ISN Forefronts Symposium 2016
The Metabolome and Microbiome
in Kidney Disease
September 23-25 2016
San Diego (CA), USA

Program

Friday

Welcome & Opening Lecture

Chairs: Kumar Sharma, USA, Katalin Susztak, USA, Subramaniam Pennathur, USA

09:00 - 09:05   Welcome Address by the Symposium Co-Chair
Kumar Sharma, USA

09:05 - 09:10   Welcome Address by the UCSD School of Medicine Dean
David Brenner, USA

09:10 - 10:00   Keynote Lecture I:
Intersection of mitochondria and metabolism in human disease in the
21st century
Ronald Evans, USA

Session 1:   *Moderator: Kumar Sharma, USA*

Glimpse into the future of metabolomics

10:00 - 10:25   Digitizing the chemistry of microbes
Pieter Dorrestein, USA

10:25 - 10:50   The panoramic view, new application, and implications of large scale global
kidney cancer metabolism
James Hsieh, USA

10:50 - 11:15   Human microbiome and gut diversity
Rob Knight, USA

11:15 - 11:40   Genetic influences of metabolism in CKD
Anna Koettgen, Germany

11:40 - 11:55   Oral presentation from abstract submissions: *Poster Board: P13*
Genome-wide association studies of metabolites in chronic kidney disease:
Methodological aspects
Anna Koettgen, Germany

11:55 - 13:20   *Networking Lunch & Poster Viewing*

Session 2:

Moderators: Moshe Levi, USA and Pieter Dorrestein, USA

Microbiome as the determinant of disease

13:20 - 13:45   The microbiome and metabolome in uremia
Tim Meyer, USA

13:45 - 14:10   Gut and urine microbiome linked to urinary disorders
Rembert Pieper, USA

14:10 - 14:35   Gut microbiome as a target and treatment of CKD/CVD
Wai Hong Wilson Tang, USA

14:35 - 14:50   Oral presentation from abstract submissions: *Poster Board: P04*
Kidney stones: A product of dynamic interaction between the microbiome
and mineral precipitation
Jessica Saw, USA

14:50 - 15:30   *Coffee Break & Poster Viewing*

Session 3:

Moderators: James Hsieh, USA and Mohit Jain, USA

Metabolism and cancer biology

15:30 - 15:55   Metabolic flux analysis and metabolic phenotypes of transformed cells
Roland Nilsson, Sweden

15:55 - 16:20   Crossroads between the metabolome and genetic susceptibility
Gabriele Kastenmüller, Germany

16:20 - 16:45   Prostate, breast, racial disparity in cancer: Role of metabolomics
Arun Sreekumar, USA

16:45 - 17:00   Oral presentation from abstract submissions: *Poster Board: P01*
Mass spectrometry imaging reveals elevated glomerular ATP/AMP in
diabetic mice and identifies sphingomyelin as a key mediator in regulation of
AMPK activity
Satoshi Miyamoto, Japan

17:00 - 18:30   *Welcome & Networking Reception*

Saturday

Session 4:

Moderators: Jeremy Duffield, USA, Uwe Sauer, Switzerland

Metabolism and obesity

08:10 - 09:00   **Keynote Lecture II:**
Metabolomics as a hypothesis generator for microbe-host interactions
Uwe Sauer, Switzerland

09:00 - 09:25   Mitochondrial signaling and diabetes
Josephine Forbes, Australia

09:25 - 09:50   Modified Warburg effect in CKD
Kumar Sharma, USA

09:50 - 10:15   Metabolism and clinical applications
David Wishart, Canada

10:15 - 10:30   Oral presentation from abstract submissions: *Poster Board: P17*
Metabolic flux analysis reveals a central role for tubular dysfunction in mediating altered plasma nucleoside levels in diabetic kidney disease
Anna Mathew, USA

10:30 - 11:00   *Coffee Break & Poster Viewing*

Session 5:

Moderators: Subramaniam Pennathur, USA and Theodore Alexandrov, Germany

Lipidomics

11:00 - 11:25   Targeting sphingolipid metabolism in the treatment of rare and common renal disease
James Shayman, USA

11:25 - 11:50   Lipidomics and inflammation
Oswald Quehenberger, USA

11:50 - 12:15   Chemical mechanisms of diabetic cardiomyopathy
Richard Gross, USA

12:15 - 12:40   Epidemiological and genetic-epidemiological studies on apolipoprotein A-IV as a marker of kidney impairment
Florian Kronenberg, Austria

12:40 - 12:55   Oral presentation from abstract submissions: *Poster Board: P09*
Shotgun lipidomics reveals dynamic changes to plasma lipidome with advancing chronic kidney disease
Farshad Afshinnia, USA

12:55 - 14:10   Networking Lunch & Poster Viewing

Session 6:
Moderators: Rob Knight, USA and Richard Gross, USA

Metabolism / microbiome and kidney disease

14:10 - 14:35   Metabolic flux analysis in CKD
Subramaniam Pennathur, USA

14:35 - 15:00   Fatty acid metabolism in CKD
Katalin Susztak, USA

15:00 - 15:25   Lipid metabolism, microbiome and CKD
Moshe Levi, USA

15:25 - 15:50   Mitochondrial function in CKD
Jeremy Duffield, USA

15:50 - 16:05   Oral presentation from abstract submissions: *Poster Board: P25*
Excessive proliferator-activated receptor gamma coactivator 1α expression
and mitochondrial biogenesis in podocytes results in cell cycle entry and
collapsing glomerulosclerosis
Szu-Yuan Li, USA

