Cambridge Healthtech Institute’s Second Annual

Biomarker Data Analysis

Systems Biology Approach to Integrate Biomarker Data and Establish Biological and Clinical Relevance

September 29-October 1, 2008
Loews Philadelphia Hotel • Philadelphia, Pennsylvania

Coverage Includes:

- Establishing Biomarker Utility
- Gene Expression Profiling of Health and Disease: Bridging Statistics and Biology
- Bridging Omic and Clinical Data
- Systems Biology Approaches to Biomarker Discovery
- Integrating Semantic and Omic Approaches for Biomarker Discovery
- Data Analysis for Single-Analyte Markers, Panels, and Profiles
- Bridging Silos: Integrating Omic Data

KEY FEATURES:

- 4 tracks
- 400+ delegates
- 75+ speakers
- 30+ exhibits
- 30+ posters

Coverage Includes:

- Fourth Annual Genomic Biomarkers
- Sixth Annual Protein Biomarkers
- Ninth Annual Metabolic Biomarkers
- Second Annual Biomarker Data Analysis

www.BiomarkerDiscoverySummit.com

Part of:

Biomarker Discovery Summit 2008
Bridging the Silos in Biomarker Discovery and Validation

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Discounted Room Rate: $189 s/d
Reduced Room Rate Cutoff: September 8, 2008
To reserve your hotel room, please call the hotel directly at 215-627-1200. Identify yourself
as a Cambridge Healthtech Institute conference attendee to receive the reduced room
rate. 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.

TRAVEL INFORMATION
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Biomarker Data Analysis Meeting is part of:

BIOMARKER DISCOVERY SUMMIT 2008
Bridging the Silos in Biomarker Discovery and Validation

FOUR TRACKS:
Fourth Annual Genomic Biomarkers
Delivering on the Promise of Personalized Medicine

Sixth Annual Protein Biomarkers
The Translational Challenge

Ninth Annual Metabolic Biomarkers
Clinical Metabolomics for Drug and Diagnostic Development

Second Annual Biomarker Data Analysis
Systems Biology Approach to Integrate Biomarker Data and
Establish Biological and Clinical Relevance

Pre-Conference Events:
• Fit-for-Purpose Biomarker Assay Development and Validation
• Novel Approaches to Cancer Biomarkers
• microRNA as Cancer Biomarkers
• Technology Advances for Protein Biomarker Discovery

Why attend Biomarker Discovery Summit 2008:
• Network with 400+ delegates
• Get access to four established meetings and 70+
presentations under one roof
• Choose from four pre-conference workshops
• Learn about new tools at the expanded exhibit hall
and new technology showcase

Please visit www.BiomarkerDiscoverySummit.com
for complete program information.
Monday, September 29

**Pre-Conference Events** (separate registration required):
- Fit-for-Purpose Biomarker Assay Development and Validation
- Novel Approaches to Cancer Biomarkers
- Technology Advances for Protein Biomarker Discovery

Visit www.BiomarkerDiscoverySummit.com for full agenda.

3:00-4:00  Conference Registration
4:00-4:10  Welcoming Remarks from Conference Director
Julia Boguslavsky, Cambridge Healthtech Institute

**ESTABLISHING BIOMARKER UTILITY**

4:10-4:15  Chairperson’s Opening Remarks
4:15-4:40  Five Characteristics of a Biomarker to be Useful for Personalizing Medicine
Felix Frauh, Ph.D., Vice President, Research and Development, Personalized Medicine, Medco Health Solutions, Inc.

4:40-5:05  Biomarkers for What? Diagnostic, Prognostic or Predictive?
Sudhir Srivastava, Ph.D., Chief, Cancer Biomarkers Research Group, NIH National Cancer Institute

5:05-5:30  Building a Biomarker Information Pipeline and Enabling Translational and Personalized Medicine: Leveraging Industry Standard to Bring Omics Closer to Medicine
Martin D. Leach, Ph.D., Executive Director, Basic Research & Biomarker IT, Merck & Co., Inc.

