Program

40th ANNIVERSARY SYMPOSIUM

July 19 - 22, 2026 | Boston, Massachusetts

The Protein Society

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 40 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.

THE PROTEIN SOCIETY

40th ANNIVERSARY SYMPOSIUM

July 19 - 22, 2026 | Boston, Massachusetts

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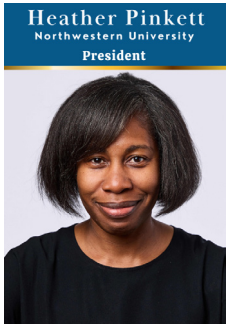


We are excited to bring you this year's Annual Symposium program consisting of 12 outstanding scientific sessions, highlighting the wide range of scientific achievements in the field of protein science. The program showcases cutting-edge discoveries, transformative technologies and new frontiers that are shaping the future of the field. Our Program Planning Committee includes Janice Robertson, Washington University; Josh Wand, Texas A&M University (Co-Chairs); Aitziber Lopez-Cortajarena, CIC biomaGUNE, Hyun-Ho Lim, Korea Brain Research Institute, Catherine Royer, Rensselaer Polytechnic Institute, and Jay Ponder, Washington University. They have assembled a line-up of engaging speakers working at the forefront of protein science research.

This year's Symposium continues our commitment to open participation with additional talks from abstract submissions across every session, including a member-contributed session. We are also pleased to showcase an exciting line-up of poster presentations and recognize outstanding young scientists through special sessions and awards. Protein Society Award recipients will present their work throughout the meeting, and selected contributions will appear in a future special issue of Protein Science.

As we celebrate 4 decades of impact in the field of protein science, we reaffirm our commitment to scientific excellence, public engagement and advancing diversity, equity, and inclusivity across all Society activities. We encourage you to engage in meaningful dialogue within our community and beyond about the vital role of scientific research. Thank you for joining us at the 2026 40th Anniversary Symposium in Boston. We welcome your feedback through the post-conference survey, which directly informs future meetings. I wish you an engaging and collaborative Symposium, and invite you to introduce yourselves to me and the Executive Council. We look forward to connecting with you.

Kind Regards,

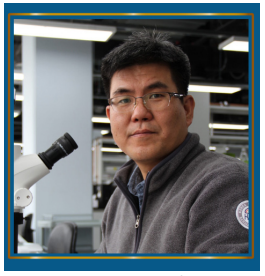
Heather Pinkett, Ph.D.
President

Program Planning Committee

Janice Robertson, Co-Chair
Washington University

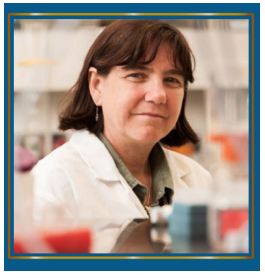
Josh Wand, Co-Chair
Texas A&M University

Aitziber Lopez-Cortajarena
CIC biomaGUNE



Hyun-Ho Lim
Korea Brain Research Institute

Jay Ponder
Washington University



Catherine Royer
Rensselaer Polytechnic Institute

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

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Thank you for helping us celebrate 40 years of impact.

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Northwestern University

Fellows

The Protein Society Fellows program, established in 2025, aims to recognize current or past members of the Society who have demonstrated excellent science and service to the Society and the protein science community. Fellows are honored at The Protein Society Annual Symposium.

The Society welcomes nominations of members for the distinction of TPS Fellows from diverse backgrounds and in all areas of the protein science. Check our website for more information.

Deadline for 2027 Nominations: **November 1, 2026**

Registration

Pick Up Your Badge

Though the registration desk will be open throughout the Symposium, we encourage you to pick up your badge on Saturday, July 18, from 4 - 8:30 p.m. in the Grand Ballroom Foyer (**and be entered to win one of three $100 gift cards**). This allows you plenty of time to get a seat for the Opening Plenary.

Attendees are required to wear their badge at all times. In addition to being a means of identification, your badge is required for admission to all scientific sessions, networking/social events, and exhibits. Don't forget to show your badge at selected food outlets for a 10% discount.

Registration Hours

Saturday, July 18:	5 - 8:30 p.m.
Sunday, July 19:	7:30 a.m. - 4 p.m.
Monday, July 20:	8 a.m. - 4 p.m.
Tuesday, July 21:	8 a.m. - 4 p.m.
Wednesday, July 22:	8 - 11:30 a.m.

Get Your Swag Here!

Be sure to stop by The Protein Society/Wiley exhibit booth (Booth #1) next to registration, chat with TPS staff, and pick up some cool swag!

Posters

Poster Set Up & Removal

All posters will be displayed in the **Grand Ballroom Foyer and Pavilion**, and will be available for viewing during lunch hours and for presentations on the following days:

Sunday, July 19:	4:30 - 6:30 p.m.
Monday, July 20:	4:30 - 6:30 p.m.
Tuesday, July 21:	3:30 - 5:30 p.m.

Poster competition and prizes - there will be up to 30 winners who will receive a $250 check and TPS-branded gift.

Instructions for Preparing Posters

Posters are displayed on a standard poster board with the dimensions of 90 inches (2.3 meters) wide by 42 inches (1.1 meters) high of usable space.

This year, due to the high number of posters submissions received, some poster boards will have 2 presenters per board, and each poster will be up for 1 day only. It is important that you install your poster the day of of your presentation, starting at noon, and remove it after the end of the entire session. If it is not removed by the end of the day, remaining posters will be kept at the registration desk on the following day.

Contests

PS40 Contests

Registration Desk: Pick up your badge on July 18 and be entered to win one of four $50 gift cards.

Exhibitor Passport: Collect a stamp from every exhibitor and turn in completed passport to TPS booth by 5:30 p.m. on July 21 for a First Prize of Bose QuietComfort SC Noise Cancelling Headphones and a Second Prize of a $100 Gift Card.

Bingo: Participate in this game at the pre-conference mixer and be entered to win TPS limited-edition swag or a $25 gift card.

Social Media Contests (LinkedIn, Bluesky, Instagram)

1. Daily Trivia – (July 19 - 21)
Hashtag #TPS40DailyTrivia
Each morning of the conference a question about TPS history or general Boston trivia will be posted to the social media accounts. The first ten people to e-mail the correct answers to socialmedia@proteinsociety.org will be entered into the TPS40 raffle.

2. Attendee Spotlight – (July 18 - 21)
Hashtag #TPS40Spotlight
Attendees can post photos of themselves at the conference. They must have some type of PS40 signage in the post and use the tags #TPS40. Attendees who use the hashtags will be entered into the TPS40 Raffle.

3. TPS Booth Selfie – (July 18 - 21)
Hashtag #SayHiTPS40
Attendees will post selfies at the TPS booth using the props provided and the tag #TPS40. Attendees who use the hashtags will be entered into the TPS40 Raffle.

4. AI Proteins Industry Visits Spotlight – (July 18)
Hashtag #TPS40IndustryVisit
Attendees going on industry visits will post (approved) photos of the visits and use the tag #TPS40. Attendees who use the hashtags will be entered into the TPS40 Raffle.

5. Most Popular/Reactions Post - (July 19 - 21)
Hashtag #TPS40
Attendee with the post that has the most views, tagged with #TPS40
Winner: Limited Edition TPS swag (4 pieces)

Winners will be posted on our social media accounts throughout the conference.

Raffle Prizes for Contests 1 - 5

Win one of seven fabulous prizes. Winners receive entries as described for each contest. Prizes include:

TPS CEO's Favorite Things: What does Protein Science and the World Cup have in common? This prize is especially designed by Our TPS CEO.
Value: Priceless (Actual value $200+)

Bose Soundlink Flex SE Portable Speaker

Minolta MND23 SelfShot Digital Camera

Fujifilm instax mini 12 Camera

3 x $50 Gift Cards

Winners will be chosen on July 22 at 10 a.m. at the TPS/Wiley booth. Must be present to win.

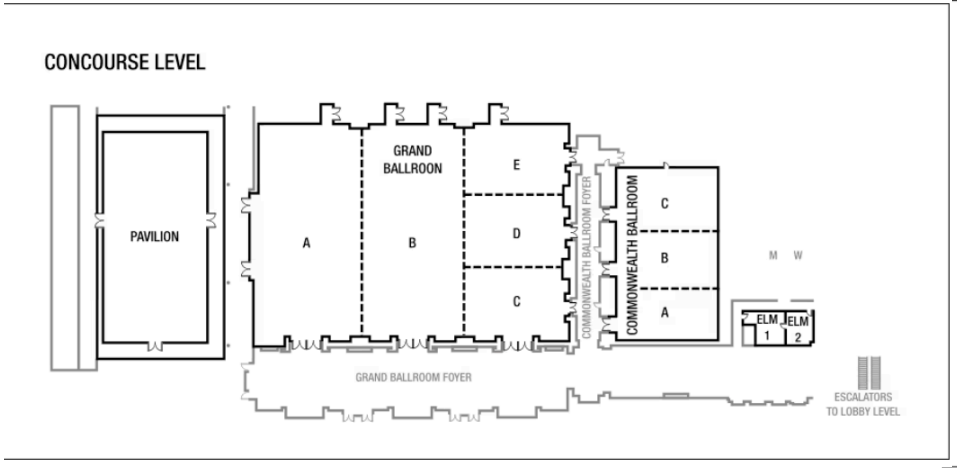
Survey - PS40 Symposium Survey
1 x $50 gift card

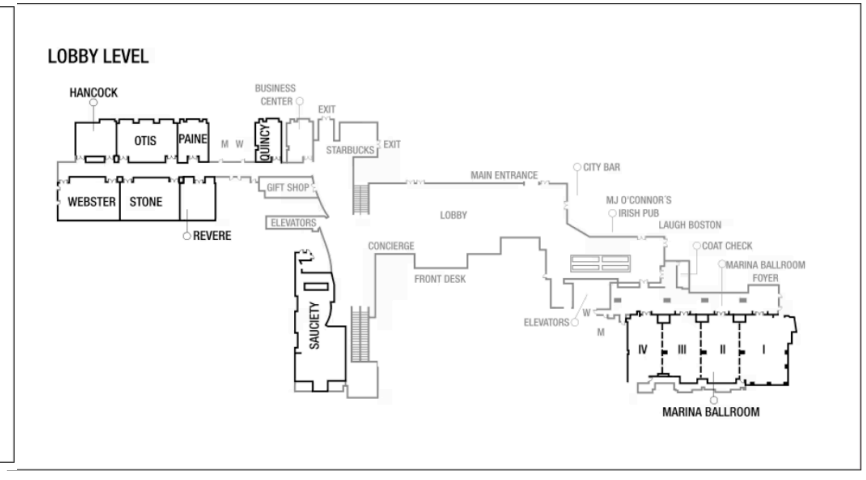
Social Media

Follow @proteinsociety.bsky.social on Bluesky, @the-protein-society on LinkedIn, and @the_protein_society on Instagram for Symposium updates and coverage during the event. You can contribute to the conversation by using the hashtag #ps40.

Hotel Floor Plan

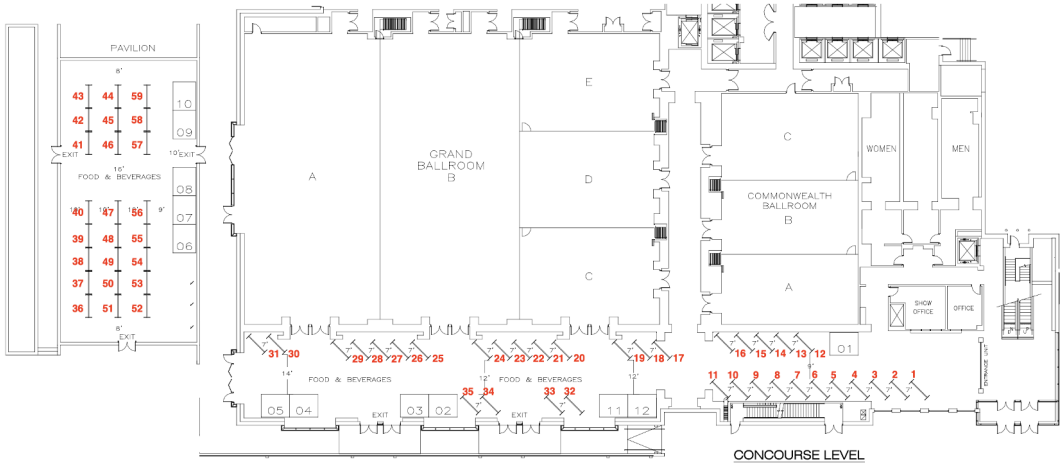
Westin Seaport Boston
425 Summer Street
Boston, Massachusetts 02210





Hotel Floor Plan

TPS40 Poster Numbers Map



TPS40 Meeting Space Map

General Info

Safety

As with any large city, there can be problems with petty theft on the public transit systems. Crowded buses, or mass transit stops, make for the perfect environment for those stealing purses, bags or wallets. You will doubtless notice a number of people experiencing homelessness in areas around the hotel. We recommend you exercise the same safety precautions as you would visiting any unfamiliar city. Keep the following common sense tips in mind when moving around the city:

- Keep an eye on your belongings when out and about.
- Carry wallets in your front pockets.
- Be award of your surroundings.
- Don't carry expensive or unnecessary items with you.
- Park in an attended garage.

Live Mobile App

The NEW PS40 Mobile App (search Protein Society Symposium) provides on-the-go Symposium information including a program planner, poster presentations info, exhibitor list, social media updates, #PS40 alerts, and maps. The Protein Society's "PS40" mobile application is available for download in the Apple App Store and Google Play. You can view/create schedules; view abstracts, and interact virtually with speakers using the app. Use the QR code at right to dowload, for both iPhone and Android.

Username: Log in using your TPS website username (in most cases this is the e-mail you used to register for the meeting).

Password: Check the latest Know Before You Go, or reach out to staff@proteinsociety.org for the universal password

- Scan the QR code and download the Core-apps Events App to your mobile Device.
- Select the TPS40 2026 event and click Download
- At the Login screen, log in using your TPS website username
- For questions and support, contact staff@proteinsociety.org

General Info

Mobile Devices

As a courtesy to your fellow attendees, please silence all cell phones prior to entering a session room.

Cameras/Video Recording

The unauthorized use of cameras/video recording inside session rooms or among the posters is prohibited.

Certificates of Attendance

All attendees will receive a certificate of attendance via email after the Symposium.

Internet Access

There is complimentary wi-fi internet access for the Symposium in the meeting space. **Please use the following information to gain access:**

Network Name: Westin_Conference Password: TPS40

Photography

Registration for the meeting implies consent to having photographs taken and to their use by officials of The Protein Society, or their representatives, for editorial and promotional purposes, on the Society website, social media outlets, and publications. Recordings of any kind (audio taping, videotaping, camera, tablets, or cell phones) in the session rooms, Exhibit Hall, and poster areas are strictly prohibited, unless accompanied by a member of the Society staff. Any individual seen taking photographs of any session or presentation will be escorted out by security.

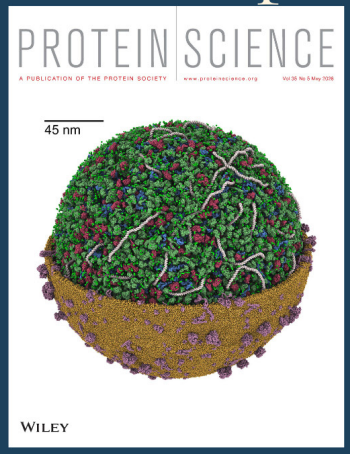
Meeting Survey

Please be sure to fill out our meeting survey post Symposium (you'll find it in the App). It will only take a few minutes to complete, and your feedback is crucial to the ongoing success of our meetings.

Exhibitor Passport

Don't forget to participate in our exhibitor passport contest. It's easy - collect stamps from all the exhibitors that you visit. Once you complete your passport, turn it in at the Registration desk, and we will enter you into a drawing for prizes!