16:05 - 16:35   Coffee Break & Poster Viewing

Session 7:
Moderators: Katalin Susztak, USA and Matthias Nahrendorf, USA

Metabolism and CVD

16:35 - 17:00   Novel metabolic crosstalk with the vasculature
Zoltan Arany, USA

17:00 - 17:25   Cardiovascular disease and metabolism
Mohit Jain, USA

17:25 - 17:50   Translating big data from spatial metabolomics into molecular knowledge
Theodore Alexandrov, Germany

17:50 - 18:15   Metabolomics and lipidomics as disease markers
Shankar Subramaniam, USA

Saturday, September 24

Session 8:
Moderators: David Wishart, Canada and Matthias Kretzler, USA

Systems biology approaches, circadian rhythm and flux studies

08:15 - 09:05
Keynote Lecture III:
Imaging at the intersection of molecular and organ systems
Matthias Nahrendorf, USA

09:05 - 09:30
Circadian rhythms and eating pattern in regulating metabolic homeostasis
Satchidananda Panda, USA

09:30 - 09:55
Understanding the interplay between amino acid and lipid metabolism
Christian Metallo, USA

09:55 - 10:20
System-level metabolomics and renal metabolism
Eugene Rhee, USA

10:20 - 10:35
Oral presentation from abstract submissions:
Poster Board: P29
Multi-omics and systems analysis reveal a novel role of MDM2 in diabetic nephropathy
Rintaro Saito, USA

10:35 - 11:10 *Coffee Break & Poster Viewing*

Session 9:
Moderators: Eugene Rhee, USA and Satchidananda Panda, USA

Integration and tools for personalized medicine

11:10 - 11:35
Cytoscape and novel tools for integrative biology
Trey Ideker, USA

11:35 - 12:00
Multi-scala data integration in CKD
Matthias Kretlzer, USA

12:00 - 12:25
Metabolic reprogramming in renal cell cancer
Robert Weiss, USA

12:25 - 12:40
Oral presentation from abstract submissions:
Poster Board: P10
Lipidomic analysis reveals a complex regulatory network in the diabetic kidney
Kelli Sas, USA

12:40 - 12:45	Closing Remarks

Kumar Sharma, USA
Pennathur Subramaniam, USA
Katalin Susztak, USA

Biographies

Theodore Alexandrov

Theodore Alexandrov received a PhD in maths in Russia in 2007, did his postdoc at the University of Bremen, Germany, where he became a group leader at the Center for Industrial Mathematics and the head of MALDI Imaging Lab. In 2010-2015, he was a visiting researcher at University of California San Diego (UCSD), mainly at the Dorrestein lab, Skaggs School of Pharmacy. Since 2012, he is a co-founder and the scientific director of the company SCiLS GmbH, Germany. Since 2014, he is a team leader at European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany, with a research program on spatial metabolomics and the head of the EMBL Metabolomics Core Facility. Since 2015 he is the Assistant Adjunct Professor at the Skaggs School of Pharmacy, UCSD. The Alexandrov team at EMBL develops novel tools of computational biology that reveal spatial organization of metabolic processes by exploiting high-throughput metabolic imaging and by translating the generated big data into molecular knowledge.

Zoltan Arany

Zoltan (Zolt) Arany, MD, PhD is an Associate Professor of Medicine at the Perelman School of Medicine at the University of Pennsylvania. Dr. Arany recently joined the Penn faculty within the Division of Cardiovascular Medicine and the Cardiovascular Institute after several years serving as a faculty member at the Harvard Medical School and at the Beth Israel Deaconess Medical Center. Dr. Arany trained in Internal Medicine at Massachusetts General Hospital and performed his cardiology fellowship at the Brigham and Women's Hospital in Boston, Massachusetts. He received his Bachelor's degree, his PhD in Biological and Biomedical Sciences, and his MD in Medicine from Harvard University. Dr. Arany is a recipient of several awards including the American Heart Association Established Investigator Award in 2012, the Hal Dvorak Young Investigator Award in Translational Research, and the prestigious Inaugural Yale Calabresi Prize in 2014, given to Dr. Arany in recognition for his work on cardiovascular metabolism. He was recently elected to the American Society of Clinical Investigators. Dr. Arany has published more than 75 research papers in prominent journals such as Nature, Cell, The New England Journal of Medicine, PNAS, Cell Metabolism, and Genes & Development. Dr. Arany's active laboratory focuses on the regulatory mechanisms that underlie metabolic pathophysiology in the skeletal and cardiovascular system. Dr. Arany is also an active clinical cardiologist. In addition, he devotes considerable interest and effort to teach and mentor, in the classroom, in the clinical setting, and in his own laboratory, and has received a number of teaching and mentoring awards.

Pieter Dorrestein

Dr. Dorrestein is Professor at the University of California - San Diego. He is the Director of the Collaborative Mass Spectrometry Innovation Center and a Co-Director, Institute for Metabolomics Medicine in the Skaggs School of Pharmacy & Pharmaceutical Sciences, and Department of Pharmacology. Since his arrival to UCSD in 2006, Dr. Dorrestein has been pioneering the development of mass spectrometry methods to study the chemical ecological crosstalk between populations of microorganisms, including host interactions for agricultural, diagnostic and therapeutic applications.

