

VIRTUAL SYMPOSIUM

JULY 7 - 9, 12 - 14, 2021



35TH ANNUAL SYMPOSIUM PROGRAM

Join Our Gold Sponsor



on July 12

for their Webinar

5:15 - 5:45 p.m. EST

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MISSION

The Protein Society is a not-for-profit scholarly society with a mission to advance state-of-the-art science through international forums that promote communication, cooperation, and collaboration among scientists involved in the study of proteins.

For 35 years, The Protein Society has served as the intellectual home of investigators across all disciplines - and from around the world - involved in the study of protein structure, function, and design. The Society provides forums for scientific collaboration and communication and supports professional growth of young investigators through workshops, networking opportunities, and by encouraging junior researchers to participate fully in the Annual Symposium. In addition to our Symposium, the Society's prestigious journal, *Protein Science*, serves as an ideal platform to further the science of proteins in the broadest sense possible.

#PS35

1986 - 2021



WELCOME



Welcome to 35th Annual Symposium of the Protein Society!

The Protein Society is proud to present our first virtual symposium. Although a virtual meeting cannot replace all of the rewarding interactions that we enjoy when we meet in person, this format will nevertheless bring outstanding protein science and meaningful connections to members and other symposium registrants around the world.

Our 6-day program will feature contributed talks by junior and senior investigators, Protein Society award talks, and presentations by invited speakers. Our program committee, chaired by Jeanne Hardy, Ph.D., has convened a host of stimulating speakers who will address current topics related to protein structure, function, dynamics, evolution, modification, degradation, and design. Our successful 2020-2021 webinar series has taught us that on-line dissemination and discussion of content can work very well.

When you aren't enjoying some of the 50+ talks, we invite you to engage with interactive activities including live posters - some of which will be featured in flash talks - and professional networking events. There will be occasions to meet Protein Society executive councilors and partners from academia and industry and to learn about professional opportunities and trajectories from members at different career stages.

Diversity, equity and inclusion are important to The Protein Society and we aspire to broaden participation among our membership and symposium participants. In addition to our Anniversary Awards (formerly travel grants), we are introducing new initiatives such as the TPS Diversity Awards, which will support meeting registration for members at all levels who are working to make our community increasingly welcoming to all.

I hope you will take advantage of everything our on-line meeting has to offer and give us your opinions about what you like and what we can do better. We are committed to strengthening our events to meet the needs of our constituents, and your honest feedback will directly shape future programming, including our 2022 annual symposium in San Francisco.

I wish you a fruitful and engaging virtual experience, full of eye-opening moments, exciting new ideas, and connections with colleagues and friends old and new.

Kind Regards,

Amy E. Keating, Ph.D.
President

Uber Eats Vouchers have been hidden in some poster sessions. Go to the scheduled poster sessions in Fourwaves to find them!

Once you find a voucher, click on the link to claim it. Make sure you have an Uber Eats account to place the voucher in your Uber Eats wallet.

To use the voucher, put items in your Uber Eats cart and head to checkout. From there, click on your Uber Eats wallet and select the voucher you wish to apply to your order.

You will be able to use your voucher from July 7th, 12:00 AM EDT to July 14th, 11:59 PM.

Participation in the PS35 Scavenger Hunt is not necessary to participate in this incentive game.



35th Anniversary Symposium July 7 - 9, 12 - 14, 2021

Meeting Access Fact Sheet

The Anniversary Symposium will be delivered via the SOCIO virtual event platform (web app to access the program, scientific sessions, attendee information, sponsors, webinars, networking events, society info, and other material), and accompanied by FOURWAVES for posters, available to view at any time, and for interactive sessions as indicated in the schedule.

VIRTUAL MEETING PLATFORM SOCIO Instructions

SOCIO (Web App)

Access the PS35 platform by using this registrant-only [website](#), using the SAME EMAIL used during the Symposium registration process. Access will be available within 48 hours after you have registered on [The Protein Society website](#) and payment has been processed.

Mobile-App Access

- Download the PS35 Mobile App for [iPhone](#) or [Android](#).
- After App is installed, sign up. Use the SAME EMAIL that you used to register.
- Create your profile (if you already created an account via the Virtual Platform, use the same login).
- Search for PS35.

If you need assistance related to the web or mobile app, please email support: eventapp@socio.events
For general meeting support, please email: lrobitaille@agoraopus3.com.

Need Help Keeping Track of Your Logins?
Jot them down here!

#PS35 SOCIO Email: _____

#PS35 SOCIO Password: _____

#PS35 FOURWAVES Email: _____

#PS35 FOURWAVES Password: _____



ABSTRACTS & LIVE POSTER SESSIONS FOURWAVES Instructions

- Register [here](#) by entering your name and e-mail.
- You will receive a confirmation e-mail with a link to activate your account.
- Browse & find posters [here](#) starting **June 15**. Live poster presentations will take place on **July 7 and July 9, from 2:30 - 4:00 PM EDT** and on **July 8 and 13 from 6:30-10 EDT**.
- Note: If you've already registered to submit your abstract on the platform, you do not need to register again.
- Note: You will need to download the Zoom app on your phone if you plan to view posters that way. If viewing on a computer, you can view them via browser if you don't wish to download the app.

If you need assistance related to the abstract platform, contact: info@fourwaves.com
For general meeting support, please email: lrobitaille@agoraopus3.com

PROGRAM PLANNING COMMITTEE

Virtual Symposium | July 7-9, 12-14, 2021



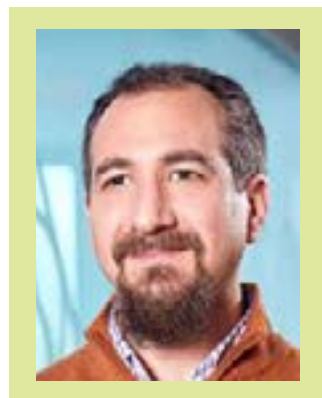
Jeanne Hardy, Ph.D.
CHAIR,
University of
Massachusetts Amherst



Gabriel Lander, Ph.D.
CO-CHAIR,
Scripps Research Institute



Charlotte Deane, Ph.D.
University of Oxford



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CORPORATE SUPPORT

The Protein Society is extremely grateful to the following sponsors for their generosity and continued support.

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Thank you for helping us celebrate 35 years of impact.



AT A GLANCE

Subject to Change

On Demand session content will be available for 3 months post-symposium.