PROTEIN SCIENCE Workshop



July 20 | 12:15 - 1:25 p.m. | RSVP Only

Chairs: John Kuriyan, Editor-in-Chief, *Protein Science*, Margaret Donnelly, Wiley

Commonwealth Ballroom

Discount on Food & Beverage

We are glad to be able to offer TPS attendees a discount on select food and beverage inside the hotel. **Just show your badge upon purchase for 10% off!** The Westin Seaport Boston offers four restaurants to choose from:

Sauciety:

Mon - Fri 6:30 a.m. - 2 p.m.
Sat - Sun 7 a.m. - 2 p.m.

Birch Bar

Open Everyday Daily 4 p.m. - 12 a.m.

TPS Membership

Member Rates

	TPS Membership (Jan 1 - Dec 31)			Meeting Reg (Before June 1)		Meeting Reg (After June 1)	
	1-Year	2-Year	5-Year	Member	Non-Member	Member	Non-Member
Undergraduate	$30	$50		FREE	$50	FREE	$60
Graduate	$30	$50		$100	$200	$120	$240
Early Career	$75	$130	$300	$250	$400	$300	$480
Lab Staff	$50	$85	$200	$100	$250	$120	$300
Emeritus	$30	$50	$120	$100	$200	$120	$240
Full	$150	$255	$600	$350	$600	$420	$720
Corporate	$150	$255	$600	$600	$850	$700	$1,000

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

Annual Symposium and Awards

- Members save as much as 50% for the Annual Symposium.
- Get funding for your local protein-centered mini-symposium, workshop, or other event with a Member Mini-Grant.
- Connect with TPS leaders and have a say in the direction of your Society.
- Nominate your colleagues for one of eight prestigious TPS awards.
- Eligibility to submit a contributed talk or be considered for a Young Investigator Talk.

Protein Science Journal Benefits

- Complimentary online access to the premier Journal focused on all aspects of protein science.
- $250 discount on publication fees.
- Pain-Free Publishing: Fast turnaround under the guidance of Editor-in-Chief John Kuriyan and Senior Editors Aitziber Lopez Cortajerena, Lynn Kamerlin and Nir Ben-Tal, and Zengyi Chang.
- Reduced open-access fees from publisher Wiley Blackwell.

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

2026 Award Winners

Paula Booth, Ph.D. | King's College London
2026 Christian B. Anfinsen Award

Paula Booth
2026 Christian B. Anfinsen Award
King's College London

Dr. Booth is not able to attend this year's Symposium.

Previous Winners

2025 - Jan Steyaert
2024 - Neil Kelleher
2023 - Mei Hong
2022 - Jin Zhang
2021 - Petra Fromme
2020 - Stephen Sligar
2019 - Anthony Kossiakoff
2018 - Yifan Cheng
2017 - Lewis Kay
2016 - Andreas Pluckthun
2015 - Sachdev Sidhu
2014 - Robert Tycko
2013 - Tom Alber
2012 - Barry Honig
2011 - Wayne Bolen
2010 - Yoshinori Fujiyoshi
2009 - Wayne Hubbell
2008 - Carol Robinson
2007 - Carl Frieden
2006 - John R. Yates, III
2005 - Matthias Mann
2004 - Meir Wilchek
2003 - Ada Yonath
2002 - Roger Tsien
2001 - Martin Karplus
2000 - Stephen Benkovic
1999 - Alan Fersht
1998 - James Wells
1997 - Wayne Hendrickson
1996 - Donald Hunt

The **Christian B. Anfinsen Award**, sponsored by The Protein Society, recognizes technological achievement or significant methodological advances in the field of protein science. The 2026 recipient of this award is **Professor Paula Booth** (King's College London). Dr. Booth is a pioneer in the study of membrane protein folding, particularly membrane protein kinetics. She is recognized for her formidable scientific creativity and problem-solving ability, as well as her dedication for more than 30 years to scientific rigor and sustaining a leading presence on the cutting edge of the membrane protein folding field.

Peng Chen, Ph.D. | Peking University
2026 Emil Thomas Kaiser Award

Peng Chen
2026 Emil Thomas Kaiser Award
Peking University

Plenary: July 21:
2:50 - 3:20 p.m.

Previous Winners

2025 - Brian Kuhlman
2024 - David Craik
2023 - Jason Gestwicki
2022 - Philipp Kukura
2021 - Lei Wang
2020 - Shuguang Zhang
2019 - Shahriar Mobashery
2018 - Michael Rosen
2017- Thomas Muir
2016 - Charles Craik
2015 - Anna Mapp
2014 - Carol Fierke
2013 - Wilfred van der Donk
2012 - No Award Given This Year
2011 - Jeffery Kelly
2010 - Suzanne Walker
2009 - Donald Hilvert
2008 - JoAnne Stubbe
2007 - Michael Marletta;
2006 - Barbara Imperiali

Previous recipients, sponsored by SynPep Corporaion:

2005 - Ronald Raines
2004 - Homme Hellinga
2003 - Michael Hecht
2002 - Steve Kent

The **Emil Thomas Kaiser Award**, sponsored by generous individual contributions, recognizes a recent, highly-significant contribution to the application of chemistry in the study of proteins. The 2026 recipient is **Dr. Peng Chen** (Peking University). Dr. Chen is an international leader in chemical biology, including his key innovative chemistry-based contributions to studying proteins in living cells as with control of time and position. His methods to target specific amino acids and/or subcellular compartments in cells and animals represents enabling technology for understanding and treating human diseases.

2026 Award Winners

Marius Clore, Ph. D. | National Institute of Health
2026 Stein & Moore Award

Marius Clore

2026 Stein & Moore Award
National Institute of Health

Plenary: July 22
11:35 a.m. - 12:05 p.m.

Previous Winners

2025 - Timothy Springer
2024 - Jeffery Kelly
2023 - Kevin Gardner
2022 - Daniel Hershlag
2021 - David Agard
2020 - Jim Bowie
2019 - Dame Carol Robinson
2018 - Raymond Stevens
2017 - John Kuriyan
2016 - Jane Clarke
2015 - William DeGrado
2014 - Nikolaus Pfanner
2013 - Robert T. Sauer
2012 - No Award This Year
2011 - Gerhard Wagner
2010 - Peter Wright
2009 - Peter Walter
2008 - Susan Lindquist
2007 - Paul Schimmel
2006 - Arthur Horwich & F. Ulrich Hartl
2005 - Avram Hershko & Alexander Varshavsky
2004 - Wolfgang Baumeister
2003 - Chris Dobson
2002 - Paul Sigler
2001 - Alan Fersht
2000 - Brian Matthews
1999 - Mo Cleland
1998 - David Davies
1997 - Mildred Cohn
1996 - David Eisenberg
1995 - Harold Scheraga
1994 - Michael Rossman
1993 - Walter Kauzmann
1992 - Robert Baldwin
1991 - Russell Doolittle
1990 - Kurt Wuthrich
1989 - Hans Neurath
1988 - Fred Richards
1987 - Emil Smith

The **Stein & Moore Award**, sponsored by The Protein Society and with support from Wiley, is named for Nobel laureates Dr. William Stein and Dr. Stanford Moore. The award recognizes eminent leaders in protein science who have made sustained, high-impact research contributions to the field. The 2026 recipient is **Professor Marius Clore** (National Institute of Health). Dr. Clore is one of the pioneers in developing Nuclear Magnetic Resonance (NMR) into the powerful tool it is today for studying the structure and dynamics of proteins. For over 35 years, he has consistently extended the capabilities of NMR by developing highly innovative approaches and applying them to important problems in biophysics.

Laura Dassama, Ph. D. | Stanford University
2026 Protein Science Young Investigator Award

Laura Dassama

2026 Protein Science Young Investigator Award
Stanford University

Plenary: July 21
12:45 - 1:15 p.m.

Previous Winners

2025 - Christopher Barnes & Jamie Spangler
2024 - Gabriela Schlau-Cohen
2023 - Polly Fordyce
2022 - Nicolas Fawzi
2021 - Bruno Correia
2020 - Mohammad Seyedsayamdost
2019 - Gabriel Lander
2018 - Brandon Ruotolo
2017 - David Pagliarini
2016 - Benjamin Garcia
2015 - Nieng Yan
2014 - M. Madan Babu
2012 - Mei Hong & Tarun M. Kapoor
2011 - Shu-ou Shan
2013 - Feng Shao
2010 - Charalampos Kalodimos
2009 - Virginia Cornish
2008 - Jamie H. Doudna Cate
2007 - Benjamin Cravatt, III
2006 - Vijay Pande
2005 - Thomas Muir
2004 - Erin O'Shea & Jonathan Weissman
2003 - Yigong Shi
2002 - Carolyn Bertozzi
2001 - Kevan Shokat
2000 - David Baker
1999 - Jeffery Kelly
1998 - Nikola Pavletich
1997 - John Kuriyan
1996 - Michael Summers
1995 - Stuart Schreiber
1994 - Peter Kim
1993 - Ad Bax & Marius Clore
1992 - Peter Schultz
1991 - Carl Pabo
1990 - Rachel Klevit
1989 - William DeGrado

The ***Protein Science* Young Investigator Award**, sponsored by Wiley, recognizes scientists within their first 8 years of an independent career at the time of nomination who have made an important contribution to the study of proteins. The 2026 recipient is **Professor Laura Dassama** (Stanford University). Dr. Dassama is an emerging leader in the field of chemical biology with a particular focus on understanding and mitigating bacterial multidrug resistance (MDR). Dassama's work has focused on identifying novel classes of sterol and other lipid binding proteins in poorly characterized bacteria, and the approach spans computational, biochemical, analytical, and structure determination.

2026 Award Winners

Stephen Fesik, Ph. D. | Vanderbilt University
2026 Marie Maynard Daly Award

Stephen Fesik
2026 Marie Maynard Daly Award
Vanderbilt University

Plenary: July 21
1:15 - 1:45 p.m.

Previous Winners

2025 - Yuh Min Chook
2024 - Alexandra Newton
2023 - Renã Robinson

The **Marie Maynard Daly Award**, the newest award sponsored by The Protein Society, established in 2023, recognizes groundbreaking research at the interface between protein science and human health. The 2026 recipient is **Professor Stephen Fesik** (Vanderbilt University). Dr. Fesik is a world leader in the development and utilization of chemical fragment and structure-based drug design approaches to develop new therapeutics targeting "undruggable" proteins. His innovative and pioneering research has revolutionized our methods for finding new cancer therapeutics and yielded critically important discoveries about cancer biology.

Charalampos Babis Kalodimos, Ph.D. | St. Jude Children's Research Hospital
2026 Hans Neurath Award

Previous Winners

2025 - Antonina Roll-Mecak
2024 - David Cortez
2023 - Elena Conti
2022 - Squire Booker
2021 - Toshiya Endo & Amy Rosenzweig
2020 - Martin Gruebele
2019 - Dave Thirumalai
2018 - David Baker
2017 - Kazuhiro Nagata
2016 - H. Eric Xu
2015 - Marina Rodnina
2014 - James Hurley
2013 - Jennifer Doudna & Chuck Sanders
2012 - Charles Brooks
2011 - Johannes Buchner
2010 - Wendell Lim
2009 - William Eaton
2008 - Robert Stroud
2007 - Robert Sauer
2006 - Christopher Dobson
2005 - Roderick MacKinnon
2004 - Carlos Bustamante
2003 - James Wells
2002 - Ad Bax
2001 - Arthur Horwich
2000 - Janet Thornton
1999 - Peter Kim
1998 - Ken Dill

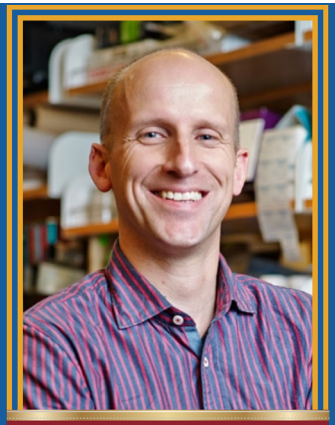
Charalampos Babis Kalodimos
2026 Hans Neurath Award
St. Jude Children's Research Hospital

Plenary: July 21
2:20 - 2:50 p.m.

The **Hans Neurath Award**, sponsored by the Hans Neurath Foundation, honors individuals who have made a recent contribution of exceptional merit to basic protein research. The 2026 recipient is **Professor Charalampos Babis Kalodimos** (St. Jude Children's Research Hospital). For more than 2 decades Dr. Kalodimos has been at the leading edge of the development and application of novel and powerful NMR methods for studies of protein structural dynamics, including allostery, and conformationally rare states of biomolecules that have profound implications to human health and disease.

2026 Award Winners

Andreas Martin, Ph.D. | University of California Berkeley
2026 Dorothy Crowfoot Hodgkin Award



Andreas Martin
2026 Dorothy Crowfoot Hodgkin Award
University of California Berkeley

Plenary: July 22
12:05 - 12:35 p.m.

Previous Winners

2025 - Andy LiWang
2024 - Margaret Sunde
2023 - Patricia Clark
2022 - Sun Hur
2021 - Janet Smith
2020 - Catherine Drennan
2019 - Hao Wu
2018 - Susan Marqusee
2017 - Juli Feigon & Manajit Hayer-Hartl
2016 - Rachel Klevit
2015 - Eva Nogales;
2014 - Judith Frydman
2013 - Christopher Hill & Cynthia Wolberger
2012 - Mark Lemmon
2011 - Brenda Schulman & Wei Yang
2010 - Lila Gierasch
2009 - Janet Thornton
2008 - Douglas Rees
2007 - Leemor Joshua-Tor

The **Dorothy Crowfoot Hodgkin Award**, sponsored by Rigaku Corporation, is granted in recognition of exceptional contributions in protein science that profoundly influence our understanding of biology. The 2026 recipient is **Professor Andreas Martin** (University of California, Berkeley). Dr. Martin has advanced our understanding of the macromolecular assemblies that mediate protein degradation and translocation, particularly the eukaryotic proteasome. Through ingenious biochemical reconstitution, single-molecule assays, and structural analyses, he has made the proteasome one of the most thoroughly understood molecular machines in biology.

Neil Osheroff, Ph.D. | Vanderbilt University
2026 Carl Brändén Award

Previous Winners

2025 - James Fraser
2024 - Tamir Gonen
2023 - Arthur Lesk
2022 - David Goodsell
2021 - Sheila Jaswal
2020 - Karen Fleming
2019 - Minoru Kanehisa
2018 - Jane & Dave Richardson
2017 - Billy Hudson
2016 - Gary Pielak
2015 - C. Robert Matthews
2014 - Stephen White
2013 - Sheena Radford
2012 - Helen Berman
2011 - Michael Summers
2010 - Nobuhiro Go
2009 - Bruce Alberts
2008 - Howard Schachman
2007 - Lubert Stryer

Neil Osheroff
2026 Carl Brändén Award
Vanderbilt University

Plenary: July 22
12:35 - 1:05 p.m.

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 to the field. The 2026 recipient of this award is **Professor Neil Osheroff** (Vanderbilt University). Dr. Osheroff is an exceptional protein biochemist whose pioneering research has profoundly advanced our understanding of DNA topoisomerases and their roles as targets for critical anticancer and antibacterial drugs. Over his 42-year career at Vanderbilt University, he has taught and mentored more than 4,000 physicians and scientists, earning numerous awards for his contributions to medical and biochemical education.

The Protein Society

...presents eight awards each year to distinguished scientists. They recognize excellence and outstanding achievements in the multidisciplinary fields of protein science, and honor contributions in the areas of leadership, education & service.

We will present awards for the following at our 41st Annual Symposium in San Francisco, California, July 9 - 12, 2027.

Carl Brändén Award
Christian B. Anfinsen Award
Dorothy Crowfoot Hodgkin Award
Emil Thomas Kaiser Award
Hans Neurath Award
Marie Maynard-Daly Award
Stein & Moore Award
Protein Science Young Investigator Award

Nominations for all eight TPS awards are now open.