5:30-6:30  Opening Reception in the Exhibit Hall

Tuesday, September 30

7:00  Registration Open
7:30-8:15  Morning Coffee or Technology Workshops
(Sponsorship Available. Contact Ilana Schwartz at 781-972-5457 or ischwartz@healthtech.com.)

**GENE EXPRESSION PROFILING OF HEALTH AND DISEASE: BRIDGING STATISTICS AND BIOLOGY**

8:30-8:35  Chairperson’s Opening Remarks
8:35-9:00  Biomarkers: Understanding the Disease Process
Michael N. Liebman, Ph.D., Senior Institute Fellow, Windber Research Institute; Managing Director, Strategic Medicine, Inc.

Measurement of gene expression data presents an opportunity to further classify patients and their disease using biological specimens, robust experimental methods and statistical analysis to enhance clinical decision making. It is critical, however, to appropriately evaluate this perspective on patient and/or disease stratification in terms of the complexity of the disease process and clinical need, rather than solely on the concept of a disease state. This presentation will describe both the conceptual framework for understanding the relationship between biomarkers and the disease process and results from its application in breast cancer.

9:00-9:25  Biomarkers for Metabolic Disease: Predicting Weight Loss From Serotranscriptomics
Sujoy Ghosh, Ph.D., Advisor, Metabolic Diseases, Center of Excellence for Drug Discovery, Clinical Pharmacology & Discovery Medicine, GlaxoSmithKline

Serotranscriptomics refers to the study of gene expression in blood samples. We have examined gene expression profiles in whole blood from obese subjects who lost weight at significantly different rates in response to a fixed, low calorie diet. Gene expression profiles were analyzed to identify biological pathways that discriminate between obese and lean subjects and between obese, diet-sensitive (ODS) and obese, diet-resistant (ODR) subjects. Additionally, candidate biomarkers of the rate of weight loss were identified and confirmed by quantitative real-time PCR. This approach qualifies whole-blood transcriptome analysis for unraveling the biology underlying obesity and weight-loss. Blood-based biomarkers predictive of the rate of weight loss also opens a promising avenue for individualizing weight-loss therapy by caloric restriction alone or in combination with pharmacotherapy.

9:25-9:50  Ingenuity Pathways Analysis: Prioritization of Biomarker Candidates from Omics Data Based on Phenotypic Association
Deborah Riley, Ph.D., Senior Application Scientist, Ingenuity Systems

Sponsored by Ingenuity Systems

9:50-10:15  Defining Health at the Molecular Level
Martin Grigorov, Ph.D., Head of Bioinformatics, Nestlé Research Center

The challenge for the Life Sciences in the new century resides in promoting health and in preventing disease. In order to meet this challenge, knowledge should be built to define and better understand the function of the molecular markers which define the healthy status of a biological system. The aim of the present study was to generate a map of gene expression patterns along the human healthy adult gastro-intestinal tract in order to use such sets of biomarkers as references when screening for pathological deviations. Nearly 150 marker genes were found to perfectly discriminate the five major GI regions considered. Fourteen had never been described in the GI tract, and six were novel genes. This work offers a perspective on nutrition-specific biomarkers discovery programs. It shows such studies to be complementary to typical drug development programs focusing on disease-specific biomarkers, rather than on the molecular signatures of health.

10:15-11:10  Networking Coffee Break, Poster and Exhibit Viewing

**BRIDGING OMIC AND CLINICAL DATA**

11:10-11:35  Advances in Bioinformatics for Next Generation Clinical Research and Biomarker Development Studies
James Lyons-Weiler, Ph.D., Director, Bioinformatics Analysis Core, Genomics and Proteomics Core Laboratories, Department of Biomedical Informatics, Department of Pathology, University of Pittsburgh Cancer Institute

