapeutics, and 3) an understanding of the relationship of human genetic variation to drug efficacy.

Enteroendocrine Drug Discovery for Treatment of Metabolic Diseases

Paul L. Feldman, Ph.D., Senior Vice President, GlaxoSmithKline

The Enteroendocrine Discovery Performance Unit at GlaxoSmithKline is focused on discovering and developing medicines that mimic the efficacy of Roux-en-Y gastric bypass surgery to treat metabolic diseases. Our strategy emanates from the findings that there are significant metabolic benefits to obese and obese diabetic patients that undergo Roux-en-Y gastric bypass surgery. In general, these patients experience ~30% weight loss while >80% of obese diabetics who undergo this surgery have complete "remission" of diabetes. Our strategy is focused on three areas: 1) enteroendocrine science: discovery efforts focused on targets expressed on the luminal surface of the GI tract and peptides secreted from the GI tract or other peptides known to have metabolic effects, 2) combination therapies: by first intent progress combinations of assets that work synergistically to manifest significant, differentiated metabolic efficacy, and 3) assets that minimize safety risks: peptide based therapeutics and GI luminally restricted small molecules. In this presentation, I will describe the strategy our Unit has taken to discover novel combination peptide-based and GI luminally restricted small molecule therapeutics.

3:10-3:50 pm Refreshment Break in the Exhibit Hall with Poster Viewing

3:50 Close of Conference

Functional Genomics Screening Strategies

Part Two: Exploring Novel Screening Platforms and Cellular Models for Next-Generation Screens

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WEDNESDAY, SEPTEMBER 25

11:50 am Registration

SYNERGISTIC USE OF RNAi AND CHEMICAL GENOMICS SCREENS

1:30 pm Chairperson's Opening Remarks

1:40 PLENARY KEYNOTE PRESENTATION

See Page 6 for Information

3:10-3:50 Refreshment Break in the Exhibit Hall with Poster Viewing

3:50 Chairperson's Opening Remarks

4:00 The Role and Positioning of RNAi in Our Approach to Target and Biomarker Discovery

John N. Feder, Ph.D., Associate Director, Genome Biology, Applied Genomics, Bristol-Myers Squibb Co.

4:30 Sponsored Presentations *(Opportunities Available)*

5:00 Utilization of siRNA and Small Molecule Screens to Elucidate Cellular Pathways Involved in HPV-Associated Cancers

Jennifer Smith, Ph.D., Assistant Director, ICCB-Longwood Screening Facility, Harvard Medical School

Infection with 'high-risk' human papillomavirus (HPV) is considered the primary cause of cervical cancer. HPV DNA is found in a variety of other anogenital cancers and ~20% of head and neck cancers. Two viral oncogenes, E6 and E7, are implicated in HPV-associated carcinogenesis. To identify cellular genes and pathways as potential therapeutic targets, RNAi screens were conducted. Small molecule HTS was also performed to identify compounds tool compounds and potential lead compounds for a therapeutic against HPV-associated cancers and precancerous persistent infections.

5:30 Compound Synergy via Genomics and Combinatorics

Matthew Tudor, Ph.D., Principal Scientist, Screening & Protein Sciences, Merck Research Laboratories

Exploration of some methods used to identify and characterize compound interactions. Exploiting rich readouts, RNAi, and novel applications of drug screening tools, we demonstrate several approaches to find 'molecular partners'.

6:00 Size Exclusion Chromatography Target Identification (SEC-TID): A Label-Free Method for Small Molecule Target Identification

Gregory Michaud, Ph.D., Senior Investigator I, Developmental & Molecular Pathways, Novartis Institutes for BioMedical Research

Bioactive small molecules are an invaluable source of therapeutics and chemical probes for exploring biological pathways. Yet, significant hurdles in drug discovery often come from lacking a comprehensive view of the target(s) for both early tool molecules and even late stage drugs. To address this challenge, a method is provided which allows for assessing the interactions of small molecules with thousands of targets without any need to modify the small molecule of interest or attach any component to a surface.