Deadline to submit 2028 award nomination packages is:

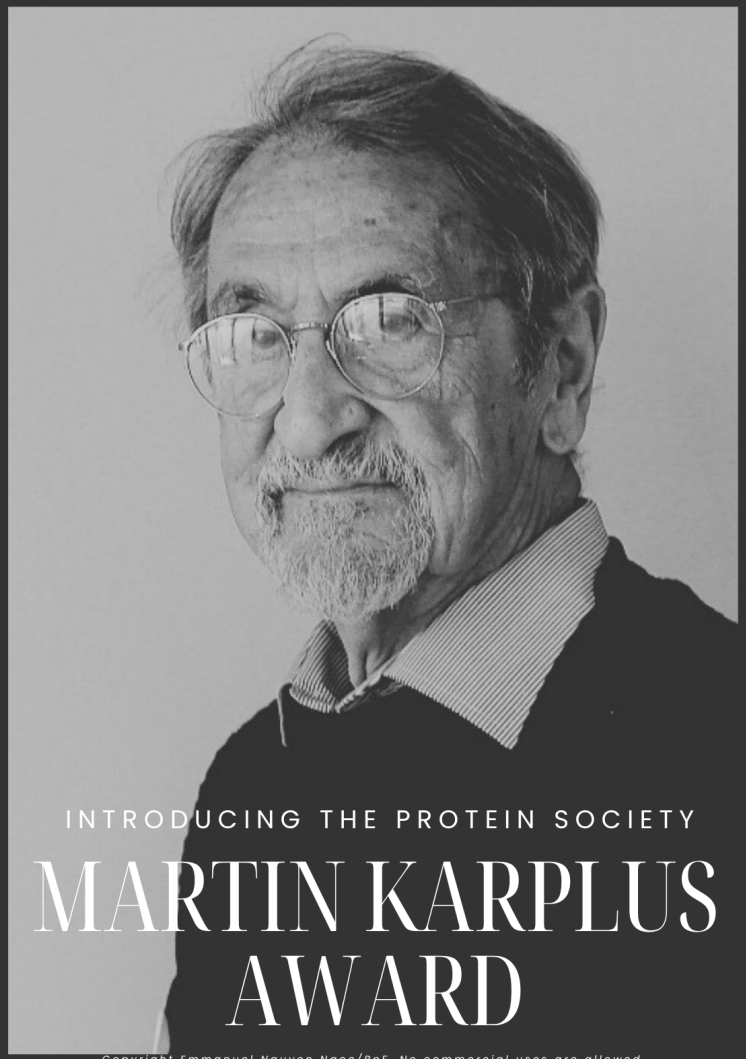
Noon EDT on November 1, 2027.

2027 call for nominations







INTRODUCING THE PROTEIN SOCIETY

MARTIN KARPLUS AWARD

The Martin Karplus Award, established in 2026, honors scientists' outstanding contributions to theoretical biophysics.

THE PROTEIN SOCIETY

2025 Best Paper Winners

Valeria Italia

As a PhD student in a cotutelle program between Swansea University and Université Grenoble-Alpes **Valeria Italia** focused her research on Ultrabithorax (Ubx) protein and its ability to form materials through a multistep assembly process. She demonstrated that simple parameters, such as protein concentration and buffer conditions, can be tuned to create new Ubx-based materials with distinct structural properties in a fast and cost-effective way.

Her mentor, Mauro Cortese, shared: "I am truly pleased to learn that Valeria has received this recognition. Her approach to work clearly reflects the scientific method, rigor and analytical mindset she developed through her academic and PhD experience. Valeria combines strong professional discipline with genuine empathy in the way she manages relationships with colleagues, enabling her to build trust, connect multidisciplinary expertise and drive projects toward valuable outcomes. Her determination, relational intelligence and ability to work across different technical specialties make her a highly effective contributor, both in project management and in achieving meaningful technical results.

Zoltan Kovacs

Zoltan Kovacs is a Ph.D. graduate in the Department of Physiology and Membrane Biology at the University of California Davis. In his work there, they show that the genome maintenance factor human single-stranded DNA binding protein 2 (hSSB2) undergoes DNA-dependent phase separation, revealing a mechanism by which DNA-modifying complexes can be organized on single-stranded DNA stretches during genome metabolism. Together with previous work, these findings suggest that SSB-driven phase separation is an evolutionarily conserved strategy to regulate DNA metabolic processes.

His PI, Mihály Kovács, shared: "This work highlights how intrinsically disordered regions and nucleic acid interactions of proteins can drive the formation of functional biomolecular condensates in eukaryotic systems. Our results bear implications on how genome maintenance machineries are dynamically organized, and how genome metabolic processes can be adapted across different biological contexts."

Welcome Mixers

July 18, 2026

Welcome/Orientation for Students
7:30 - 8:30 p.m.
Commonwealth Ballroom

Pre-Conference Mixer
8:30 - 9:30 p.m.
Commonwealth Ballroom

Hosted by **Dr. Meg Stratton**, Associate Professor, University of Massachusetts Amherst, and **Dr. Heather Pinkett**, Northwestern University, TPS President

2026 Travel Award Winners

Congratulations to the following outstanding students and early-career investigators for receiving travel assistance to attend The 40th Annual Symposium of The Protein Society.

Under the strong belief that our Symposia presents an invaluable opportunity for future protein scientists, The Protein Society is committed to making it possible for young scientists to participate and benefit from our Annual Meeting by awarding **Finn Wold Travel Awards, *Protein Science* Young Investigator Awards**, and **Community Opportunity and Action (COA) Awards**. The leadership and Executive Council of The Protein Society also thank the recent donors to the Finn Wold Travel Awards Fund.

Finn Wold Award Winners

Sahra Baran | Czech Academy of Sciences
Mamata Basnet | The Ohio State University
Karol Buda | University of British Columbia
Evan Buechel | Northwestern University
Priscilla Chinchilla | Rutgers University
Priya Das Sinha | Cleveland Clinic Research
Kyoka Deguchi | Waseda University
Gladys Díaz Vázquez | Washington University in Saint Louis
Ivan Escobar-Chavez | Centro de Investigacion en Alimentacion y Desarrollo
Laura Guerrero | Stanford University
Trang Hoang | Korea Polar Research Institute
Nicole Houppermans | University of Massachusetts, Amherst
Shosei Imai | The University of Tokyo
Natalie Jaeger | University of Oregon
Laura Jung | University of Texas at Austin
Matthew Kirby | University of Manitoba
Oguz Koc | University of Massachusetts Amherst
Albert Lee | Stanford University
Maria Oliveira Batista | University of Sao Paulo
Isaac Paddy | Stanford School of Medicine
Neo Padi | University of the Witwatersrand
Zhihui Qi | Harvard University
Fatima Rizwan | CUNY Advanced Science Research Center

Lee Schnaider | University of California San Francisco
Sydney Shuster | Yale University
Aruesha Srivastava | California Institute of Technology
Katherine Stefanski | Vanderbilt University
Yuta Uto | The University of Tokyo
Andrew Voss | University of Montana
Haoyue Wang | Cornell University
Rachel Ward | Furman University
Momono Yamauchi | Kyoto University
Zhuangyu Zhao | Massachusetts Institute of Technology

Protein Science Young Investigator Award Winners

Ruth Adafia | University of Massachusetts Amherst
Wei Chen | The Pennsylvania State University
Anna Curtis | Yale University
Rajatabha Das | Georgia Institute of Technology
Kanika Dhiman | University of North Carolina at Charlotte
Aninda Dutta | University of Virginia
Montserrat Escobar-Rosales | Universitat Ramon Llull
Natalia Fernandes Frota | McGill University
KC Gabriel | Yale University
Michael Gillman | University of Texas Austin
Aransa Griñen | Pontificia Universidad Catolica de Chile
Gabriela Guedes | University of Cambridge
MD Hossain | Jawaharlal Nehru University
Lauren Hughes | Wichita State University
Toma Ikeda | Institute of Science Tokyo
Chloe Jackson | Northwestern University
Alper Karagöl | Istanbul University
Taner Karagöl | Istanbul University
Nelli Khudaverdyan | University of California, Riverside
Jean Kim | University of Pennsylvania
Xiaohuan Lu | Clark University
Eryn Lundrigan | University of Ottawa
Ailsa MacRae | The University of Birmingham
Zefeng Nie | Dartmouth College
Jamie Northup | University of Massachusetts Amherst
Carlos Oliva | Center for Scientific Research & Higher Education at

2026 Travel Award Winners

Ensenada
Isabella Perez | San Jose State University
Muhammad Rahat | University of Massachusetts Amherst
Dharshika Rajalingam | University of Notre Dame
Raibat Sarker | Yale University
Sachithra Senanayake | University of Nebraska-Lincoln
Daphney Sihwa | University of California, Merced
Ryan Singer | University of Michigan
Lauren Sweeney University of Massachusetts Amherst
Rain Tela | University of Richmond
Molly Wise | University of Richmond
Julian Zhang | Vanderbilt University

Community, Opportunity and Action Award Winners

Saleha Anwar | Ajman University
Marisa Barilla | Yale University
Grace Baron | California Institute of Technology
Indu Bhatia | Vanderbilt University
Nicole Cheung | University of California Los Angeles
Elijah Dunn | Georgia Institute of Technology
Sydni Alexis Elebra | Emory University
Fatoumata Gnine Fofana | African Center of Excellence in Bioinformatics and Data Science (ACE-Mali) / University of Sciences, Techniques and Technologies of Bamako (USTTB)
Jordan Ford | University of California Los Angeles
Mani Gupta | Jawaharlal Nehru University
Farah Haque | Massachusetts General Hospital & Harvard Medical School
James Hutchison | Yale School of Medicine & Yale Cancer Biology Institute
Nora Jaber | Rutgers University
Virginia Jiang | Princeton University
Lydia Kenney | Northwestern University
Emme Leão | University of Massachusetts Amherst
Laura Nataly Lozano | Universidad Nacional Autónoma de México
Gino Magalang | University of California, Santa Cruz
Katherina Martinez | University of California Merced
Bethany McManus | Presbyterian College
Winnie Mirembe | Texas Woman's University
Sarah Najera | Dartmouth College
Grace Nieukirk | University of North Carolina at Chapel Hill
Blessing Oyiogu | University of the Witwatersrand
Phuc Phan | University of Arkansas
Yawei Qi | University of Cambridge
Yousuf Ramahi | University of Toronto Mississauga
Irina Ritsch | Scripps Research Institute
Nirsanka Roy | Arizona State University
Kathryn Shelley | University of Washington
Caroline Slaughter | Colorado State University
Clarice Stumpf | University of Massachusetts Amherst
Areesha Tariq | University of California, Merced
Emily Walsh | University of Arkansas
Briana Whitehead | Bowie State University

At A Glance

The Protein Society 40th Anniversary Symposium

July 19 - 22, 2026

Boston, Massachusetts | Westin Seaport Boston

	July 18	July 19 | Sunday		July 20 | Monday		July 21 | Tuesday		July 22 | Wednesday	
7:30 a.m.		**Registration** 7:30 a.m. - 4 p.m. | Grand Ballroom Foyer		**Registration** 8 a.m. - 4 p.m. | Grand Ballroom Foyer		**Registration** 8 a.m. - 4 p.m. | Grand Ballroom Foyer		**TPS Business Meeting/New Member Breakfast (RSVP Required) |** 7:45 - 8:15 a.m. | Commonwealth Ballroom	
8:15 a.m.				**Nicoya Breakfast Workshop** 8:15 - 8:50 a.m. | Commonwealth Ballroom				**Registration** 8 - 11:30 a.m. | Grand Ballroom Foyer	
8:30 a.m.						**Session 9:** **New Problems in Protein Folding** Grand Ballroom	**Session 10:** **Proteins at the Membrane** Grand Ballroom	**Session 11:** **Proteins Evolution** Grand Ballroom	**Session 12:** **Proteins in Agriculture** Grand Ballroom
9 a.m.		**Session 1:** **Macromolecular Complexes in Biology** Grand Ballroom	**Session 2:** **Engineering Protein Biologics** Grand Ballroom	**Session 5:** **Function & Behavior of Intrinsically Disordered Proteins** Grand Ballroom	**Session 6:** **Machine Learning & AI in Protein Science** Grand Ballroom				
9:15 a.m.									
11:30 a.m.						**Undergrad Research Session (RSVP Only)** 11:30 a.m. - 12:30 p.m. | Commonwealth Ballroom		**Plenary Awards** 11:30 a.m. - 1:10 p.m. | Grand Ballroom **2026 Stein & Moore** **Marius Clore** | National Institute of Health **2026 Dorothy Crowfoot Hodgkin** **Andreas Martin** | University of California Berkeley **2026 Carl Brändén** **Neil Osheroff** | Vanderbilt University	
12:15 p.m.		**Networking Tables w/Community, Opportunity & Action Committee (RSVP Only)** 12:15 - 1:25 p.m. | Commonwealth Ballroom		**Protein Science Workshop (RSVP Only)** 12:15 - 1:25 p.m. | Commonwealth Ballroom					
12:35 p.m.						**Plenary Awards** 12:35 - 3:25 p.m. | Grand Ballroom **2026 Protein Science Young Investigator** **Laura Dassama** | Stanford University **2026 Marie Maynard Daly** **Stephen Fesik** | Vanderbilt University **2026 Hans Neurath** **Charalampos Babis Kalodimos** | St. Jude Children's Research Hospital **2026 Emil Thomas Kaiser** | **Peng Chen** | Peking University			
1:10 p.m.									
1:30 p.m.		**Session 3:** **Protein Allostery & Biophysics** Grand Ballroom	**Session 4:** **Protein Nanotechnology** Grand Ballroom	**Session 7:** **Cellular Protein Dynamics & Distribution** Grand Ballroom	**Session 8:** **Physics-Based Computation in Protein Science** Grand Ballroom				
2 p.m.									
3:30 p.m.						**Posters and Exhibitor Reception |** 3:30 - 5:30 p.m. | Ballroom Foyer and Pavilion			
4:30 p.m.									
5 p.m.	**Registration** 5 - 8:30 p.m. | Grand Ballroom Foyer	**Posters and Exhibitor Reception |** 4:30 - 6:30 p.m. | Ballroom Foyer and Pavilion		**Posters and Exhibitor Reception |** 4:30 - 6:30 p.m. | Ballroom Foyer and Pavilion					
6:45 p.m.						**PS40 Reception at AI Proteins** **(RSVP Required)** **6 - 7 p.m. | One Kenmore Square** **Red Sox Baseball Game** **(RSVP & Tickets Required)** 7:10 p.m. | Fenway Park			
7:30 p.m.	**Student Welcome (RSVP Only)** 7:30 - 8:30 p.m. Commonwealth Ballroom								
8:30 p.m.	**Pre-Conference Mixer** 8:30 - 9:30 p.m. Commonwealth Ballroom								

Networking WORKSHOP

July 19 | 12:15 - 1:25 p.m. | RSVP Only
Commonwealth Ballroom

Chair:
Dr. Meg Stratton, UMass Amherst

Community, Opportunity & Action

Our COA Statement:

Protein science is an integrative and inclusive endeavor that utilizes concepts and methods from a diverse array of disciplines to strive for a more complete understanding of the role that proteins play in biological structure and function across many levels. As a membership-based society and leader in its field, The Protein Society values and is committed to diversity, equity, and inclusion in all aspects of its societal endeavors. We, therefore, strive to provide a safe and supportive environment for all of our constituents, where everyone is treated with respect and is encouraged to contribute their unique strengths and abilities to our shared mission. We are committed to acting on these principles for the betterment of the field of protein science and all activities with which The Protein Society is engaged.

We Care About Your Pronouns!

Stop by The Protein Society's booth outside of the Exhibit Hall and grab a pronoun sticker for your name badge!

These let us all know how to address one another, and help everyone feel more comfortable.

When you meet someone, look for their pronoun sticker!

