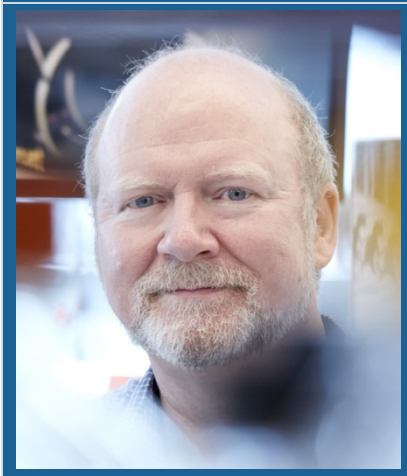
NYC-ISB23

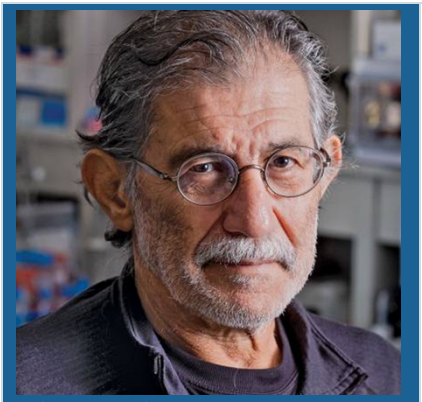
Speaker biographies

KEYNOTE SPEAKER

Keynote	Setting the scene for integrative structural biology
 Mike Rout George and Ruby de Stevens Professor, Head of Laboratory Laboratory of Cellular and Structural Biology Rockefeller University	I studied as a graduate student at the Laboratory for Molecular Biology in Cambridge, where I developed techniques for the subfractionation of the yeast nucleus. As a postdoctoral researcher at the Rockefeller University, I studied the Nuclear Pore Complex (NPC), which mediates trafficking between the cytoplasm and nucleoplasm, and also plays key roles in other crucial cellular processes. Using highly enriched yeast NPC fractions for a biochemical and structural approach, we generated the first inventories of its components. This work also demonstrated that there are distinct transport pathways, with many different but partially redundant and overlapping transport pathways all converging at the NPC. In 1997 I started my own laboratory at the Rockefeller University, the main focus of which remains the NPC. The studies of my laboratory and our collaborators have led to the first maps of the three-dimensional architecture of the NPC and the position of all its components, revealing the common evolutionary origins of this structure with vesicle coating proteins, and suggesting a model explaining the overall transport mechanism. We have also studied the kinetics of transport, revealing roles for binding and competition in the mechanism of the NPC, and how multiple and extremely rapid interactions between cargo-carrying transport factors and proteins in the NPC mediate both fast and specific nuclear trafficking. We ultimately aim to generate dynamic maps of the transporting NPC at the atomic and nanosecond level of resolution. We have also applied many of the approaches we have developed and refined to a wide range of cell biology, interactomic and therapeutic studies.

PLENARY SPEAKERS

Session 1	S4 - Size, shape, stoichiometry, and signals



Brian Chait
Rockefeller University

Professor Brian T. Chait of the Rockefeller University received the 2015 ASMS Award for a Distinguished Contribution in Mass Spectrometry at the 63rd Conference on Mass Spectrometry and Allied Topics in St. Louis. Brian received B.Sc. degrees in natural sciences (1969) and physics (1970) from the University of Cape Town, and in 1976 was awarded the D. Phil. degree in nuclear physics from the University of Oxford. After postdoctoral study at the University of Manitoba, he joined the Rockefeller University in 1979, where he is now a Camille and Henry Dreyfus Professor and Head of the Laboratory of Mass Spectrometry and Gaseous Ion Chemistry. Brian has received numerous awards, including the Newcombe-Cleveland Prize, Bijvoet Medal (Utrecht University), Field and Franklin Award, HUPO Discovery Award in Proteomics Sciences, and the Pehr Edman Award.

Anthony Fitzpatrick
Columbia University

Trained as a biophysicist by Prof. Sir Christopher M. Dobson, F.R.S., at the University of Cambridge, Prof. Fitzpatrick balanced protein misfolding research with playing semiprofessional rugby (Cambridge "Blue" '07) to earn a Ph.D. in the structure and biophysics of protein aggregates, solving the first atomic structure of an amyloid fibril (in close collaboration with Prof. Helen R. Saibil, F.R.S., at Birkbeck College, and Prof. Robert G. Griffin, at MIT). As an outgoing international Marie Curie Fellow at CalTech, he and Prof. Ahmed H. Zewail, Nobel Laureate, pioneered ultrafast time-resolved cryo-electron crystallography of proteins by combining electron and laser optics. During the Marie Curie incoming phase, he worked with Profs. Sjors Scheres, F.R.S., and Michel Goedert, F.R.S., at the MRC Laboratory of Molecular Biology during the tremendously exciting early days of the cryo-electron microscopy "resolution revolution." With improvements in cryoelectron microscopy, Prof. Fitzpatrick and colleagues solved the first ex vivo atomic models of Alzheimer's disease-related tau filaments, paving the way for the investigation of these previously intractable and important structures in a range of neurodegenerative diseases. The Fitzpatrick lab continues to solve brain-derived filaments implicated in neurodegeneration. In addition, his lab has assembled a cryo-electron tomography pipeline to explore the effects of amyloid formation in neurons and glia and is currently developing the world's first ultrafast pulsed laser phase plate to enhance contrast in cryoelectron tomograms.