Jeremy Duffield

Dr. Duffield is Vice President of Research and Senior Research Fellow at Biogen, Inc in Cambridge MA. Biogen is a Fortune 500 biotechnology company developing therapies for Immunological, Hematological and Neurological Diseases. Jeremy is also adjunct Professor of Medicine at University of Washington, is a practicing physician at Massachusetts General Hospital, and serves on NIH study sections. Jeremy directs a research group and oversees programs identifying new targets for potential therapeutics. The group is working in three major areas. Mechanisms of fibrosis, cell stress pathways and mechanisms of regeneration. Previously, the group identified pericytes and MSCs as major populations of precursor cells of pathological fibroblasts. Major pathways in fibroblast activation including innate immunity and WNT pathway are areas of active research. The group identified microRNA21 as a major target for the treatment of Alport syndrome, and helped develop a drug blocking this microRNA which is now in clinical trials. MicroRNA21 suppresses many metabolic functions including mitochondrial biogenesis. The lab is actively engaged in dissecting molecular mechanisms controlling mitochondrial function, autophagy and metabolic changes in chronic diseases.

Ronald Evans

Ronald Evans is an authority on hormones, both their normal activities and their roles in disease. A major achievement in Evans' lab was the discovery of a large family of molecules, called nuclear hormone receptors, which respond to various steroid hormones, vitamin A and thyroid hormones. These hormones help control sugar, salt, calcium and fat metabolism, affecting our daily health as well as treatment of disease. The receptors Evans discovered are primary targets in the treatment of breast cancer, prostate cancer, pancreatic cancer and leukemia, as well as osteoporosis and asthma. In addition, Evans' studies led to a new class of drugs called exercise mimetics, which promote the benefits of fitness without the need to train. Exercise mimetics represent one of the newest and most important advances in addressing problems arising from excess weight and obesity, such as frailty, muscular dystrophy and the potential treatment of adult onset diabetes (type 2 diabetes).

Josephine Forbes

Prof. Forbes completed her PhD in Paediatric Nephrology in 1999 at the University of Melbourne and Royal Children's Hospital in Melbourne, Australia. In 2012, she became a Professorial Fellow at the Mater Research Institute-UQ in Brisbane, Australia. She holds research grants from NH&MRC of Australia, Kidney Health Australia, NIH/NIDDK and the Juvenile Diabetes Research Foundation (JDRF). She is board member of the Australian Diabetes Society and is the co-chair of the Diabetes Australia Research Program and a Founding Council Member of the EASD Reactive Metabolites Study Group. Her work to date has resulted in more than 140 publications in highly ranked journals which have been cited > 5500 times (H-index of 41). Her primary research focuses on the biochemical processes of advanced glycation and mitochondrial energy production and their contribution to diabetes and kidney disease. She has received numerous awards for her research including the Commonwealth Health Minister's Award for Excellence in Medical Research in Australia and an ISN APR Young Researcher Award.

Richard Gross

Dr. Gross' research has focused on the molecular mechanisms through which biologic membranes participate in cellular signaling and bioenergetics in health and disease. In his earliest studies, he purified and characterized the first two intracellular phospholipases that are now recognized as the founding members of the cPLA2 and iPLA2 families of intracellular phospholipases. Dr. Gross' lab has purified, cloned and expressed multiple members of these families of phospholipases and determined their biologic significance through genetic ablation, tissue-specific transgenic expression and enantioselective mechanism-based inhibition. Recent work has highlighted the importance of these enzymes in human disease. For example, missense genetic mutations in iPLA2b results in Infantile Neuronal Axonal Dystrophy (INAD) and adult onset Parkinson's disease while genetic deletion of iPLA2g (proband with double stop mutation) results in mitochondrial dysfunction and neuronal degeneration.In 1984, the Gross laboratory developed methods for the soft ionization of phospholipids using neutral Xenon beams that enabled the facile determination of amount and structure of the many hundreds of lipids in mammalian cells. These early studies were remarkable for identifying the predominance of plasmalogens in sarcolemma and that plasmalogens were the major storage depot for arachidonic acid in myocardial sarcolemma.Throughout his career, Dr. Gross has utilized basic chemical principles to understand the importance of biologic membranes in cellular signaling and bioenergetics. Through extending the frontiers of multiple technologies, his laboratory continues to study the impact of alterations in membrane structure and function to understand the molecular mechanisms underlying the major medical problems of the 21st century.

James Hsieh
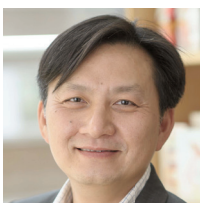
As a medical student taking care of cancer patients in 1990, Dr. James Hsieh witnessed the hopelessness metastatic cancer patients faced and decided to devote his life to the fight against cancer. His Ph.D. thesis concluded the mechanisms by which EBV EBNA2 hijacks Notch signaling for tumorigenesis and earned him the Young Investigator Award at Johns Hopkins Medical School in 1996. Dr. Hsieh completed Internal Medicine and Medical Oncology training at Washington University and DFCI, respectively. Dr. Hsieh studied under the late Dr. Korsmeyer in 2000, and discovered proteolytic processing of MLL, purified the protease, and named it "Taspase1" in 2003. As NCI K01 Howard Temin Awardee, Dr. Hsieh joined the faculty at Wash U. in 2004. Dr. Hsieh was inducted into ASCI in 2010. As a physician taking care of metastatic kidney cancer patients, Hsieh joined MSKCC to integrate his research and clinical interests. He founded the Translational Kidney Cancer Research Program (TKCRP) in 2011 to enable seamless collaboration among basic, preclinical, and clinical scientists. His team employs state-of-art platforms and clinical trial materials to integrate kidney cancer genomics, transcriptomics, proteomics, metabolomics, and therapeutics. His group pioneers a novel metabolic analytic algorithm (Metabologram) to interrogate human cancer metabolism in 2016. Dr. Hsieh proposed a novel paradigm-the Braided Cancer River Model-in 2015, capitalizing phenotypically, mechanistically convergent events to guide effective cancer therapy and overcome treatment-resistance. He wishes to develop novel mechanism-based, personalized therapeutics to prevent recurrence in high-risk patients and provide cure to significant number of metastatic kidney cancer patients.