COA Committee

Sheila Jaswal, Co-Chair
Amherst College

Raquel Lieberman, Co-Chair
Georgia Institute of Technology

Committee Members

Shannan Cunniffe
The Protein Society

Jamaine Davis
Belmont University

Pernilla Wittung-Stafshede
Chalmers University of Technology

Program

Saturday, July 18, 2026		
2 - 4 p.m.	**Industry Visit: AI PROTEINS** (Offsite, Transportation Not Provided) (RSVP only)	
5 - 8 p.m.	**Registration** *Grand Ballroom Foyer | BR (Concourse Level)* Pick up your badge on July 18 and be entered to win one of four $50 gift cards.	
7:30 - 8:30 p.m.	**Welcome/Orientation for Students** *Commonwealth Ballroom | Concourse Level* Hosted by **Dr. Margaret Stratton**, UMass Amherst, Executive Council Member Take advantage of the PS40 orientation, where hosts will share insider information related to the program and opportunities offered at the meeting. Network and mingle with other attendees, and play PS40 Bingo to win prizes! Recommended for undergraduate, graduate students and postdocs, and all Travel Award winners.	
8:30 -9:30 p.m.	**Pre-Conference Mixer** *Commonwealth Ballroom | Concourse Level* Hosted by **Dr. Heather Pinkett**, Northwestern University, President, The Protein Society Recommended for early and full career attendees, but all welcome!	
Sunday, July 19, 2026		
7:30 a.m. - 4 p.m.	**Registration** | *Grand Ballroom Foyer | (Coucourse Level)*	
9 - 11:55 a.m.	**Parallel Session 1 |** *Grand Ballroom* ***Macromolecular Complexes in Biology*** Session Co-Chair: **Yifan Cheng**, UCSF; **Josh Wand**, Texas A&M University	**Parallel Session 2** | *Grand Ballroom* ***Engineering Protein Biologics*** Session Chair: **Chris Bahl**, AI Proteins | Session Co-Chair: **Heather Pinkett**, Northwestern University, President, The Protein Society
9:05 - 9:35 a.m.	**Erica Ollmann Saphire |** La Jolla Institute for Immunology | *New Antibodies Against an Old Threat - The Structural Roadmap*	**Tanja Kortemme |** University of California San Francisco | *De novo Design of Programmable Protein Dynamics*
9:35 - 10:05 a.m.	**Walter Chazin,** Vanderbilt University | *Watching Active Nucleotide Excision Repair Machinery as it Repairs a DNA Lesion*	**Shohei Koide |** New York University | *Direct and Selective Targeting of Cancer-driver Mutants With Synthetic Binding Proteins*
10:05 - 10:20 a.m.	**Juan Caceres Vergara |** HHMI/MIT | *Cryo-EM snapshots of Ribonucleotide Reductase Inhibition by the Anticancer Agent Gemcitabine Diphosphate*	**Valeria Italia**, M.P.G Instruments | *Tuning Protein-Based Materials Through Control of Early Assembly Conditions*
10:20 - 10:45 a.m.	**Coffee Break & Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*	
10:46 - 10:49 a.m.	**Laura Nataly Mesa Lozano |** Universidad Nacional Autónoma de México | *Biochemical Characterization of a Recombinant Chimeric Antigen from Mycobacterium tuberculosis Produced in Pichia pastoris (Komagataella phaffii)*	**Montserrat Escobar-Rosales |** Universitat Ramon Llull | *Engineering a Generalizable Strategy for Conditionally-active Biotherapeutics Via de novo Peptide Mask Design*
10:49 - 10:52 a.m.	**Casey Wing |** UT Southwestern Med Center | *Intrinsic XPO1 Allostery Determines Whether Inhibitors Block Export or Drive ASB8-dependent Degradation*	**Foster Birnbaum |** MIT | *StructMPNN: A Next-generation Sequence Design Model That Learns Many-to-Many Sequence-structure Mappings By Supervising Foldability*
10:52 - 10:55 a.m.	**Motahareh Ghahari Larimi |** National Institutes of Health | *Structural Studies of SARS-CoV-2 Nucleocapsid Protein RNA Complexes*	**Hanzhi Zhang |** AstraZeneca | *HDX-MS-Guided Computational Modeling for Rapid & Accurate Antibody-Antigen Interface Mapping*
10:55 - 11:25 a.m.	**Ruchi Anand**, Indian Institute of Technology | *Combatting Ribosomal Methylation Based Antibiotic Resistance: A War at the Microscopic Level*	**Lindsay Hammack**, Merck | *De Novo Designed Protein Agonist Targeting a Heterodimer Without a Solved Structure*
11:25 - 11:55 a.m.	**Kendra Frederick**, UT Southwestern Med Center | *Determining Protein Conformations Inside Cells Using DNP-Enhanced Solid-State NMR*	**Dane Wittrup |** MIT | *Knotpin Libraries: Diverse b-hairpin Paratopes Grafted Into Knottin/Cyclotide Scaffolds*
12 - 1:30 p.m.	**Workshop & Exhibits |** *Commonwealth Ballroom, Grand Ballroom Foyer & Outdoor Pavilion*	

Program

12:15 - 1:25 p.m.	**Networking Tables (RSVP Required) |** Commonwealth Ballroom **Chair: Dr. Margaret Stratton,** University of Massachusetts Amherst This networking event is a unique experience that brings students and early career attendees up close and personal with protein science veterans and peers to discuss various topics. Table leaders include **Dr. Anne Gershenson**, Program Director, NIH and the Community, Action and Opportunity Committee.	
1:30 - 4:30 p.m.	**Parallel Session 3 |** *Grand Ballroom A, B* ***Protein Allostery & Biophysics*** Session Chair: **Margaret Stratton**, UMass Amherst, I Session Co-Chair: **Amy Keating**, MIT	**Parallel Session 4 |** *Grand Ballroom C, D, E* ***Protein Nanotechnology*** Session Chair: **Aitziber Lopez Cortajarena**, CLC Biomagune I Session Co-Chair: **Kevin Gardner,** CUNY
1:35 - 2:05 p.m.	**Breann L. Brown |** Vanderbilt University I *Uncovering the Role of Protein Structure & Dynamics in the Regulation of Heme Biosynthesis*	**Alena Khmelinskaia |** Ludwig-Maximilians-Universität München I *Function-driven Design of Protein Assemblies*
2:05 - 2:35 p.m.	**Vince J. Hilser |** Johns Hopkins University I *A Code For Ensemble Molecular Mimicry and Antibody Cross-reactivity*	**Jin Montclare |** New York University I *Designing Protein-Based Nanomaterials: From Sequence to Functional Biomaterials*
2:35 - 2:50 p.m.	**Harrison Wang |** Harvard University I *Atomic-resolution Observation of Force Propagation in a Human Enzyme*	**Gabriela Guedes |** University of Cambridge I *Engineered CTPR Protein Scaffolds-Based Nanoparticles as Versatile Theranostic Agents*
2:50 - 3:20 p.m.	**Coffee Break & Exhibits |** *Commonwealth Ballroom*	
3:22 - 3:24 p.m.	**Anna Bock |** Brown University I *Atomic-level Insights Into Long-range Effects of Specificity Enhancing Mutations on the Active Site of CRISPR-Cas9 HNH Nuclease*	**Caroline Slaughter |** Colorado State University I *Enzymatic Ligation and Restriction for Dynamic Reconstruction of Biomolecular Co-Crystals*
3:24 - 3:26 p.m.	**Lee Schnaider |** UCSF I *Enfolds: Stimuli-Responsive Protein Switches for Cue-Gated Bioactive Peptide Masking and Release*	**Taner Karagöl |** Istanbul University I *Systematic Redesign of Synaptic Vesicle Proteins Into Water-Soluble Variants via the QTY-Code Reveals Key Conformational & Evolutionary Dynamics*
3:26 - 3:28 p.m.	**Nirsanka Roy |** Arizona State University I *Structural Determination of the Elevator-type Movement of ZIP proteins*	**Rama Edaibis |** University of Toronto I *Developing Next-Generation Drugs from Designer Proteins*
3:28 - 3:30 p.m.	**Susu He |** Dartmouth College I *Cysteine Sensing Allostery of CifR, a TetR Regulator of the Virulent Epoxide Hydrolase Circuit in Pseudomonas Aeruginosa*	
3:30 - 4 p.m.	**Lakshmi Wijeyewickrema |** La Trobe University I *Exosite-mediated Regulation of Complement Protease Activity Reveals Distinct Mechanisms Controlling C3 Proconvertase Assembly*	**Alice Ma |** Cube Biotech I *Membrane Proteins at Scale: Automated Copolymer Nanodisc Purification for Structure & Function*
4 - 4:30 p.m.	**Julien Roche |** Iowa State University I *High-pressure NMR Study of Biological Systems*	**Adam Caparco |** Northeastern University I *Protein Nanoassemblies for Biocatalysis & Nucleic Acid Delivery*
4:30 - 6:30 p.m.	**Reception: Posters & Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*	

Monday, July 20, 2026

8 a.m. - 4 p.m.	**Registration** I *Grand Ballroom Foyer	(Concourse Level)*	
8:15 - 8:50 a.m.	**Breakfast and Learn - Nicoya Workshop (RSVP preferred) |** *Commonwealth Ballroom*	
9 - 11:55 a.m.	**Parallel Session 5 |** *Grand Ballroom C, D, E* ***Function & Behavior of Intrinsically-Disordered Proteins*** Session Chair: **Afua Nyarko**, Oregon State I Session Co-Chair: **Gary Pielak**, UNC	**Parallel Session 6 |** *Grand Ballroom A, B* ***Machine Learning & AI in Protein Science*** Session Chair: **Bill DeGrado**, UCSF I Session Co-Chair: **Janice Robertson**, Washington University
9:05 - 9:35 a.m.	**Priya Banerjee |** University at Buffalo I *From Sequence to Selectivity: How Disordered Prion-Like Domains Orchestrate Co-Condensation of Transcriptional Regulators*	**Stephanie Wankowicz |** Vanderbilt University I *From Possibility to Precision in Macromolecular Ensemble Prediction*

Program

9:35 - 10:05 a.m.	**Andrea Soranno |** Washington University	*Single-molecule Spectroscopy of Disordered Regions & Nucleic Acids in Bacterial Transcription*	**Minkyung Baek |** Seoul National University **|** *AI-based Antigen–Antibody Complex Structure Prediction & Design*
10:05 - 10:20 a.m.	**Mriganka Parasar |** MIT	*Investigating Tau Fibrillization Intermediates Using 19F & 13C Solid-State NMR*	**Susan Tsutakawa |** Lawrence Berkeley National Laboratory	*AlphaSAXS: Integrating OpenFold with Physiologically Relevant Conformations from X-ray Scattering Data*
10:20 - 10:45 a.m.	**Coffee Break & Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*	
10:46 - 10:49 a.m.	**Clarice Stumpf |** University of Massachusetts Amherst	*Automated Protocol For Large-Scale Reconstruction of Amyloid Fuzzy Coats*	**Zheyu Zhang |** Northeastern University	*Large Language Models for Ligand Annotation in the Protein Data Bank: A Benchmark Study*
10:49 - 10:52 a.m.	**Marisa Barilla |** Yale University	*Protective Mechanisms of CAHS IDPs in Tardigrades*	**Emma Magna |** Colorado State University	*Computational Protein Design for a Novel Porous DNA-Protein Co-Crystal*
10:52 - 10:55 a.m.	**Nora Jaber |** Rutgers University	*Protein-Membrane Interactions in Cell-to-Cell Transmission of Huntingtin Protein*	**Zhihui Qi |** Harvard University	*Inferring Protein Dynamics from Evolutionary Sequence Embeddings*
10:55 - 11:25 a.m.	**Rebecca Berlow |** University of North Carolina	*Uncovering Hidden Conformations & Funtions of Intrinsically Disordered Proteins*	**Kuen-Phon Wu |** Academia Sinica	*Mesostructured Water Enhances Stability of AI-designed Proteins*
11:25 - 11:55 a.m.	**Ute A. Hellmich |** Friedrich Schiller University	*Regulation Through Disorder: Lipid Signalling Through Unstructured Regions Shapes Ion Channel Function in Health & Disease*	**Jean-Philip Piquemal |** Sorbonne Universite	*A Quantum Foundation Model for Accurate Atomistic Simulations in Drug Design*
12 - 1:30 p.m.	**Workshop & Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*	

12:15 - 1:25 p.m.	***Protein Science Journal Workshop (RSVP Required) |*** *Commonwealth Ballroom* ***Effective Strategies for Writing & Publishing in Protein Science*** Join Editor-in-Chief Dr. John Kuryian and his team of Senior Editors and Associate Editors as they discuss what makes a paper great for Protein Science. You'll come away with a better understanding of the submission and publication process, insights into what the editors look for in a research paper, and how you can strengthen your submission to Protein Science. Organizers: ***Margaret Donnelly,*** Senior Publisher, Wiley and ***John Kuriyan,*** Editor in Chief, Protein Science	
1:30 - 4:30 p.m.	**Parallel Session 7 |** *Grand Ballroom C, D, E* ***Protein Nanopores: Sequencing & Sensing*** Session Chair: **Shao-Qing Zhang**, Center for Excellence in Molecular Cell Science |Session Co-Chair: **Laura Dassama**, Stanford School of Medicine CAS	**Parallel Session 8 |** *Grand Ballroom A, B* ***Physics-based Computation in Protein Science*** Session Chair: **Qiang Cuin**, Boston University | Session Co-Chair: **Charles L. Brooks III**, University of Michigan
1:35 - 2:05 p.m.	**Vicki Wysocki |** Georgia Institute of Technology	*Native MS of Protein Complexes, AAVs, and VLPs*	**Joan-Emma Shea |** University of California Santa Barbara	*Self-Assembly of the Tau Protein: Liquid-Liquid Phase Separation and Fibrillization*
2:05 - 2:35 p.m.	**Masaharu Somiya |** Tohoku University **|** *Post-translational Editing of Protein Sequences*	**Dan Herschlag |** Stanford University	*Ensemble-function Analysis Accounts for Mysteries of Phosphoryl Transfer Catalysis: Transitioning From Empirical Analyses to Physics-based Evaluation*
2:35 - 2:50 p.m.	**Raibat Sarker |** Yale University	*WW Domain Folding in Living Cells*	**George Wanes |** Northeastern University	*Physical-Chemical Principles of Ribosome Dynamics in Translation & Trans-Translation*
2:50 - 3:20 p.m.	**Coffee Break & Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*	
3:21 - 3:24 p.m.	**Moriah Beck |** Wichita State University	*Condensates as Cytoskeletal Control Centers: Palladin's Emerging Role in Actin Dynamics*	**Virginia Jiang |** Princeton University	*A Multiscale Framework For Designing Synthetic Membrane-associated Condensates as Microreactors*

Program

3:24 - 3:27 p.m.	**Isaac Paddy |** Stanford School of Medicine | *Deciphering the Molecular and Structural Framework of Bacterial HMG-CoA reductases in isoprenoid biosynthesis*	**Yousuf Ramahi |** University of Toronto | *Changes in Protein Dynamics Quantified by Inter-residue Contact Lifetimes: A Molecular Dynamics Simulation Analysis*
3:27 - 3:29 p.m.	**Ruth Adafia |** University of Massachusetts Amherst | *Using Cryo-EM to Decipher Calcium Sensitivity of CaMKII Variants*	**Jacopo Zattoni |** University of Alberta | *Matchmaking at the Molecular Level: the PLI-Scanner as a Machine Learning Framework*
3:30 - 4 p.m.	**Hirofumi Kosuge**, University of Tokyo | *Molecular Basis for Intrinsically Low-affinity Interactions of PRELP With Multiple Proteins Modulated via ECM Localization*	**Carol B. Post |** Purdue University | *Atomistic Mechanism of a Unique Entropy-driven Allosteric Mechanism to 'Tone Down' High Affinity Binding of Syk Kinase to Membrane Receptors*
4 - 4:30 p.m.	**Elizabeth Hinde |** University of Melbourne | *Quantitative Imaging of Live Cell Nuclear Architecture and Dynamics*	**Benoit Roux |** University of Chicago | *Theoretical & Computational Treatments of Molecular Binding in the Context of Lipid Membranes*
4:30 - 6:30 p.m.	**Reception: Posters and Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*	

