VAGELOS COLLEGE OF PHYSICIANS & SURGEONS,
COLUMBIA PRECISION MEDICINE INITIATIVE,
IRVING INSTITUTE FOR CLINICAL AND
TRANSLATIONAL RESEARCH, AND THE
HERBERT IRVING COMPREHENSIVE CANCER CENTER

# PRECISION MEDICINE SCHOLARS' DAY

Friday, November 3, 2023
9:00 a.m.–1:00 p.m.
Vagelos College of Physicians and Surgeons
630 West 168th Street, 4th Floor, Faculty Club

COLUMBIA | PRECISION MEDICINE

# Schedule

**9:00 a.m. Opening Remarks: Christine Garcia, MD, PhD**

**9:10 a.m. Opening Remarks: Muredach Reilly, MD**

**9:20 a.m. Marie-Pierre St-Onge, PhD / Christian Dye, PhD**

**9:45 a.m. Raju Tomer, PhD**

**10:10 a.m. Kelley Yan, MD / Arnold Han, MD, PhD**

**10:35 a.m. Ibrahim Batal, MD**

**11:00 a.m. Brent Stockwell, PhD**

**11:25 a.m. Keynote: Tarjinder (TJ) Singh, PhD**

**12:10 p.m. Closing Remarks: Anil Rustgi, MD**

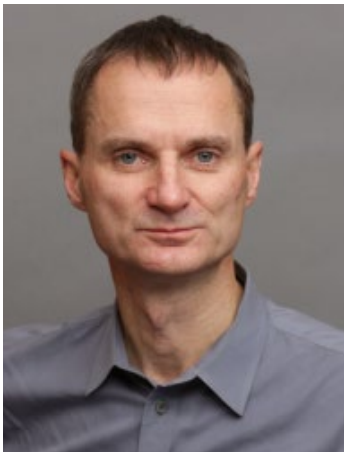
**12:30 p.m. Poster Session and Lunch**

This is a private meeting for Columbia researchers. By participating in this meeting, you agree to treat all information disclosed during the meeting as solely for Columbia internal use for academic purposes.

## Christine Garcia, MD, PhD

Frode Jensen Professor of Medicine
Director, Columbia Precision Medicine Initiative
Chief, Division of Pulmonary, Allergy and Critical Medicine
Department of Medicine
Vagelos College of Physicians and Surgeons
Columbia University Irving Medical Center

Christine Kim Garcia is the Frode Jensen Professor of Medicine, director of the Columbia Precision Medicine Initiative, and chief of the Division of Pulmonary, Allergy and Critical Medicine within the Department of Medicine at Columbia University Irving Medical Center. Her laboratory studies the genetic basis of monogenic lung disease, with a specific focus on familial pulmonary fibrosis. Her group has identified several rare variants in genes belonging to the telomere, surfactant, and spindle pathways. She received her MD and PhD from the University of Texas Southwestern Medical Center, where she completed her residency in internal medicine and fellowship in pulmonary and critical care medicine. In 2019 she moved to Columbia and has been a member of the Center for Precision Medicine and Genomics and an affiliate of the Institute for Genomic Medicine. Dr. Garcia has received a number of awards and honors, including the Irene and Arthur Fishberg Prize from VP&S (2022), American Society for Clinical Investigation (2012), Doris Duke Charitable Foundation Clinical Scientist Development Award (2008), President's Research Council Distinguished Young Investigator Award from University of Texas Southwestern Medical Center (2006), Charles E. Culpeper Foundation Medical Scholar Award (2004), Parker B. Francis Fellowship Award in Pulmonary Research (2003), and Alpha Omega Alpha (1991). She currently co-chairs the NIH Clinical Genetic (ClinGen) Pulmonary Domain Executive Committee.