Trey Ideker

Trey Ideker, Ph.D. is a Professor of Genetics and Bioengineering in the Department of Medicine at the University of California at San Diego. He serves as Director of the National Resource for Network Biology, Director of the San Diego Center for Systems Biology, and Co-Director of the Cancer Cell Mapping Initiative. Additionally, he is an Adjunct Professor of Computer Science and Bioengineering, and a member of the Moores Cancer Center at UC San Diego. Dr. Ideker received his Bachelor's and Master's degrees from MIT in Electrical Engineering and Computer Science and his Ph.D. from the University of Washington in Molecular Biology under the supervision of Dr. Leroy Hood. Dr. Ideker's research is led by the vision that given the right experimentation and analysis, it will be possible to automatically assemble maps of pathways just as we now assemble maps of genomes. During graduate work, he developed a general iterative framework for how biological systems can be systematically perturbed, interrogated and modeled. This framework laid the foundation for many studies in the discipline of Systems Biology. He demonstrated that biological networks could be integrated with gene expression to systematically map pathways and aligned, like sequences, to reveal conserved

Biographies

and divergent functions. He showed that the best biomarkers of disease are typically not single proteins but aggregates of proteins in networks. Dr. Ideker has founded influential bioinformatic tools including Cytoscape, a popular network analysis platform which has been cited >12,000 times. Ideker serves on the Editorial Boards for Cell, Cell Reports, Nature Scientific Data, EMBO Molecular Systems Biology, and PLoS Computational Biology and is a Fellow of AAAS and AIMBE. He was named one of the Top 10 Innovators of 2006 by Technology Review magazine and was the recipient of the 2009 Overton Prize from the International Society for Computational Biology. His work has been featured in news outlets such as The Scientist, the San Diego Union Tribune, Forbes magazine, and the New York Times.

Mohit Jain

Mo Jain obtained his M.D. and Ph.D. from Boston University School of Medicine, with his graduate work in physiology and metabolic biochemistry focusing on the enzyme, glucose-6-phosphate dehydrogenase and its role in cardiac physiology and redox metabolism. He subsequently performed training in clinical biomedicine including Internal Medicine and Cardiology at Brigham and Women's Hospital. His postdoctoral work was performed at the Broad Institute and Harvard Medical School Department of Systems Biology in the HHMI laboratory of Dr. Vamsi Mootha, developing methods for large scale LC-MS based metabolomics and integrative computational analysis, and the application of these approaches to define the role of metabolism in normal tissue physiology and human disease pathophysiology. Dr. Jain's work continues to focus on leveraging his background in physiology, biomedicine and mass spectrometry based metabolomics to understand global metabolic dysregulation and to identify metabolic target for disease intervention. The Jain laboratory at UC San Diego consists of an interdisciplinary team with diverse expertise encompassing analytical chemistry, high-throughput biology, computational biology, metabolic biochemistry, cellular biology, biomedical and clinical epidemiology. Our work is performed in close collaboration with a team of investigators based at UC (San Diego), Harvard Medical School (Boston) and Karoliska Institute (Stockholm).

Gabriele Kastenmüller

Gabi Kastenmüller heads the Metabolomics Group at the Institute of Bioinformatics and Systems Biology (IBIS), Helmholtz Zentrum München, Germany, and is an Honorary Lecturer in the Department of Twin Research, King's College London, UK. Holding master's degrees in chemistry and computer science, she moved into bioinformatics for her PhD, which she obtained from the Technische Universität München in 2009 for her work on in silico prediction and comparison of metabolic capabilities from sequenced genomes. In the same year, she joined Karsten Suhre's lab at IBIS, where she was involved in the bioinformatic analysis of various large-scale metabolomics experiments. In 2010, she spent four months at the metabolomics company Metabolon, Inc, USA, as a visiting scientist, delving into metabolite identification and the interpretation of spectral data. In 2011, she took over her current position as head of the Metabolomics Group at IBIS. Her group mainly focuses on the analysis and interpretation of high-throughput metabolomics data sets from clinical as well as epidemiological projects by the means of bioinformatics and systems biology. To this end, the group also develops novel approaches for integrating metabolomics data with data from further omics layers and for facilitating metabolomics data interpretation in the context of biochemical pathways. In particular, the group is interested in the inborn metabolic individuality in human populations and how this individuality affects predisposition to diseases and response to treatments.

Rob Knight

Rob Knight is Professor of Pediatrics and Computer Science & Engineering at the University of California, San Diego, and author of "Follow Your Gut: The Enormous Impact of Tiny Microbes". His TED talk on the human microbiome has been viewed over 1 million times. His work combines microbiology, DNA sequencing, ecology and computer science to understand the vast numbers of microbes that inhabit our bodies and our planet.