Algorithms have been central to most advances in bioinformatics and its role in basic and clinical research. In this presentation, I will (a) provide a glimpse into the potential future of biomarker development via Integrative Translational Research, (b) examine why a revolution is needed in survivorship prediction modeling, including a description of the first phases of that revolution, and (c) examine how and why adaptive study designs may or may not be able to boost biomarker development studies. Early case studies will be provided. Software that implements each of these developments is either now available, or is under construction at the Bioinformatics Analysis Core at the University of Pittsburgh.
Monday, October 1

8:30-8:50 Chairperson's Opening Remarks

9:00-9:15 Targeting Omics and Clinical Data to Better Understand Disease Mechanism and Predict Treatment Outcome
A. Jamie Cuticchia, Ph.D., Director, Duke Bioinformatics, Duke Institute for Genome Sciences & Policy, Duke University Comprehensive Cancer Center
With the continuing maturity of the collection of Omics data and a better understanding of interpretation methodologies, the relationship between these data and clinical phenotypes are becoming a growing component of modern healthcare. This is more than just gene association studies or personal genomes. It is an opportunity to better understand the underlying mechanisms of disease and predict the outcomes of treatment. Large studies such as the Framingham heart study are indicative of the value of collecting longitudinal clinical data. When such processes are combined with underlying Omics data, the value of such datasets become exponentially valuable.

9:20-9:35 High-Throughput Functional Proteomics Facilitates a Systems Biology Approach to Personalized Medicine
Jake Chen, Ph.D., Assistant Professor, Informatics, Indiana University; Computer Science, Purdue University; Director, Indiana Center for Systems Biology and Personalized Medicine; Founder and Chief Executive Officer, MedoLinx, LLC
Translational systems biology is an emerging research area that aims to help biomedical researchers derive novel insights on drug targets and biomarkers with the rapid development of computational models and systems biology informatics software tools. Key questions that we need to address for biomarker discoveries are how to incorporate prior knowledge into these models and tools, with which we can improve the interpretation of complex experimental Omics data sets. In our lab and the new Indiana Center for Systems Biology and Personalized Medicine, we have developed several new software tools such as HAPPI (a comprehensive human protein interactome database), C-maps (a disease drug target mining web server), HIP2 (a database of all plasma proteins detected in healthy human with tandem mass spectrometry techniques), and GeneTerrain (a visualization software tool for panel expression biomarker discoveries). We show the concept behind these tools and how they can be integrated for panel biomarker discovery applications.

9:40-10:00 Wide-Field Neuroimaging of the Human Brain: From Magnetic Resonance Imaging to Functional Connectivity
Rajesh Rao, Ph.D., Assistant Professor, Electrical Engineering and Computer Science & Policy, Duke University Comprehensive Cancer Center
Despite advances in our powers of observation, the ability to determine biological mechanisms from large-scale multi-omic technologies continues to be a major bottleneck in the discovery of biomarkers of disease progression and drug response. The marriage of computational learning methods that identify directly from the data the circuits and connections between drug-affected molecular constituents and physiological observables. The implementation of personalized healthcare requires the development of mechanistic diagnostics to enable the matching of a patient’s disease to the right therapeutic regimen. To meet this demand, Genestra has implemented a Causal Network Modeling (CNM) framework capable of using any Omics data source to develop mechanistic models of disease and drug action, and to define mechanistic biomarkers. Mechanistic Biomarkers are distinct from conventional, correlative biomarkers by their placement within a molecular mechanism explaining how the Mechanistic Biomarker relates to the pathophysiology in question or to the efficacious response triggered by a successful therapeutic. Similarly, mechanistic toxicity biomarkers can measure undesirable molecular networks affected by drug treatment, as applicable. In all cases, a Mechanistic Biomarker research program starts by building Causal Network Models for disease progression and drug response to map the molecular networks controlling the biological processes relevant to the disease. A data-driven approach to understanding the causal network topology governing a disease state or underlying an efficacious drug response is the critical starting point for the discovery of Mechanistic Biomarkers.