## Muredach Reilly, MD

Professor of Medicine
Director, Irving Institute for Clinical and Translational Research
Associate Dean for Clinical and Translational Research
Director, Cardiometabolic Precision Medicine Program

As professor of medicine at Columbia University, Muredach Reilly has experience in human genetics and functional genomics, genetic epidemiology, mechanistic translational research, and cardiometabolic medicine. His research program is dedicated to translational genomic studies and focused on (1) cell specific (e.g., adipocyte and macrophage) genomic and transcriptomic contributions to human cardiometabolic disorders; (2) the functions of adipose tissue in insulin resistance and atherosclerotic risk; (3) novel mechanisms of human atherosclerosis underlying recent GWAS discoveries; and (4) the role of innate immunity in promoting cardiometabolic disease. His team employs a translational and genomic approach including human functional genomics, human-induced pluripotent stem cell (hiPSC) technology and gene-editing, animal-based mechanistic studies, and patient-oriented interrogation as well as large-scale genetic epidemiological studies. In his role as director of the Irving Institute for Clinical and Translational Research at Columbia, he also builds programs in clinical and translational research and in precision medicine while continuing his research program in cardiometabolic diseases. Dr. Reilly has nearly 20 years in NIH grant funding experience and publications as well as mentorship and teaching activities.

## Marie-Pierre St-Onge, PhD

Associate Professor of Nutritional Medicine
Director, Center of Excellence for Sleep & Circadian Research, Division of General Medicine, Department of Medicine, Vagelos College of Physicians and Surgeons
Columbia University Irving Medical Center

Marie-Pierre St-Onge is the founding director of the Center of Excellence for Sleep & Circadian Research at Columbia University Irving Medical Center. The overall focus of her research is the study of the impact of lifestyle, specifically sleep and diet, on cardiometabolic risk factors. Dr. St-Onge has been NIH-funded since 2008, conducting innovative, cutting-edge clinical research combining her expertise on sleep, nutrition, and energy balance regulation to address questions related to the role of circadian rhythms—including sleep duration and timing as well as meal timing and eating patterns—on cardiometabolic risk. She has strong expertise in the conduct of controlled inpatient and outpatient studies of sleep and dietary manipulations. Dr. St-Onge was center director for the American Heart Association–funded Go Red for Women Strategically Focused Research Center, aimed at determining the causality of the relation between sleep and cardiovascular disease and the specific role that sleep plays in the health of women throughout the life cycle. She is a pioneer in this field, having chaired the first scientific statements endorsed by the AHA on sleep and cardiometabolic health as well as meal timing and frequency and cardiovascular disease risk prevention. She is the recipient of an NHLBI Outstanding Investigator Award and a standing member of the Human Studies of Diabetes and Obesity Study Section at the NIH.

# Christian Dye, PhD

Postdoctoral Research Fellow, Department of Environmental Health Sciences
Mailman School of Public Health

Christian Ka'ikekūponoaloha Dye is a postdoctoral research fellow in the Laboratory of Precision Environmental Health, under the direction of Andrea Baccarelli.

His research focuses on the interface between environmental exposures and metabolic diseases, utilizing epigenetic information to develop novel biomarkers of disease risk. Further, by utilizing epigenetic data, he seeks to elucidate the potential epigenetic mechanisms of disease pathogenesis.

Dr. Dye received his PhD in molecular biosciences and bioengineering from the University of Hawai'i at Mānoa, under the mentorship of Alika Maunakea, where he focused on identifying immunoepigenetic signatures in monocytes of chronic disorders, particularly insulin resistance syndrome, type 2 diabetes mellitus, and dementia. His long-standing interest in chronic diseases stems from his passion for his Native Hawaiian community, as his community is disproportionately at risk for adverse health outcomes. Dr. Dye seeks to eventually bridge his work in epigenetic epidemiology with inclusive community-based research with underrepresented populations, including Native Hawaiians and Pacific Islanders.

## Prolonged Mild Sleep Restriction Results in Specific Alterations in Genome-Wide DNA Methylation: A Randomized Crossover Trial

### ABSTRACT

Rocío Barragán[1,2,3], Oscar Coltell[2,4], Christian K. Dye[5], Bin Cheng[6], Lawrence S. Honig[7], Dolores Corella[1,2], Marie Pierre St-Onge[3,8,9]

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8. Division of General Medicine, Department of Medicine, Columbia University Irving Medical Center, New York, NY, USA.

9. New York Nutrition Obesity Research Center Columbia University Irving Medical Center New York NY, USA.

INTRODUCTION: Short sleep duration is associated with increased cardiometabolic risk. DNA methylation plays a critical role in the regulation of gene expression, and studies suggest that sleep deprivation may alter DNA-methylation patterns. However, most findings are from acute sleep deprivation or short duration studies.