Anna Koettgen

Dr. Anna Koettgen is a Professor of Genetic Epidemiology at the University of Freiburg, Germany, and an Adjunct Assistant Professor at the Johns Hopkins Bloomberg School of Public Health. She obtained an MD from the University of Freiburg and an MPH from the Johns Hopkins University. Her research focuses on the use of epidemiological methods to understand kidney function in health and disease. For this purpose, her group uses both population- and patient-based studies to employ both targeted and unbiased genetic and metabolomic approaches to identify determinants and correlates of kidney function and disease. A special focus of the Koettgen group is the identification and characterization of genes associated with complex kidney diseases, and the investigation of the kidney's role in the handling of small molecules in health and disease. The ultimate goal of this research is to better understand mechanisms underlying complex kidney diseases, and to identify novel treatment targets for chronic kidney disease.

Matthias Kretzler

Dr. Kretzler is the Warner-Lambert/Parke-Davis Professor of Internal Medicine/Nephrology and Computational Medicine and Bioinformatics. He has 15 years of experience in integration of bioinformatics, molecular and clinical approaches in more than 180 collaborative studies on molecular analysis of renal disease. His research team has established a tract record on interdisciplinary data integration of large-scale data sets. He has initiated consortia for translational research in glomerular disease including NEPTUNE, CureGN, C-PROBE and ERCB and participates with translational studies with H3CKD Africa, CRIC, GENIE, FIND and SLEGENE. He focuses with his research team on the analysis of molecular mechanism of glomerular damage, defining regulatory networks in glomerular diseases in human cohorts and integrates them with genetic, proteomic, metabolomic, histological and clinical information. Key disease drivers along the genotype-phenotype continuum are used to identify novel disease predictors and targets molecular therapies in glomerular diseases from diabetic nephropathy to rare glomerular diseases.

Florian Kronenberg

Florian Kronenberg, MD is specialized in Medical Genetics and is a Full Professor for Genetic Epidemiology at the Innsbruck Medical University. He heads the Department of Medical Genetics, Molecular and Clinical Pharmacology. Florian Kronenberg served as principal investigator in several studies on genetic risk factors for atherosclerosis and biomarkers for the progression of chronic kidney disease including the «Mild to Moderate Kidney Disease Study» (MMKD). He is a Co-PI of the "German Chronic Kidney Disease" (GCKD) study. He was a workgroup member of the NKF K/DOQI Guidelines on «Cardiovascular Disease in Dialysis Patients» and the KDIGO Clinical Practice Guideline for Lipid Management in Chronic Kidney Disease. He has published roughly 300 papers and his research interests are genetic and clinical epidemiological studies on lipoprotein(a) as well as genetics of complex diseases such as atherosclerosis, kidney diseases, diabetes mellitus and related intermediate phenotypes

Moshe Levi

Moshe Levi received his degrees in Chemical Engineering from Northwestern University (B.S.) and Stanford University (M.S.) followed by medical degree from Albert Einstein College of Medicine. He completed his Internship and Residency training at Cornell Medical College followed by Nephrology Fellowship at the University of Colorado. He was on the faculty at UT Southwestern Medical School from 1884-2002 and he returned to University of Colorado since then. His research interests include i) regulation of renal, intestinal, and vascular phosphate transport, ii) role of nuclear receptors, G protein coupled receptors, and transcription factors in regulation of lipid metabolism, kidney, liver, and cardiovascular disease in obesity, diabetes, and aging, and iii) application of high resolution microscopy techniques for imaging lipids, metabolism, and fibrosis.

Christian Metallo

Christian Metallo joined the University of California, San Diego in 2011 and is currently an assistant professor in the Department of Bioengineering. He received his bachelor's in chemical engineering from the University of Pennsylvania in 2000 before joining Merck Research Laboratories to conduct bioprocess engineering research. He received his Ph.D. from the University of Wisconsin-Madison Department of Chemical and Biological Engineering in 2008 and was an American Cancer Society Postdoctoral Fellow in Chemical Engineering at the Massachusetts Institute of Technology. Christian was the recipient of the Biomedical Engineering Society Rita Schaffer Young Investigator Award in 2012, a 2013 Searle Scholar Award, and a 2015 NSF CAREER Award.

Tim Meyer

Tim Meyer undertook his medical school training at Harvard followed by medical residency at Stanford. He then did his nephrology fellowship with Dr. Barry Brenner at the Brigham and Women's Hospital before joining the faculty at Stanford where he has remained since. His research efforts over the past decade have been directed toward identifying retained solutes responsible for uremic illness, with a focus on those derived from colon microbes. He has worked on quantifying and improving removal of these solutes by dialysis and related therapies, and more recently toward suppressing their production.

Matthias Nahrendorf

Dr. Nahrendorf is currently an associate professor at Harvard Medical School and director of the Mouse Imaging Program at the Center for Systems Biology at MGH. He completed his joint Ph.D. and M.D. studies at the University of Heidelberg in Germany before moving to the University of Würzburg where he did his residency, fellowship and postdoctoral training. Dr. Nahrendorf joined Harvard Medical School in 2004. His laboratory focuses on the cellular and molecular processes in atherosclerosis and after myocardial infarction, using the entire spectrum of imaging modalities, including MRI, nuclear, and optical imaging techniques, with a special interest in multimodal imaging. These technologies are embedded in a biologically driven research program that aims at a systematic understanding of inflammation at a basic level while keeping a rigorous translational perspective.