Tuesday, July 21, 2026

8 a.m. - 4 p.m.	**Registration** | *Grand Ballroom Foyer | (Concourse Level)*	
8:30 a.m. - 11:25 a.m.	**Parallel Session 9 |** *Grand Ballroom A,B* ***New Problems in Protein Folding*** Session Chair: **George Rose**, Johns Hopkins University | Session Co-Chair: **Caitlin Davis**, Yale University	**Parallel Session 10 |** *Grand Ballroom C, D, E* ***Proteins At the Membrane*** Session Chair: **Rachelle Gaudet**, Harvard University | Session Co-Chair: **Huong Kratchovil**, University of North Carolina Chapel Hill
8:35 - 9:05 a.m.	**Tobin Sosnick |** University of Chicago | *Structural Energetics as a Framework for Rationalizing Protein Function*	**Rosemary Cater |** University of Queensland | *Structural & Molecular Basis of Choline Uptake Into the Brain by FLVCR2*
9:05 - 9:35 a.m.	**Brian F. Volkman |** Medical College of Wisconsin | *Cold Denaturation in the Adaptive Evolution of Metamorphic Proteins*	**Camilo Perez |** University of Georgia **|** *Mechanistic Basis of Transport Processes in Bacterial Cell Wall Biopolymer Synthesis*
9:35 - 9:50 a.m.	**Kathryn Shelley |** University of Washington | *De novo Design of Light-driven Protein Motor Domains*	**Grace Baron |** California Institute of Technology | *The Structure of the Lipid II flippase from E. coli in a Native Lipid Environment*
9:50 - 10:15 a.m.	**Coffee Break & Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*	
10:16 - 10:19 a.m.	**Juaneisha Finnie |** University of Virginia | *Signal Peptides Govern Effective Targeting, Folding, and Insertion of Outer Membrane Proteins in the E. coli Outer Membrane*	**Ryan Singer |** University of Michigan | *Engineering Genetically Encoded Tools For Activation of Endogenous Melanocortin Receptors with High Spaciotemporal Resolution*
10:19 - 10:22 a.m.	**Ian Neidigh |** Yale University | *Quantifying Protein Folding & Dynamics of VlsE in Differentiated Tissues of Living Zebrafish Embryos*	**Momono Yamauchi |** Kyoto University | *Structural Insights Into the G Protein Subtype Selectivity Revealed by Human Sphingosine-1-Phosphate Receptor 3-Gq Complexes*
10:22 - 10:25 a.m.	**Mohammad Shamsi |** Ajman University | *Molecular & Biophysical Insights into the Interaction of Hordenine with Human Lactoferrin*	**Phuc Phan |** University of Arkansas | *PKC Phosphorylation Modulates Kv7.2–Calmodulin Interactions*
10:25 - 10:55 a.m.	**Stephen Fried |** Johns Hopkins University | *Protein Folding in the AI Era: What's Left to Discover?*	**Ming-Feng Tsai |** Affiliation | *Molecular Mechanisms of Mitochondrial Calcium Transport*
10:55 - 11:25 a.m.	**Duyoung Min |** Ulsan National Institute of Research | *Single-molecule Tweezers Decode Hidden Patterns of Membrane Protein Folding and Interactions*	**Brian Fuglestad |** Virginia Commonwealth University **|** *Molecular Control of Proteins at the Membrane Interface*
11:25 a.m. - 12:35 p.m.	**Workshop & Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*	
11:30 a.m. - 12:30 p.m.	**Undergrad Research Session (RSVP Required) |** *Commonwealth Ballroom* **Chair: Dr. Matthew Gage,** University of Massachusetts Lowell **Speakers: Ivan Escobar-Chavez,** Centro de Investigacion en Alimentacion y Desarrollo **| Sydney Mager,** University of Massachusetts Amherst **| Mary Harutyunyan,** University of Massachusetts Lowell **| KC Gabriel,** Yale University	

Program

12:35 - 3:25 p.m.	**Plenary Awards and Best Poster Presentations |** *Grand Ballroom*
12:35 - 12:45 p.m.	**2025 and 2026 Fellows Recognition by TPS President Heather Pinkett,** Northwestern University
12:45 - 1:15 p.m.	**2026 Protein Science Young Investigator Award** **Laura Dassama**, Stanford University | *Uncovering Opportunity Targets in Bacterial Pathogens*
1:15 - 1:45 p.m.	**2026 Marie Maynard Daly Award** **Stephen Fesik**, Vanderbilt University | *Drugging the Undruggable: Targeting MYC for Cancer Therapy*
1:45 - 1:55 p.m.	**Martin Karplus Award, Marci Karplus**
1:55 - 2:20 p.m.	**Coffee Break and Exhibits |** Grand *Ballroom Foyer & Outdoor Pavilion*
2:20 - 2:50 p.m.	**2026 Hans Neurath Award** **Charalampos Babis Kalodimos**, St. Jude Children's Research Hospital | *Exploring and Exploiting the Conformational Landscape of Protein Kinases*
2:50 - 3:20 p.m.	**2026 Emil Thomas Kaiser Award** **Peng Chen**, Peking University | *Live-cell Protein Chemistry in Health & Disease*
3:20 - 3:30 p.m.	**Best Poster Competition Winners | Dr. Kay Perry,** Cornell University; and **Dr. Meghan Breen**, Furman University
3:30 - 5:30 p.m.	**Reception: Posters and Exhibits |** *Grand Ballroom Foyer & Outdoor Pavilion*
6 - 7 p.m.	**PS40 Reception (RSVP Required) |** *One Kenmore Square (Citgo Building)*
7:10 p.m.	**Baseball Game (RSVP and Tickets Required) |** *Fenway Park*
Wednesday, July 22, 2026	
8 - 11:30 a.m.	**Registration |** *Grand Ballroom Foyer*
7:45 - 8:20 a.m.	**TPS Business Meeting (RSVP required) |** *Commonwealth Ballroom*

8:30 - 11:20 a.m.	**Parallel Session 11 |** *Grand Ballroom A, B* ***Proteins Evolution*** Session Chair: **Karen Allen**, Boston University | Session Co-Chair: **Liskin Swint Kruse**, University of Kansas Medical Center	**Parallel Session 12 |** *Grand Ballroom C, D, E* ***Proteins in Agriculture*** Session Chair: **Katie Stewart**, Corteva Agriscience | Session Co-Chair: **Josh Wand**, Texas A&M University
8:35 - 9:05 a.m.	**Mike Harms,** University of Oregon | *The Evolution of Multi-conformation Proteins*	**Katie Stewart,** Corteva Agriscience | *Plant Derived Insecticidal Proteins for Protection of Crop Plants*
9:05 - 9:35 a.m.	**Anum Glasgow,** Columbia University | *Evolutionary Conservation of Functional Allostery in Protein Families*	**Sheng Yang He,** HHMI/ Duke University | *Biochemical Functions of Bacterial Pathogen Effectors: Implications for Plant Disease Control*
9:35 - 9:50 a.m.	**Hannes Ludewig |** HHMI, Brandeis University | *Comparing the Evolvability of an Ancestrally Reconstructed & Modern Adenylate kinase*	
9:50 - 10:10 a.m.	**Coffee Break |** *Grand Ballroom Foyer*	
10:11 - 10:14 a.m.	**Farah Haque |** Massachusetts General Hospital & Harvard Medical School | *Repurposing the Kinesin Fold: How KIF7 Adapts Conserved Kinesin Design Principles for its Function in Hedgehog Signaling*	
10:14 - 10:17 a.m.	**Stephanie Halim |** Massachusetts Institute of Technology | *Upregulated Chaperone Networks in Cancer Increase p53's Mutational Tolerance*	
10:17 - 10:20 a.m.	**Alper Karagöl |** Istanbul University, Istanbul Faculty of Medicine | *Multi-level Comparative Analysis Reveals Evolutionary Influence of Truncated Isoforms in Glutamate Transporters*	

Program

10:20 - 10:50 a.m.	**Colin Jackson |** Australian National University | *Enthalpyentropy Trade-offs in the Evolution of Ligand Specificity in a Superfamily of Transcription Factors*	**Christopher Fleming |** Syngenta | *Beyond Nature's Arsenal: Engineering the Next Generation of Insecticidal Proteins*
10:50 - 11:20 a.m.	**Dominique Madern |** CNRS-Grenoble | *Unraveling Unexpected Links Between Extremophilic Adaptation and Latent Allostery Using Archaeal Malate Dehydrogenases*	**Matthew Dwyer |** Michigan State University | *Repurposing Protein-based Organelles of Bacteria for Applications in Agriculture*
11:30 a.m. - 1:15 p.m.	**Plenary Awards and Closing |** *Grand Ballroom*	
11:35 a.m. - 12:05 p.m.	**2026 Stein & Moore Award** **Marius Clore**, National Institute of Health | *Probing Excited States, Structural Transitions and Kinetics in Fold-switching & Aggregation by NMR Exchange Spectroscopy*	
12:05 - 12:35 p.m.	**2026 Dorothy Crowfoot Hodgkin Award** **Andreas Martin**, University of California Berkeley | *Asymmetrically Firing on all Cylinders – Assembly, Structure, and Function of the Proteasome Molecular Machine*	
12:35 - 1:05 p.m.	**2026 Carl Brändén Award** **Neil Osheroff**, Vanderbilt University | *Catalyzing Change: From Enzymology to Medical Education*	
1:05 - 1:15 p.m.	**Service Awards and Closing, Dr. Heather Pinkett,** Northwestern University | President, The Protein Society	
2 - 4 p.m.	**Industry Visit: GINKGO BIOWORKS**, (Offsite, Transportation Not Provided) (RSVP only)	
2:30 - 4 p.m.	**Industry Visit: JNANA**, followed by Mixer, (Offsite, Transportation Not Provided) (RSVP only)	
2:30 - 4:30 p.m.	**Industry Visit: NOVARTIS**, (Offsite, Transportation Not Provided) (RSVP only)	
2:30 - 4:30 p.m.	**Industry Visit: SANOFI**, (Offsite, Transportation Not Provided) (RSVP only)	

UNDERGRAD RESEARCH SESSION

Speakers:

Ivan Escobar-Chavez

Centro de Investigacion en Alimentacion y Desarrollo

Sydney Mager

University of Massachusetts Amherst

Mary Harutyunyan

University of Massachusetts Lowell

KC Gabriel

Yale University

CHAIR: Matthew Gage, U Mass Lowell

July 21 | 11:30 a.m. - 12:30 p.m. | RSVP Only

Commonwealth Ballroom

Exhibitor List

The Protein Society/Wiley	**Booth 1**
SLAC National Accelerator Laboratory	**Booth 2**
SciTide	**Booth 3**
PromoChrom Technologies	**Booth 4**
Brookhaven Instruments	**Booth 5**
Brookhaven National Laboratory	**Booth 6**
Dartmouth University	**Booth 7**
CubeBioTech	**Booth 8**
Bruker	**Booth 9**
Waters Wyatt	**Booth 10**
UT Southwestern Medical Center	**Booth 11**
Exciting Instruments	**Booth 12**

Exhibitor Hours

July 19 and 20
Coffee Breaks:
10:20 - 10:45 a.m.
2:50 - 3:20 p.m.

Lunch:
12 - 1:30 p.m.

Exhibitor & Poster Reception:*
4:30 - 6:30 p.m.

July 21
Coffee Breaks:
9:50 - 10:15 a.m.
1:55 - 2:20 p.m.

Lunch:
11:25 a.m. - 12:35 p.m.

Exhibitor & Poster Reception:*
3:30 - 5:30 p.m.

*Reception will feature snacks/bar

Exhibitor Directory

Wiley: Booth #1
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Exhibitor Directory

SLAC National Accelerator Laboratory: Booth #2
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Exhibitor Directory

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NICOYA WORKSHOP

July 20 | 8:15 - 8:50 a.m.
Commonwealth Ballroom

BREAKFAST AND LEARN

Protein stability is foundational to successful discovery and development. Join us for breakfast and a live SUPR-DSF demonstration to see how researchers are generating rapid stability and binding insights using minimal sample and high-throughput workflows.

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THE PROTEIN SOCIETY

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TPS BUSINESS MEETING

JULY 22 | 7:45 - 8:20 AM | RSVP ONLY
COMMONWEALTH BALLROOM

Abstracts

TPS Award Winners

Laura Dassama, Ph.D. | Stanford University
2026 Protein Science Young Investigator Award | Sponsored by Wiley

Plenary: July 21 | 12:45 - 1:15 p.m.

Uncovering Opportunity Targets in Bacterial Pathogens
Laura Dassama1
1 Stanford University

Increased human exposure to pathogens couples with rising antibiotic resistance and slow antibiotic development to pose a nearly insurmountable human health challenge. My work aims to discover proteins critical for pathogen survival. We then reveal important insights into their mechanisms of action and develop chemical tools that precisely modulate their functions. By focusing on pathogens with limited or unique metabolic capabilities, we aim to discover novel biomarkers and antibiotic targets that are less likely to evade inhibitors. This talk will describe our use of informatics and other "omics" methods along with protein biochemistry and biophysics to accelerate the proteome-wide discovery of essential metabolite synthesis and handling proteins in human pathogens.

Stephen Fesik, Ph.D. | Vanderbilt University
2026 Marie Maynard Daly Award | Sponsored by The Protein Society

Plenary: July 21 | 1:15 - 1:45 p.m.

Drugging the Undruggable. Targeting MYC for Cancer Therapy
Stephen Fesik1
1 Vanderbilt University

MYC is a highly validated cancer target that is expressed in 50% of all cancers and responsible for over 100,000 deaths in the US annually. Despite much effort, MYC has been difficult or impossible to drug. Using fragment-based methods and structure-based design, we discovered orally active small molecules targeting the MYC cofactor WDR5 which disrupt chromatin engagement. We have also targeted the MYC/MAX dimer to block DNA binding. These efforts have produced potent MYC pathway inhibitors that show promise for treating patients with MYC-driven tumors.

Babis Kalodimos, Ph.D. | St. Jude Children's Research Hospital
2026 Hans Neurath Award | Sponsored by The Hans Neurath Foundation

Plenary: July 21 | 2:20 - 2:50 p.m.

Exploring and Exploiting the Conformational Landscape of Protein Kinases
Babis Kalodimos1
1 St. Jude Children's Research Hospital

Protein kinases are not static switches but dynamic systems whose function emerges from a complex conformational landscape. Our work establishes a framework to experimentally define and quantitatively map these landscapes, revealing sparsely populated, transient states that are invisible to conventional structural approaches yet central to regulation, catalysis, and drug response. Using NMR, integrated with complementary structural and biochemical methods, we uncover how kinase activity is encoded in shifts in state populations and exchange kinetics. These insights redefine kinase regulation as a tunable equilibrium rather than a binary process, and enable a new paradigm for ligand discovery by targeting transient, functionally critical conformations. This approach opens a path to systematically explore and exploit the dynamic kinome.

Peng Chen, Ph.D. | Peking University
2026 Emil Thomas Kaiser Award

Plenary: July 21 | 2:50 - 3:20 p.m.

Live-cell Protein Chemistry in Health and Disease
Peng Chen1
1 Peking University

Investigating the functional mechanisms of proteins within their "native environment"—living cells or animals—represents a challenging scientific conundrum as well as an interdisciplinary frontier spanning chemistry, life sciences and medicine. My group has been interested in the development and applications of live-cell chemistry for mechanistic study as well as therapeutic engineering of proteins. We have established a chemical reaction repertoire that can be genetically encoded on proteins in living systems. For example, we have pioneered the development and applications of "bond-cleavage" bioorthogonal reactions (termed "bioorthogonal cleavage reactions"), which opened a new direction for gain-of-function study of proteins under physiological as well as pathological settings. These in vivo chemical protein technologies have yielded interesting biological discoveries, revealing the crosstalk and remodeling of the tumor-immune microenvironment mediated by protein kinases, hydrolases, as well as transmembrane proteins such as GPCRs. In addition, we further integrated multiple bioorthogonal reactions as a combinatorial chemistry strategy that has enabled the modular conjugation and release of various therapeutic modalities. By recruiting various immune cells, our strategy demonstrated superior anti-tumor activity and tumor-specific immune responses in patient-derived organoids of solid tumors.

Abstracts

TPS Award Winners

Marius Clore, Ph.D. | NIH
2026 Stein & Moore Award | Sponsored by The Protein Society and Wiley

Plenary: July 22 | 11:35 a.m. - 12:05 p.m.