HYPOTHESIS: Prolonged sleep restriction study that mimics real-life situations is associated with differentially methylated CpG loci (DML) in the core-clock candidate genes and across the epigenome in an epigenome-wide association study (EWAS).

METHODS: Sixty participants (65% women) aged 21–73 y were included in randomized crossover studies with 2 phases of 6 weeks each. Phases differed in sleep duration: either adequate sleep (AS; sleep ≥7h/night) or sleep restriction (SR; -1.5h/night relative to AS). DNA was isolated from whole blood at wk 0 and wk 6 of each phase. DNA methylation (DNAm) was quantified the Illumina Infinium MethylationEPIC BeadChip array v.2.0 (>900K methylation sites) and Partek Genomic Suite v.720.0831. After quality control and normalization, several global and stratified EWASs were performed to test the impact of sleep condition on DNAm. Analyses were adjusted for week, phase, sex, age, BMI, and cell-type composition. We also focused on methylation changes of the selected core-clock candidate genes *(RORA, CRY1, NR1D2, TIMELESS, NPAS2, NFIL3, RORB, PER3, CSNK1E, ARNTL2, CRY2, CLOCK, ARNTL, RORC, PER2, BHLHE40, NR1D1, CSNK1D, BHLHE41, and PER1*).

RESULTS: In the candidate gene approach, we detected several significant DML. Top-ranked DML in selected core-clock genes with significant interactions between condition and time were: cg02394126 at *ARNTL* (p<0.001), cg23506964 at *CLOCK* (p=0.001), cg03701037 at NPAS2 (p=0.009), cg06606972 at *NPAS2* (p=0.009), and cg13576304 at *RORA* (p=0.008). Hypermethylation was primarily observed after 6 wk of SR vs AS for cg02394126, cg23506964, cg03701037, and cg06606972, while hypomethylation was observed at cg13576304 (*RORA*). In our EWAS, we detected some suggestive significant condition and time interactions in cg23738833 at SNHG3-*RCC1* (p=1,34E-06), cg13280380 in the *FAF1* gene (p=2,25E-05), cg03179866 in the *MMP12* gene (p=2,78E-05), and cg13063696 (p=3,21E-05). All but cg23738833 (*SNHG3-RCC1*) showed hypermethylation after 6 wk of SR vs AS.

CONCLUSION: Six weeks of mild SR was associated with changes in DNAm in core-clock candidate genes and in other genes in the EWAS. However, further studies are needed to confirm these findings and determine the functional pathways.

## Raju Tomer, PhD

Assistant Professor of Biological Sciences

Raju Tomer is an associate professor of biological sciences with research interests in developing complex in vitro 3D neuronal systems that can recapitulate some of the higher-order network elements underlying cognitive brain functions, and their applications in brain diseases. Dr. Tomer has a strong interdisciplinary research record encompassing brain evolution, advanced microscopy development, high-resolution whole brain mapping, brain organoids development, and advanced data analysis. In the last years, the Tomer lab has been focused on advancing the field of 3D neuronal cultures for in vitro modeling of network dysfunctions associated with schizophrenia.

## Toward Precision Psychiatry: An In Vitro Model of Schizophrenia-Associated Network Pathophysiology


### ABSTRACT

Brain diseases are the leading cause of disability and the second leading cause of death worldwide. The therapeutic options for most neurological conditions remain severely limited. This is partly due to the lack of an accurate understanding of the etiology and progression of brain diseases, primarily based on research conducted in animal models and, to a lesser extent, on the analysis of patient pathophysiology. However, despite evolutionarily conserved similarities between animal models and humans in terms of basic neuronal features like ion channels, neuron types, and developmental patterning, there are substantial differences in neural computations and cognitive processes. Consequently, many hypotheses that appear promising in preclinical studies often fail during clinical trials or, at best, provide only palliative relief. Therefore, there is an urgent need for better models with robust predictive value for human conditions.