WEEK 1	DAY 1	DAY 2	DAY 3	WEEK 2 - DAY 4	DAY 5	DAY 6
Time Zone Boston 10 - 10:50 AM Los Angeles 7 - 7:50 AM Tokyo 11 - 11:50 PM London 3 - 3:50 PM Rome 4 - 4:50 PM	7-Jul	8-Jul	9-Jul	12-Jul	13-Jul	14-Jul
		Malvern Panalytical Webinar 10 - 10:30 a.m.	Gender Power Hour	St. Jude Children's Hospital Webinar 10 - 10:30 a.m.	Refeyn Webinar 10 - 10:30 a.m.	PLENARY # 12: Dr. Janet Smith, University of Michigan, 2021 Dorothy Crowfoot Hodgkin Award Winner
Boston 11 - 11:50 AM Los Angeles 8 - 8:50 AM Tokyo 12 - 12:50 AM London 4 - 4:50 PM Rome 5 - 5:50 PM	PLENARY # 1 Dr. Martin Gruebele, University of Illinois Urbana- Champaign, 2020 Hans Neurath Award Winner	PLENARY # 3: Dr. Stephen Sligar, University of Illinois Urbana- Champaign, 2020 Christian B. Anfinson Award Winner	PLENARY # 5: Dr. Amy C Rosenzweig, Northwestern University, 2021 Hans Neurath Award Winner	PLENARY # 7: Dr. Sheila Jaswal, Amherst College, 2021 Carl Brändén Award Winner	PLENARY # 9: Dr. Bruno Correia, EPFL, 2021 Protein Science Young Investigator Award Winner	PLENARY # 13: Dr. Catherine Drennan, MIT, 2020 Dorothy Crowfoot Hodgkin Award Winner
BREAK Boston 12 - 2:00 PM Los Angeles 9 - 11:00 AM Tokyo 1 - 3:00 AM London 5 - 7:00 PM Rome 6 - 8:00 PM	Concurring Session 1: Protein Structures Through the Lens of Machine Learning	Concurring Session 1: Novel Approaches to Observe Proteins in Their Natural Environment	Concurring Session 1: Designer Proteins Through Genetic Code Expansion	Networking and Career Discussion Tables Boston 12 - 1:25 p.m. Los Angeles 9 - 10:25 a.m. Tokyo 1 - 2:25 p.m. London 5 - 6:25 p.m. Rome 6 - 7:25 p.m.	Concurring Session 1: Protein Evolution, Design and Selection	Concurring Session 1: Allostery & Dynamics in Protein Function
	Concurring Session 2: Quaternary Structure: Shape Shifting in the Control of Protein Function	Concurring Session 2: New Protein Post-Translational Modifications 12 - 2:20 p.m.	Concurring Session 2: Measuring Forces of Biological Systems	Diversity Power Hour Boston 1:30 - 2:15 p.m. Los Angeles 10:30 - 11:15 a.m. Tokyo 2:30 - 3:15 p.m. London 6:30 - 7:15 p.m. Rome 7:30 - 8:15 p.m.	Concurring Session 2: Undergraduate Research Session	Concurring Session 2: Targeted Protein Degradation
BREAK Boston 2:30 - 4:00 PM Los Angeles 11:30 - 1:00 PM Tokyo 3:30 - 5:00 AM London 7:30 - 9:00 PM Rome 8:30 - 10:00 PM	POSTER PRESENTATIONS	PLENARY # 4: Dr. Shuguang Zhang, MIT, 2020 Emil Thomas Kaiser Award Winner Protein Science Best Paper Winners	POSTER PRESENTATIONS	Diversity in Protein Science II	Plenary #10: Dr. Mohammad Seyedsayamdost, Princeton University, 2020 Protein Science Young Investigator Award Winner Plenary # 11: Dr. Lei Wang, University of California, San Francisco, 2021 Emil Thomas Kaiser Award Winner	Plenary # 14: Dr. Karen Fleming, Johns Hopkins University, 2020 Carl Brändén Award Winner Protein Science Journal, a Conversation with Editor-in-Chief, Brian Matthews, University of Oregon & Incoming Editor-in-Chief, John Kuriyan, University of California, Berkeley
Boston 4 - 5:00 PM Los Angeles 1 - 2:00 PM Tokyo 5 - 6:00 AM London 9 - 10:00 PM Rome 10- 11:00 PM	Industry Visit: Novartis	Industry Visit: Silicon Therapeutics	Industry Visit: Scholar Rock	Diversity: Mentoring Event	Industry Visit: C4 Therapeutics	Industry Visit: Ginkgo Bioworks
	6 p.m. Shuimu BioSciences Webinar			5:15 p.m. PerkinElmer Webinar		
Boston 6:30 - 8:30 PM Los Angeles 3:30 - 5:30 PM Tokyo 7:30 - 9:30 AM London 11:30 PM - 1:30 AM Rome 12:30 - 2:30 AM	PLENARY # 2: Dr. Minoru Kanehisa, Kyoto University, 2019 Carl Brändén Award Winner Protein Science Best Paper Winners	POSTERS PRESENTATIONS 6:30 - 10 p.m.	PLENARY # 6: Dr. Toshiya Endo, Kyoto Sangyo University, 2021 Hans Neurath Award Winner	Concurring Session 1: Cryo-EM: Beyond Single Particle Reconstruction Concurring Session 2: Diffraction Methods are Alive and Well	POSTER PRESENTATIONS 6:30 - 10 p.m.	

PROGRAM

July 7

Plenary Awards Session #1: 11 - 11:50 a.m.

Dr. Marlin Gruebele, University of Illinois at Urbana-Champaign,

2020 Hans Neurath Award Winner

Talk Title: Protein Folding And Interactions: From The Computer Into The Test Tube And On To The Cell

Welcome from Chair of The Program Planning Committee - Dr. Jeanne A. Hardy, University of Massachusetts Amherst

Intro & welcome from The Protein Society President - Dr. Amy E. Keating, MIT

Dr. Gruebele is widely known for introducing the advanced technology of flash heating and ultrafast spectroscopy to study protein folding. His work showed that early stages of protein folding, including initial collapse and formation of secondary structures can occur in microseconds. These advances allowed the first direct comparisons between folding rates determined experimentally and folding rates estimated from simulations. More recently, Dr. Gruebele showed that fast folding can be studied in live cells. His work established that in vivo folding, while following similar physicochemical rules as in vitro folding, is significantly modulated by the different cellular environments in different parts of the cell. Dr. Gruebele's work brings the highest level of experimental innovation, experimental precision, and conceptual rigor to protein biophysics.

The Protein Society Hans Neurath Award

Hans Neurath played an integral role in the early life of the Society, as a founding member and later -at age 81- as founding editor of Protein Science. His contributions to the early success of the Society were surpassed only by his larger contributions to the field of biochemistry and our early understanding of proteins. Reflective of his prolific contributions to the understanding of the physical chemistry of proteins, The Hans Neurath Award, sponsored by the Hans Neurath Foundation, seeks to honor individuals who have made a recent contribution of exceptional merit to basic protein research.

Specific Requirement: A recent contribution of unusual merit to basic protein science.

Concurring Session 1: 12 - 2 p.m.

Protein Structures Through the Lens of Machine Learning

Session Sponsor: [Shuimu Biosciences](#)

Session Chair:

Session Speakers:

John Jumper, DeepMind

Talk Title: High Accuracy Protein Structure Prediction Using Deep Learning

David Koes, University of Pittsburgh

Talk Title: An Atomistic View Of Deep Protein Structure Prediction

Heather Kulik, MIT

Talk Title: What Can Machine Learning And Big Data Teach Us About Metalloenzymes?

Daniel Schmidt, University of Minnesota

Talk Title: Applying Machine Learning To Understand The Biophysical Basis Of Protein Domain Compatibility

Carlos Outeiral Rubiera, University of Oxford

Talk Title: How Good Are Protein Structure Prediction Methods At Predicting Folding Pathways?

Flash Talks:

Fabian Liessmann, Leipzig University

Homology Modeling of GPR114/ADGRG5 With Rosetta Elucidates Possible Interactions Between ECL2 And GAIN Domain

Wonmuk Hwang, Texas A&M University

Simultaneous Tracking Of Multiple Dynamic Microtubules Decorated By The Microtubule-Associated Protein Ebi

Susan Tsutakawa, LBNL

Experimental Validation Of Predicted Protein Structures By Small Angle X-Ray Scattering

Ryan Hayes, University of Michigan

Bringing Statistical Mechanical Rigor to Protein Design in Large Sequence Spaces with Multisite λ Dynamics

PROGRAM (CONT.)

July 7

Concurring Session 2: 12 - 2 p.m.

Quaternary Structure: Shape Shifting in the Control of Protein Function

Session Chair: Eileen Jaffe, Fox Chase Cancer Center

Session Speakers:

Yimon Aye, EPFL

Talk Title: Unmasking Proteins' Moonlighting Behaviors Shaped By Ligand-Driven Changes In Functional Networks

Constance Jeffrey, University of Illinois Chicago

Talk Title: Shapeshifting Moonlighting Proteins

Acacia Dishman, Medical College of Wisconsin

Talk title: Evolution of Fold-Switching in the Metamorphic Protein XCL1

Kushol Gupta, University of Pennsylvania

Talk Title: Solution Conformations of Dimeric Phenylalanine Hydroxylase

LORNE REPRESENTATIVE

Bostjan Kobe, University of Queensland

Talk Title: Signaling By Cooperative Assembly Formation (Scaf) In Innate Immunity And Cell-Death Pathways

Flash Talks

Silvia Borkosky, Fundacion Instituto Leloi

Talk Title: Liquid-Like Condensates of p53 Are Modulated by Interaction with the Papillomavirus E2 Master Regulator

Elizabeth Dragonova, Tufts University

Talk Title: Structural Basis for NEC Coat Formation During HSV-1 Nuclear Egress

Live Poster Presentations

2:30 - 4 p.m.

All live poster presentations will take place on an external platform and can be accessed [here](#) (account registration is required if you have not yet registered in Fourwaves). All accepted abstracts can be browsed by theme and schedule on the platform.

Industry Visit - Novartis

4 - 5 p.m.

Shuimu Biosciences Webinar: 6 - 6:30 p.m.

The Next Generation Specimen Supporting Focused Ion Beam for High-Resolution Cryo-EM Analysis

Plenary Awards Session 2: 6:30 - 8:30 p.m.

