The ultimate vision for the National Heart, Lung, and Blood Institute's Proteomics Centers is to help better understand heart, lung, and blood disease biology. Hence, the goal of the NHLBI Proteomics Centers Contract Program is to promote the application of proteomic technologies to gain a greater understanding of physiologic pathways for defined clinical questions. The Program supports the development of new tools and a knowledgebase to facilitate translation of innovative proteomic approaches to clinical utility. The new tools will be used to gain a greater understanding of physiological pathways, molecular interactions, and regulatory signals related to heart, lung, blood diseases and disorders. The transdisciplinary expertise of each Center encompasses three components to make an interactive team and includes proteomic technology development, molecular mechanistic and functional studies as well as application of proteomic approaches and technologies to clinical questions. Importantly, many of the Centers will leverage existing NIH resources and programs. The Centers will not only help fill existing knowledge gaps, but will also contribute to the integration and creation of a knowledgebase linking changes in proteomes with molecular phenotypes of disease. Tools developed through the Proteomics Program will be made available to the larger community to further advance heart, lung, and blood research.

National Heart, Lung, and Blood Institute
National Institutes of Health

www.NHLBI-Proteomics.org
Robert (Bob) James Cotter, a Johns Hopkins scientist and Professor, died on November 12th, 2012 in Baltimore, Maryland. Best known for his work in mass spectrometry, during his career Dr. Cotter made a number of discoveries in both the health and science fields.

Dr. Cotter was an amazing chemist and one of the leading mass spectrometrist of his generation. Dr. Cotter’s research led to many advances in the field of time-of-flight mass spectrometry, diagnostic medicine, and biological chemistry. Of these, the most notable include the invention of the curved-field reflectron to improve mass resolution during time-of-flight mass spectrometry, the miniaturization of mass spectrometers for use in environmental surveys, clinical settings, and space exploration, and the development of a technique to quantitate protein acetylation.

From 1978 until his death in 2012, Robert Cotter served as a faculty member at the Johns Hopkins School of Medicine with the Department of Pharmacology and Molecular Sciences. Dr. Cotter also held joint appointments with the Department of Biophysics and Biochemistry and with the Johns Hopkins University Applied Physics Laboratory. Most recently, Dr. Cotter was serving as a co-investigator on the Mars Organic Molecule Analyzer (MOMA) project, developing a miniaturized, low power ion trap/time-of-flight mass spectrometer intended for the ExoMars Rover. At the time of his death, Cotter was also a key investigator at the Johns Hopkins University Proteomic Innovation Center in Heart Failure.

In addition to his wife, Dr. Catherine Fenselau Cotter, Robert Cotter is survived by his mother, five siblings, three children, and four grandchildren.

Notable Awards/Honors:
ASMS Award for Distinguished Contribution in Mass Spectrometry (June, 2011)
Frank H. Field & Joe L. Franklin Award for Outstanding Achievement in Mass Spectrometry (January, 2011)
American Chemical Society Division of Analytical Chemistry Award in Chemical Instrumentation (2009)

Books Authored:

Time-of-flight Mass Spectrometry.
Robert J. Cotter (Ed); ACS Symposium Series 549, American Chemical Society. Washington DC. 1994

Selection of Recent Publications:


NHLBI Proteomics Coordinating and Administration Center

The NHLBI Proteomics Coordinating and Administration Center coordinates information from the seven National Heart, Lung, and Blood Institute Proteomics Centers to provide consistent and up-to-date information about their achievements and to share the innovative proteomics resources they produce. CLICK HERE TO LEARN MORE: http://www.nhlbi-proteomics.org

Recent Events

The NHLBI Proteomics Centers’ Fifth PI Meeting was successfully adjourned on March 6th, 2013 in Stanford, CA. From March 5th – 6th, 2013, the NHLBI Proteomics Centers’ Fifth PI Meeting was held at the Li Ka Shing Center for Learning and Knowledge at Stanford University School of Medicine in Stanford, CA. Representatives from each of the seven Centers delivered presentations summarizing their significant accomplishments and milestones since the award inception three years ago. Thank you to Dr. Garry Nolan for hosting this event at Stanford University, and a special thank you to Mr. Howard Guss of Dr. Nolan’s lab for assisting the NHLBI Proteomics Coordinating and Administration Center in the organization of this meeting.