Human-induced pluripotent stem cell (iPSC)-derived 3D neuronal cultures, known as brain organoids, have emerged as a valuable bridge between insights gained from animal models and limited human studies. These approaches generally aim to mimic the trajectory of embryonic development by using growth factors, differentiation cues, and culture conditions and have found success in applications related to neurodegenerative and neurodevelopmental disorders. However, the physiological relevance of brain organoids for adult human brain function and dysfunction remains highly limited due to the lack of mature neuronal networks. This limitation severely hinders their applicability to psychiatric conditions resulting from brain network dysfunctions, such as schizophrenia.

Our goal is to pioneer novel human iPSC-derived 3D neuronal culture methods that can overcome the physiological limitations of brain organoids. To this end, we have developed an innovative framework centered around the concept of creating a network of interconnected brain organoid-like modules, termed modular neuronal networks (MoNNets). This approach aims

to better reflect the architecture, signaling, and dynamics of the adult brain, shifting from merely reproducing early developmental pathways to faithfully recapitulating the known network properties of the cognitive brain. Over the past year, we have worked on developing, characterizing, and applying MoNNets to model network dysfunctions associated with schizophrenia. I will present these advances, as well as the new closed-loop techniques we are developing to capture, manipulate, and analyze the complex activity of these modular networks. Overall, the MoNNets framework has the potential to yield more predictive human in vitro models of brain disorders involving neural network dysfunctions.

## Kelley Yan, MD

Herbert Irving Assistant Professor of Medicine and Warner-Lambert Assistant Professor of Medicine (in the Columbia Center for Human Development)
Assistant Professor of Genetics and Development

Kelley Yan is the Warner-Lambert Assistant Professor and the Herbert Irving Assistant Professor of Medicine, with a joint appointment in the Department of Genetics & Development. She is a physician-scientist who received her MD and PhD degrees from Mount Sinai School of Medicine, where she conducted graduate studies in structural biology. She completed her clinical training in internal medicine and gastroenterology at Stanford University. She joined the lab of Calvin Kuo, a pioneer in organoid platforms, for postdoctoral training. In 2016 she launched her lab at Columbia that studies intestinal stem cell biology using interdisciplinary approaches. She is the founding co-director of the Organoid Core facility in Columbia's new P30-funded Digestive & Liver Diseases Research Center.

## Arnold Han, MD, PHD

Assistant Professor of Medicine in Digestive and Liver Diseases and Microbiology & Immunology

Arnold Han is Robert F. Loeb Assistant Professor of Medicine and of Microbiology & Immunology. Dr. Han is a physician-scientist whose laboratory studies T cell immunology as it pertains to human diseases. Dr. Han practices adult gastroenterology at Columbia University Irving Medical Center. He received his BA from Columbia College and his MD and PhD from Mount Sinai School of Medicine. As a graduate student, he trained in the laboratory of Michel Nussenzweig at Rockefeller University, where he studied B cell development. He completed his clinical training in internal medicine and gastroenterology at Stanford University. While at Stanford, he did his postdoctoral training in the laboratory of Mark Davis, where he studied T cells in celiac disease and cancer. He joined the faculty in 2016, where he has continued to study T cell function as it pertains to human intestinal diseases, including autoimmune disease and gastrointestinal cancers.

## Central Memory T Cells in the Human Colorectal Cancer Immune Microenvironment


### ABSTRACT

Colorectal cancer (CRC) is a leading cause of cancer and cancer deaths in the US. Although T cell populations are strongly associated with outcomes in CRC, current immunotherapies have had only limited success in CRC. One current barrier to our understanding is our inability to define tumor-reactive T cells in solid tumors, including CRC. Through close collaboration with Kelley Yan's lab, we are using patient-derived organoids to study human cancer ex vivo. Through these studies, we aim to define a signature of tumor-reactive T cells and their antigen targets. Our approach differs from most conventional approaches in that we begin from the perspective of the T cell rather than from the tumors. If successful, we could directly enable precision approaches where T cell immunotherapies are tailored to individual cancers.