Roland Nilsson
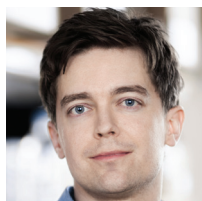
I am an assistant professor at the Karolinska Institute (Stockholm, Sweden) studying cellular metabolism using a blend of computational and experimental methods. My background is in computational biology, with a focus on cellular metabolism and metabolic disorders. I have made some contributions in statistical methods for whole-genome expression analysis, data integration methods for identifying novel components of metabolic pathways, and more recently metabolomics studies of cancer cells. The current focus of my lab at Karolinska is on mass spectrometry-based isotope tracing methods for studing activity of metabolic enzymes in living cells, particularly in one-carbon metabolism.

Biographies

Satchidananda Panda

Satchin Panda received his PhD from the Scripps Research Institute, San Diego and did postdoctoral research at the Genomics Institute of Novartis Research Foundation, San Diego. He has been a faculty at the Salk Institute (San Diego) since 2004, where his lab focuses on the circadian regulation of behavior, physiology and metabolism in model organisms and in human subjects. Satchin Panda's major scientific achievements include key discoveries of molecules, mechanisms and principles underlying the diurnal rhythms in metazoans. He discovered the role of a novel blue-light sensitive photopigment melanopsin in adapting mammalian circadian clock and non-image forming behavior to ambient lighting condition. This has led to public policy and commercial products aimed at dynamically managing lighting in built environment to optimize human health. His research identified genome-scale circadian regulation of thousands of genes in a tissue specific manner, which led to the subsequent discoveries of several core clock components, and molecular mechanisms. Recently, his lab demonstrated that the feeding-fasting cycle is a dominant determinant of diurnal rhythms in gene expression and function in peripheral organs independent of ambient lighting. Health relevance of this finding was demonstrated in a pre-clinical animal model that a robust feeding-fasting cycle without altering nutrient quality and quantity can prevent several chronic metabolic diseases. Based on a feasibility study in humans, his lab is currently carrying out a smartphone based study (www.mycircadianclock.org) to assess the extent of circadian disruption among adults.

Subramaniam Pennathur
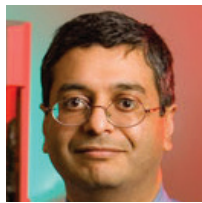
Dr. Pennathur is an Associate Professor, Division of Nephrology, University of Michigan. He completed his medical school in Madurai University, India and subsequently did his clinical training in internal medicine and nephrology at Washington University, Saint Louis and research fellowships at Mass General Hospital and University of Washington, Seattle. His laboratory has made extensive use of mass spectrometric methods to study oxidant injury mechanisms, metabolomics, lipidomics and proteomics in animal models and humans with diabetic complications. He leads the Molecular Phenotyping and Metabolomics, at the University of Michigan Nutrition and Obesity Center and Diabetes Centers and serves as the Co-Director, Michigan Regional Comprehensive Metabolomics Resource and Applied Systems Biology Core, George O'Brien Kidney Center.

Rembert Pieper

Rembert Pieper is a Professor for Infectious Diseases/Systems Biology and Director of the campus of the J. Craig Venter Institute (JCVI) in Rockville, Maryland. His research interests are cellular and molecular interactions of pathogens and microbial commensal organisms with the human host and the investigation of host-pathogen interactions. Dr. Pieper also directs protein biomarker discovery efforts of JCVI's proteomics laboratory. He has current research projects on urethral catheter biofilms, acute and latent infections by Mycobacterium tuberculosis in the context of the oral/nasal microbiome and antibiotic resistance, and mechanisms and biomarkers for infectious and other inflammatory diseases of the urinary tract and kidneys. In addition, he is involved in genomics and proteomics training programs for students and research fellows in developing nations. He has a Ph.D. in molecular biology/biochemistry from Berlin Technical University which was followed by research fellowships at Stanford University and the National Cancer Institute. He joined The Institute of Genomic Research, a legacy organization of the JCVI, in 2003.

Oswald Quehenberger

Oswald Quehenberger received his M.S. in Chemistry and his Ph.D. in Biochemistry from the University of Graz, Austria. Subsequently, he conducted his postdoctoral work at the The Scripps Research Institute, La Jolla, where he received his training in Immunology. In 1993, Dr. Quehenberger joined the faculty at University of California, San Diego and currently holds the position of Professor at the Department of Medicine. Dr. Quehenberger is the recipient of an Established Investigator Award from the American Heart Association, is an elected Fellow of the AHA and a Recognized Member of the American Stroke Association. He severed on numerous review committees for the NIH and other government granting agencies and as an editorial board member of scientific journals. Dr. Quehenberger has had a long-standing scientific interest in immunity and inflammation, with specific expertise in research pertaining to cardiovascular disease and metabolic syndrome with underlying acute, chronic and subclinical inflammation. His most recent studies have used novel lipidomics approaches to develop lipid signatures in health and disease.