6:30 Close of Day

THURSDAY, SEPTEMBER 26

7:30 am Registration

USE OF 3D CELL CULTURES FOR FUNCTIONAL SCREENING

8:00 Breakfast Interactive Breakout Discussion Groups

9:05 Chairperson's Opening Remarks

9:10 Disease & Risk On Chips: 3D Culture to Improve Development and Assessment of Drugs for Prevention and Treatment of Breast Cancers

Sophie Lelièvre, D.V.M., L.L.M., Ph.D., Associate Professor, Department of Basic Medical Sciences; Associate Director, Discovery Groups, NCI-Designated Purdue Center for Cancer Research, Purdue University

Heterogeneity within tissues targeted to prevent or treat cancer necessitates improved therapeutic efficacy via phenotyping. For prevention, 3D culture and organ-on-a-chip models mimicking tissues at risk for cancer provide high-throughput assessment of tissue features linked to epigenetic changes necessary for tumor onset. For treatment, disease-on-a-chip models enable comparison of tumor and non-tumor cell sensitivity to therapies based on epigenetic profiles. Moreover, on-a-chip models permit the design of methods for targeted drug delivery in anatomical context.

9:40 Targeting Cancer Stem Cells: A Model Demonstrating the Advantages and Disadvantages of 3D qHTS Technology *in vitro*

Lesley Mathews, Ph.D., Research Scientist, Biomolecular Screening and Profiling/Probe Development Group, National Center for Advancing Translational Sciences, NIH

10:10 Coffee Break in the Exhibit Hall with Poster Viewing

10:55 Multi-Cellular 3D Tumor Spheroid Models for High-Throughput Screening in Cancer Biology

Geoffrey A. Bartholomeusz, Ph.D., Assistant Professor and Director, siRNA Core Facility, Department of Experimental Therapeutics, Division of Cancer Medicine, The University of Texas MD Anderson Cancer Center

The intrinsic limitations associated with 2D cell culture systems have prompted the development of 3D spheroid models with cellular organization emulating the heterogeneity of solid tumors with necrosis and hypoxic regions. The ease at which spheroid models can be applied in high-throughput screens has resulted in the realization of their importance to address relevant questions in tumor biology. The design of spheroid-based models for target identification utilizing high-throughput RNAi screens will be discussed.

11:25 Image Analysis Workflows for High Throughput 2D/3D Screens

Arvind Rao, Ph.D., Assistant Professor, Department of Bioinformatics and Computational Biology, The University of Texas MD Anderson Cancer Center

High-throughput screening is routinely used to identify the role of RNAi in altering cellular phenotype as well as to study the effects of therapeutics on diseased cell morphology. A high-throughput kinome siRNA screen (880 kinases) was carried out to study their effects on tumor architecture and hypoxic response induced in 3D tumor spheroids. We present a workflow to identify and interpret gene function in such large scale 3D RNAi experiments by analyzing such image-derived data in the context of associated molecular data.

11:55 PANEL DISCUSSION: Pros and Cons of Working with 3D Cell Cultures

Moderator: Geoffrey A. Bartholomeusz, Ph.D., Assistant Professor and Director, siRNA Core Facility, The University of Texas MD Anderson Cancer Center

Panelists: Session Speakers

12:25 pm Sponsored Presentation *(Opportunity Available)*

12:55 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

IN VIVO RNAi SCREENING

2:25 Chairperson's Opening Remarks

2:30 Pooled RNAi Screens in Xenograft Mouse Models

Sponsored by CELLECTA Discovery is *Yours*.

Donato Tedesco, Ph.D., Lead Research Scientist, Cellecta, Inc.

We will present results of clonal analysis studies aimed at characterizing the heterogeneity of cancer cell growth in xenograft models. We developed an RNAi screening platform designed to improve the sensitivity and reproducibility of xenograft "drop-out" screens. Preliminary data from a panel of tumorigenic cell lines, including human breast, ovarian and colon carcinomas will be presented.

3:00 RNAi Mouse Models: Revolutionizing Drug Discovery *in vivo*

Sponsored by MIRIMUS

Prem K. Premsrirut, Ph.D., President & CEO, Mirimus, Inc.

We developed a cost-effective pipeline for the production of RNA interference (RNAi) transgenic mice with enormous predictive power that will shape our development of better tolerated therapies. Unlike traditional knockout models, gene inhibition by RNAi is reversible, allowing us to mimic drug therapy. By using this system, we are able to pinpoint toxicities associated with gene inhibition in mice and identify potential effective targets as well as those that will cause harmful and intolerable effects in patients.

