# Genomics and Proteomics Hands On Workshop

## From Sample Preparation to Data Analysis

**SEATING IS LIMITED**

## July 8 – 17, 2009

A 10-day intensive hands-on workshop designed to provide a comprehensive view of proteomics, genomics, and bioinformatics to investigators who are currently utilizing, or are considering utilizing these methods in their own research.

## Location: University of Colorado Denver and National Jewish Health, Denver, CO

**Organizers:** Nichole Reisdorph, PhD, Chris Coldren, PhD, Katerina Kechris, PhD, and Tzu Phang, PhD

**www.nationaljewish.org/NHLBIworkshop**

National Jewish Health™
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University of Colorado Denver

"The NHLBI Proteomics and Genomics Workshop was an ideal mix of theory-based and practical hands-on training"

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# Twenty slots are available

## Deadline for applications is April 17, 2009

Applicants will be notified in late May. Unsuccessful applicants will have the option of being placed on a waiting list in the event that additional slots become open.

## Who should apply

This course is appropriate for individuals with little to no experience in genomics and proteomics who are considering or are currently utilizing these technologies in their research. Minorities and women are strongly encouraged to apply. National Jewish Health and The University of Colorado are committed to diversity and equality in education and employment.

## Specific target audience

Basic and clinical scientists, principle investigators, post-doctoral fellows, graduate students in their final year of training, "omics" core users, bioinformaticists, and others who need to be familiar with typical "omics" workflows. Applicants with current NHLBI funding or NHLBI supported positions (e.g., medical post-doctoral fellows) will be given priority in filling the training slots. Individuals with current NIH funding in the areas of interest to NHLBI (diseases of the heart, lung, blood, and sleep disorders) are also be encouraged to apply.

## Requirements

Applicants are not expected to have prior experience in using "omics" approaches but a more general background in molecular approaches to research problems and laboratory methods is preferred. Primary appointment must be in the United States as faculty (principal investigator or research faculty), post-doctoral student, or graduate student in his/her final year upon course completion. Applicants must agree to submit follow-up surveys and that pre-requisites will be met prior to the course. (For more information on pre-requisites, please visit our website)

## Application Material

**Please visit www.nationaljewish.org/NHLBIworkshop to apply on-line.** Applicants will be required to submit the following: a cover letter, current curriculum vitae, and the application form which includes a clear justification for and a concise description on how these technologies will be incorporated into his/her research program. Graduate and post-doctoral students must provide 3 strong letters of support. *Please note that last years applications were highly competitive!*

Scholarship application: Those who wish to apply for a scholarship (free tuition plus lodging/travel allowance up to $1500) should indicate this on their application. Scholarship applicants will be required to submit additional information and will be contacted after their application has been received.

## Course location

The workshop will be held at the University of Colorado at Denver Aurora campus and National Jewish Health in Denver, Colorado.

## Miscellaneous Information

Prerequisite material, in the form of readings and on-line tutorials/courses, must be completed prior to attending the workshop.

Hotel and lodging information will be available in May for course participants.

A detailed curriculum is available on-line

A listing of planned social and group events, as well as local attractions, will be made available in May.

"The small class size permitted one-on-one interaction with instructors..."

**Scholarships are available**

# WORKSHOP PROGRAM

## Proteomics

**Lecture Topics:** Introduction to Mass Spectrometry, Introduction to Database Searching, Front-End Technologies, Advanced Technologies, and Quantitative Proteomics.

**Laboratories** are divided into 3 stations where participants receive hands-on experience in:

**Station I:** Sample Preparation: protein digestion and sample cleanup, phosphopeptide enrichment, peptide labeling

**Station II:** Instrumentation: includes high performance liquid chromatography (HPLC) and 3 mass spectrometers: ion trap, quadrupole time-of-flight, and electrospray time-of-flight. Students use multiple instruments to analyze their own peptide digests, generated during the sample preparation laboratories.

**Station III:** Practical Proteomics: introduction to database searching, off-line fractionation techniques, and spectral Interpretation.

**Database Searching:** The proteomics module culminates with a ½ day database searching laboratory where students analyze data they acquired on the mass spectrometers during the course. Includes: basic MS and MS/MS searching using MASCOT and Spectrum Mill, and spectral review and validation.

## Bioinformatics and Biostatistics:

**Bioinformatics lecture and hands-on laboratory sessions:**

- Gene and Protein Annotation
- Promoter Analysis
- Gene Interactions and Pathway Analysis
- Introduction to Protein Domain and Structure Databases
- Exploring the Genomic Context of Genes
- Database Resources for Genetic Variations and Disorders

**Biostatistics lectures include experimental design and common statistical functions. The optional Biostatistics workshop session will include hands-on experience with appropriate usage of common data analysis techniques.**

## Genomics

**Lectures:**

Principles and Applications of DNA Microarray Technology, Advancing Translational Medicine with DNA Microarrays, Beyond Transcription Profiling: Genetic and Epigenetic applications of DNA Microarray Technology.