Probing Excited States, Structural Transitions and Kinetics in Fold-switching and Aggregation by NMR Exchange Spectroscopy
G. Marius Clore1
1 Laboratory of Chemical Physics, NIDDK, National Institutes of Health

In this talk for the Stein & Moore Award, I will highlight how exchange-based NMR can bring into view the sparsely populated, transient conformational states that often determine biological outcome. Using these approaches, my laboratory has characterized the hidden intermediates and kinetics underlying two very different but conceptually related problems: fold switching in the generalized transcription factor RfaH and fibril formation by the huntingtin exon 1 protein. In RfaH, we have delineated the sequence of excited states that connects the all-β C-terminal domain to the α-helical hairpin adopted in full-length RfaH, thereby defining the structural transitions and kinetics along the fold-switching pathway. These findings resolve a hierarchy of transient intermediates and show how a metamorphic protein traverses a rugged energy landscape to interconvert between two distinct functional states. For huntingtin exon-1 protein, responsible for Huntington's disease, an autosomal dominant fatal neurodegenerative condition, our work shows that fibrillization on the hours timescale is mechanistically linked to microsecond transient pre-nucleation oligomerization, with the N-terminal segment driving dimer and tetramer formation that promotes polyQ nucleation, followed by elongation and secondary nucleation. These studies further show how aggregation can be inhibited either by blocking productive tetramerization or by sub-stoichiometric sequestration of fibril ends. Together, they illustrate a unifying theme: rare, invisible states—biological "dark matter"—can control both protein function and protein misfolding.

Andreas Martin, Ph.D. | University of California Berkeley
2026 Dorothy Crowfoot Hodgkin Award | Sponsored by Rigaku Corporation

Plenary: July 22 | 12:05 - 12:35 p.m.

Asymmetrically Firing on all Cylinders – Assembly, Structure, and Function of the Proteasome Molecular Machine
Andreas Martin1
1 Department of Molecular & Cell Biology, Howard Hughes Medical Institute, and California Institute for Quantitative Biosciences, University of California at Berkeley

The ubiquitin-proteasome system is the major degradation pathway for protein quality control and the regulation of many vital processes in eukaryotic cells, and it therefore also plays important roles in the development of various human diseases. Elucidating the principles for 26S proteasome biogenesis, substrate recruitment, and mechanical processing is thus critical for advancing our understanding the proteasome's numerous cellular functions. Our biochemical, single-molecule, and cryo-EM structural studies of the 26S proteasome give mechanistic insights into the assembly of the proteasomal ATPase motor, the recognition of protein substrates in ubiquitin-dependent and -independent manners, and their ATP-dependent degradation. Visualizing the hetero-hexameric ATPase motor in different conformations and nucleotide states, and monitoring its movements by single-molecule FRET give a glimpse of the mechanochemical coupling that drives substrate translocation by asymmetric firing of the six cylinders. These studies not only advance our understanding of the basic principles that underlie substrate degradation by the 26S proteasome and related ATPase motor proteins, but may also help in developing new therapeutic strategies to modulate proteasomal activities or target unwanted proteins for degradation.

Neil Osheroff, Ph.D. | Vanderbilt University
2026 Carl Brändén Award Award | Sponsored by Rigaku Corporation

Plenary: July 22 | 12:35 - 1:05 p.m.

Catalyzing Change: From Enzymology to Medical Education
Neil Osheroff1
1 Vanderbilt University

I have pursued a deliberately bifurcated career in biochemistry: research and education. Trained in the era of the "one person – one polypeptide" paradigm, I have led a research program focused on DNA topoisomerases. Beyond their critical cellular functions, these essential enzymes are also targets for some of the most widely prescribed antibacterial and anticancer agents worldwide. The culmination of more than four decades of work from my laboratory is a comprehensive understanding of enzyme and drug mechanism. This work directly contributed to the FDA approval of gepotidacin, the first new class of antibacterials for the treatment of urinary tract infections and gonorrhea in more than 3 decades.

Abstracts

TPS Invited Speakers

Session 1: Macromolecular Protein Complexes in Biology

Erica Ollmann Saphire | La Jolla Institute for Immunology

Human Neutralizing Antibodies Against Measles Virus From an MMR Vaccine

Marissa Acciani1, Dawid Zyla1, Gele Niemeyer1, 2, Stephanie Harkins1, Diptiben Parekh1, Emily Pawlack3, Davide Lacarbonara4, Dhvanir Kansara5, Margaret E. Ackerman6, Stefan Niewiesk3, Matteo Porotto4,7,8, Kathryn M. Hastie1, Erica Ollmann Saphire1
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Measles virus (MeV), a highly transmissible paramyxovirus, causes disease that can lead to severe complications and death, particularly in babies and young children. Deployment of the durable, highly effective, live-attenuated measles vaccine has saved an estimated 94 million lives in the past 50 years, yet the immunological explanation for this vaccine's unique success and its landscape of antibody recognition remains unclear. Here we report the first panel of human monoclonal antibodies (mAbs) specific for the MeV hemagglutinin (H) and fusion (F) surface proteins, derived from the memory B cells of an MMR vaccinee. From over 100 cloned human mAbs, we mapped four major epitope clusters on H and another five major clusters on F, and structurally characterized 17 representative mAbs including one or more examples of each of the nine epitope clusters on the two surface antigens. We find that antibodies against both H and F can lead to potent virus neutralization and reduction of viral loads in vivo , including one mAb against F that reduces viral loads to below the limit of detection for all animals. High-resolution cryo-EM reveals contact sites of the most protective antibodies against both surface antigens. Discovery, characterization, and in vitro and in vivo success of these fully human mAbs now provide new avenues for prophylactic or therapeutic intervention against this re-emerging virus.

Kai Zhang | University of Science and Technology of China

High-resolution in situ Cryo-EM of Complexes within Mitochondria and Chloroplasts

Jiao Li1, Wan Zheng 2, Eduard Elias3, Pengxin Chai 2,4, Roberta Croce3, Jiapeng Zhu5, Kai Zhang 1,2
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2 Department of Molecular Biophysics and Biochemistry, Yale University
3 Department of Physics and Astronomy and Institute for Lasers, Life and Biophotonics, Faculty of Sciences, Vrije Universiteit Amsterdam
4 Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School
5 Department of Hepatobiliary Surgery, The First Affiliated Hospital of Anhui Medical University

Cellular energy conversion in mitochondria and chloroplasts depends on complex molecular assemblies embedded in native membranes, yet their organization and functional states remain poorly understood in physiological contexts. Here, we develop high-resolution in situ cryo-electron microscopy to directly visualize energy-converting complexes within mitochondria and chloroplasts. We resolve diverse supercomplex architectures at near-atomic resolution and uncover their native organization, protein-membrane interactions, and dynamic functional states. Our work establishes a unified in situ structural framework for understanding complex cellular energy systems across multiple scales.

Session 2: Engineering Protein Biologics

Tanja Kortemme | University of California, San Francisco

De novo Design of Programmable Protein Dynamics

Tanja Kortemme1
1 Department of Bioengineering and Therapeutic Sciences, University of California, San Francisco, United States of America

Methods from artificial intelligence (AI) have led to transformative advances in designing proteins de novo. Highly stable and static de novo proteins can now be robustly designed to bind to many protein targets with high affinity. However, many protein functions - those critical for signal processing, energy conversion, and multistep catalytic transformations - require defined structural transitions between dynamically interconverting protein conformations. These functions are currently challenging to design de novo even with advanced AI models, because these are trained to predict and design static structures. I will describe our recent progress with (i) designing dynamic proteins and (ii) developing advanced AI methods that can generate proteins with multiple conformational states and physically realistic paths between them. I will also show recent results demonstrating the design of diverse, de novo protein conformational changes in a single protein fold, suggesting that protein motions might be more designable than previously thought. Finally, since suitable and large-scale experimental data on protein dynamics are a big limitation in developing improved models, I

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will describe how we are designing and experimentally characterizing hundreds of predicted protein conformational switches in high-throughput.

Shohei Koide | New York University

Direct and Selective Targeting of Cancer-Driver Mutants with Synthetic Binding Proteins

Shohei Koide1,2
1 Department of Biochemistry and Molecular Pharmacology, New York University Grossman School of Medicine
2 Perlmutter Cancer Center, New York University Langone Health

Effective anti-cancer therapy depends on the ability to specifically inhibit and/or kill cancer cells while sparing healthy cells. Many cancers are driven by hyperactive point mutants, most of which remain undruggable by the conventional small-molecule drugs. These mutated proteins are potential sources of cancer-specific neoantigens. I will discuss protein-engineering strategies to effectively target cancer drivers, including the development of biologics that are exquisitely selective to hotspot mutations and the use of small-molecule inhibitors to create synthetic neoantigens that can be targeted with biologics.

Valeria Italia | Swansea University

Tuning Protein-Based Materials through Control of Early Assembly Conditions

Valeria Italia1, Amanda Jons2,3, Bhavika Kaparthi2, Britt Faulk4,5, Marco Maccarini6, Paolo Bertoncello7, Ken Meissner1, Donald K. Martin6, Sarah E. Bondos2,3,4
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5 Department of Biochemistry and Biophysics, Texas A&M University, College Station, Texas, USA
6 University Grenoble Alpes, SyNaBi, TIMC-IMAG/CNRS/INSERM, UMR 5525, Grenoble, France
7 Department of Chemical Engineering, Swansea University, Swansea, UK

The intrinsically disordered protein Ultrabithorax (Ubx) from Drosophila can assemble into materials through a multistep process. It starts with weak interactions between individual molecules, which form liquid-like droplets and gradually evolve into solid structures stabilized by covalent bonds. In this work, we investigate how simple parameters—such as protein concentration, assembly time, and buffer composition—influence the early stages of this process. We show that, under low-salt conditions, it is possible to create a new class of Ubx-based materials using significantly less protein and much shorter assembly times. These materials differ from conventional Ubx fibers in both surface structure and molecular organization. In particular, they display distinct surface patterns and a higher level of covalent cross-linking, even without relying on specific residues previously considered essential. Overall, our results demonstrate that simply tuning assembly conditions offers an effective and low-cost strategy to design new protein-based materials with unique properties.

Session 3: Protein Allostery & Biophysics

Julien Roche | Iowa State University

High-pressure NMR Study of Biological Systems

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1 Iowa State University
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High pressure is a powerful, reversible perturbation for studying protein stability, folding, dynamics, and assembly. By favoring conformational states with smaller partial molar volumes, pressure destabilizes solvent-excluded cavities, weak hydrophobic contacts, and protein–protein interfaces. When coupled with NMR spectroscopy, this perturbation provides residue-resolved access to equilibrium populations, volume changes, and conformational exchange processes across the protein energy landscape. This talk will introduce the thermodynamic basis of pressure-induced conformational changes and highlight key differences between pressure perturbation, temperature variation, and chemical denaturation. Pressure offers a local probe of the native-state ensemble, revealing structural features such as cavities, packing defects, and low-lying excited states that are often invisible under ambient conditions. I will discuss how high-pressure NMR can be used to monitor pressure-induced unfolding, quantify residue-specific volume changes, and combine equilibrium measurements with real-time pressure-jump experiments to reconstruct folding pathways and transition-state features. Additional examples will illustrate applications to intrinsically disordered and low-complexity protein domains, as well as to tight protein complexes in which pressure can stabilize otherwise inaccessible monomeric states.

Vincent Hilser | Johns Hopkins University

A Code For Ensemble Molecular Mimicry and Antibody Cross-reactivity

Vincent Hilser1
1 Department of Biology, Johns Hopkins University, 3400 N. Charles St. Baltimore, MD 21218

The ability of organisms to diverge and adapt to different environmental niches is a hallmark of evolution. We are interested in how proteins adapt to their environments, whether these adaptive mechanisms are general, and whether these processes are in any way connected to more fundamental mechanisms that drove the expansion and evolution of news folds. Here we reveal that fluctuations are much more extreme than previously believed, that they provide a 'thermodynamic yardstick' for classifying folds, and that this

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yardstick can be used to reveal similarities and predictable structural transitions between different folds. This information in turn, provides important insights about the evolution of new folds and even the origins of viral induced auto-immunity.

Breann Brown | Vanderbilt University

Uncovering the Role of Protein Structure and Dynamics in the Regulation of Heme Biosynthesis

Breann Brown1
1 Vanderbilt University

Heme is an essential biomolecule used by nearly all organisms, with critical cellular roles including oxygen transport in humans. Because dysregulation of heme levels is linked to multiple diseases, its biosynthesis must be tightly controlled. The first and rate-limiting step in heme production is catalyzed by the pyridoxal 5′-phosphate (PLP)-dependent enzyme aminolevulinic acid synthase (ALAS). Despite high sequence similarity among ALAS enzymes, organism-specific differences in regulation and protein assembly remain poorly understood. Here, we combine structural biology, biophysical and cellular assays, enzymology, and molecular dynamics simulations to investigate the structure, dynamics, and regulation of eukaryotic ALAS from Saccharomyces cerevisiae (scALAS). Our studies reveal key conformational changes associated with substrate binding and catalysis, as well as previously uncharacterized interactions with accessory proteins. Additionally, evolution-guided engineering of scALAS variants demonstrates how alterations in conserved and divergent regions affect catalytic activity and cellular metabolism. Together, these findings establish critical structure–function relationships governing ALAS regulation, provide insight into the molecular basis of heme biosynthesis and erythropoiesis, and lay the groundwork for developing targeted therapeutic strategies for heme-related disorders.

Lakshmi Wijeyewickrema | La Trobe University, Melbourne

Exosite-mediated Regulation of Complement Protease Activity Reveals Distinct Mechanisms Controlling C3 Proconvertase Assembly

Lakshmi Wijeyewickrema1
1 La Trobe University, Melbourne

Assembly of the classical and lectin pathway C3 proconvertases depends on the precisely coordinated proteolytic activation of C2 by the complement proteases C1s and MASP-2. Although catalysis occurs within the serine protease active site, efficient C2 cleavage relies on exosite-mediated molecular recognition, raising fundamental questions about how these protein–protein interactions dictate catalytic efficiency and pathway specificity. Here, we combine structure-guided mutagenesis with functional and kinetic analyses to define the contribution of a conserved anion-binding exosite within the serine protease domains of C1s and MASP-2 to C2 activation. We demonstrate that this surface is essential for efficient cleavage of C2 by both enzymes and identify the von Willebrand factor A domain of C2 as the principal interaction platform. Despite the structural similarity of the two proteases, they exhibit distinct requirements for electrostatic recognition, with C1s and MASP-2 engaging different anionic surfaces on C2 to achieve productive catalysis. These findings reveal mechanistic divergence in substrate recognition while preserving a common functional outcome. We further present new data demonstrating how MASP-1 contributes to C2 activation and functionally compensates for reduced MASP-2 activity, providing new insight into the robustness and regulation of lectin pathway initiation. Together, these studies establish exosite-mediated molecular recognition as a central determinant of complement protease function and illustrate how subtle differences in protein surface interactions tune catalytic efficiency, pathway specificity, and biological resilience. Beyond complement biology, this work highlights general principles by which multidomain serine proteases achieve selective substrate recognition through allosterically coupled interaction surfaces.

Session 4: Protein Nanotechnology

Alena Khmelinskaia | Ludwig-Maximilians-Universität München

Function-driven Design of Protein Assemblies

Alena Khmelinskaia1
1 Ludwig-Maximilians-Universität München

Recent computational methods have been developed for designing novel protein assemblies with atomic-level accuracy. Yet, when compared to their natural counterparts, the structural and functional space covered by de novo designed assemblies remains limited. I will share with you our ongoing efforts in diversifying the structural repertoire of protein assemblies and developing strategies to dynamically control protein assembly state. First, I will describe our approaches to the diversify assembly geometries beyond simple polyhedral geometries, such as linked architectures assembled from rigid building blocks following quasi-equivalence principles. Then, I will present our generalizable interface-seeded design approach for the generation of environemnt responsive oligomers driven by ion-mediate, small molecule-dependent or phosphorylation-triggered protein-protein interfaces. By leveraging novel architectures and a diversity of endogenous and exogenous signals, we aim to generate orthogonal, programmable control elements for synthetic biology.