10:05-10:30 Achieving Confidence in Mechanism for Biomarker Discovery and Accelerated Drug Development
Colin Hill, Ph.D., Chief Executive Officer and President, Gene Network Sciences
Despite advances in our powers of observation, the ability to determine biological mechanisms from large-scale multi-omic technologies continues to be a major bottleneck in the discovery of biomarkers of disease progression and drug response. This can be overcome by utilizing computational learning methods that identify directly from the data the circuits and connections between drug-affected molecular constituents and physiological observables. The marriage of multi-omics technologies with reverse engineering approaches can provide missing insights needed to improve drug development success rates.

10:35-10:50 Closing Remarks

11:00-12:00 Luncheon Technology Showcases (Sponsorship Available. Contact Ilana Schwartz at 781-972-5457 or ischwartz@healthtech.com) Visit www.BiomarkerDiscoverySummit.com for a list of confirmed presentations.

12:00-1:40 Systems Biology Approaches to Biomarker Discovery
1:40-1:45 Chairperson's Opening Remarks
1:45-2:10 A Translational Systems Biology Approach to Panel Biomarker Discoveries
Jake Chen, Ph.D., Assistant Professor, Informatics, Indiana University; Computer Science, Purdue University; Director, Indiana Center for Systems Biology and Personalized Medicine; Founder and Chief Executive Officer, MedoLinx, LLC
Translational systems biology is an emerging research area that aims to help biomedical researchers derive novel insights on drug targets and biomarkers with the rapid development of computational models and systems biology informatics software tools. Key questions that we need to address for biomarker discoveries are how to incorporate prior knowledge into these models and tools, with which we can improve the interpretation of complex experimental Omics data sets. In our lab and the new Indiana Center for Systems Biology and Personalized Medicine, we have developed several new software tools such as HAPPI (a comprehensive human protein interactome database), C-maps (a disease drug target mining web server), HIP2 (a database of all plasma proteins detected in healthy human with tandem mass spectrometry techniques), and GeneTerrain (a visualization software tool for panel expression biomarker discoveries). We show the concept behind these tools and how they can be integrated for panel biomarker discovery applications.

2:10-2:35 High-Throughput Functional Proteomics Facilitates a Systems Biology Approach to Personalized Medicine
Gordon B. Mills, M.D., Ph.D., Chair, Department of Systems Biology, Professor of Medicine, The University of Texas, M. D. Anderson Cancer Center
Systems biology is the study of the emergence of functional properties that are present in a biological system but that are not obvious from a study of its individual components. Systems biology is a data-driven process requiring comprehensive databases at the DNA, RNA, and protein level to integrate systems biology with cancer biology. Combining these patient and model-based databases with the ability to interrogate functional networks by a systematic analysis using siRNA libraries and chemical genomics provides an ability to link in silico modeling, computational biology, and intervention approaches to develop robust predictive models applicable to patient management.

2:35-3:00 Identification of Candidate Biomarkers Using Large-Scale Mathematical Models
Aranath Kadambi, Ph.D., Senior Scientist, Entelos, Inc.
Entelos develops large-scale mathematical models of human physiology known as PhysioLab platforms, and applies them to support the pharmaceutical drug discovery and development process. This talk will discuss the application of Entelos PhysioLab platforms to the discovery of candidate biomarkers. First, the development of virtual populations will be discussed; these virtual populations reproduce the diversity in both underlying patient biology and phenotype seen in clinical trial populations. Second, case studies will be shown to describe the application of virtual populations to the identification of candidate biomarkers. These biomarkers can both predict compound efficacy and characterize responder/non-responder sub-populations.