On June 19th and 20th, 2012, NHLBI and NCI jointly hosted a workshop on "Omnics Integration in Biology and Medicine" at the Cloisters, Building 60 of NIH campus, in Bethesda, Maryland. The two day workshop was attended by 400+ scientists worldwide, NIH program directors, and staff members with stimulating discussions. Click here for the live video cast.

2013 Upcoming Scientific Events

ASMS Conference on Mass Spectrometry and Allied Topics
June 9th – 13th, 2013, Minneapolis Convention Center, Minneapolis, MN
http://www.asms.org/conferences/annual-conference

Basic Cardiovascular Sciences 2013 Scientific Sessions
July 22nd – 25th, 2013, Las Vegas, Las Vegas, NV
http://my.americanheart.org/professional/Sessions/BCVS/BCVS_UCM_316903_SubHomePage.jsp

HUPO 12th Annual World Congress, Yokohama
September 14th – 18th, 2013, Yokohama, Japan
http://www.hupo.org

SGP (Society of General Physiologists)
September 4th – 8th, 2013, Woods Hole, MA
http://www.sgpweb.org/symposium2013.html

American Heart Association’s Scientific Sessions
November 16th – 20th, 2013, Dallas Convention Center, Dallas, TX
http://my.americanheart.org/professional/Sessions/ScientificSessions/Scientific-Sessions_UCM_316900_SubHomePage.jsp

NHLBI Proteomics Coordinating and Administration Center
www.NHLBI-Proteomics.org

Dr. Jun Zhang,
Director

Ms. Kimberly Bunje,
Sr. Administrative Analyst
Boston University Cardiovascular Proteomics Center

The Boston University Cardiovascular Proteomics Center (CPC) is a research institute studying oxidative stress using proteomics technologies. The CPC is investigating post-translational modifications of proteins that are of high importance in signaling mechanisms and altered by oxidative chemical reactions in cardiovascular disease. The CPC is developing and applying new proteomics methodologies and instrumentation for the analysis of known and novel proteins and the qualitative and quantitative determinations of their post-translational modifications. 

CLICK HERE TO LEARN MORE: http://www.nhlbi-proteomics.org/pages/centers-bos

Recent Publications

Energy-dependent electron activated dissociation of metal-adducted permethylated oligosaccharides. Yu X, Huang Y, Lin C, Costello CE. Anal Chem. 2012 Sep 4;84(17):7487-94. The effects of varying the electron energy and cationizing agents on electron activated dissociation (ExD) of metal-adducted oligosaccharides were explored using permethylated maltoheptaose as the model system. Across the examined range of electron energy, the metal-adducted oligosaccharide exhibited several fragmentation processes, including electron capture dissociation (ECD) at low energies, hot-ECD at intermediate energies, and electronic excitation dissociation (EED) at high energies. The dissociation threshold depended on the metal charge carrier(s), whereas the types and sequence spans of product ions were influenced by the metal-oligosaccharide binding pattern. Click on Link to Read Full Article: http://pubs.acs.org/doi/full/10.1021/ac301589z

Nox4- and Nox2-dependent oxidant production is required for VEGF-induced SERCA cysteine-674 S-glutathiolation and endothelial cell migration. Evangelista AM, Thompson MB, Bolotina VM, Tong X, Cohen RA. Free Radic Biol Med. 2012 Oct 23;53(12):2327-2334. Endothelial cell (EC) migration in response to vascular endothelial growth factor (VEGF) is a critical step in both physiological and pathological angiogenesis. Although VEGF signaling has been extensively studied, the mechanisms by which VEGF-dependent reactive oxygen species (ROS) production affects EC signaling are not well understood. The aim of this study was to elucidate the involvement of Nox2- and Nox4-dependent ROS in VEGF-mediated EC Ca(2+) regulation and migration. VEGF-induced migration of human aortic ECs into a scratch wound over 6 hours, which was inhibited by overexpression of either catalase or superoxide dismutase (SOD). EC stimulation by micromolar concentrations of H(2)O(2) was inhibited by catalase but also, unexpectedly, by SOD. Both VEGF and H(2)O(2) increased S-glutathiolation of SERCA2b and increased Ca(2+) influx into EC, and these events could be blocked by overexpression of catalase or overexpression of SERCA2b, in which the reactive cysteine-674 was mutated to a serine. Click on Link to Read Full Article: http://www.sciencedirect.com/science/article/pii/S0891584912017777