Dr. Minoru Kanehisa, Kyoto University, 2019 Carl Brändén Award Winner

Talk Title: Toward Understanding The Origin And Evolution Of Cellular Organisms And Viruses

Intro from The Protein Society President - Dr. Amy E. Keating, MIT

The 2019 recipient of this award is Professor Minoru Kanehisa (Kyoto University). Professor Kanehisa is one of the world leaders in the bioinformatics field. The KEGG (Kyoto Encyclopedia of Genes and Genomes) database, which he established in 1995 and continues to develop, provides a very original and useful data resource not only in the protein science field, but also in much wider fields of general biology and medicine. KEGG integrates information on biological systems from the organismal-level, to the cell-level, to the molecular level and includes genomic, chemical, and human health data both for understanding biological systems and practical applications in society. Professor Kanehisa will receive his award and be recognized at the 2020 World Conference on Protein Science in Sapporo, Japan, a joint symposium organized by The Protein Society, the PSSJ (Protein Science Society of Japan), and Asia Pacific Protein Association (APPA).

The Protein Society Carl Brändén Award

In the tradition of Carl Brändén, pioneer in structural biology, co-author of the seminal text Introduction to Protein Structure, and leader of the world-class synchrotron facility at Grenoble, the Carl Brändén Award, sponsored by Rigaku Corporation, honors an outstanding protein scientist who has also made exceptional contributions in the areas of education and/or service.

Specific Requirement: Sustained, high-impact research contributions to the field.

2019 Protein Science Best Paper Award Winner: Tatsuya Niwa, Tokyo Institute of Technology

Talk Title: Translation-Coupled Protein Folding Assay Using a Protease to Monitor the Folding Status

2020 Protein Science Best Paper Award Winners: Samuel Junod and Joseph Kelich, Temple University

Talk Title: Nucleocytoplasmic Transport of Intrinsically Disordered Proteins Studied by High-Speed Super-Resolution Microscopy

PROGRAM (CONT.)

July 8

Malvern Panalytical Webinar: 10 - 10:30 a.m.

Protein Activity and Stability - Two Sides of the Same Coin

Plenary Awards Session 3: 11 - 11:50 p.m.

Dr. Stephen Sligar, University of Illinois Urbana-Champaign, 2020 Christian B. Anfinsen Award Winner

Talk Title: Revealing the Structure and Function of Membrane Proteins

Intro From The Protein Society President-Elect Dr. Chuck Sanders, Vanderbilt University

Dr. Sligar's academic career has featured the discovery, development, and use of chemical and biophysical tools to understand fundamental problems in protein biochemistry and biophysics. Of relevance to the Anfinsen Award is his development of nanodiscs, which are patches of lipid membrane stabilized by a "belt" of membrane scaffolding proteins. By using nanodiscs, signaling proteins and macromolecular complexes that rely on a membrane can be readily studied in a native bilayer that is solubilized in an aqueous environment. Dr. Sligar's commitment to wide dissemination of the nanodisc technology has led to its use by hundreds of laboratories, amplifying the impact of his advances and broadly benefitting the field of protein science.

The Protein Society Christian B. Anfinsen Award

Established in 1996 and named for Nobel laureate Christian Boehmer Anfinsen, whose research on the structure and function of enzyme proteins contributed to the general acceptance of the "thermodynamic hypothesis," The Christian B. Anfinsen Award recognizes significant technological achievements and/or methodological advancements in protein research. *Specific Requirement: Technological achievement or significant methodological advances.*

Concurring Session 1: 12 - 2 p.m.

Novel Approaches to Observe Proteins in Their Natural Environment

Session Chair: Dr. Gabriel Lander, Scripps Research Institute

Session Speakers:

Rina Rosenzweig, Weizmann Institute of Science

Talk title: The Roles of Hsp40 Chaperones in Health and Disease

Miroslava Schaffer, Max Planck Martinsreid

Talk Title: Cryo-Fib Sample Preparation Methods For Tissue And Cells In Structure Biology Studies At Molecular Resolution

Lisa Jones, University of Maryland

Talk Title: Development Of In-Cell Protein Footprinting Coupled With Mass Spectrometry For Proteome-Wide Biology

Stephen D Fried, Johns Hopkins University

Talk Title: Probing the Proteome's Refoldability under Cellular-like Conditions with Mass Spectrometry

Whitney Costello, UT Southwestern Medical Center

Talk Title: Enabling Structural Studies Of Metastable Proteins Within Cellular Milieu Via Dynamic Nuclear Polarization Nmr

Flash Talks:

Farha Khan, UCLA

Effect Of Voltage On Transport Kinetics And Conformation Of The Sodium Dependent Sugar Transporter Vsglt

Yiling Xiao, UT Southwestern Medical Center

Optimizing DNP-Assisted NMR in Living Cells

Rachel Hutchinson, University of Wisconsin-Madison

Selective Tuning of Solubility and Structural Accuracy of Newly-Synthesized Proteins by the Hsp70 Chaperone System

Concurring Session 2: 12 - 2:20 p.m.

New Protein Post-Translational Modifications

Session Chair: Dr. Jean Baum, Rutgers University

Session Speakers:

Eranthie Weerapana, Boston College

Talk Title: Chemical-Proteomic Strategies To Investigate Reactive Cysteines

Ian Maze, Icahn School of Medicine

Talk Title: Protein Monoamination In Brain: Novel Mechanisms Of Neural Development, Plasticity And Disease

Hening Lin, Cornell University

Talk Title: Post-Translational Modification Cycles In Cell Signaling And Disease

Renā A. S. Robinson, Vanderbilt University

Talk title: Proteomic Platforms for Endogenous Measurement of S-Nitrosylation in Aging Models

Sonya Neal, University of California, San Diego

Talk Title: The Role of Derlin Rhomboid Pseudoproteases in ERADicating Misfolded Membrane Proteins

PROGRAM (CONT.)

July 8

Alex Guseman, University of Pittsburgh

Talk Title: Assessing The Structures And Interactions Of Fd-Crystallin Deamidation Variants

Flash Talks:

Jared Edwards, Michigan Technological University

Talk Title: Rapid Detection and Purification of Glycosylated Proteins and Their Receptors

Mina Yu, Princeton University

An Alternative Photoacclimation Response In Cryptophyte Algae Through Differential Chromophorylation Of Their Phycobiliproteins

Plenary Award Session #4: 2:30 - 4 p.m.

Dr. Shuguang Zhang, MIT, 2020 Emil Thomas Kaiser Award Winner

Talk Title: Self-Assembling Peptides: From A Discovery In A Yeast Protein To Diverse Uses And Beyond

Intro from The Protein Society President - Dr. Amy E. Keating, MIT

Dr. Zhang is widely seen as a founder of the field of peptide nanomaterials. He discovered a class of ionic self-complementary peptides that undergo molecular self-assembly to form well-ordered nanofibers and membranous structures. Dr. Zhang went on to show many important applications of this class of peptide materials as carriers for controlled drug delivery and as the building blocks of scaffolds for tissue regeneration and accelerated wound healing. He was at the forefront of showing that 3-D cell culture offers a more realistic micro- and local-environment than 2-D culture, and he demonstrated the utility of 3-D culture in basic cell biology, tumor biology, high-content drug screening, and regenerative medicine. His contributions have transformed our basic understanding of the biochemical basis of molecular self-assembly and its application in the field of biomedical engineering.

The Protein Society Emil Thomas Kaiser Award

In 2002, The Protein Society established The Emil Thomas Kaiser Award. Dr. Kaiser's highly original research, including the profoundly significant discovery of the necessity amphiphilic helices to biological life, can be said to have introduced a new field of chemistry. In this tradition, The Emil Thomas Kaiser Award recognizes a recent, highly significant contribution in applying chemistry to the study of proteins.
Specific Requirement: Application of chemistry to the study of proteins.

2019 Protein Science Best Paper Winner

Talk Title: Structures of single-layer β -sheet proteins evolved from β -hairpin repeats

2019 Protein Science Best Paper Co-Winners: Qingping Xu, Argonne National Laboratory and Matthew Biancalana

Industry Visit - Silicon Therapeutics and Roivant Discovery Webinar

4 - 5 p.m.

Live Poster Presentations

6:30 - 10 p.m.

All live poster presentations will take place on an external platform and can be accessed [here](#) (account registration is required if you have not yet registered in Fourwaves). All accepted abstracts can be browsed by theme and schedule on the platform.

PROGRAM (CONT.)

July 9

Gender Power Hour
10 - 10:50 a.m.

Plenary Awards Session #5: 11 - 11:50 a.m.