3:30 Ice Cream Refreshment Break in the Exhibit Hall with Poster Viewing

STEM CELL AND LONG NON-CODING RNA (lncRNA)-BASED SCREENS

4:00 Functional Genomics, a Novel Stem Cell-Based Screening Platform

Scott Noggle, Ph.D., Director and Charles Evans Senior Research Fellow for Alzheimer's Disease, The New York Stem Cell Foundation

Integrating advances in genomics with stem cell technology, The New York Stem Cell Foundation (NYSCF) has developed the first fully automated robotic technology to derive a full array of induced pluripotent stem (iPS) cell lines. Researchers can use the thousands of cells generated on this Global Stem Cell Array to directly test, screen, and de-risk drugs on thousands of genetically and disease diverse cells *in vitro*. The Array provides a means to streamline the drug research and discovery process, ushering in an age of truly personalized medicine.

4:30 Primary Neural Stem Cell-based High Throughput High Content Phenotypic Screening for Multiple Sclerosis

Mei Zhang, M.D., Ph.D., Senior Scientist, Molecular Pharmacology, Small Molecule Platforms, EMD Serono Research and Development Institute, Inc.

We have established spheroid-based primary stem cell culture, scaled it up to bio-mass production and applied the culture platform to further differentiate lineages towards oligodendrocyte progenitor cells (OPC), potentially the myelin generating cells. By using partially differentiated OPC cells, we have conducted robot-supported live cell phenotypic High Content Screening (HCS) for 100k small molecules and identified promising hits for next stage of drug discovery.

5:00 Long Non-Coding RNAs as Targets for High-Throughput Functional Screens

Marcel Dinger, Ph.D., Head, Genome Informatics, The Kinghorn Cancer Centre, Garvan Institute for Medical Research; Associate Professor, Faculty of Medicine, University of New South Wales, Sydney, Australia

Recent transcriptomic studies have revealed 10,000s of long non-coding RNAs are transcribed from mammalian genomes in a tissue- and developmentally-specific manner. However, the function of the vast majority remains unknown and whether or not the majority are indeed of biological importance has to date been controversial. I will present evidence supporting the notion that the majority of long non-coding RNAs are functional and will show data from our ectopic expression and siRNA knockdown screens of long non-coding RNAs in various cell lines.

5:30 Presentation to be Announced

6:00 Close of Conference

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CHI offers comprehensive sponsorship packages which include presentation opportunities, exhibit space and branding, as well as the use of the pre and post-show delegate lists. Customizable sponsorship packages allow you to achieve your objectives before, during, and long after the event. Signing on early will allow you to maximize your exposure to hard-to-reach decision makers!

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Showcase your solutions to a guaranteed, highly-targeted audience. Package includes a 15 or 30-minute podium presentation within the scientific agenda, exhibit space, on-site branding and access to cooperative marketing efforts by CHI.

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Opportunity includes a 30-minute podium presentation. Boxed lunches are delivered directly into the main session room, which guarantees audience attendance and participation. A limited number of presentations are available for sponsorship and they will sell out quickly. Sign on early to secure your talk!

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Sponsors will select their top prospects from the conference pre-registration list for an evening of networking at the hotel or at a choice local venue. CHI will extend invitations and deliver prospects. Evening will be customized according to sponsor's objectives (i.e. purely social, focus group, reception style or plated dinner with specific conversation focus).

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The Intro-Net offers you the opportunity to set up meetings with selected attendees before, during and after this conference, allowing you to connect to the key people you want to meet. This online system was designed with your privacy in mind and is available only to registered session attendees of this event. Registered conference attendees will receive more information on accessing the Intro-Net in the weeks leading up to the event!

HOTEL & TRAVEL INFORMATION

Conference Hotel:

Westin Boston Waterfront
425 Summer St.
Boston, MA 02210
T: 617-532-4600

Discounted Room Rate: $269 s/d

Discounted Room Rate Cut-off Date: August 26, 2013

Please visit our conference website or call the hotel directly to reserve your sleeping accommodations. You will need to identify yourself as a Cambridge Healthtech Institute conference attendee to receive the discounted room rate with the host hotel. Reservations made after the cut-off date or after the group room block has been filled (whichever comes first) will be accepted on a space and rate-availability basis. Rooms are limited, so please book early.