Relationship of plasma galectin-3 to renal function in patients with heart failure: effects of clinical status, pathophysiology of heart failure, and presence or absence of heart failure. Gopal DM, Kommineni M, Ayalon N, Koelbl C, Ayalon R, Biolo A, Dember LM, Downing J, Siwik DA, Liang CS, Colucci WS. J Am Heart Assoc. 2012 Oct;1(5):e000760. BACKGROUND: Galectin-3 (GAL-3), a β-galactoside-binding protein, is a new clinical biomarker believed to reflect cardiac remodeling/fibrosis in patients with heart failure (HF). Plasma GAL-3 is inversely related to renal function. It is not known whether the relationship between renal function and GAL-3 is influenced by clinical decompensation, type of HF, or the presence or absence of clinical HF. METHODS AND RESULTS: Patients were prospectively categorized as having acute decompensated HF or stable HF on the basis of clinical status and as having HF with reduced left ventricular ejection fraction or HF with preserved left ventricular ejection fraction. Click on Link to Read Full Article: http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3541630/
The central philosophy of the Johns Hopkins Proteomic Innovation Center is that innovative technologies in proteomics will be essential to pursue compelling biological and clinical questions. The highly collaborative and integrated nature of our investigator team allows us to keep focused on clinically-relevant problems and provide rapid paths to translational medicine.

CLICK HERE TO LEARN MORE: http://www.nhlbi-proteomics.org/pages/centers-jh

Jennifer E. Van Eyk, PhD
Director, Johns Hopkins NHLBI Proteomics Innovation Center in Heart Failure
JHU Bayview Proteomics Center.
Professor of Medicine, Biological Chemistry and Biomedical Engineering,
Johns Hopkins University

Anne Murphy, MD
Co-PI, Johns Hopkins NHLBI Proteomics Innovation Center in Heart Failure
Professor, School of Medicine
Johns Hopkins University

Key Investigators

Robert Cole, PhD
Dept. Biological Chemistry, School of Medicine

Josef Coresh, MD, PhD
Dept. Epidemiology, School of Public Health

David Graham, PhD
Dept. Mol. and Comp. Pathobiology, School of Medicine

Gerald Hart, PhD
Dept. Biological Chemistry, School of Medicine

David Kass, MD
Dept. Medicine, School of Medicine

Edgar Miller, MD, PhD
Dept. Medicine, School of Medicine

Brian O’Rourke, PhD
Dept. Medicine, School of Medicine

Akhilesh Pandey, MD, PhD
Institute of Genetic Medicine, School of Medicine

Gregg Semenza, MD, PhD
Dept. Pediatrics, School of Medicine

Hui Zhang, PhD
Dept. Pathology, School of Medicine

Recent Publications

Multiple reaction monitoring to identify site-specific troponin I phosphorylated residues in the failing human heart.
Six novel phosphorylation sites of cardiac troponin I, a key regulatory protein in heart, were identified using MRM, an absolute quantitative targeted MS method. The extent of phosphorylation of each known and novel residue of troponin I was quantified in control versus failing human cardiac muscle. This methodology has been moved to serum where alterations in specific phosphorylation sites may serve as biomarker for heart failure.
Click on Link to Read Full Article: http://circ.ahajournals.org/content/126/15/1828.long

Cysteine oxidative posttranslational modifications: emerging regulation in the cardiovascular system.
Chung HS, Wang SB, Venkatraman V, Murray CI, Van Eyk JE.
In the cardiovascular system, changes in oxidative balance can affect many aspects of cellular physiology through redox-signaling. Depending on the magnitude, fluctuations in the cell’s production of reactive oxygen and nitrogen species can regulate normal metabolic processes, activate protective mechanisms, or be cytotoxic. Reactive oxygen and nitrogen species can have many effects including the posttranslational modification of proteins at critical cysteine thiols. A subset can act as redox-switches, which elicit functional effects in response to changes in oxidative state. Although the general concepts of redox-signaling have been established, the identity and function of many regulatory switches remain unclear.
Click on Link to Read Full Article: http://circres.ahajournals.org/content/112/2/382.long