Dr. Amy C. Rosenzweig, Northwestern University, 2021 Hans Neurath Award Winner

Talk Title: Copper-Dependent Biological Methane Oxidation

Professor Rosenzweig is a preeminent protein biochemist who tackles problems at the forefront of bioinorganic chemistry. Her lab studies metal-dependent methane oxidation, oxygen activation, and metal uptake and transport using structural, spectroscopic, biochemical, genetic, and bioinformatics approaches. Her contributions characterizing the membrane-bound methane monooxygenase have inspired new ways to harness the energy of methane, a potent greenhouse gas, as an alternative liquid fuel source. Other work from Professor Rosenzweig on copper uptake may hold therapeutic potential in Wilson's disease, a genetic disorder leading to copper overload in humans.

Concurring Session 1: 12 - 2 p.m.

Designer Proteins Through Genetic Code Expansion

Session Chair: Dr. Meghan Breen, Furman University

Session Speakers:

Kathrin Lang, ETH Zurich

Talk Title: Expanding The Genetic Code - Novel Chemistries In Living Systems

Abhishek Chatterjee, Boston College

Talk Title: Genetically Encoded Chemistries to Read and Write Biology

Nediljko Budisa, University of Manitoba

Talk Title: Recent Advances in Genetic Code Engineering with Non-canonical Aromatic Amino Acids in Escherichia Coli

Amy Ryan, University of Pittsburgh

Talk Title: Optogenetic Approaches for Acute Control of Protein Localization and Degradation

Ahmed Badran, Broad Institute

Talk Title: Teaching Old Machines New Activities: Novel Technologies For Engineering Cellular Protein Translation

Francesca Anson, University of Massachusetts Amherst

Talk Title: Weaponizing Caspases: Investigations To Exploit Caspase-Induced Apoptosis Via Intracellular Delivery

Flash Talks:

Mariha Islam, Tufts University

Diversifying Simple Synthetic Antibody Chemistries

Stephanie Breunig, California Institute of Technology

Modification of Insulin Lispro by Incorporation of Non-canonical Proline Residues

Concurring Session 2: 12 - 2 p.m.

Measuring Forces of Biological Systems

Session Chair: Dr. Chuck (Charles) Sanders, Vanderbilt University

Session Speakers:

Michelle Wang, Cornell University

Talk Title: DNA Mechanics in Fundamental Processes

Andrea Candelli, LUMICK

Talk Title: Force-Dependent Biological Mechanisms Across Scales: From Single-Molecules To Single-Cells

Khalid Salaita, Emory University

Talk Title: Using The Force: Molecular Tension Probes Reveal How Forces Boost The Fidelity Of Information Transfer In Signaling

Colleen Kelly, University of Massachusetts, Lowell

Talk Title: Protein Folding Across Methods

Ibraheem Alshareedah, University at Buffalo

Talk Title: Protein-Rna Phase-Separated Condensates Are Viscoelastic Fluids With Tunable Material Properties

Flash Talks:

Rachel Bender, Emory University

An Indestructible Tension Probe for Measuring High-Force Mechanical Events in Cells

Jie Shi, Texas A&M University

Coupling Between Local Hydration And Protein Motion In Determining The Free Energy Of Ligand Binding

PROGRAM (CONT.)

July 9

Live Poster Presentations

2:30 - 4 p.m.

All live poster presentations will take place on an external platform and can be accessed [here](#) (account registration is required if you have not yet registered in Fourwaves). All accepted abstracts can be browsed by theme and schedule on the platform.

Industry Visit - Scholar Rock

4 - 5 p.m.

Plenary Awards Session #6: 6:30 - 7:30 p.m.

Dr. Toshia Endo, Kyoto Sangyo University, 2021 Hans Neurath Award Winner

Talk Title: Protein Machineries That Make And Maintain Mitochondria

Introduction from The Protein Society President-Elect Charles (Chuck) R. Sanders, Vanderbilt University

Professor Endo has made outstanding contributions to the fields of intracellular protein sorting and mitochondrial biology and is an international leader in the area of structure-function studies of cell organelles. His work combines biochemical, structural, and molecular biological approaches in a highly innovative and productive manner to solve major problems of protein research. The molecular understanding of the mitochondrial protein import machinery elucidated by Professor Endo is a highlight of mitochondrial research and provides an essential basis for understanding diseases of mitochondrial dysfunction.

July 12

St. Jude Children's Hospital Webinar: 10 - 10:30 a.m.

Postdoc Opportunities at St. Jude Children's Hospital

Plenary Awards Session #7: 11 - 11:50 a.m.

Dr. Sheila Jaswal, Amherst College, 2021 Carl Brändén Award Winner

Talk Title: A Quarter Century of Being Human in Protein Science

Welcome from Chair of The Program Planning Committee - Dr. Jeanne A. Hardy, University of Massachusetts Amherst

Professor Jaswal is an expert on kinetic and thermodynamic mechanisms for protein stabilization and an award-winning teacher. With a team of undergraduates, she has developed tools to better understand the diversity of protein folding kinetics and provided a theoretical framework for mapping energy landscapes under native conditions using hydrogen-exchange mass spectrometry. In response to a 2015 campus-wide Black Lives Matter protest, she collaborated with students to develop "Being Human in STEM" (HSTEM). In this moment of unprecedented recognition of racism in science, the HSTEM model offers a structure that welcomes participants in their complex intersecting identities, educates them about racism, and gives them practice with having difficult conversations, collaborating across differences, and making realistic and effective change.

Networking & Career Discussion, Gathertown

12 - 1:25 p.m.

Chaired by Dr. Mary Munson, University of Massachusetts Medical School

Diversity Power Hour, Gathertown

1:30 - 2:15 p.m.

Diversity in Protein Science II

2:30 - 4 p.m.

Diversity Mentoring Event, Gathertown

4 - 5 p.m.

Perkin Elmer Webinar: 5:15 - 5:45 p.m.

PROGRAM (CONT.)

July 12

Concurring Session 1: 6:30 - 8:30 p.m.

Cryo-EM: Beyond Single Particle Reconstruction

Session Sponsor: BioViz Studio

Session Chair: Gabriel Lander, Scripps Research Institute

Session Speakers:

Mimi Ho, Columbia University

Talk Title: Endogenous Structural Biology Approaches For Challenging Systems

Amédée des Georges, CUNY

Talk Title: Peering Into Conformational Ensembles Of The Ryanodine Receptor With Cryo-Em

Radostin Danev, University of Tokyo

Talk Title: Pushing The Limits Of Cryo-Em For G Protein-Coupled Receptors

Jungsan (J.) Sohn, Johns Hopkins University

Talk Title: The Signaling Direction, Order, And Specificity Of The Aim2-Asc Inflammasome

Katarina Meze, Cold Spring Harbor Laboratory

Talk Title: The 3'-5' Exonuclease Dis3l2 Undergoes Conformational Dynamics During Structured Rna Degradation

Flash Talks:

Daniel Gestaut, Stanford University

A Very Special Chaperonin: How Does Tric/Cct Achieve Tubulin Folding?

Piotr Kolata Vlaam, Instituut voor Biotechnologie

Structure of Escherichia coli Respiratory Complex I Reconstituted into Lipid Nanodiscs Reveals an Uncoupled Conformation

Siyu Chen, Northwestern University

Structural Basis Of Long-Range To Short-Range Synaptic Transition In Nhej

Ryoichi Arai, Shinshu University

Icosahedral 60-Meric Porous Structure Of Designed Protein Nanoparticle Tip60

Concurring Session 2: 6:30 - 8:30 p.m.

Diffraction Methods are Alive and Well

Session Sponsor: MiTeGen

Session Chair: Sarah Perry, University of Massachusetts, Amherst

Session Speakers:

Jose Rodríguez, UCLA

Talk Title: New Approaches In Electron Diffraction For Visualizing Molecules With Atomic Detail

Carolyn Larabell, UCSF/LBNL

Talk Title: Imaging Membraneless Organelles And Biomolecular Condensates In The Native State

Eriko Nango, Tohoku University

Talk Title: Protein Structural Dynamics Revealed By Molecular Movie Analysis

Karsten Melcher, Van Andel Institute

Talk Title: Structure Of The Ampk Complex In Its Inactive Atp-Bound State

Michelle Fry, California Institute of Technology

Talk Title: The Atpase Cycle Of Gef3 From A Human Pathogen

Flash Talks:

Lindsey Backman, Massachusetts Institute of Technology

Structural Characterization of a Hydroxyproline Dehydratase from C. difficile

Tolou Golkar, McGill University

Structural Basis for Plazomicin Antibiotic Action and Resistance

Xiaolong Li, Dana-Farber Cancer Institute

Crystallographically Resolved Pretrc-Pmhc Complexes Reveal The Structural Basis Of B Selection During Early T Cell Development

PROGRAM (CONT.)