Shifra Lansky
Weill Cornell Medical College

Shifra completed a PhD in chemistry and structural biology under the supervision of Prof. Gil Shoham from the Hebrew University (Jerusalem, Israel), where she used X-ray crystallography to study the structure-function relationships of diverse proteins involved in the hemicellulose utilization systems of the G. stearothermophilus bacterium. She then went on to research membrane protein structural dynamics in the Bio-AFM-Lab of Prof. Simon Scheuring in Weill Cornell Medicine (Cornell University, NY), where she is currently completing her postdoc. During her postdoc, Shifra discovered, using high-speed atomic force microscopy (HS-AFM), a rare pentameric state for the TRPV3 channel, and determined the cryo-EM structure of the pentamer. Her results correlate the pentamer state to the structurally-elusive pore-dilated state, and lay the foundation for many new direction in TRP channel research in particular, and in ion channel research in general.

Alisha 'Jonesy' Jones
New York University

My academic research interests are centered around using interdisciplinary techniques to investigate the conformational dynamics of RNA structure and how this influences protein binding events. I am particularly interested in the interactions between RNA-binding proteins (RBPs) and long noncoding RNAs (lncRNAs), a class of transcripts for which nearly 50,000 RNAs have been identified, but for which details of structure and RBP recognition have yet to be extensively explored. Gaining an understanding of the molecular mechanisms that underlie recognition of structured lncRNAs by RBPs will improve our knowledge of the numerous biological processes regulated by these transcripts and allow us to therapeutically target the structures that are implicated in disease.

Ruben Gonzalez
Columbia University

I have a long-standing interest in the translational control of gene expression. As a graduate student with Prof. Ignacio Tinoco at UC at Berkeley, I used biochemical and biophysical methods to investigate the structure and dynamics of an RNA pseudoknot involved in the translational regulation of several viral RNAs. Subsequently, as a postdoctoral fellow with Profs. Jody Puglisi and Steven Chu at Stanford, I helped pioneer the first singlemolecule fluorescence studies of the ribosome and the associated cellular translation machinery (TM). Since 2006, my independent research group at Columbia has used single-molecule fluorescence methods in combination with molecular biological, biochemical, spectroscopic, and structural approaches to characterize the structure-dynamics-function relationships of the TM that drive and regulate protein synthesis. Most notably, my group has helped elucidate how the conformational dynamics of the TM contribute to the mechanisms through which the TM accurately assembles at the start codon of an mRNA during translation initiation; selects the correct, mRNA-encoded aminoacyl-tRNA and guides tRNA movements from one ribosomal binding site to the next during translation elongation; and directs the release of the newly synthesized protein and the disassembly of the TM at a stop codon during translation termination and ribosome recycling.

Session 2	Bridging scales from atoms to cells

Chris Lima
Memorial Sloan Kettering Cancer Center

Christopher D. Lima is a Howard Hughes Medical Institute Investigator at the Sloan Kettering Institute in New York City where he is Chair and Member of the Structural Biology Program. He holds an Alfred P. Sloan endowed chair and is a Professor in the Weill Cornell and Sloan Kettering Graduate Schools. He received his PhD from Northwestern University for resolving the structure of DNA topoisomerase I. As a Helen Hay Whitney Fellow at Columbia University, his postdoctoral studies focused on resolving mechanisms underlying nucleotidyl transferases. He joined the faculty at Weill Cornell in 1998 and moved his lab to Sloan Kettering in 2003. His research investigates pathways that contribute to RNA processing and post-translational modification by ubiquitin-like proteins. He was a Beckman Young Investigator and Rita Allen Scholar and was selected as an HHMI Investigator in 2013. He was elected to the American Academy of Arts and Sciences in 2017 and the National Academy of Sciences in 2020.