**Interactive Discussion:** How to Apply Microarray-based Transcript Profiling in Your Research: Strategies, Quality and Costs

Advancing Translational Medicine with DNA Microarrays

Beyond Transcription Profiling: Genetic and Epigenetic applications of DNA Microarray Technology

**Laboratories:**

**Microarray analysis:** Converting RNA into cDNA and cleanup, in vitro transcription reaction (biotin-labeling cRNA), and to be announced

**SNP Analysis:** SNP analysis using genome wide arrays and quantitative PCR

**Gene Expression Data Analysis:**

- Introduction and Installation of ArrayTools Components
- Compiling Gene Expression Datasets
- Normalization, Scaling, Data Filtering
- Class Averages and Fold-Change
- Cluster Analysis and other Visualization Tools
- Classifiers and Predictors
- Output for Figures and Presentations

## Miscellaneous topics and events:

- Optional workshops
  - Additional hands-on experience on several instruments
  - Two-dimensional gel electrophoresis and DiGE
  - Literature review sessions, statistics, grant writing
- Bioinformatics
- Responsible conduct in research
- Informal receptions
- Social and group events (rafting, hiking, scenic walks)

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Training is provided through a generous grant from the National Heart, Lung, and Blood Institute (NHLBI T15 HL086386-01)

# REGISTRATION

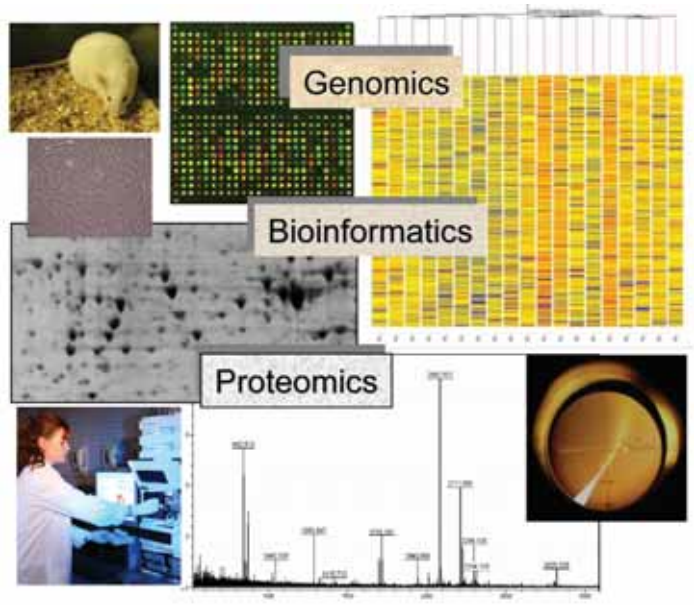
## Fees and registration

The tuition fee is $1,000 and covers items not allowable by NIH funding including: transportation to and from course facilities, lunch, continental breakfast, snacks and 4 dinners. Applicants are responsible for their own travel and lodging; negotiated hotel rates will be between $40 and $150 per night depending on the number of individuals per room.

If accepted, applicants must officially register at least 30 days prior to the class (last date to register is June 10, 2009). A $250 non-refundable registration fee will be charged. Applicants can withdraw from the class 14 days prior to the class (last date to withdraw is July 24, 2009) and receive their tuition minus the registration fee. Applicants withdrawing less than 14 days prior to the class will lose the entire tuition fee.

Three scholarships will be awarded to individuals who submit a strong application along with a justification for need. Scholarship awardees will receive a travel and lodging allowance (up to $1500) and free tuition. To apply for a scholarship, please check the appropriate box on the application.

Registration information will be sent to applicants who are accepted into the program




## Guest Speakers

**Keynote Speaker**

**David Schwartz, MD**

Professor,
Department of Medicine

Head, Division of Pulmonary and Critical Care Medicine

Director, Center for Genetics and Therapeutics

National Jewish Health

**David Erle, MD**

Professor of Medicine
University of California,
San Francisco

Director of UCSF NHLBI Shared Microarray Facility

UCSF Clinical and Translational Sciences Institute's Bioinformatics Program

**Mark Geraci, MD**

Professor of Medicine;
Division Head of Pulmonary Sciences/Critical Care Unit

University of Colorado at Denver

Director, UCD Microarray Facility

**Kevin Schey, PhD**

Professor of Biochemistry
Mass Spectrometry
Research Center

Vanderbilt University

**Alexey Nesvizhskii, PhD**

Assistant Professor of Pathology

University of Michigan