July 13

Webinar: 10 - 10:50 a.m.

Mass Photometry - A New Tool to Study Biomolecules

Plenary Awards Session #8: 11 - 11:50 a.m.

Dr. Bruno Correia, EPFL, 2021 Protein Science Young Investigator Award Winner

Talk Title: Expanding the Universe of Functional Proteins by Computational Design - Examples on Antigen Design and Cell Engineering

The 2021 recipient is Professor Bruno Correia. During his time at EPFL, Professor Correia has combined computational science with experimental studies in the area of protein design. He developed methods for the de novo design of proteins that present native binding epitopes, and he led a collaborative team to demonstrate that designed proteins can induce neutralizing antibodies against respiratory syncytial virus. Professor Correia has also pioneered impactful computational methods using machine learning to advance our understanding of molecular recognition

Protein Science Young Investigator Award

The Protein Science Young Investigator Award, sponsored by Wiley, formerly known as The Irving Sigal Young Investigator Award, recognizes a scientist in the first 8 years of an independent career who has made an important contribution to the study of proteins.**With allowances for familial leave or other exigent circumstance.

Specific Requirement: Within 8 years of starting an independent career.

Concurring Session 1: 12 - 2 p.m.

Protein Evolution, Design and Selection

Session Chair: Nikolay V. Dokholyan, Penn State College of Medicine

Session Speakers:

Donald Hilvert, ETH Zurich

Talk Title: Evolving Virus-Like Nucleocapsids From A Bacterial Enzyme

Janet Thornton, EMBL

Talk Title: Computational Enzymology: The Structure, Function And Evolution Of Enzymes

Lydia M. Contreras, University of Texas at Austin

Talk Title: New Approaches For Identifying And Designing Novel Rna Readers

Liangcai Gu, University of Washington

Talk title: Efficient, Generalizable Approaches for Creating Chemogenetic

and Optogenetic Sensors

LAPS REPRESENTATIVE

Sergio Romero-Romero, University of Bayreuth

Talk Title: Exploring The Stability Panorama Of De Novo Tim Barrels By Protein Design

Flash Talks:

Nicholas Callahan, IBBR

Developing Protein Tools For Single-Molecule Protein Sequencing

Saacnicteh Toledo Patino, OIST

Lost & Found. Indel-Mediated Cofactor Specificity Switch From Nad To Sam

Kateryna Maskysenko, Max Planck Institute for Developmental Biology

De Novo Protein Design Of Vascular Endothelial Growth Factor Inhibitors

Jaewan Jang, University of Toronto

New Binding Partners To Cyanobacteriochromes For Optogenetic Applications

Concurring Session 2: 12 - 2 p.m.

Undergraduate Research Session

Session Sponsor: Refeyn

Learn about groundbreaking research from undergraduate scholars.

Session chaired by Dr. Matt Gage, University of Massachusetts Lowell.

Speakers:

Katherine Lee, University of Connecticut

Matthew Zackin, Tufts University

Samuel Fredericksen, University of Massachusetts, Lowell

Isabella Bakestani, University of Ottawa

Emily Schaffter, University of Massachusetts Lowell

Thomas Grant, University of Ottawa

Xi Chen, University of Wisconsin - Madison

Jacob Parres-Gold, California State University, Los Angeles

Plenary Awards Session #9: 2:20 - 3:10 p.m.

Dr. Mohammad Seyedsayamdost, Princeton University,

2020 Protein Science Young Investigator Award winner

Talk Title: New Reactions Catalyzed by Metalloenzymes in Natural Product Biosynthetic Pathways

Intro & welcome from The Protein Society President - Dr. Amy E. Keating, MIT

Dr. Seyedsayamdost has conducted pioneering work on novel biochemical pathways. He uses a creative combination of bioinformatics and chemical

PROGRAM (CONT.)

July 13

genetics to activate cryptic biosynthetic pathways in microbial systems and determine their products. This has led him to discover the vast - and previously overlooked - biosynthetic potential of many bacteria and to determine the effects that bacterially-produced molecules have on other microbes. Pathways that he has discovered produce previously unknown natural products using reactions catalyzed by hitherto uncharacterized proteins. His insights are already having a substantial impact on protein science, as these pathways include novel transformations catalyzed by newly discovered metalloenzymes.

Plenary Awards Session #10 : 3:10 - 4 p.m.

Dr. Lei Wang, University of California, San Francisco, 2021 Emil Thomas Kaiser Award Winner

Talk Title: Genetically Encoded Latent Bioreactive Amino Acids: New Covalent Bonds for Proteins and Covalent Protein Drugs

Intro & welcome from The Protein Society President - Dr. Amy E. Keating, MIT

Professor Wang has advanced the genetic introduction of unnatural amino acids into proteins in living systems. Professor Wang pioneered the concept of proximity-enabled bioreactivity, in which an unnatural amino acid selectively reacts with a nearby target natural amino acid, introducing a new covalent bond into a protein. Such modifications can confer exceptional stability, affinity, and optical control on targeted proteins. Technology that Professor Wang developed makes it possible to identify elusive protein interactions in living cells, and provides a route to covalent protein therapeutics. His contributions open up a new field with impacts on biological studies, biotherapeutics, and synthetic biology.

Emil Thomas Kaiser Award

In 2002, The Protein Society established The Emil Thomas Kaiser Award. Dr. Kaiser's highly original research, including the profoundly significant discovery of the necessity amphiphilic helices to biological life, can be said to have introduced a new field of chemistry. In this tradition, The Emil Thomas Kaiser Award recognizes a recent, highly significant contribution in applying chemistry to the study of proteins.

Specific Requirement: Application of chemistry to the study of proteins.

Industry Visit - C4 Therapeutics

4 - 5 p.m.

Live Poster Presentations

6:30 - 10 p.m.

July 14

Plenary Awards Session #11: 10 - 10:50 a.m.

Dr. Janet Smith, University of Michigan, 2021 Dorothy Crowfoot Hodgkin Award Winner

Talk Title: Flavivirus NS1: New Fold and New Functions for an Enigmatic Virulence Factor

Intro & welcome from The Protein Society President - Dr. Amy E. Keating, MIT

Professor Smith is recognized for exceptional contributions to our understanding of the biological function of proteins through knowledge of their 3D structures. In major studies of natural-product biosynthetic enzymes, she demonstrated how macrolactones form, how biosynthetic assembly lines function, and how nature has adapted enzymes from primary metabolism for surprising chemical transformations such as cyclopropane formation. Her recent investigations of viral proteins and host antiviral proteins led to an understanding of how the flavivirus NS1 protein increases the virulence of dengue and Zika viruses, and how the zinc-finger antiviral protein recognizes viral RNA.

Dorothy Crowfoot Hodgkin Award

Dorothy Crowfoot Hodgkin was a founder of protein crystallography as well as a Nobel laureate. The Dorothy Crowfoot Hodgkin Award, sponsored by Genentech, is granted in recognition of exceptional contributions in protein science which profoundly influence our understanding of biology. *Specific Requirement: Profound influence on our understanding of biology.*

Plenary Awards Session #12: 11 - 11:50 a.m.

Dr. Catherine Drennan, MIT, 2020 Dorothy Crowfoot Hodgkin Award Winner

Talk Title: Capturing Snapshots of Ribonucleotide Reductase in Action

Intro & welcome from The Protein Society President - Dr. Amy E. Keating, MIT

Dr. Drennan has made enormous contributions by solving high-resolution structures of proteins and protein complexes that enhance our understanding of the biology of metalloproteins. Dorothy Crowfoot Hodgkin was famous for using X-ray crystallography to determine the structure of Vitamin B12, and Dr. Drennan has provided monumental insights into the structure and function of proteins that bind to B12. Dr. Drennan is known for going beyond single proteins and elucidating structures that illuminate entire pathways, capturing multiple snapshots of enzymes as they proceed through their reaction cycles. Among her many notable accomplishments, Dr. Drennan determined the first structure of the cobalamin-dependent ribonucleotide reductase, one of the three enzymes that catalyze the final step in production of deoxyribonucleotides in all organisms. Dr. Drennan's insights are solidly etched into textbooks and the fabric of our field. Drennan is also an outstanding and widely recognized educator and a tireless advocate for inclusion and equity in science.