Eugene Rhee

Eugene Rhee is a PI at the Massachusetts General Hospital, an Assistant Professor of Medicine at Harvard Medical School, and an Associate Member of the Broad Institute of MIT and Harvard. His laboratory is jointly supported by the Endocrine and Nephrology Divisions of the Department of Medicine at MGH. Dr. Rhee's studies on metabolism and renal disease extend naturally from this collaboration and span epidemiologic, physiologic, and experimental approaches, with an emphasis on liquid chromatography, mass spectrometry based metabolomics. Current projects include: 1.) discovery of metabolite predictors of incident CKD, CKD progression, and cardiovascular outcomes in well-characterized clinical cohorts, 2.) identification of the genetic determinants of the blood metabolome, 3.) characterization of novel renal metabolic functions using samples acquired with invasive catheterization, and 4.) animal and cell based studies to test the functional effects of select metabolites and metabolic pathways. His laboratory is interested both in metabolites that are important locally for maintaining kidney cell health as well as metabolites that may have a systemic role in metabolism.

Uwe Sauer

Uwe Sauer received a Ph.D. in Microbiology from the University of Göttingen in 1992. He is currently Professor of Systems Biology at the Institute of Molecular Systems Biology of the ETH Zurich (Switzerland) with a research focus on complex regulation processes that control cellular metabolism. His lab has pioneered the development of quantitative mass spectrometry-based methods for metabolomics and flux analysis with a particular focus on high-throughput methods. Combining the skills of physicists, biologists, engineers and computer scientists, his interdisciplinary lab specializes in developing original computational and modeling approaches to generate testable hypotheses from large-scale metabolomics data. Prof. Sauer has about 70 publications in peer-reviewed journals over the last 5 years, and is a member of various editorial boards, scientific steering and advisory committees of international organizations and companies in systems biology and biotechnology.

Biographies

Kumar Sharma

Dr. Sharma's research efforts have focused on the pathogenesis of diabetic kidney disease (DN). His laboratory helped define the central role of the cytokine Transforming Growth Factor-b (TGF-b) in DN using cell culture and animal models and has translated these findings to the human condition. These studies contributed to the development of the highly innovative anti-fibrotic approaches that are currently being tested in clinical research trial. Recently, Dr. Sharma has focused his attention on the contribution of the kidney to cardiovascular disease in diabetes and obesity using metabolomics and systems biology approaches. His group was the first to describe the role of adiponectin on podocyte function. His group has also identified that reduced mitochondrial function is a major contributor in diabetic complications and that stimulation of energy sensing pathways are beneficial in diabetic and obesity-related kidney disease. The goal of his research efforts is to develop new diagnostic and therapeutic approaches for personalized medicine in diabetes complications and chronic kidney disease. He has been continuously funded with grants from the NIH and private foundations. He serves as the Chair of the ISN Nexus Core Committee. Clinical Interests: Dr. Sharma has maintained a strong clinical practice with a focus on patients with type 1 and type 2 diabetes and kidney disease. He has conducted NIH-funded and industry supported investigator-initiated clinical trials. He has a major interest in the development of clinical biomarkers of kidney disease progression.

James Shayman

James Shayman, M.D. received his undergraduate degree from Cornell University and medical degree from Washington University in St. Louis. Following clinical training in internal medicine and nephrology at Barnes Hospital, post-doctoral training was received in the Department of Pharmacology. He joined the University of Michigan in 1986 where he is currently professor of internal medicine and pharmacology. His primary research has focused on the development of small molecule therapeutics for lysosomal storage diseases. To this end, his group has targeted glucosylceramide synthase as potential treatments for Gaucher and Fabry disease. Eliglustat tartrate, now approved worldwide for Gaucher disease type 1, is a result of this effort. His group has studied the mechanistic basis of the vasculopathy associated with Fabry disease. Most recently, his work has focused on the development of CNS permeant glycolipid synthesis inhibitors and is funded through the NIH Blueprint for Neurosciences program. His group also discovered and characterized a novel lysosomal hydrolase, group XV phospholipase A2. This lipase functions in surfactant catabolism, host defense to mycobacterial infection, clearance of apoptotic cells, and is the target of cationic amphiphilic drugs that cause phospholipidosis. Dr. Shayman has published over 140 peer reviewed papers and is an inventor on more than 60 US and international patents. He has served as the associate chair for research in the department of internal medicine and associate vice-president for research, health sciences. Recently, he was recipient of the 2016 University of Michigan Distinguished Innovator award.

Arun Sreekumar

Dr Arun Sreekumar is a Professor and Director of Metabolomics at Baylor College of Medicine, Houston. He completed his PhD from Indian Institute of Science, Bangalore, India in 2000 and his post-doctoral training from University of Michigan under the mentorship of Dr Arul Chinnaiyan in 2004. In 2008, he started his own research group while at the University of Michigan before moving to the Medical College of Georgia (MCG) Cancer Center in 2009. He joined as an Associate Professor at Baylor College of Medicine (BCM) in 2011. Dr Sreekumar's research focuses on understanding metabolic re-wiring in prostate and breast cancer. Since joining BCM, he has established their state-of-the-art mass spectrometry-based metabolomic profiling platform, and is the first to publish the unbiased metabolic profile of prostate cancer in Nature, 2009. Recently, in collaboration with colleagues at the University of Michigan, Dr Sreekumar published a paper in Nature Communications that described altered metabolic networks associated with castration resistant prostate cancer. In addition to these, he has published a number of high impact papers in journals such as New England Journal of Medicine, Journal of Clinical Investigation, Cell Reports etc. Dr Sreekumar's research is funded by grants from the National Cancer Institute, Department of Defense, Cancer Prevention Research Institute of Texas, National Science Foundation, Helis Foundation and Agilent Foundation. Dr Sreekumar's laboratory was recently designated the Agilent Center for Global Mass Spectrometry Excellence.