Histone demethylase JMJD2C is a coactivator for hypoxia-inducible factor 1 that is required for breast cancer progression.
SILAC cell based labeling was used to identify unique regulators of transactivation of HIF-1 and HIF-2, in collaboration with the Pandey lab. This led to the discovery that histone demethylase JMJD2C selectively interacts with HIF-1a, but not HIF-2a. HIF-1a mediates recruitment of JMJD2C to the hypoxia response elements of HIF-1 target genes. JMJD2C decreases trimethylation of histone H3 at lysine 9 enhancing HIF-1 binding to hypoxia response elements, thereby activating transcription of genes encoding proteins required for metabolic reprogramming and the extracellular matrix. This establishes an important epigenetic mechanism that stimulates HIF-1-mediated transcription.
Click on Link to Read Full Article: http://www.pnas.org/content/109/49/E3367.long
Harvard-Broad Proteomics Center

The overall goal of our Center is to identify novel pathways and biomarkers of ischemic heart disease. Our Center’s approach integrates three core components: 1) Proteomic Technology Development, led by Dr. Steven Carr (Broad Institute); 2) Molecular Mechanistic and Functional Studies, led by Drs. Anthony Rosenzweig and Robert Gerszten; and 3) Application of Proteomics Approaches to Clinical Questions, led by Drs. Marc Sabatine and Robert Gerszten. The overall goal is to identify new metabolites and proteins that mark disease activity, shed insight into disease progression, and ultimately provide targets for therapeutic intervention.

CLICK HERE TO LEARN MORE: http://www.nhlbi-proteomics.org/pages/centers-harvard

Robert Gerszten, MD
Director, Translational Research in the Cardiology Division
Director, Harvard – Broad Proteomics Center
Associate Professor of Medicine, Harvard Medical School

Co-PIs

Steven Carr, PhD
Broad Institute
Director, Proteomics Platform at the Broad Institute of MIT and Harvard

Anthony Rosenzweig, MD
Beth Israel Deaconess Medical Center
Director, Cardiovascular Research
Associate Chief of Cardiology

Marc S. Sabatine, MD, MPH
Brigham & Women's Hospital
Associate Professor of Medicine

Key Investigators

Gregory Lewis, MD
Massachusetts General Hospital
Associate Director of the MGH Cardiopulmonary Exercise Laboratory

Michelle L. O'Donoghue, MD
Brigham & Women's Hospital
Instructor in Medicine

Recent Publications

Click on Link to Read Full Article: http://www.nature.com/nbt/journal/v29/n7/full/nbt.1899.html

Click on Link to Read Full Article: http://www.mcponline.org/content/11/6/M111.014423.long

Click on Link to Read Full Article: http://www.mcponline.org/content/12/3/825.long

Click on Link to Read Full Article: http://www.nature.com/nmeth/journal/v10/n1/full/nmeth.2309.html

Click on Link to Read Full Article: http://www.sciencemag.org/content/338/6114/1549.long
The Stanford NHLBI Proteomics Center brings together an experienced interdisciplinary group of scientists with significant track records in the areas of PAH and autoimmunity, organized around several Cores and five Projects.

**Project 1 (led by Drs. Rabinovitch/Nicolls)** is investigating the role of viral triggers and inflammatory cells in PAH pathogenesis by using rodent models and patient samples.

**Project 2 (led by Dr. Nolan)** is developing Phospho-Flow cytometry and mass spectrometry for the isotope-based analysis of signaling pathways at the single-cell level.

**Project 3 (led by Dr. Robinson)** is characterizing serum autoantibodies and cytokines to define the autoimmune targets associated with disease initiation and progression, with the ultimate goal of developing "clinically actionable" diagnostics for PAH.

**Project 4 (led by Dr. Utz)** is evaluating the contribution of cytokines, chemokines, growth factors, and signaling pathways to PAH in animals and patients by using the High-throughput Immunophenotyping using Transcription (HIT) and reverse phase lysate microarray proteomics platforms.

**Project 5 (led by Dr. Kodadek)** is developing peptoids as antagonists to perturb cells and as detector molecules to profile lineage-specific cell surface molecules and serum autoantibodies.