PROGRAM (CONT.)

July 14

Concurring Session 1: 12 - 2 p.m.

Allostery & Dynamics in Protein Function

Session Chair: Woody Sherman, Silicon Therapeutics

Session Speakers:

Andrew Woolley, University of Toronto

Talk Title: Harnessing Photo-Switchable Proteins

Rachelle Gaudet, Harvard University

Talk Title: Mechanics Of An Nrapm Family Transition Metal Transporter

Corey Wilson, Georgia Tech

Talk Title: Transcriptional Programming - Engineering Intelligent Biological Systems

David Boehr, The Pennsylvania State University

Talk Title: Differences In Conformational Dynamics Between A Virus Polyprotein And Its Fully Processed Counterparts Expands The Functional Proteome

Heather Masson-Forsythe, Oregon State University

Talk title: A Dancing Duplex: The SARS-CoV-2 Nucleocapsid Phosphoprotein's Multivalent Binding to RNA

Flash Talks:

Irina Shlosman, Harvard Medical School

Uncovering The Conformational Dynamics Of A Bacterial Cell Wall Synthase Using Smfret

Aaron Cruz Navarrete, University of Sheffield

Substrate Discrimination Via A Proline Switch In An Allomorphic Enzyme

Rama Reddy, University of California, Merced

Functional Role of Protein Disorder in Eukaryotic Gene Regulation

Gabriel Rosenblum, Weizmann Institute of Science

Allostery Through DNA Drives Phenotype Switching

Concurring Session 2: 12 - 2 p.m.

Targeted Protein Degradation

Session Chair: Dr. Jeanne Hardy, University of Massachusetts, Amherst

Session Speakers:

Katelyn Cassidy, Astra-Zeneca

Talk Title: Ms-Based Proteomics: A Central, Multifaceted Resource For The Advancement Of Targeted Protein Degradation Projects

Angela Cacace, Arvinas

Talk Title: Arvinas Targeted Degradation Discovery Engine

Nicolas Thomä, Friedrich Miescher Institute

Talk Title: Haven't Got A Glue: Translating Molecular Insights On Chromatin And Ubiquitin Ligases Into Novel Therapeutics

Scott Eron, C4 Therapeutics

Talk Title: Finding a Way Out of the Labyrinth: Degradation-Induced Ternary Complex Modelling

Jiale Du, University of Massachusetts Amherst

Talk Title: A Cryptic K48 Ubiquitin Chain-Specific Site On The Proteasome-Associated Deubiquitinase Uch37/Uchl5 Is Required For Degradation

Flash Talks:

Cynthia Okoye, University of Cambridge

Harnessing the APC/C for Targeted Protein Degradation

Anton Sorkin, University of Moscow

A System of Auxin-inducible Degradation of Human Ku70 Protein to Study Its Role in HIV-1 Replication

Plenary Awards Session #13: 2:30 - 3:20 p.m.

Dr. Karen Fleming, Johns Hopkins University, 2020 Carl Brändén Award Winner

Talk Title: Chaperoning Unfolded Membrane Proteins

Intro & welcome from The Protein Society President-Elect - Dr. Charles (Chuck) R. Sanders, Vanderbilt University

Professor Karen Fleming is a pioneer and leader in the field of membrane protein folding. Her contributions include making some of the first rigorous thermodynamic measurements for membrane protein folding, introducing the hydrophobicity scale that is now most widely used to describe amino-acid side chain partitioning into bilayers, and elucidating the thermodynamic principles governing the coupled trafficking and folding of Gram-negative beta-barrel membrane proteins. Dr. Fleming has also tirelessly served the scientific community, devoting major service to scientific societies and co-founding (with Stein and Moore awardee James Bowie) the Gordon Research Conference on Membrane Protein Folding. Dr. Fleming is also an eloquent and outspoken advocate for women in

PROGRAM (CONT.)

July 14

science, with a particular passion for illuminating and neutralizing hidden biases commonly held by both men and women.

Protein Science Journal: A Conversation with Editor-in-Chief Brian Matthews, University of Oregon and incoming Editor-in-Chief, John Kuriyan, University of California, Berkeley
3:20 - 4 p.m.

Industry visit - GinkgoBioworks
4 - 5 p.m.



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- * Register here: <https://event.fourwaves.com/ps35/registration> by entering name and email.
- * Activate account using link in confirmation email. Browse & find posters here starting July 1: <https://event.fourwaves.com/ps35/schedule>
- * Live poster presentations take place July 7 and July 9, from 2:30 - 4 p.m. EDT, and July 8 and 13 from 6:30 - 8:30 p.m. EDT.

Access the Official PS35 Virtual Platform here: <https://app.socio.events/ODMONw/authby> using the registrant-only website & entering the SAME EMAIL used during the registration process.








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How to Connect

Access the platform using the link that will be sent to you by email.



Enter your full name and set up your Avatar.



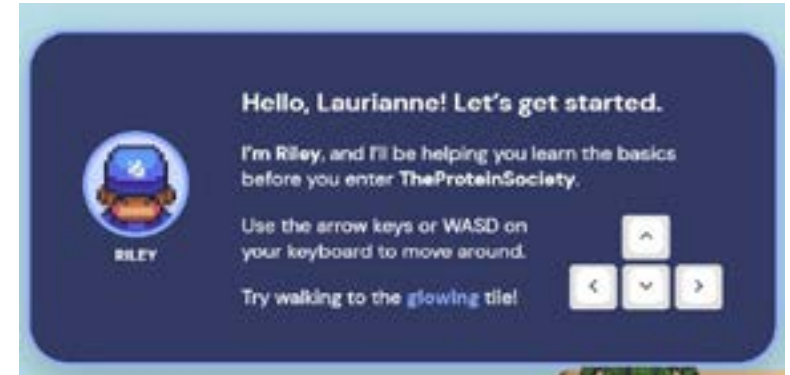
When you connect you will be asked to select your **camera**, **microphone** and **speaker**, you can then click on "Join the gathering."

You do not have to turn on your microphone or your camera.

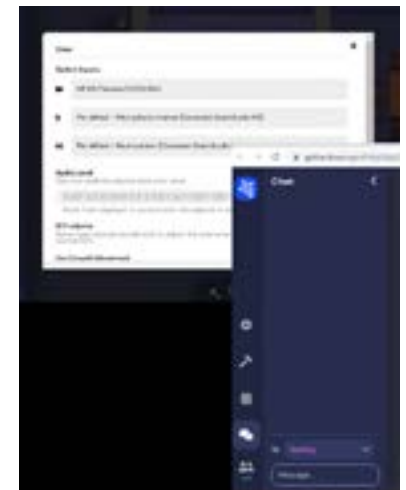
From the platform you can **deactivate** your microphone and camera at any time.

How to navigate through gather town

Once on the platform, move using the **arrows** on your computer keyboard. When you see a **glowing object**, press the X key on your keyboard to access it. Once on the platform, you can join **private spaces** to chat with different people.



In the left band of your screen, you have access to the **settings**, the **calendar** and the **chat**. The **settings** will allow you to modify your switch inputs. The **calendar** will allow you to consult the schedule. The **chat** will allow you to get in touch with other people.



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	1 Year Price/ Discount Code	2 Year Price/ Discount Code	5 Year Price/ Discount Code
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Graduate	Regular Rate: \$50 Reduced Rate: \$40 Code: vt8bupqd	Regular Rate: \$90 Reduced Rate: \$63 Code: xdhxha4	
Early-Career	Regular Rate: \$100 Reduced Rate: \$80 Code: ppb3r6vt	Regular Rate: \$180 Reduced Rate: \$126 Code: vhnclmwn	Regular Rate: \$475 Reduced Rate: \$333 Code: ujnucurf
Lab Staff	Regular Rate: \$50 Reduced Rate: \$40 Code: axkbrhu	Regular Rate: \$90 Reduced Rate: \$63 Code: azsjdkhf	Regular Rate: \$230 Reduced Rate: \$161 Code: gjkfzfb
Full	Regular Rate: \$200 Reduced Rate: \$150 Code: zkmbg6wx	Regular Rate: \$380 Reduced Rate: \$266 Code: 7sj9cxrk	Regular Rate: \$950 Reduced Rate: \$665 Code: kzxgwn99
Emeritus	Regular Rate: \$25 Reduced Rate: \$20 Code: 7d4dmat9	Regular Rate: \$50 Reduced Rate: \$35 Code: wurmkky	Regular Rate: \$115 Reduced Rate: \$81 Code: 6c6wvweax
Corporate	Regular Rate: \$300 Reduced Rate: \$250 Code: r87jux2g	Regular Rate: \$470 Reduced Rate: \$400 Code: mahtw2q6	Regular Rate: \$1,150 Reduced Rate: \$1,000 Code: 4ptmdf49

Individual Memberships

TPS members represent an international community of all those who share an interest in the structure, function, design, synthesis, and utilization of proteins. In fact, it is this diversity of disciplines and perspectives represented by TPS members that is the group's defining characteristic.