Biographies

Shankar Subramaniam
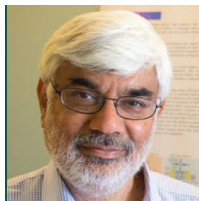
Subramaniam is a distinguished professor of Bioengineering, Computer Science & Engineering, Cellular & Molecular Medicine and Nanoengineering and the Joan and Irwin Jacobs Endowed Chair in Bioengineering and Systems Biology, at UC San Diego. Dr. Subramaniam's innovative work has major impact on research and development in academia and industry by allowing the synthesis of complex biological and medical information from genes and molecules into integrated knowledge at cellular and system levels, thus providing important basis for drug discovery and innovation. He has fostered training and research in systems biology and bioinformatics at the national level, serving on the NIH Director's Advisory Committee on Bioinformatics and played a key role in the formulation of the NIH Director's Roadmap which places a major emphasis on the use of quantitative approaches of engineering to biomedical research in health and disease. He founded the UCSD Bioinformatics program and was Chair of the nationally top-ranked bioengineering program from 2008-2013. Dr. Subramaniam has collaborated with colleagues in clinical medicine to elucidate the molecular and genomic basis of the pathogenesis of several diseases. His research is focused on understanding mechanisms, reconstructing networks, building quantitative models and predicting phenotypes in mammalian systems. Towards this end, he and his laboratory develop novel methods and technologies, carry out information-rich assays and build temporal and context-specific pathways and models leading to cellular and physiological end points. The work in his laboratory now spans several systems medicine projects including work on human brain, liver, skeletal muscle, and vascular and immune systems.

Katalin Susztak

Katalin Susztak is a physician-scientist, Associate Professor of Medicine and Genetics at the University of Pennsylvania. Dr. Susztak received integrated training as an MD/PhD followed by post-graduate training in Internal Medicine and in Nephrology. She also completed a Master of Clinical Research program to better understand clinical research study design and analysis. Currently Dr. Susztak practices medicine and runs a research laboratory. Work in my laboratory is aimed towards the understanding of molecular pathways that govern chronic kidney disease development. We have two general areas of interest: hypothesis generating (high trough-put, translational) and mechanistic studies. Over the past 10 years we banked and analyzed (combined genetic, epigenetic and genomic approaches) a large number of healthy and diseased human kidney tissue samples. We hypothesize that integrative analysis of epigenetic and genetic settings in diseased cells can provide a rational basis for more accurately modeling the critical biological pathways involved in mediating the progressive phenotype in individual patients. We also predict that epigenomic integrative analysis can be used to determine the identity of chromatin and transcription factors that contribute mechanistically to aberrant transcriptional programming in chronic kidney disease, and that this information can be used for designing therapeutic strategies. We are specifically interested in defining cis-regulatory modules (promoters, enhancers and repressors) that govern the normal and altered epithelial phenotype in diseased kidneys. In addition, we use genetic approaches and mouse as a model organism to test the role of candidate signaling molecules and regulatory pathways directly in vivo. Work in the Susztak lab is supported by industry sponsors, non-profit organizations and by the National Institute of Health.

Wai Hong Wilson Tang

Dr. Tang is Professor of Medicine at Cleveland Clinic Lerner College of Medicine at Case Western Reserve University, and the Director of the Center for Clinical Genetics at the Cleveland Clinic. He has been elected as member of the American Society of Clinical Investigation in 2013. As a clinician-scientist and practicing heart failure/transplant cardiologist, Dr. Tang's translational research focuses on understanding the cellular and molecular mechanisms that contribute to disease progression in heart failure, specific cardiomyopathies, cardio-renal diseases and more recently the contributing role of microbiome in cardiovascular diseases.

Robert Weiss

Dr. Robert H. Weiss is a clinician/scientist nephrologist and cell biologist and is Professor of Medicine at UC Davis and Chief of Nephrology at the Sacramento VA Medical Center. His training was all at several campuses of the University of California. His clinical and research interests are broad and include vascular and hereditary renal disease, as well as both breast and kidney cancer. He was among the first to characterize the role of the cyclin kinase inhibitors in cancer and is the first to utilize metabolomics to search for urinary biomarkers and therapeutic targets in kidney cancer and polycystic kidney diseases. He has an active clinical practice as well as a productive basic science laboratory.

David Wishart

Dr. David Wishart (PhD Yale, 1991) is a Professor in the Departments of Biological Sciences and Computing Science at the University of Alberta. He currently directs the Metabolomics Innovation Centre (TMIC), Canada's national metabolomics laboratory. Dr. Wishart's research interests span many areas including metabolomics, bioinformatics, structural biology and nanotechnology. For the past 10 years, Dr. Wishart has led the "Human Metabolome Project" (HMP), a multi-university, multi-investigator project that catalogued all of the known metabolites in human tissues and biofluids. Using advanced methods in NMR spectroscopy, mass spectrometry, multi-dimensional chromatography and machine learning Dr. Wishart and his colleagues have identified or found evidence for more than 42,000 metabolites in the human body. This information has been archived on a freely accessible web-resource called the Human Metabolome Database (HMDB). Dr. Wishart is actively using the resources arising from TMIC and HMP towards a variety of clinical applications including cancer, heart disease, kidney diseases and organ transplantation.