3:00-4:00 Networking Refreshment Break with Poster and Exhibit Viewing

4:00-4:25 System-Wide Peripheral Biomarker Discovery Through an Information-Theoretic Framework
Gil Alterovitz, Ph.D., Research Fellow, Children’s Hospital Informatics Program, Harvard/MIT Division of Health Sciences and Technology; Research Affiliate, Massachusetts Institute of Technology, Computer Science and Artificial Intelligence
The identification of reliable peripheral biomarkers for clinical diagnosis, patient prognosis, and biological functional studies would allow for access to biological information currently available only through invasive methods. Here, we introduce an information-theoretic framework for biomarker discovery, integrating biofluid and tissue information. This approach was applied to the analysis of 204 tissue/biofluid pairs to determine the quantitative predictive ability of certain biofluids for specific tissues via relative entropy calculation of proteomes mapped onto functional space. A network of significant biofluid-tissue relationships interconnected via functional protein biomarker proxies, namely the biofluidome network, resulted. Over 200 unique candidate biomarker proxies were identified, including novel ones that were validated via gene expression. This work offers a novel method of biomarker discovery, providing an efficient way of selecting proteins to analyze and validate experimentally for eventual diagnostic and prognostic use.

4:25-4:50 Using Causal Network Models for Mechanistic Biomarker Discovery and Development
Keith Ellison, Ph.D., President & Chief Executive Officer, Genestra, Inc.
The development of personalized medicine requires a detailed understanding of the molecular mechanisms of disease, and of drug action. The implementation of personalized healthcare requires the development of mechanistic diagnostics to enable the matching of a patient’s disease to the right therapeutic regimen. To meet this demand, Genestra has implemented a Causal Network Modeling (CNM) framework capable of using any Omics data source to develop mechanistic models of disease and drug action, and to define mechanistic biomarkers. Mechanistic Biomarkers are distinct from conventional, correlative biomarkers by their placement within a molecular mechanism explaining how the Mechanistic Biomarker relates to the pathophysiology in question or to the efficacious response triggered by a successful therapeutic. Similarly, mechanistic toxicity biomarkers can measure undesirable molecular networks affected by drug treatment, as applicable. In all cases, a Mechanistic Biomarker research program starts by building Causal Network Models for disease progression and drug response to map the molecular networks controlling the biological processes relevant to the disease. A data-driven approach to understanding the causal network topology governing a disease state or underlying an efficacious drug response is the critical starting point for the discovery of Mechanistic Biomarkers.

4:50-5:15 Achieving Confidence in Mechanism for Biomarker Discovery and Accelerated Drug Development
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5:15 Close of Day

Wednesday, October 1

7:00 Registration Open

7:30-8:15 Morning Coffee or Technology Workshops (Sponsorship Available. Contact Ilana Schwartz at 781-972-5457 or ischwartz@healthtech.com)

8:00-8:15 Chairperson’s Opening Remarks

8:15-8:35 MOA Biomarker Discovery for IKKb Inhibition Program: An Interdisciplinary Approach
Zhenhao Qi, Ph.D., Senior Principal Scientist, Translational Sciences, Boehringer Ingelheim Pharmaceuticals, Inc.
There is increasing demand for Mechanism of Action (MOA) biomarker(s) in Phase I clinical trials to demonstrate compound hits the target in vivo, thus allowing better decision making at early phase. In this IKKb inhibition MOA biomarker program, we employed an interdisciplinary approach to combine statistical genome-wide search on in-house established gene expression database and literature/text mining to narrow down to a set of biologically relevant genes. Our statistics-driven in vitro LPS whole blood assay allowed us to find optimal inhibition window for
**BRIDGING SILOS: INTEGRATING OMIC DATA**

1:10-1:15  
Chairperson’s Opening Remarks

1:15-1:40  
Integration of Metabolic and Transcriptomic Profiling for Understanding of Diabetes and Obesity Mechanisms  
Christopher B. Newgard, Ph.D., Director, Sarah W. Stedman Nutrition and Metabolism Center, Duke University Medical Center  
Type 2 diabetes is a disease that occurs as a result of metabolic dysfunction in multiple tissues, including most prominently liver, skeletal muscle, and the pancreatic islets of Langerhans. An understanding of the transcriptional and metabolic networks that control normal functions in these tissues, and identification of the network elements that are perturbed during development of type 2 diabetes, are essential steps in the development of new therapies for the disease. The value of targeted mass spectrometry-based profiling of key clusters of intermediary metabolites for identifying specific network perturbations will be highlighted, as well recent examples of integration of metabolomic and transcriptomic profiling for identifying heretofore unrecognized regulatory pathways.