## Ibrahim Batal, MD

Associate Professor of Pathology & Cell Biology, Columbia University Irving Medical Center

Ibrahim Batal is a renal pathologist at Columbia University in New York, one of the largest national kidney pathology laboratories, which processes more than 5,000 renal biopsies annually. He is the recipient of the 2019 Gloria Gallo Research Award by the Renal Pathology Society and is a member of the Banff Working Groups to improve histologic classification of kidney and liver allograft biopsies. As a PI, he managed several faculty development grants and, more recently, an NIH-based grant. He acquired extensive experience in transplantation and kidney pathology during his clinical training in transplantation pathology at the University of Pittsburgh in Pittsburgh, Pennsylvania, and kidney pathology at the Brigham and Women's Hospital/ Harvard Medical School (BWH/HMS) in Boston, Massachusetts. In addition, Dr. Batal acquired solid experience in translational research immunology during his postdoctoral training at BWH/ HMS. He also developed experience in implementing multicenter studies with nationally and internationally known collaborators. His research focuses on assessing the pathogenesis of glomerular diseases in the kidney allograft. Kidney transplantation offers a unique environment to dissect culprit factors from recipients and donors that contribute to the histologic manifestations of glomerular diseases. Kidney pathology at Columbia University has been historically, and continues to be, a leader in advancing kidney pathology research. The Transplant Center at Columbia University is one of the largest centers in the nation and provides unique biopsy material and scientific environment to carry out Dr. Batal's research.

## Defining Genomic and Inflammatory Predictors of Post-Transplant Kidney Diseases Related to *APOL1* Status of the Donor

### ABSTRACT

Dr. Batal's group was the first to show an association of *APOL1* high-risk genotype in the donor with increased risk and inferior prognosis of collapsing glomerulopathy in the kidney allograft. They also demonstrated that developing collapsing glomerulopathy was the main factor leading to worse allograft survival in transplant patients receiving a kidney allograft from Black donors.

To pursue this further, Dr. Batal's team assembled the largest retrospective tissue-based cohort of transplant recipients of a kidney from Black donors with prolonged follow-up. They are currently (a) studying transcriptome signals from kidney allograft biopsies to identify inflammatory signals that predict occurrence and prognosis of collapsing glomerulopathy and (b) using Image Analysis to quantitatively assess the evolution of chronic histologic changes in the kidney allograft over time in patients who did not develop collapsing glomerulopathy.

## Brent Stockwell, PhD

William R. Kenan Jr. Professor of Biological Sciences and Chair of the Department of Biological Sciences
Professor of Chemistry and Professor of Pathology and Cell Biology, Vagelos College of Physicians and Surgeons, Columbia University Irving Medical Center

Brent R. Stockwell is the William R. Kenan Jr. Professor of Biological Sciences and chair of the Department of Biological Sciences; professor of chemistry; and professor of pathology and cell biology at Vagelos College of Physicians and Surgeons, Columbia University Irving Medical Center.

His research involves the discovery of small molecules that can be used to understand and treat cancer and neurodegeneration, with a focus on biochemical mechanisms governing cell death. In a series of papers from 2003 to 2012, Dr. Stockwell reported on discovering a new form of cell death known as ferroptosis. Since then, his lab has defined the major mechanisms governing ferroptosis, as well as key reagents for studying this new form of cell death.

Dr. Stockwell has received numerous honors, including being elected to the National Academy of Medicine and receiving a Burroughs Wellcome Fund Career Award at the Scientific Interface, a Beckman Young Investigator Award, an HHMI Early Career Scientist Award, the BioAccelerate NYC Prize, the Lenfest Distinguished Columbia Faculty Award, the Great Teacher of Columbia College Award from the Society of Columbia Graduates, the Dean Peter Awn Commitment to the LGBTQ Community Faculty Award, and an NCI R35 Outstanding Investigator Award. He has been in the top one percent of highly cited researchers the last three years and was named as one of the 50 most influential life science individuals in New York.

He has developed a new blended learning approach to teaching biochemistry, performed randomized controlled trials to examine the effectiveness of teaching methods, and introduced the use of virtual reality and augmented and mixed reality into his biochemistry course. Dr. Stockwell has given more than 150 seminars around the world; trained more than 100 undergraduate and graduate students, technicians, and postdoctoral scientists; published more than 180 scientific articles; been awarded 23 US patents; and received over 50 research grants for over $40 million. He founded the biopharmaceutical companies CombinatoRx Incorporated, Inzen Therapeutics, ProJenX, Inc., and Exarta Therapeutics; he is the author of *The Quest for the Cure: The Science and Stories Behind the Next Generation of Medicines* and is a top-ranked writer on Medium.