Jin Montclare | NYU Tandon School of Engineering

Designing Protein-Based Nanomaterials: From Sequence to Functional Biomaterials

Dustin Britton1, Lindsay Hill2, Hao-Wei-Shih1
1 Department of Chemical and Biomolecular Engineering, NYU Tandon School of Engineering
2 Department of Biomedical Engineering, NYU Tandon School of Engineering

Inspired by nature's biopolymers, we engineer artificial protein materials with entirely

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new properties and function. We employ synthetic and chemical biology to construct our materials and endow them with stimuli-responsiveness. In particular, we have fabricated protein-derived nanomaterials that assemble into nanofibers and hydrogels. We investigate the fundamental self-assembly and molecular recognition capabilities of these systems. More importantly, we are able to harness these structures to interface with tissues enabling delivery of therapeutic exosomes and small molecules as well as non-invasively image them.

Adam Caparco | Northeastern University
Protein Nanoassemblies for Biocatalysis and Nucleic Acid Delivery
Adam Caparco1,2,3
1 Northeastern University Chemical Engineering Department
2 Northeastern University Chemistry and Chemical Biology
3 Northeastern University Institute for Plant-Human Interface

Protein-based nanoassemblies are programmable scaffolds for organizing molecular cargo with spatial precision. Our work uses viral and non-viral protein architectures, combined with genetically encoded fusion domains, to address enzyme immobilization for biocatalysis and nucleic acid delivery to plants. We have shown that plant virus-derived spherical nanoparticles can encapsulate double-stranded RNA and small-molecule payloads, and are extending this approach to rod-shaped assemblies based on tobacco mild green mosaic virus (TMGMV) for programmable RNA packaging. For biocatalysis, we build on earlier work using leucine zipper coiled-coil fusions to load enzymes onto protein-inorganic nanomaterials, and are now exploring bacterial microcompartment shell proteins as self-assembling cages for multi-enzyme co-localization. Across both efforts, proteins and their fusion variants serve as modular building blocks that connect nanoscale architecture to function.

Session 5: Function & Behavior of Intrinsically Disordered Proteins

Priya Banerjee | The State University of New York at Buffalo
From Sequence to Selectivity: How Disordered Prion-Like Domains Orchestrate Co-Condensation of Transcriptional Regulators
Anushka Supakar1, Richoo Davis1, Priya R. Banerjee1
1 Department of Physics, The State University of New York at Buffalo

Prion-like low-complexity domains (PLCDs) are intrinsically disordered regions that drive the assembly of biomolecular condensates central to gene regulation. Chromosomal fusions that link FET family PLCDs to transcription factor DNA-binding domains generate potent oncogenic drivers, yet the molecular grammar governing their functional interactions remains poorly understood. Here, we systematically map the molecular grammar–function landscape of FET PLCDs using a library of ~70 sequence variants that feature distinct aromatic content, spacer composition, and charge patterning. Integrating in vitro reconstitution, live-cell imaging, and quantitative modeling, we uncover how specific arrangements of aromatic, aliphatic, and charged amino acids define the energetic and kinetic principles governing co-condensation with chromatin remodelers such as the mSWI/SNF complex. We identify a tunable regime of interaction strength, encoded by the PLCD sequence grammar, that enables dynamic, functional condensates, whereas excessive cohesive interactions drive dynamical arrest and deregulation of transcriptional activity. These findings establish a new molecular grammar for disorder-mediated interactions in transcriptional control and reveal how FET oncoproteins exploit this grammar to rewire gene expression in cancer.

Andrea Soranno | Washington University
Single-molecule Spectroscopy of Disordered Regions and Nucleic Acids in Bacterial Transcription
Drake Jensen, Melissa D. Stuchell-Brereton, Alex Holehouse, Eric Galburt, Andrea Soranno1
1 Washington University

In bacteria, sigma factors (σ) associate with core RNA polymerase (RNAP) to form the holoenzyme and initiate transcription of specific promoters. In Mycobacterium tuberculosis, the housekeeping σA contains a ~200-amino-acid N-terminal IDR with highly segregated charges. Removing this IDR strongly reduces transcription under multi-round conditions, suggesting a role in RNAP holoenzyme formation and recycling. Using fluorescence correlation spectroscopy (FCS) and single-molecule FRET, we find that the IDR enhances RNAP binding, adopts salt-dependent conformations, and remains highly dynamic in both free and bound states. Notably, it expands upon RNAP binding but re-compacts in the transcriptionally competent complex. Our results show that σA–RNAP–DNA assembly competes with non-specific DNA interactions and suggest that conserved IDR sequence features across Actinobacteria provide a general mechanism for modulating bacterial transcription.

Ute Hellmich | Friedrich Schiller University Jena
Regulation Through Disorder: Lipid Signalling Through Unstructured Regions Shapes Ion Channel Function in Health and Disease
Yasmine S. Damayanti1, Charlotte Guhl1, Jean-Martin Harder1, Christoph Wiedemann1, Benedikt Goretzki1, Ute A. Hellmich1
1 Friedrich Schiller University Jena, Institute of Organic and Macromolecular Chemistry & Cluster of Excellence "Balance of the Microvers"

Cells rely on membrane receptors to detect and integrate diverse environmental signals. Ligands such as small molecules, peptides or ions trigger conformational changes that regulate downstream signaling cascades. However, many membrane receptors, including most Transient Receptor Potential (TRP) channels, also contain large intrinsically disordered regions (IDRs) whose dynamic nature has severely hampered structural characterization. Although nearly half of the human proteome is predicted to be disordered,

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the contribution of IDRs to signal sensing remains poorly understood. TRP channels contribute to almost every physiological process in the human body, including thermo- and osmosensation, nociception, as well as to the molecular basis of both genetic and infectious diseases, yet the molecular basis of their multimodal sensing remains elusive. Using an integrated structural biology approach, we unravel how disordered regions contribute to multipartite signalling networks, and how TRP channel properties are dynamically modulated by lipids, posttranslational modifications and disease mutations. Together, our studies advance our understanding how intrinsic disorder coordinates cellular signal sensing.

Session 6: Machine Learning & AI in Protein Science

Stephanie Wankowicz | Vanderbilt University
From Possibility to Precision in Macromolecular Ensemble Prediction
Stephanie Wankowicz1
1 Friedrich Schiller University Jena, Institute of Organic and Macromolecular Chemistry & Cluster of Excellence "Balance of the Microvers"

Cells rely on membrane receptors to detect and integrate diverse environmental signals. Ligands such as small molecules, peptides or ions trigger conformational changes that regulate downstream signaling cascades. However, many membrane receptors, including most Transient Receptor Potential (TRP) channels, also contain large intrinsically disordered regions (IDRs) whose dynamic nature has severely hampered structural characterization. Although nearly half of the human proteome is predicted to be disordered, the contribution of IDRs to signal sensing remains poorly understood. TRP channels contribute to almost every physiological process in the human body, including thermo- and osmosensation, nociception, as well as to the molecular basis of both genetic and infectious diseases, yet the molecular basis of their multimodal sensing remains elusive. Using an integrated structural biology approach, we unravel how disordered regions contribute to multipartite signalling networks, and how TRP channel properties are dynamically modulated by lipids, posttranslational modifications and disease mutations. Together, our studies advance our understanding how intrinsic disorder coordinates cellular signal sensing.

Minkyung Baek | Seoul National University
AI-based Antigen–Antibody Complex Structure Prediction and Design
Minkyung Baek1
1 Department of Biological Sciences, Interdisciplinary Program in Artificial Intelligence, Seoul National University

Recent advances in deep learning have opened new possibilities for antibody research and development, enabling computational approaches that were previously intractable. Despite remarkable progress in protein structure prediction, the rational design of therapeutic antibodies remains challenging, as it requires not only accurate modeling of antigen–antibody interactions but also practical considerations such as expression and manufacturability. In this talk, I will present an integrated AI-driven framework that addresses the full spectrum of this challenge. Our approach moves seamlessly from understanding how antibodies bind to designing entirely new ones. By mapping plausible binding interfaces on antigen surfaces through epitope scanning, we establish a structurally informed foundation for the design process. Building on this, we explore vast regions of antibody sequence space to propose de novo candidates with target-specific binding properties, well beyond what existing libraries can offer. Crucially, we also ensure that computationally designed candidates meet the practical requirements of therapeutic development by optimizing for antibody expression levels. Through benchmarking and case studies across diverse antigen targets, we demonstrate that tightly coupling structure prediction, de novo design, and expression optimization within a unified pipeline can substantially accelerate the discovery and development of therapeutic antibodies.

Jean-Philip Piquemal | Sorbonne Université
A Quantum Foundation Model for Accurate Atomistic Simulations in Drug Design
Jean-Philip Piquemal1
1 Laboratoire de Chimie Théorique, Sorbonne Université

While artificial intelligence has revolutionized the prediction of static protein structures, characterizing their dynamics and interactions with drug candidates remains a computational bottleneck. Here, we introduce FeNNix-Bio1, a foundation machine learning model designed to power accurate, reactive atomistic simulations of biological systems at an unprecedented speed and scalability. Trained exclusively on synthetic quantum chemistry data, FeNNix-Bio1 accurately captures complex condensed-phase phenomena such as ion solvation and subtle liquid water properties for which it outperforms state-of-the-art specialized force fields. In this presentation, I will illustrate its versatility across a full spectrum of drug design applications, including the calculation of hydration free energies (HFEs), the reversible folding of small proteins, the simulation of protein-ligand absolute binding free energies and chemical reactions. Notably, FeNNix-Bio1 sets a new standard for the precise prediction of HFEs for the more than 600 molecules of the Freesolv dataset, providing sub-kcal/mol accuracy. By enabling scalable, quantum-accurate molecular dynamics without the need for manual parametrization, FeNNix-Bio1 bridges the gap between static structure prediction and dynamic biological reality.

Abstracts

TPS Invited Speakers

Session 7: Cellular Protein Dynamics & Distribution

Lisa Jones | University of California San Diego

Characterizing Drug Downstream and Off Target Effects Using Proteome-Wide Structural Biology

Lisa Jones1
1 Department of Biochemistry and Molecular Biophysics, University of California San Diego

In recent years, protein footprinting coupled with mass spectrometry has been used to identify protein-protein interaction sites and regions of conformational change through modification of solvent accessible sites in proteins. Fast photochemical oxidation of proteins (FPOP) is a footprinting method that utilizes hydroxyl radicals to oxidatively modify solvent accessible amino acids. FPOP has traditionally been used in vitro on relatively pure protein systems. We have further extended the FPOP method for in-cell analysis of proteins, a method entitled in-cell FPOP (IC-FPOP). This allows for the study of proteins in their native cellular environment. A major application of IC-FPOP is for proteome-wide structural biology as the method can oxidatively modify over 2000 proteins in a single experiment. In one such application, we used IC-FPOP to identify on and off targets of the anti-cancer drug methotrexate in leukemia cells. We examined the interaction of methotrexate with its target protein DHFR and found long range conformational changes that occur upon drug binding. We also identified protein interaction and conformation changes on 50 other proteins in the folate acid pathway where DHFR is located. Further, we were able to identify off target structural changes that occur in several different biological pathways including pathways related to DNA repair, DNA replication, metabolism, and immune system amongst several others. A better understanding of the off-target effects of drugs will inform on the potential side effects that patients will face. We have also further extended the FPOP method for analysis in C. elegans, a member of the nematode family. This allows us to study protein structure directly in animal model for human disease. These methods have the potential to become a powerful tool in the structural biology toolbox.

Elizabeth Hinde | University of Melbourne

Tracking DNA Repair Protein Control of Chromatin Dynamics in Living Cells

Jieqiong Lou1, Julissa Sanchez-Velasquez1, Saul Menendez Cardenas1, Xiaomeng Zhang1, Elizabeth Hinde1,2
1 School of Physics, University of Melbourne, Australia
2 School of Chemistry, University of Melbourne, Australia

DNA double-strand breaks (DSBs) are among the most deleterious forms of DNA damage and must be repaired within the highly organised chromatin environment of the living cell nucleus. While the molecular mechanisms governing DSB repair are well established, how chromatin organisation influences repair pathway choice and repair fidelity remains poorly understood due to the diffraction limit of light microscopy. To address this problem, we combined phasor-based fluorescence lifetime imaging microscopy (FLIM) of histone Förster resonance energy transfer (histone FRET) with single-particle tracking (SPT) of DSB mobility, enabling simultaneous measurement of chromatin compaction and mobility during DNA repair at nanometre scales in living cells. Using this integrated imaging framework, we investigated how the antagonistic DNA repair proteins breast cancer gene 1 (BRCA1) and p53-binding protein 1 (53BP1) regulate chromatin dynamics during the DNA damage response. We found that DSB repair pathway choice is associated with distinct chromatin compaction and mobility states that are differentially regulated by BRCA1 and 53BP1. Collectively, these findings reveal a previously unrecognised mechanism by which DNA repair proteins regulate chromatin architecture, linking chromatin compaction and mobility to DNA repair pathway function in living cells.

Session 8: Physics-Based Computation in Protein Science

Joan Emma Shea | University of California Santa Barbara

Self-Assembly of the Tau Protein: Liquid-Liquid Phase Separation and Fibrillization

Joan Emma Shea1
1 Department of Chemistry and Biochemistry, University of California Santa Barbara

Intrinsically disordered proteins (IDPs) belong to a class of proteins that do not fold to a well-defined, three-dimensional structure, but rather co-exist between interconverting, partially structured conformations. In the crowded cellular milieu, IDPs can form liquid droplets through liquid-liquid phase separation or self-assemble into beta-sheet enriched amyloid fibrils, processes linked to normal physiological functions and various pathologies. In this talk, we present a new computational framework that scores amyloid and LLPS propensities from protein language model (pLM) embeddings, thereby enabling rapid proteome-wide annotation of peptides and residues. We apply this framework to the Tau protein, an intrinsically disordered protein that plays an important role in stabilizing microtubules, and identify segments of Tau that have a propensity to phase separate or form fibrils. Using a multiscale approach combining atomistic, coarse-grained, and field-theoretic simulations, we further characterize the mechanisms of fibrillization and phase separation of these fragments and shed light on the sequence characteristics linked with these two modes of assembly.

Abstracts

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Dan Herschlag | Stanford University

Ensemble-function Analysis Accounts For Mysteries of Phosphoryl Transfer Catalysis: Transitioning From Empirical Analyses to Physics-based Evaluation

Dan Herschlag1, Fanny Sunden1, Siyuan Du1
1 Department of Biochemistry, Stanford University School of Medicine

Structure-function has dominated biochemistry and biophysics for decades, and there has been enormous value in learning to infer what proteins due based on structural information and corresponding functional studies. Yet, function is not just what a protein does, but also how fast it interacts and catalyzes reactions, how specifically, and how strongly it interacts with other proteins and effectors. Thus, function is quantitative, and ultimate understanding of function will be in terms of fundamental chemical interactions forces. Here we extend ensemble–function analysis from our prior dissection of serine protease catalysis (Du et al. Science 387, eado5068 [2025]) to another common catalytic strategy, two-metal ion catalysis of phosphoryl transfer. Ensemble-function comparisons of the enzymatic reaction pathway and non-enzymatic interactions reveal several new, unexpected catalytic contributions that bring us closer to understanding the overall catalysis of >1027 by these enzymes. Ensemble–function analysis provides a fundamental framework to dissect protein function and can be applied to many systems in the future.