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**Recent Publications**

**Garry Nolan, PhD**
Director, Proteomics Center at Stanford University

Rachford and Carlota A. Harris
Professor, Microbiology & Immunology,
Baxter Laboratory for Stem Cell Biology

COP9 signalosome component JAB1/CSN5 is necessary for T cell signaling through LFA-1 and HIV-1 replication. Kinoshita SM, Krutzik PO, Nolan GP.
Click on Link to Read Full Article:

**Marlene Rabinovitch, MD**
Professor, Pediatrics – Cardiology
Member, Bio-X

Molecular pathogenesis of pulmonary arterial hypertension. Rabinovitch M.
Click on Link to Read Full Article:
[http://www.jci.org/articles/view/60658](http://www.jci.org/articles/view/60658)

**Mark Nicolls, MD**
Associate Professor, Medicine – Pulmonary and Critical Care Medicine
Member, Child Health Research Institute

Developing better biomarkers for connective tissue disease-associated interstitial lung disease: Citrullinated HSP-90 autoantibodies in rheumatoid arthritis. Deane KD, Nicolls MR.
Click on Link to Read Full Article:

**William H. Robinson, MD, PhD**
Associate Professor, Medicine – Immunology & Rheumatology
Member, Bio-X

Response to ‘Plasma proteins present in osteoarthritic synovial fluid can stimulate cytokine production via Toll-like receptor 4’ - authors’ reply.
Sohn DH, Sokolove J, Sharpe O, Erhart JC, Chandra PE, Lahey LJ, Lindstrom TM, Hwang I, Bayer KA, Andriacchi TP, Robinson WH.
Click on Link to Read Full Article:
[http://arthritis-research.com/content/14/5/406](http://arthritis-research.com/content/14/5/406)

**Paul J. Utz, MD**
Professor, Medicine – Immunology & Rheumatology
Member, Bio-X

Correction: Specific post-translational histone modifications of neutrophil extracellular traps as immunogens and potential targets of lupus autoantibodies. Liu CL, Tangsombatvisit S, Rosenberg JM, Mandelbaum G, Gillespie EC, Gozani OP, Alizadeh AA, Utz PJ.
Click on Link to Read Full Article:
[http://arthritis-research.com/content/14/4/403](http://arthritis-research.com/content/14/4/403)

**Thomas Kodadek, PhD**
Professor
Vice Chair, Department of Chemistry
Department of Chemistry
Scripps Florida Campus

Synthesis of libraries of peptidomimetic compounds containing a 2-oxopiperazine unit in the main chain. Suwal S, Kodadek T.
Click on Link to Read Full Article:
[http://pubs.rsc.org/en/Content/ArticleLanding/2013/OB/c3ob27476d](http://pubs.rsc.org/en/Content/ArticleLanding/2013/OB/c3ob27476d)
Congratulations to Merry L. Lindsey, PhD, on her new position as Director of the Jackson Center for Heart Research at the University of Mississippi Medical Center. Dr. Lindsey remains the Principal Investigator of the UT Health Science Center at San Antonio Cardiovascular Proteomics Center, but Dr. Lindsey’s move to Jackson created changes at the San Antonio Cardiovascular Proteomics Center, which is now under the direction of Co-PI, Richard A. Lange, MD. Dr. Lange is Professor and Executive Vice Chairman of Medicine and Director of the Office of Educational Programs.

CLICK HERE TO LEARN MORE: http://www.nhlbi-proteomics.org/pages/centers-uthsc

**Merry Lindsey, PhD, FAHA, FAPS**
Principal Investigator
Director, Jackson Center for Heart Research
Department of Physiology & Biophysics
University of Mississippi Medical Center

**Richard A. Lange, MD, MBA**
Co-Principal Investigator
Professor & Executive Vice Chair of Medicine
Department of Medicine
UT Health Science Center at San Antonio

Dr. Lindsey participated in a podcast interview with AJP Heart and Circulatory Physiology regarding the review article, “The history of matrix metalloproteinases: milestones, myths, and misperceptions”, by Iyer et al, published in Oct 2012. Joining Dr. Lindsey were Editor in Chief Dr. William Stanley and expert Dr. Loren Wold from the Research Institute at Nationwide Children’s Hospital.