## Optimization of Small Molecules That Restore Enzyme Activity to R152H GPX4

### ABSTRACT

Glutathione Peroxidase 4 (GPX4) is distinguished from other members of the GPX family as the only enzyme capable of reducing phospholipid hydroperoxide within cellular members and therefore protecting cells from ferroptosis, a form of iron-driven, oxidative cell death

involving lipid peroxidation. We previously identified a homozygous point mutation in the GPX4 gene, resulting in an R152H coding mutation and a substantial loss of GPX4 enzymatic activity, in patients with Sedaghatian-type spondylometaphyseal dysplasia (SSMD), an ultra-rare progressive disorder. Aiming to develop precision therapy for these patients, we screened 2.8 billion compounds in a DNA-encoded chemical library for compounds that selectively enriched on the R152H variant (GPX4R152H) over the wildtype (GPX4WT), and therefore identified top screening hits that could bind to GPX4R152H with remarkably higher binding affinities than to GPX4WT. Encouragingly, we found the most promising hit compounds could selectively elevate the enzyme activity of GPX4R152H and specifically increase the viability of fibroblast and lymphoblast cells developed from a SSMD patient with the R152H variation, but not control cells from his healthy parent or HEK293T cells treated with a GPX4 inhibitor. Our subsequent structural optimization of hit compounds led to discovery of analogs with improved therapeutic potency for R152H patients. Here we present an innovative, low-cost, high-throughput, and general approach to identify targeted small-molecule therapeutics for patients with missense mutations, which features the potential to be broadly applied to diseases that bear point mutations on crucial proteins and biological macromolecules.

## Tarjinder (TJ) Singh, PhD

Assistant Professor of Computational and Statistical Genomics, affiliated with Columbia University's Department of Psychiatry and the New York State Psychiatric Institute (NYSPI)
Associate Member, New York Genome Center (NYGC)

Tarjinder (TJ) Singh is an assistant professor of computational and statistical genomics affiliated with Columbia University's Department of Psychiatry and the New York State Psychiatric Institute (NYSPI). Additionally, he holds an associate faculty position at the New York Genome Center (NYGC). Furthermore, he has an interdisciplinary appointment at Columbia University's Zuckerman Mind Brain Behavior Institute. He earned his bachelor's in biology, mathematics, and economics from Williams College. Subsequently, he pursued his graduate studies under the guidance of Dr. Jeffrey Barrett at the University of Cambridge and the Wellcome Trust Sanger Institute. He underwent further training at the Analytical and Translational Unit of the Massachusetts General Hospital and the Stanley Center for Psychiatric Research at the Broad Institute of Harvard and M.I.T. He served as a post-doctoral fellow and Instructor at Harvard Medical School under the mentorship of Dr. Mark Daly and Dr. Benjamin Neale. Throughout his career, he actively participated in global collaborative initiatives, analyzing large-scale sequence data to identify protein-coding variants associated with significant risk for psychiatric disorders. His primary focus revolves around using genome sequencing as a fundamental tool to gain insights into the origins of mental illnesses.

## Insights into the Etiology of Psychiatric Disorders through Leveraging Population-Scale Sequencing and Functional Genomics

### ABSTRACT

In the last decade, genomic technologies and concerted worldwide efforts to create well-powered studies have helped characterize our knowledge of the genetic basis of mental disorders. In particular, the decreased cost of whole-exome and whole-genome sequencing has enabled the characterization and study of common to ultra-rare genetic variants. This talk will discuss insights from global collaborative efforts to analyze sequence data from schizophrenia patients to advance gene discovery. We will explore the genetic architecture of psychiatric disorders and how different variants have pinpointed specific genes associated with a specific diagnosis. We will discuss how genetics can be integrated with other data modalities to gain additional insights into disease biology. Finally, we will discuss possible ways forward as sample sizes dramatically increase in the next decade.