Members include chemists, biologists, physicists, and mathematicians - researchers of all stripes, whose collaboration and communication comprise the Society's core mission. They represent academia, industry, government, non-profits, and leading institutions in more than 50 nations.

BENEFITS INCLUDE:

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- Connect with TPS leaders and have a say in the direction of your Society.
- Only members are able to submit or sponsor an abstract for the Best Poster Competition, or be considered for a Young Investigator Talk.
- Nominate your colleagues for one of seven prestigious TPS awards.
- Apply for a travel/ anniversary award
- Eligibility to submit a contributed talk.

Webinars

Members have priority free registration for our virtual workshops and can [design their own webinars](#).

Networking and Leadership

- Connect and collaborate privately with other members through the Member Directory or the members-only LinkedIn group.
- Be eligible to vote – or stand yourself – for TPS Executive Council, Nominating Committee, and other leadership roles.
- Stay informed with the monthly member e-news.

2021 Protein Society AWARD WINNERS

Toshiya Endo, Ph.D., Kyoto Sangyo University
2021 Hans Neurath Award Winner



Professor Endo has made outstanding contributions to the fields of intracellular protein sorting and mitochondrial biology and is an international leader in the area of structure-function studies of cell organelles. His work combines biochemical, structural, and molecular biological approaches in a highly innovative and productive manner to solve major problems of protein research. The molecular understanding of the mitochondrial protein import machinery elucidated by Professor Endo is a highlight of mitochondrial research and provides an essential basis for understanding diseases of mitochondrial dysfunction.

Amy Rosenzweig, Ph.D., Northwestern University
2021 Hans Neurath Award Winner



Professor Rosenzweig is a preeminent protein biochemist who tackles problems at the forefront of bioinorganic chemistry. Her lab studies metal-dependent methane oxidation, oxygen activation, and metal uptake and transport using structural, spectroscopic, biochemical, genetic, and bioinformatics approaches. Her contributions characterizing the membrane-bound methane monooxygenase have inspired new ways to harness the energy of methane, a potent greenhouse gas, as an alternative liquid fuel source. Other work from Professor Rosenzweig on copper uptake may hold therapeutic potential in Wilson's disease, a genetic disorder leading to copper overload in humans.

David Agard, Ph. D., University of California, San Francisco
2021 Stein & Moore Award Winner



The 2021 recipient is Professor David Agard. Professor Agard's contributions cover a broad array of scientific areas, from protein folding to chaperone mechanisms, and from cytoskeletal structure and function to the structure of the centrosome. His recent determination of the structural details of complexes of Hsp90 with substrates, partner chaperones, and co-chaperones have yielded unprecedented insights into client loading, remodeling, and maturation by this system. He has made important methodological contributions to the development of cryoEM and has integrated structural biology and biophysics to interrogate dynamic protein systems, opening up previously uncharted domains of cell biology. Professor Agard is also recognized for exceptional mentoring and advocacy for the field of protein science. Dr. Agard will speak at PS36 in San Francisco, July 7 - 10, 2022.

Sheila Jaswal, Ph.D., Amherst College
2021 Carl Brändén Award Winner - Sponsored by Rigaku Corporation



The 2021 recipient of this award is Professor Sheila Jaswal. Professor Jaswal is an expert on kinetic and thermodynamic mechanisms for protein stabilization and an award-winning teacher. With a team of undergraduates, she has developed tools to better understand the diversity of protein folding kinetics and provided a theoretical framework for mapping energy landscapes under native conditions using hydrogen-exchange mass spectrometry. In response to a 2015 campus-wide Black Lives Matter protest, she collaborated with students to develop "Being Human in STEM" (HSTEM). In this moment of unprecedented recognition of racism in science, the HSTEM model offers a structure that welcomes participants in their complex intersecting identities, educates them about racism, and gives them practice with having difficult conversations, collaborating across differences, and making realistic and effective change.

2021 Protein Society AWARD WINNERS

Petra Fromme, Ph.D., Arizona State University

2021 Christian B. Anfinsen Award Winner - Sponsored by Rigaku Corp.



The recipient of this award in 2021 is Professor Petra Fromme. Professor Fromme is a world leader in developing and applying novel technology for determining the structures of proteins, including the most challenging among them: membrane proteins. She has led this field by assembling a large network of collaborators spanning chemistry, physics, data science, biology, materials science, and engineering to pioneer the method of serial femtosecond crystallography (SFX), which is used to collect snapshots of molecules in action. She has made important contributions to the structural biology of large membrane protein complexes, especially those involved in light capture and energy conversion. Dr. Fromme will speak at PS36 in San Francisco, July 7 - 10, 2022.

Janet Smith, Ph.D., University of Michigan

2021 Dorothy Crowfoot Hodgkin Award Winner- Sponsored by Genentech



The 2021 recipient is Professor Janet Smith. Professor Smith is recognized for exceptional contributions to our understanding of the biological function of proteins through knowledge of their 3D structures. In major studies of natural-product biosynthetic enzymes, she demonstrated how macrolactones form, how biosynthetic assembly lines function, and how nature has adapted enzymes from primary metabolism for surprising chemical transformations such as cyclopropane formation. Her recent investigations of viral proteins and host antiviral proteins led to an understanding of how the flavivirus NS1 protein increases the virulence of dengue and Zika viruses, and how the zinc-finger antiviral protein recognizes viral RNA.

Lei Wang, Ph.D., University of California, San Francisco

2021 Emil Thomas Kaiser Award Winner



The 2021 recipient is Professor Lei Wang. Professor Wang has advanced the genetic introduction of unnatural amino acids into proteins in living systems. Professor Wang pioneered the concept of proximity-enabled bioreactivity, in which an unnatural amino acid selectively reacts with a nearby target natural amino acid, introducing a new covalent bond into a protein. Such modifications can confer exceptional stability, affinity, and optical control on targeted proteins. Technology that Professor Wang developed makes it possible to identify elusive protein interactions in living cells, and provides a route to covalent protein therapeutics. His contributions open up a new field with impacts on biological studies, biotherapeutics, and synthetic biology.

Bruno Correia, Ph.D., EPFL

2021 Protein Science Young Investigator Award Winner - Sponsored by Wiley



The 2021 recipient is Professor Bruno Correia. During his time at EPFL, Professor Correia has combined computational science with experimental studies in the area of protein design. He developed methods for the de novo design of proteins that present native binding epitopes, and he led a collaborative team to demonstrate that designed proteins can induce neutralizing antibodies against respiratory syncytial virus. Professor Correia has also pioneered impactful computational methods using machine learning to advance our understanding of molecular recognition.