Olga Boudker
Weill Cornell School of Medicine

Olga went to Novosibirsk State University in Russia before obtaining her MSc from Weizmann Institute of Science in Israel, working with Anthony Futerman on sphingolipid biochemistry. She received her PhD from the Johns Hopkins University, where she worked on protein folding with Ernesto Freire. Olga then trained as a postdoctoral fellow with Peter Kim at MIT and Eric Gouaux at Columbia University. There, she became interested in the structure and mechanism of membrane transporters. She started her lab at Weill Cornell Medical College in 2005.

Brinda Vallat
Rutgers University
PDB-Dev Project Lead

I am a computational biologist interested in understanding the molecular basis of life. My research interests include modeling and analysis of biomolecular structure and function using data obtained from experimental and theoretical methods. I currently lead the PDB-Dev project, which is focused on building the infrastructure for archiving integrative structural models of macromolecules. Integrative modeling methods combine complementary information from various experimental and computational techniques to determine the structures of complex macromolecular assemblies. The complexities of handling different data types involved in integrative modeling provide challenging opportunities for data acquisition, standardization, archiving, validation and dissemination.

Priyasha Deshpande
City University of New York

bio coming soon

Alex de Marco
New York Structural Biology Center

Alex is a distinguished electron microscopist known for innovative research in the field of cryo-electron tomography. He earned his Ph.D. from EMBL and Heidelberg University (Germany) specializing in cryo-electron tomography and image processing. His work resulted in the first structural description of the viral maturation in HIV-1 and the first sub-nm structure ever solved using sub-tomographic averaging. He then worked as Product Manager at FEI Company (now Thermo Fisher) and introduced solutions for cryo-FIB milling and correlative microscopy. In 2016 he returned to academic research starting his group at Monash University. His research focused on methods and technology development for high resolution in situ cryo-electron microscopy while maintaining an interest in the development of non-linear micro-optics. In 2023, he became director of the Simons Electron Microscopy Center at the New York Structural Biology Center.

Session 3	Computational approaches to analyze multi-scale data

Amédée des Georges
City University of New York

Since his first class on the subject, Amedee Des Georges has been fascinated by protein structures and allosteric control. He found electron microscopy to be a compelling tool to study their function and dynamics, and joined Linda Amos at the MRC Laboratory of Molecular Biology in Cambridge, UK for his Ph.D. to learn its techniques. He subsequently pursued postdoctoral studies with Joachim Frank at Columbia University to decipher the structure and dynamics of large macromolecular complexes by the single-particle technique. He joined CUNY ASRC as an assistant professor in 2015. Still excited by cryo-EM's ability to visualize proteins directly, he continues to foray into the study of protein dynamics, deciphering the allosteric modulation of membrane proteins and the role this plays in cell signaling.

Pilar Cossio
Flatiron Institute

Pilar Cossio joined the Center for Computational Mathematics in April 2021 as the Research Scientist and Project Leader for Structural and Molecular Biophysics (SMB). Previously, Cossio was Max Planck Tandem Group Leader associated with the University of Antioquia (Colombia) and the Max Planck Institute of Biophysics (Germany). She also has held postdoctoral positions at the National Institute of Health (NIH, USA) and the Max Planck Institute of Biophysics. She focuses on the development of mathematical and computational methods to characterize biomolecular structures and dynamics from cryo-electron microscopy, single-molecule spectroscopy and biomolecular simulations. She holds a Ph.D. in Physics and Chemistry of Biological Systems from the International School for Advanced Studies (SISSA) in Italy and a B.S. in Physics from the University of Antioquia.

Augustine Chimezie Onyema City Univerisity of New York	*bio coming soon*

Poster presenter	TBD

Hashim M. Al-Hashimi
Columbia University

Al-Hashimi was born in Beirut, Lebanon, and grew up in Greece, Italy, Jordan, and the UK. As a graduate student at Yale, Al-Hashimi helped develop residual dipolar coupling methodology, which revolutionized the study of protein structure and dynamics by NMR. As a postdoctoral fellow at the Memorial Sloan Kettering Cancer Center, Al-Hashimi expanded the domain of applicability of these methods to nucleic acids. As a principal investigator, Al-Hashimi and his trainees discovered many of the ubiquitous motional modes underlying the biological activities of nucleic acids, with important implications for drug discovery and for understanding the mechanisms that cause genome instability and cancer. These motions include transitions between Watson-Crick and Hoogsteen base pairs, which shape the DNA protein recognition and damage landscapes; transitions between mismatch and tautomeric/anionic Watson-Crick base pairs, which are responsible for errors during replication, transcription, and translation; motions that determine proper folding of RNA; and transient changes in RNA secondary structure that underlie gene regulation and viral genomic replication by non-coding RNAs. His group developed methods harnessing the predictive power of RNA dynamic ensembles to identify small molecule inhibitors of HIV-1 replication. In 2009, Al-Hashimi co-founded Nymirum Inc to enable RNA-targeted drug discovery using RNA dynamics.

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