# Anil Rustgi, MD

Herbert and Florence Irving Professor of Medicine, Herbert Irving Comprehensive Cancer Center (HICCC); Herbert and Florence Irving Director, Herbert Irving Comprehensive Cancer Center (HICCC); Associate Dean of Oncology, Vagelos College of Physicians and Surgeons; Chief, Cancer Services, NewYork-Presbyterian Hospital/ Columbia University Irving Medical Center Campus

Anil K. Rustgi is the director of the Herbert Irving Comprehensive Cancer Center at NewYork-Presbyterian/Columbia University Irving Medical Center. Dr. Rustgi is a world-renowned leader in the field of gastrointestinal oncology. His interdisciplinary research focuses on tumor initiation, the tumor microenvironment, and tumor metastasis in the context of gastrointestinal cancers, including cancer of the esophagus, pancreas, and colon. Dr. Rustgi's lab works to translate its discoveries into improving molecular diagnostics and finding new experimental therapeutics for patients; it is funded through several grants including an NCI P01 (program project on esophageal cancer), an NCI U54 on Barrett's esophagus, two NIH R01 grants (for pancreatic cancer and colon cancer), and an American Cancer Society Research Professorship. Dr. Rustgi has more than 300 publications, and his work has appeared in high-impact journals such as *Nature, Nature Genetics, Nature Medicine, Cancer Cell, Genes and Development, Gastroenterology, Journal of Clinical Investigation, PNAS,* and *New England Journal of Medicine*.

Dr. Rustgi has been elected to the American Society of Clinical Investigation and the Association of American Physicians and is a fellow of the American Association for the Advancement of Science. Previously, he was president of the American Gastroenterological Association (17,000 members), editor-in-chief of *Gastroenterology,* and president of the International Society of Gastroenterological Carcinogenesis. Dr. Rustgi will serve as president of the American Pancreatic Association.

He has been recognized for his contributions with numerous awards, including the AGA Julius Friedenwald Lifetime Achievement in Gastroenterology Medal (2017), the AGA Distinguished Mentor Award (2016), the Ruth C. Brufsky Award for Excellence in Research in Pancreatic Cancer (2013), the Distinguished Achievement Award from the South Asian American Society for Cancer Research (2012), and an American Cancer Society Research Professorship. In addition, he received the top mentorship awards (Arthur Asbury for faculty and one from the postdoctoral fellow program) from his tenure at the University of Pennsylvania.

Dr. Rustgi graduated summa cum laude from Yale College with a bachelor's degree in molecular biophysics and biochemistry (departmental honors) and earned his medical degree at Duke University School of Medicine, where he was elected to Alpha Omega Alpha, the national medical honorary society. He completed an internal medicine residency at Beth Israel Hospital and a GI fellowship at Massachusetts General Hospital (MGH), both of which are affiliates of Harvard Medical School. He also rose to associate professor of medicine at MGH before joining the University of Pennsylvania in 1998, where he served as chief of Gastroenterology and directed two centers and NIH T32 training grants until 2018.

# Posters

## New Joint PM Awardees

**Swarnali Acharyya, PhD**
Targeting S100A9 using RA antagonists and nano ligases to treat CNS metastasis in lung cancer

**Thomas Hays, MD, PhD**
The genetic basis of small for gestational age preterm birth

**Yueqing Peng, PhD**
The impact of sleep fragmentation on memory dysfunctions in neuropsychiatric disorders

**Kathrin Schilling, MSc, PhD**
Metallomics MISSION: A comprehensive assessment of Metals, Isotopes, and SpeciatioN as disease biomarkers and therapeutic targets

**Ji-Yeon Shin, PhD**
Impaired cellular energetics and lipid metabolism in human iPSC-derived cardiomyocytes carrying cardiomyopathy-causing mutations in genes encoding nuclear envelope proteins

## Genome Editing

**Rando Allikmets, PhD;** and **Takayuki Nagasaki, PhD**
Mouse **models of Stargardt disease for hypomorphs and modifiers**

**Vincenzo Genarrino, PhD**
**Two different neurological diseases caused by different mutations in the Pumilio1 gene**

**Joseph Gogos, MD, PhD**
**Generation of mouse models of schizophrenia risk mutations in the SETD1A gene**

**John P. Morrow, MD; Gregg G. Gundersen, PhD;** and **Howard J. Worman, MD**
**Murine models of FHOD3 mutations causing hypertrophic and dilated cardiomyopathy**

**Vidhu Thaker, MD**
**Mouse model to establish the role of ARNT2 in the weight regulation pathway**

**Stephen Tsang, MD, PhD**
**Precision SNP therapeutic editing for autosomal dominant retinitis pigmentosa**