Click Here to Listen: http://ajpheart.podbean.com/2012/12/17/mmps-milestones-myths-and-misperceptions/

**Ganesh V. Halade, PhD,** presented research seminars for the Comprehensive Cardiovascular Center, Department of Medicine at the University of Alabama; for the Department of Human and Health Physiology, the College of Liberal Arts and Sciences at University of Iowa; and for the Department of Medicine at the University of Texas Health Science Center at San Antonio. His seminars emphasized Cardiac Remodeling in Response to Myocardial Infarction in Obesity and were very well-received.

**Yonggang Ma, PhD,** His manuscript entitled “Matrix Metalloproteinase-28 Deletion Exacerbates Cardiac Dysfunction and Rupture Following Myocardial Infarction in Mice by Inhibiting M2 Macrophage Activation” was published in the Feb 14 issue of Circulation Research. The article was accompanied with an editorial by Dr. Frank Spinale and has already generated several reprint requests. Nice work, Dr. Ma.

**Kristi DeLeon, PhD,** was recently awarded a two-year fellowship grant from the American Heart Association, entitled “P. Gingivalis Primes The Post-Myocardial Infarction Remodeling Response,” in the amount of $90,772. Dr. DeLeon was also awarded an APS Minority Travel Fellowship Award to attend EB 2013 in Boston from April 20-24. Dr. DeLeon was chosen out of a pool of 64 applicants, so the competition was quite tough. Join us in congratulating Dr. DeLeon for her outstanding performance.

**Elizabeth Lopez** has matched with the University of Texas Medical Branch (UTMB) in Galveston to attend medical school and will officially join the UTMB School of Medicine Class of 2017 in August of this year. Liz has been a member of the Lindsey Lab since her junior year in high school and is a co-author on 5 manuscripts (to date). We are very proud of her and will miss her.

**Andrew Voorhees,** a predoctoral candidate in the laboratory of Dr. Hai-Chao Han, was admitted to candidacy in December 2012. The title of his dissertation work is “A Multi-Scale Mechanical Analysis of Left Ventricle Extracellular Matrix Remodeling Post-Myocardial Infarction.” Congratulations and well done, Andrew.
University of Texas Medical Branch
NHLBI Proteomics Center at Galveston

The UTMB NHLBI Proteomics Center is pursuing both proteomics technology development and directed proteomics research to investigate total protein expression in order to obtain a more global understanding of biological phenomena. The overall theme of this Center is airway inflammation focusing on asthma, allergy, and respiratory viruses. CLICK HERE TO LEARN MORE: http://www.nhlbi-proteomics.org/pages/centers-utmb

Team 1: Innovative Methods Development
Team 2: Array-Based Technologies
Team 3: Protein Complexes & Signaling in Lung Mucosal Cells
Team 4: Leukocytes in Airway Inflammation
Team 5: Oxidative Stress in Asthma/COPD

Team 6: Molecular Phenotypes in Asthma/COPD
Team 7: Oxidative Lung Injury in Respiratory Viral Infections
Core A: Dynamic Cell & Tissue Imaging
Core B: Informatics/Bioinformatics
Core C: Biomarker Verification

KEY INVESTIGATORS

Alexander Kurosky, PhD
Professor
Department of Biochemistry & Molecular Biology
Director, UTMB Biomolecular Resource Facility
Director, UTMB NHLBI Proteomics Center on Airway Inflammation
Team 1 Leader: Innovative Methods Development
Team 4 Leader: Leukocytes in Airway Inflammation

Allan R. Brasier, MD
Associate Center Director, UTMB NHLBI Proteomics Center on Airway Inflammation
Team 3 Leader: Protein Complexes & Signaling in Lung Mucosal Cells
Team 6 Leader: Molecular Phenotypes in Asthma/COPD

Recent Publications

Model studies on iTRAQ modification of peptides: sequence-dependent reaction specificity.
Click on Link to Read Full Article: http://pubs.acs.org/doi/full/10.1021/pr2003165

Aptamers and the next generation of diagnostic reagents.
Click on Link to Read Full Article: http://onlinelibrary.wiley.com/doi/10.1002/prca.201200042/full

Down-regulation of 8-oxoguanine DNA glycosylase 1 expression in the airway epithelium ameliorates allergic lung inflammation.
Click on Link to Read Full Article: http://www.sciencedirect.com/science/article/pii/S1568786412002169