1:40-2:05  
Integrating Gene and Protein Expression Biomarkers in a Systems Biology Approach to Colon Cancer  
Mark R. Chance, Ph.D., Director, Case Center for Proteomics; Director, Center for Synchrotron Biosciences; Professor, Department of Physiology & Biophysics, Case Western Reserve University  
Protein interaction networks are at the heart of functional control of human disease. Network and pathway modeling driven by Omics based approaches are increasingly important to our understanding of disease progression and drug responses. However, deriving and validating network models are complex research problems requiring integration of multiple types of high-throughput data. We have recently employed a systems biology approach to find small networks of proteins discriminative of late stage human colorectal cancer (CRC). Expression proteomics studies were initially used to identify proteins differentially regulated when comparing normal and late stage tumor tissues obtained from adequately sized cohorts of human patients. Proteins identified by these experiments were used to seed a search for protein-protein interaction networks selective for biological relevance to the human colon. We chose four significant networks returned by this search and illustrated using measures of mutual information, calculated using gene expression data, that certain protein “signatures” within each network are highly discriminative of late stage cancer versus control. These signatures would not have been discovered using only proteomic data, or by merely clustering the gene expression data. Expanding these signatures by a single hop generated four sub-networks, which were analyzed for biological relevance to human CRC. A number of the proteins in these sub-networks have been shown to be critically involved in the progression of CRC. Others have been recently identified as potential markers of CRC, and still others merit follow-on experimental validation for biological significance in this disease. This general approach can be applied to network modeling for a number of diseases.

2:05-2:30  
A Systems Biology Approach to Biomarker Discovery  
Karim Rodland, Ph.D., Science Lead for NIH Programs, Pacific Northwest National Laboratory  
Efforts to identify biomarkers for early diagnosis or prognosis of cancer and other disease have often focused on a singular molecular species, with preference given to mRNA, microRNA, proteins, autoantibodies or metabolites based on available technologies and model systems. Each of these one-dimensional measurements provides a snapshot of cell function, but a dynamic understanding of disease processes really requires the integration of all these modalities to the extent possible. Particularly in the context of using biomarkers to guide therapeutic interventions, it is necessary to understand the relationship between changes in expression, and changes in function. One aspect of systems biology is the integration of heterogeneous datasets to define relationships that predict function. This talk will describe the application of this approach to models of chronic obstructive pulmonary disease.

2:30-2:55  
Connecting the Biomarker Dots in Cancer and Neurodegenerative Diseases  
Ira L. Goldknopf, Ph.D., Director, Proteomics, Power5 Medical Products, Inc.  
The application of fundamental principles to Omics integration to address unmet clinical needs will be illustrated with examples from cancer and neurodegenerative diseases. The integrations relate analytical with clinical validation across different analytical processes and platforms; clinical diagnostics with assessment of severity, disease progression, and efficacy; and data analysis integrating proteomic and genomic biomarkers, post-translational modifications, and protein isoforms. The clinical applications cover testing of blood serum for early detection of breast cancer as well as for early differential diagnosis and monitoring of the neurodegenerative diseases. The attainment of biological significance in terms of monitoring mechanisms of disease through blood testing as well as clinical practical diagnostic applications of such testing will also be discussed.

3:00  
Close of Conference
Biomarker Data Analysis

Systems Biology Approach to Integrate Biomarker Data and Establish Biological and Clinical Relevance

September 29 - October 1, 2008 • Loews Philadelphia Hotel • Philadelphia, Pennsylvania

YES! Register me for Biomarker Data Analysis

REGISTRATION INFORMATION

Mr.  Mrs.  Dr.  Prof.  YES!  Register me for Biomarker Data Analysis

**Email is not a mandatory field. However, by excluding your email you will not receive notification about online access to pre-conference presenter materials.**

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ADDITIONAL REGISTRATION DETAILS
Each registration includes all conference sessions, posters and exhibits, food functions, and a copy of the conference CD.