2019 and 2020 Protein Society **AWARD WINNERS**



Catherine Drennan, Ph.D.,
Massachusetts Institute of
Technology
**2020 Dorothy Crowfoot Hod-
gkin Award Winner**
Sponsored by Genentech



Karen Fleming, Ph.D.,
Johns Hopkins University
**2020 Carl Branden Award
Winner**



Stephen Sligar, Ph.D.
University of Illinois at
Urbana-Champaign
**2020 Christian B. Anfinsen
Award Winner**



Shuguang Zhang, Ph.D.
Massachusetts Institute of
Technology
**2020 Emil Thomas Kaiser
Award Winner**



Martin Gruebele, Ph.D.,
University of Illinois at
Urbana-Champaign
**2020 Hans Neurath Award
Winner**



Mohammad Seyedsayamdost, Ph.D.,
Princeton University
**2020 Protein Science Young
Investigator Award Winner**
Sponsored by Wiley



Minoru Kanehisa, Ph.D.,
Kyoto University
**2019 Carl Branden Award
Winner**

Protein Science Best Paper AWARD WINNERS

Yu-Ting Huang, National Chung Hsing University, Taiwan, University
2020 Best Paper Award Winner



Dr. Huang, working in the lab of Pei-Fen Liu, made the unexpected finding that ATP can alter the folding and function of human proteins through protein destabilization. This phenomenon may be relevant in studying the function of proteins that exist in the specific metabolic environment of a cancer cell. As Yu-Ting explains, she wanted to be either a doctor, a scientist, or a medical specialist. "Although I couldn't get into a medical school, I met Dr. Pei-Fen Liu when I was a graduate student in National Chung Hsing University. He gave me a chance to get closer to my dream. Nowadays, people are paying more and more attention to their health, especially in these two years. It couldn't be better if what we have found in this research can help solve the problem of drug-resistance, and contribute to medical fields. For now, I'm teaching chemistry and science for teenagers. I hope that those kids will be inspired and become leading lights in academia." Pei-Fen Liu speaks highly of the skill and determination which Yu-Ting brought to the project. "Yu-Ting is an eminent and self-motivated young scientist in protein science. She originally joined my laboratory with limited background knowledge about protein folding. Surprisingly, she picked up most of the concepts and learned the key experiments quickly. Her problem solving and logical thinking are also beyond other students' standards. We initially suffered from the protein purification and sample preparation in this project for a human protein, uridine phosphorylase I. She managed to overcome all of the obstacles step by step. Continuously, she came up with a new experimental design to study the interaction between ATP and the partially unfolded state of this protein. An exciting model was then developed to explain the correlation between protein concentration and ligand binding effect. It is a pleasure to work with her in exploring unknown subjects. I believe that she is on the way to achieving success in her career path.

Samuel Junod and Joseph Kelich, Temple University
2020 Best Paper Award Winners



Samuel Junod
Temple University

The two other Best Paper awardees, Samuel Junod and Joseph Kelich, were recognized for their studies of the nucleocytoplasmic transport of intrinsically disordered proteins. By using high-speed super-resolution fluorescence microscopy in the lab of Weidong Yang, they could measure the transport kinetics and 3D spatial locations of transport routes through the nuclear pore complexes for various intrinsically disordered proteins. They found that the roles executed for folded proteins are not followed by disordered ones. For the latter, diffusion efficiencies and routes are determined by their content ratio of charged and hydrophobic amino acids.

As Dr. Kelich explains "I am currently a post-doctoral researcher at the Wistar Institute in Philadelphia studying the role of telomeric protein defects in cancer. The project for which this award was given was conducted during my PhD studies in Weidong Yang's lab. I would also like to note that Samuel Junod and I formed a great team for this project and that the Yang lab provided a great multidisciplinary team-based approach to science that I love."

Sam also outlines his own background. "My initiation to research began during my undergraduate studies under the guidance of Dr. Weidong Yang. With Dr. Yang's mentorship I resolved the spatial location of several nuclear pore complex (NPC) scaffold proteins using nanobody-specific labeling and single-molecule microscopy. Since the NPC is a major pathway for proteins entering and exiting the nucleus, mapping the location of its scaffold proteins gave further insight into the structural composition of the important cellular complex. After a brief departure into the private sector as a chemist, I returned back to Temple University to pursue my PhD and



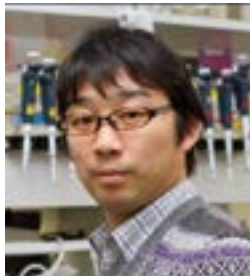
Joseph Kelich
Temple University

continue my research of the NPC with Dr. Weidong Yang. Currently, I have expanded my research of nuclear proteins to include the impact of disordered nucleoporins (Nups), characterized by the presence of phenylalanine-glycine (FG) repeats, on nucleocytoplasmic protein transport. I am very fortunate to study under Dr. Weidong Yang and to have collaborated on several projects with Dr. Joseph Kelich. I look forward to applying my knowledge of the NPC and single-molecule microscopy to other biological questions."

As Dr. Yang explains, Sam and Joe were a great team. "Samuel Junod joined my lab initially as an undergraduate student in 2014, and then a master student in 2017. Based on his great performance in research, I recommended him to the graduate committee to admit him as a PhD candidate in our department in 2018. Joseph Kelich is one of the best PhD students in my lab. He graduated from my lab in 2018 and is currently a postdoctoral fellow at the Wistar Institute of Upenn. Sam and Joe formed a good team to work on several projects including the nucleocytoplasmic transport of IDPs. In the IDP project, they had conquered the challenges of purifying and labeling various IDPs. They also took great efforts to learn single-molecule and super-resolution microscopy techniques before they successfully tracked single IDPs to move through native nuclear pores by these advanced methods."

Protein Science Best Paper AWARD WINNERS

Tatsuya Niwa, Tokyo Institute of Technology
2019 Best Paper Award Winner



For 2019 the first such paper is "Translation-coupled protein folding assay using a protease to monitor the folding status",¹ and the Best Paper awardee is Tatsuya Niwa [Fig. 1(A)].

The award-winning work of Dr. Niwa addresses two of the longest-standing questions in protein science. First, how does the amino sequence of a protein dictate its native structure and, second, how is the native structure achieved in the cell, where correct protein folding is hampered by intermediate aggregate formation? Dr. Niwa began working in this area at the University of Tokyo with Professor Hideki Taguchi and has continued at the Tokyo Institute of Technology. As a student he started a comprehensive analysis of protein aggregation and folding using a reconstituted cell-free protein synthesis approach called PURE system, developed by Professor Takuya Ueda. He plans to continue these studies in the future. As he explains, "I am also interested in 'abnormal proteins', such as intrinsically-disordered proteins and the proteins that can form liquid-liquid phase separation... These 'special' proteins may extend the conception of proteins. Ultimately, I would like to aim to find the answer to the question 'What is a protein?'."

According to Professor Taguchi "Tatsuya is a really talented and dedicated biochemist, who started his career with me and Professor Takuya Ueda at the University of Tokyo. Tatsuya conducted an epoch-making analysis of global folding and chaperone effects using a reconstituted cell-free translation system during his Ph.D. project. This work by Tatsuya opened up a new field in my lab. The translation-coupled folding assay is based on the assumption that soluble fractions following centrifugation are folded, but the soluble fractions include nonnative structures. The paper selected for a best paper award tackled the long-standing problem in the assay by adding a protease to monitor the folding status. Tatsuya literally led the research in both experiments and data analysis. I would like to emphasize that Tatsuya now has an amazing ability to analyze big data. The award encourages Tatsuya a lot for the future of his career".

Qingping Xu, Argonne National University, and
Matthew Biancalana, University of Chicago
2019 Best Paper Award Winner

The two co-recipients of the second Best Paper award, Qingping Xu and Matthew Biancalana, were brought together not so much through being in the same location as by a common research interest. Qingping obtained his undergraduate education in physics at Anqing Normal University, Anhui, China, and took his Ph.D. in biochemistry at the University of Oklahoma under the guidance of Ann West. He has determined many protein structures and worked on understanding their functions through worldwide collaborations at the Joint Center for Structural Genomics consortium at Stanford, led by Ian Wilson. Qingping currently works at the Argonne National Laboratory, where he develops software to help synchrotron users collect better data, and continues his research in protein structure and function.



Matthew Biancalana then picks up the thread: "I began my research career working in Shohei Koide's lab at the University of Chicago, where I studied the fundamental structural and dye-binding properties of amyloid fibrils. We skirted many of the technological difficulties of working with fibrils directly by using the β -sheet rich model protein Outer surface protein A (OspA). The research was compelling and inventive, and sparked my fascination with protein structure.



I subsequently conducted my Ph.D. at the University of Cambridge in Alan Fersht's group. In the course of this research, I stumbled across a structure solved by Qingping Xu that bore several similarities to the OspA variants I had worked with as an undergrad. I reached out to Qingping and we forged a long-distance collaboration to describe and analyze this unusual class of single-layer β -sheet proteins (SLBPs). Amazingly, it would take us nearly a decade to finally bring the complete story together and publish in Protein Science".

ANNIVERSARY AWARDS

Congratulations to the following outstanding students and early-career investigators for receiving assistance for the 35th Annual Symposium of The Protein Society.

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diversity awards



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Diversity Power Hour, 1:30 - 2:15 p.m. EST

Diversity in Protein Science II, 2:30 - 4 p.m. EST

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We will present the 2022 awards at our 36th Annual Symposium in San Francisco, CA, July 7 - 9, 2022. Deadline to submit complete award nomination packages is noon EDT **on November 15, 2021.**



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Please remember, you must be logged in to vote.

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PS36

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