TOP REASONS TO STAY AT THE WESTIN BOSTON WATERFRONT HOTEL:

- Take advantage of the $269 group rate!
- No Commute, since meeting takes place at hotel
- Complimentary wireless internet access in guest rooms
- Lots of new restaurants within walking distances. Waterfront is the up and coming area of Boston!

Flight Discounts:
Special discount rentals have been established with American Airlines for this conference.
- Call American Airlines 1-800-433-1790 use Conference code 2593BF.
- Go to www.aa.com/group enter Conference code 2593BF in promotion discount box.
- Contact our designated travel agent, Rona Meizler, at 617-559-3735 or rona.meizler@protravel.com

Car Rental Discounts:
Special discount rentals have been established with Hertz for this conference.
- Call Hertz 1-800-654-3131 use our Hertz Convention Number (CV): 04KL0003
- Go to www.hertz.com use our Hertz Convention Number (CV): 04KL0003

How to Register: **DiscoveryOnTarget.com**

reg@healthtech.com • P: 781.972.5400 or Toll-free in the U.S. 888.999.6288

Please use keycode **DOT4 F** when registering!

SHORT COURSES

	Commercial	Academic, Government, Hospital-affiliated
One short course	$695	$395
Two short courses	$995	$595
Three short courses	$1195	$695
Registered Conference Delegates SAVE $100	-$100	-$100

Monday, September 23

SC1: New Classes of Kinase Inhibitors: Covalent Modifiers
SC2: Practical Aspects of Structure-Based Drug Discovery with GPCRs
SC3: Biochemical and Structure-Based Approaches to Epigenetic Drug Discovery
SC4: Allosteric Modulators of GPCRs
SC5: Advancing Tools and Technologies for Fragment-Based Design
SC6: Setting Up Effective RNAi Screens: Getting From Design to Data
SC7: Production and Presentation of Integral Membrane Proteins for Antibody Discovery
SC8: Characterization and Quantification of Histone Modifications

Wednesday, September 25

SC9: Setting Up Effective Functional Screens Using 3D Cell Cultures
SC10: Tools for Epigenetic Biomarker Discovery

If you are unable to attend but would like to purchase the Discovery On Target CD for $750 (plus shipping), please visit DiscoveryOnTarget.com. Massachusetts delivery will include sales tax.

CONFERENCE PRICING

STANDARD PACKAGE *(Includes access to 2 conferences. Excludes short courses.)*

Registrations after August 23, 2013, and on-site	$2575	$1195

SINGLE CONFERENCE PACKAGE *(Includes access to 1 conference. Excludes short courses.)*

Registrations after August 23, 2013, and on-site	$1745	$975

September 24 - 25	September 25 - 26
Track 1: Targeting Epigenetic Readers	Track 7: Next-Generation Histone Deacetylase Inhibitors
Track 2: Targeting Histone Methyltransferases	Track 8: Targeting Histone Demethylases
Track 3: GPCR-Based Drug Discovery	Track 9: GPCR-Targeted Therapeutics
Track 4: Functional Genomics Screening Strategies - Part 1	Track 10: Functional Genomics Screening Strategies - Part 2
Track 5: Novel Strategies for Kinase Inhibitors	Track 11: Cardio-Metabolic Drug Targets
Track 6: Antibodies Against Membrane Protein Targets - Part 1	Track 12: Antibodies Against Membrane Protein Targets - Part 2

CONFERENCE DISCOUNTS

POSTER DISCOUNT ($50 Off) Poster abstracts are due by August 16, 2013. Once your registration has been fully processed, we will send an email containing a unique link allowing you to submit your poster abstract. If you do not receive your link within 5 business days, please contact jring@healthtech.com. ** CHI reserves the right to publish your poster title and abstract in various marketing materials and products.*

REGISTER 3 - 4th IS FREE: Individuals must register for the same conference or conference combination and submit completed registration form together for discount to apply.

ALUMNI DISCOUNT: Cambridge Healthtech Institute (CHI) appreciates your past participation at Discovery On Target. As a result of the great loyalty you have shown us, we are pleased to extend to you the exclusive opportunity to save an additional 20% off the registration rate.

GROUP DISCOUNTS: Discounts are available for multiple attendees from the same organization. For more information on group rates contact David Cunningham at +1-781-972-5472