Quantitation of the dynamic profiles of the innate immune response using multiplex selected reaction monitoring-mass spectrometry.
Click on Link to Read Full Article: http://www.mcponline.org/content/early/2013/02/15/mcp.M112.023465.long

Respiratory syncytial virus infection: mechanisms of redox control and novel therapeutic opportunities.
Click on Link to Read Full Article: http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3513983/
The NHLBI Proteomics Center at UCLA consists of an international effort led by the UCLA School of Medicine. The central scientific goal aims to provide fundamental information on the proteome biology of cardiovascular diseases, an essential component of the "Human Proteome Initiative". The diverse expertise of our investigator team integrates an array of leading technologies, model systems, and clinical studies for performing global, quantitative, and targeted proteomic analyses, including leveraging the resources offered by the UniProt Project and the Human Protein Atlas. We aim to construct a proteome knowledgebase for the scientific community to empower new discovery in cardiovascular medicine.

CLICK HERE TO LEARN MORE: http://www.nhlbi-proteomics.org/pages/centers-ucla

Recent Publications

A novel spectral library workflow to enhance protein identifications. 
Click on Link to Read Full Article: http://www.sciencedirect.com/science/article/pii/S1874391913000560

Protein Analysis by Shotgun/Bottom-up Proteomics.
Click on Link to Read Full Article: http://pubs.acs.org/doi/abs/10.1021/cr3003533

Use of Gene Ontology Annotation to understand the peroxisome proteome in humans.
Click on Link to Read Full Article: http://database.oxfordjournals.org/content/2013/bas062.long

Contribution of Antibody-based Protein Profiling to the Human Chromosome-centric Proteome Project (C-HPP).
Click on Link to Read Full Article: http://pubs.acs.org/doi/abs/10.1021/pr300924j

Achievements

Dr. Mario Deng, who is the Medical Director of Advanced Heart Failure, Mechanical Circulatory Support and Heart Transplant Program at UCLA, has been leading the clinical studies as the new clinical study Project Leader. He has revitalized the team and has played a critical role in guiding the clinical studies and in patient enrollment.

Dr. Maggie (Pui Yu) Lam has received an AHA Western States Affiliate Postdoctoral Fellowship Award in 2012. She has first authored two publications on developing a MRM strategy to characterize phosphorylation of cardiac mitochondrial proteins.

Mr. Edward Lau is a recipient of an AHA Pre-doctoral Fellowship. He also won the 2012 ISHR (American Section) Poster Competition Award in Banff, Canada.

Ms. Amanda Lin has been recruited as a new graduate student by the Molecular, Cellular, and Integrative Physiology Program at UCLA. In working with others at the Center, she has successfully co-authored two manuscripts in 2012.

Dr. Ding Wang, an Assistant Researcher at UCLA, was awarded an AHA BCVS 2012 Travel Award. He has successfully published two first-author manuscripts with Mr. Edward Lau in Circulation Research and Molecular & Cellular Proteomics in 2012.
The Boston University Cardiovascular Proteomics Center (CPC) is a research center funded by the NIH/NHLBI to analyze and identify proteins that may be modified or created by cardiovascular disease (CVD) brought on by unfavorable metabolic conditions and diseases, including obesity, diabetes, and hyperlipidemia. The CPC is developing and applying a targeted proteomic approach and bioinformatics tools to detect the effects of abnormal metabolism on proteins. The identification of a set of markers of metabolic dysfunction may afford opportunities to be used as tissue-specific biomarkers of the disease. These will provide new and powerful approaches for the detection and monitoring of metabolic CVD.

(Center Director: Catherine E. Costello, Ph.D.)

Johns Hopkins Proteomics Innovation Center in Heart Failure
www.hopkinsmedicine.org/proteomics

The mission of the Johns Hopkins Proteomics Innovation Center in Heart Failure is to apply state-of-the-art proteomic methods and develop new approaches and techniques to investigate the biological and clinical aspects of heart failure. Heart failure is a clinical syndrome in which cardiovascular function is insufficient to support the metabolic needs of the body. Many gaps in understanding heart failure remain, and it is the goal of this Center to identify how heart failure impacts signaling cascades, mitochondria, contractile apparatus, and two new subproteomes (the cell surface and secretory pathway), emphasizing post-translational modifications in order to identify novel ways by which protein modifications either contribute to disease or could be targeted to improve disease outcome.