GROUP DISCOUNTS
Special rates are available for multiple attendees from the same organization. Contact David Cunningham at 781-972-5472 to discuss your options and take advantage of the savings.

HANDICAPPED EQUAL ACCESS
In accordance with the ADA, Cambridge Healthtech Institute is pleased to arrange special accommodations for attendees with special needs. All requests for such assistance must be submitted in writing to CHI at least 30 days prior to the start of the meeting. Substitution/Cancellation Policy

In the event that you need to cancel a registration, you may:

- Transfer your registration to a colleague within your organization
- Credit your registration to another Cambridge Healthtech Institute program
- Request a refund minus a $100 processing fee per conference
- Request a refund minus the cost ($500) of ordering a conference CD.

NOTE: Cancellations will only be accepted up to two weeks prior to the conference.

Program and speakers are subject to change. Video and or audio recording of any kind is prohibited onsite at all CHI events.

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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 CD, your abstract must be submitted, accepted and registration paid in full by September 8, 2008. Register online to use the Poster Abstract Submission form or, if you register by phone, fax, or mail, you will receive Poster Abstract Submission guidelines via email. I am interested in presenting a poster at:

- Biomarker Discovery Summit 2008
- and will submit a complete one-page abstract by Sept. 8, 2008.

(Please note. Registration must be paid in full to present a poster.)

Title

Disclosure of Potential Conflicts of Interest

Dual Commitments

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Pre-Conference Events (September 29)

**Single Workshop:**

<table>
<thead>
<tr>
<th>Workshop Title</th>
<th>COMMERCIAL</th>
<th>ACADEMIC, GOVERNMENT, HOSPITAL-AFFILIATED</th>
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<tbody>
<tr>
<td>Technology Advances for Protein Biomarker Discovery (8:00 am-3:00 pm)</td>
<td>$995</td>
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**Two Workshops:**

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<tr>
<td>Novel Approaches to Cancer Biomarkers (12:00-3:00 pm)</td>
<td>$695</td>
<td>$395</td>
</tr>
</tbody>
</table>

CONFERENCE PRICING

<table>
<thead>
<tr>
<th>Main Conference</th>
<th>COMMERCIAL</th>
<th>ACADEMIC, GOVERNMENT, HOSPITAL-AFFILIATED</th>
</tr>
</thead>
<tbody>
<tr>
<td>Advance Registration until August 22, 2008</td>
<td>$1795</td>
<td>$875</td>
</tr>
<tr>
<td>Registration after August 22, 2008</td>
<td>$1995</td>
<td>$945</td>
</tr>
</tbody>
</table>

Poster Discount $50 off

**Invoices unpaid two weeks prior to conference will be billed to credit card at full registration rate. Invoices must be paid in full and checks received by the deadline date to retain registration discount. If you plan to register on site, please check with CHI beforehand for space availability.**

**Credit your registration to another Cambridge Healthtech Institute program**

**Transfer your registration to a colleague within your organization**

**Credit your registration to another Cambridge Healthtech Institute program**

**Request a refund minus the cost ($500) of ordering a conference CD.**

**NOTE: Cancellations will only be accepted up to two weeks prior to the conference.**

Program and speakers are subject to change. Video and or audio recording of any kind is prohibited onsite at all CHI events.

**FAX or MAIL your registration to:**

Cambridge Healthtech Institute
250 First Avenue, Suite 300, Needham, Massachusetts 02494
T: 781-972-5400 or toll-free in the U.S. 888-999-6288
F: 781-972-5447 • www.healthtech.com

Disclosure of Potential Conflicts of Interest

Dual Commitments

**Substitution/Cancellation Policy**

In the event that you need to cancel a registration, you may:

- Transfer your registration to a colleague within your organization
- Credit your registration to another Cambridge Healthtech Institute program
- Request a refund minus a $100 processing fee per conference
- Request a refund minus the cost ($500) of ordering a conference CD.

**NOTE: Cancellations will only be accepted up to two weeks prior to the conference.**

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