(Center Director: Jennifer E. Van Eyk, Ph.D.)

Harvard – Broad Proteomics Center
www2.massgeneral.org/crc/ translational.html

The overall goal of the Center is to establish the infrastructure necessary for the discovery and validation of novel pathways and biomarkers triggered by myocardial ischemia. Our multidisciplinary investigator team contributes expertise in basic science, diagnosis and treatment of acute coronary syndromes, epidemiology, bioinformatics, basic and clinical chemistry, and proteomics. The Center is comprised of a consortium of cooperating institutions, including the Massachusetts General Hospital, Brigham and Women’s Hospital, the Thrombolysis In Myocardial Infarction (TIMI) Study Group, Harvard Medical School, the Beth Israel Deaconess Medical Center, and the Broad Institute.

(Center Director: Robert E. Gerszten, M.D.)

Stanford University Proteomics Center
www.proteomics.stanford.edu

Pulmonary arterial hypertension (PAH) is a devastating disease that affects over 5,000 Americans. By the time patients display even vague and insidious symptoms, such as fatigue and dyspnea, they have much higher PA pressures, which eventually result in right-side heart failure. Our Center’s approach is a highly interdisciplinary effort to explore and converge results from different, innovative platform technologies that analyze intracellular and secreted proteins related to PAH with a continuing development of relational “systems” approaches that allow the integration, comparison, and correlation of different datasets generated by diverse technologies developed at the Center.

(Center Director: Garry P. Nolan, Ph.D.)

UTHSCSA Cardiovascular Proteomics Center
www.barshop.uthscsa.edu/main/science/u46

Our Center is dedicated to performing cardiovascular research that involves: 1) Developing multidimensional approaches to examine the mechanisms whereby the left ventricle responds to injury; 2) Applying the knowledge gained to develop therapeutic strategies to prevent, slow, or reverse the progression to heart failure; and 3) Disseminating our results to the general, scientific, and medical communities. The goal of the UTHSCSA Cardiovascular Proteomics Center is to develop novel proteomic technologies to identify predictive markers of adverse remodeling of the left ventricle (LV) following myocardial infarction (MI), focusing on extracellular matrix (ECM) fragment generation as a key initiating event.

(Center Director: Merryl L. Lindsey, Ph.D.)

UT Medical Branch NHLBI Proteomics Center at Galveston
www.utmb.edu/brf

The UTMB NHLBI Proteomics Center brings the power of multiple analytical technologies to proteomics research, focusing on airway inflammation relating to asthma, allergy, and respiratory viruses. The Center consists of seven multidisciplinary teams of scientists and physician-scientists to study protein expression associated with signaling pathways important in lung diseases. In addition, the Center is engaged in the development of innovative technologies for application to proteomics research. The NHLBI Proteomics Initiative was established to enhance and develop innovative proteomics technologies and apply them to biological questions relevant to heart, lung, blood, and sleep health and disease.

(Center Director: Alexander Kurosky, Ph.D.)

UCLA Proteomics Center – Global Proteomics Initiative
www.nhlbi-ucla.org

The NHLBI Proteomics Center at UCLA consists of an international effort led by the UCLA School of Medicine. The central scientific goal aims to provide fundamental information on the proteomic biology of cardiovascular diseases, an essential component for the “Human Proteome Initiative”. The diverse expertise of our investigator team integrates an array of leading technologies, model systems, and clinical studies for performing global, quantitative, and targeted proteome analyses, including leveraging the resources offered by the UniProt Project and the Human Protein Atlas. We have constructed a COPa knowledgebase (www.heartproteome.org), a resource for proteome biology configured specifically for cardiovascular investigators, to empower new discoveries in cardiovascular medicine.

(Center Director: Peipei Ping, Ph.D.)

NHLBI Proteomics Coordinating and Administration Center
www.nhlbi-proteomics.org

The NHLBI Proteomics Coordinating and Administration Center carries out administrative duties for all the NHLBI Proteomic Research Centers and is charged with raising the profile of their work. Located at the David Geffen School of Medicine at UCLA, the Administration Center is tasked with harmonizing the outputs of the seven Proteomics Centers within the Program and presenting their work to the world.

(Center Director: Jun Zhang, Ph.D.)
NHLBI Proteomics Program
Coordinating and Administration Center
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