Benoit Roux | University of Chicago

Theoretical and Computational Treatments of Molecular Binding in the Context of Lipid Membranes

Benoit Roux1
1 University of Chicago

The equilibrium dissociation constant and the binding free energy of two molecular moieties in bulk solution are two classic and extremely familiar concepts. The binding free energy of two molecular moieties in solution can be characterized experimentally and can also be computed using molecular dynamics simulations by relying on rigorously formulated free-energy simulation methodologies. In contrast, formulating these same concepts in the context of membranes requires some caution. For instance, standard computational free-energy methodologies are not applicable to integral transmembrane (TM) proteins because the association process is completely restricted to the two-dimensional space of the membrane. Another situation is that of peripheral membrane-binding proteins, where the binding process brings an unbound protein in three-dimensional bulk solution to a bound state in which it is restricted to the two-dimensional surface of the membrane. How to rigorously formulate the proper statistical mechanical description of these different situations, and design effective computational methods to treat these problems, remains a challenge. Here, rigorous statistical mechanical theoretical frameworks will be formulated for the treatment of integral transmembrane (TM) proteins and peripheral membrane-binding proteins. These new methods will be illustrated by considering the association of the glycophorin A homodimer and the binding of Bacillus thuringiensis phosphatidylinositol-specific phospholipase C (BtPI-PLC) to the membrane surface.

Session 9: New Problems in Protein Folding

Tobin Sosnick | University of Chicago

Structural Energetics as a Framework for Rationalizing Protein Function

Abigail Schroeter1, Michael Baxa1, Saba Kanwal2, Xiaoxuan Lin1, Hendrik Glauninger1, D. Allan Drummond1, Eduardo Perozo1, Heedeok Hong2
1 University of Chicago
2 Michigan State University

Central questions in the study of proteins involve the interplay between structure, energetics, dynamics, and function. Here, we introduce a procedure to quantify local folding cooperativity from hydrogen-deuterium exchange mass spectrometry (HDX-MS) data. This method measures the relationship between protein energetics and folding cooperativity, focusing on hydrogen-bonded structures throughout the protein. Central to our analysis is the recognition that deuterium uptake curves can reveal the degree of folding cooperativity among residue groups. We propose that cooperative unfolding identifies stiff segments that can support force transmission or store strain energy. In contrast, the lack of cooperativity identifies flexible regions that can help optimize binding interfaces. We apply the method to two membrane proteins, a mammalian voltage-sensitive auditory protein and a bacterial protease. Each of these proteins has a distinct pattern of local folding cooperativity, which provides insight into how its various cooperative and non-cooperative segments contribute to its function.

Brian Volkman | Medical College of Wisconsin

Cold Denaturation in the Adaptive Evolution of Metamorphic Proteins

Brian F. Volkman1, Davin R. Jensen1, Gilberto Marquez1, Acacia Mouzakitis1
1 Department of Biochemistry, Medical College of Wisconsin

Metamorphic proteins switch between different folds, defying the protein folding paradigm. It is unclear how fold switching arises during evolution. XCL1 is an unusual member of the chemokine family, whose members adopt a conserved tertiary structure. We used ancestral sequence reconstruction and nuclear magnetic resonance to examine XCL1's evolution from a single-fold ancestor to a metamorphic protein that spontaneously interconverts between two unrelated folds with different functions. Thermodynamically, dual-fold proteins are a puzzle, since most globular proteins adopt a single native conformation that corresponds to the minimum in a free energy folding landscape. Surveys of the free energy folding landscape of XCL1 and its ancestors reveal a distinct thermodynamic signature that emerges with the alternate fold. Cold denaturation at ambient temperature explains the temperature dependence of XCL1's conformational equilibrium and provides an essential clue for the design of new metamorphic proteins.

Abstracts

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Duyoung Min | Ulsan National Institute of Science and Technology (UNIST)

Single-molecule Tweezers Decode Hidden Patterns of Membrane Protein Folding and Interactions

Duyoung Min1
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Folding and interactions of membrane proteins are fundamental processes in cellular membranes, central to numerous physiological and pathological pathways, and increasingly recognized as promising therapeutic targets. These processes—particularly the conformational maturation of individual membrane protomers and the post-diffusion steps of dimerization—are highly intricate due to complex inter-residue interactions within lipid bilayers. In this talk, I present a single-molecule magnetic tweezers platform that directly profiles these hidden transitions during membrane protein folding and dimerization. This approach captures reversible structural events at the single-molecule level, revealing previously undetected intermediate states that govern both folding pathways and dimer assembly. By integrating measurements of intermediates, kinetics, and energy landscapes with molecular dynamics simulations, we delineate the underlying pathways and dissect how residue interactions and lipid bilayers shape these processes. Furthermore, our platform allows for the targeted analysis of localized perturbations—such as those induced by peptide binding or site-directed mutagenesis—demonstrating its utility for probing the mechanisms of therapeutics targeting membrane proteins at single-molecule resolution.

Session 10: Proteins at the Membrane

Rosemary Cater | The University of Queensland

Structural and Molecular Basis of Choline Uptake Into the Brain by FLVCR2

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Choline is an essential nutrient that the human body needs in vast quantities for cell membrane synthesis, epigenetic modification, and neurotransmission. The brain has a particularly high demand for choline, but how it enters the brain has eluded the field for over fifty years. The MFS transporter FLVCR1 was recently determined to be a choline transporter, and while this protein is not highly expressed at the blood-brain barrier (BBB), its relative FLVCR2 is. Previous studies have shown that mutations in human Flvcr2 cause cerebral vascular abnormalities, hydrocephalus, and embryonic lethality, but the physiological role of FLVCR2 is unknown. Here, we demonstrate both in vivo and in vitro that FLVCR2 is a BBB choline transporter and is responsible for the majority of choline uptake into the brain. We also determine the structures of choline-bound FLVCR2 in the inward- and outward-facing states using cryo-electron microscopy to 2.49 and 2.77 Å resolution, respectively. These results reveal how the brain obtains choline and provide molecular-level insights into how FLVCR2 binds choline in an aromatic cage and mediates its uptake. Building on these findings, our ongoing work focuses on therapeutically harnessing FLVCR2 and elucidating the function of its ~100–amino acid intrinsically disordered N-terminal tail.

Camilo Perez | University of Georgia

Mechanistic Basis of Transport Processes in Bacterial Cell Wall Biopolymer Synthesis

Camilo Perez1
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Bacterial infections remain a major public health challenge, increasingly exacerbated by the global rise of antimicrobial resistance. Gram-positive pathogens such as Staphylococcus aureus and Streptococcus pneumoniae are leading causes of both nosocomial and community-acquired infections. Teichoic acids are critical determinants of bacterial physiology and virulence, contributing to immune evasion, host adhesion, biofilm formation, and resistance to antimicrobial agents. Their biosynthesis depends on multiple membrane transporters that mediate the translocation of lipid-linked and soluble precursors across the membrane. Our work focuses on elucidating the molecular mechanisms of these transport systems and defining their roles in bacterial adaptation. We recently investigated the flippase TacF, a member of the multidrug/oligosaccharide-lipid/polysaccharide (MOP) superfamily, which is proposed to regulate the phosphocholine content of teichoic acids during translocation, a function whose mechanistic basis remains unresolved. Our findings provide detailed mechanistic insight into this essential flippase in S. pneumoniae pathogenesis.

Brian Fuglestad | Virginia Commonwealth University

Molecular Control of Proteins at the Membrane Interface

Brian Fuglestad1
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Peripheral membrane proteins (PMPs) are water-soluble proteins that bind to membranes, often reversibly, to perform their function. They comprise up to ~10% of the human genome and are central to a variety biological and disease processes. Despite their great biomedical importance, development of systematic approaches towards PMPs as targets for drug discovery has yet to emerge. For many PMPs, inhibition of lipid headgroup recognition and membrane anchoring may provide a therapeutic avenue. However, due to dissimilarity to traditional drug target interfaces, such as enzyme active sites, the protein-lipid and protein-membrane interface presents a significant challenge. Due to its success in inhibiting protein-protein interaction interfaces that were previously considered undruggable, we sought to utilize fragment-based inhibitor design strategies to address PMP targets. We have applied this strategy to a membrane anchoring PMP,

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p47phox, which has yielded advanceable hits that inhibit the key lipid interaction and is a promising strategy for targeting the NADPH oxidase 2 complex. However, this approach is a greater challenge for other PMP types such as membrane embedded targets. Our new reverse micelle-enabled fragment-based discovery strategy allows easy accessibility to membrane embedded protein targets. Fragment-screening of glutathione peroxidase 4 in its functionally relevant, membrane-bound state has revealed hits that bind within the lipid recognition region. Not only do these binders represent inhibitor building-blocks, but they reveal properties of small-molecule binding within the largely unexplored space of protein-membrane interfaces. Advances outlined here provide an entry point for inhibitor design of this challenging category of protein and provide tools for a better understanding of their structure and function in high-resolution.

Session 11: Proteins Evolution

Mike Harms | University of Oregon

The Evolution of Multi-conformation Proteins

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Epistasis, where the effect of a mutation depends on genetic background, is ubiquitous in proteins. It shapes evolutionary outcomes and complicates protein engineering. Our core premise is that making sense of epistasis requires understanding the mechanisms that cause it. We are particularly interested in the interplay of two mechanisms: physical interactions, where mutations are in contact within a protein structure, and emergent interactions, where mutations redistribute the energy landscape leading to nonlinear combined effects. These mechanisms have different biological consequences. For example, epistasis arising from a redistributed energy landscape depends strongly on environmental factors, while epistasis arising from direct interactions generally does not. These two mechanisms also have profoundly different implications for modeling epistasis. For example, for N mutations, the number of direct-interaction model parameters scales by N2, while the number of redistribution parameters scales by N. The relative contribution of each mechanism to epistasis in proteins remains an open question. To fill this gap, we set out to measure the relative contributions of these two mechanisms of epistasis for ~200,000 pairwise mutant cycles introduced into the E. coli lac repressor. We developed a high-throughput screen that quantitatively maps bacterial growth to DNA occupancy, then measured occupancy versus allosteric effector for the library of mutant cycles. Using the different predicted outputs of the two mechanisms of epistasis, we were able to measure the relative contributions of each mechanism. We found roughly equal contributions from direct and emergent epistasis in these mutant cycles. This suggests that both mechanisms likely shape the evolution of bacterial transcription factors. Our work also demonstrates a route to disentangle different mechanisms of epistasis in high-throughput datasets, thus improving our ability to build predictive models of combined mutational effects.

Anum Glasgow | Columbia University

Evolutionary Conservation of Functional Allostery in Protein Families

Anum Glasgow1, Malcolm Wells1, Chenlin Lu1, Daniel Sultanov1, Kyle Weber1, Erin Ahern1, Zhen Gong1, Ethan Chen1
1 Columbia University

How do protein domains with highly conserved three-dimensional folds perform radically disparate biochemical functions? To understand this, we mapped the energetic landscapes of a family of bacterial transcription factors and their anciently diverged structural homologs, the periplasmic binding proteins. Using hydrogen exchange/mass spectrometry, bioinformatics, X-ray crystallography, and molecular dynamics, we uncovered an unexpected contrast: despite binding the same sugars, the two families evolved unique "energetic blueprints" to support their distinct functional requirements. To test if differences in energetic ensembles have functional consequences, we rationally redesigned the protein fold for tunable ligand-driven transcriptional responses. We found that protein engineering guided by the family's energetic blueprint produced synthetic transcription factors with the theoretically anticipated ligand-induced transcriptional outputs. Thus, decoding energetic blueprints among conserved protein folds provides an explanation for diverse functional adaptations, paves an alternative roadmap for protein design, and offers a new approach for engineering challenging drug targets.

Dominique Madern | Institut de Biologie Structurale, Grenoble

Unraveling Unexpected Links Between Extremophilic Adaptation and Latent Allostery Using Archaeal Malate Dehydrogenases

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5 Institut de Chimie Physique d'Orsay, Orsay

We investigated the mechanisms underlying thermal adaptation in the Methanococcales—a major archaeal lineage—at both the proteome and individual enzyme levels. Our focus was on malate dehydrogenase (MalDH), a key metabolic enzyme that catalyzes the NAD(P)H-dependent interconversion of oxaloacetate and malate. Using an integrated paleoenzymology approach, we characterized both ancient and extant MalDHs, revealing unexpected phenotypes and a latent capacity for evolving allosteric regulation. First, we developed molecular thermometers to infer ancestral optimal growth temperatures (OGTs) along the evolutionary pathway. Our analysis of ancestral and modern MalDHs demonstrated a strong correlation between inferred OGTs and experimental optimal tem-

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peratures for activity (A-Topt). Strikingly, the MalDH of the Methanococcales ancestor was hyperthermostable, with an A-Topt of 80°C, consistent with a hyperthermophilic lifestyle. This ancestor gave rise to two lineages with distinct thermal adaptations: one retained hyperthermophily, while the other underwent multiple independent transitions to colder environments. Enzymes from the first lineage maintained high thermostability and A-Topt, whereas the ancestor of the second lineage exhibited robust thermostability but a significantly reduced A-Topt. This thermal shift occurred rapidly at the base of the mesophilic lineage. Additionally, we uncovered an unexpected link between thermostability and resistance to γ-irradiation-induced unfolding, suggesting this trait is ancestral. To mimic the enzyme's adaptation toward mesophily, we introduced targeted mutations that reshaped the conformational energy landscape, successfully lowering A-Topt without compromising thermostability. Crystal structures of ancestral and modern MalDHs revealed how substitutions redistribute stabilizing electrostatic interactions across lineages. Some MalDHs also displayed structural features reminiscent of the extended or compact states typical of allosteric lactate dehydrogenases. We complemented this work with molecular dynamics simulations. These simulations revealed that competent and incompetent catalytic site configurations coexist in equilibrium—akin to allosteric enzymes—with temperature-dependent conformational reorganizations.Our findings highlight an intricate link between thermal adaptation and the evolution of allostery, mediated by modulation of the protein conformational landscape.

Session 12: Proteins in Agriculture

Katie Stewart | Corteva Agriculture

Plant Derived Insecticidal Proteins for Protection of Crop Plants

Katie Stewart1
1 Corteva Agriculture

Global food security faces a dual challenge: a shrinking agricultural footprint and rising insect resistance to conventional Bt-derived toxins. To sustain crop yields, a new generation of insecticidal proteins is required. Non-seed plants offer a reservoir of unique insecticidal protein families, some with potencies comparable to Bt toxins and high specificity against key North American and Latin American pests. This presentation explores the discovery and validation of two such families, IPD083 and IPD113, highlighting their distinct structural architectures and novel modes of action, which provide a strategic advantage in overcoming existing resistance mechanisms. Our findings underscore the potential of plant-derived proteins to provide durable insect control and secure global food production.

Sheng Yang He | Duke University

Biochemical Functions of Bacterial Pathogen Effectors: Implications for Plant Disease Control

Sheng Yang He1
1 Howard Hughes Medical Institute, Department of Biology, Duke University

Bacterial plant pathogens rely on secreted effector proteins to manipulate host cellular processes and establish infection. Among these, AvrE is a widely conserved effector that plays a central role in virulence across diverse phytopathogenic bacteria by creating a water-rich apoplast in which bacteria multiply. This presentation will highlight recent progress in elucidating the biochemical activities of AvrE-family effectors and how these functions contribute to host susceptibility and disease development. AvrE-family effectors fold into a β-barrel structure that resembles bacterial porins. Electrophysiological, biochemical and genetic experiments revealed that AvrE-family channels allow the passage of water and small molecules. Targeted screening of chemical blockers based on the predicted pore size (15–20 Å) of the AvrE channel identified polyamidoamine (PAMAM) dendrimers as inhibitors. Notably, PAMAMs broadly inhibit the virulence activities of AvrE-family effectors during Erwinia amylovora and Pseudomonas syringae infections. Ongoing efforts include testing disease control by polyamidoamines in field conditions.

Matthew Dwyer | Michigan State University

Repurposing Protein-based Organelles of Bacteria for Applications in Agriculture

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Bacterial microcompartments (BMCs) are protein-based organelles that encapsulate multienzyme pathways, illustrating biological modularity. They are widely distributed across bacteria and support metabolic efficiency by co-localizing enzymes, regulating local substrate and product concentrations, isolating reactive intermediates, and enabling controlled exchange with the environment. We are engineering BMC-derived architectures (including polyhedral shells, nanotubes, and 2-D sheets) for applications in phytonanotechnology to modify and enhance plant systems. Ongoing work toward genetically deploying these assemblies as versatile nanoreactors in plants will be highlighted, along with efforts to introduce BMC-based structures directly into plant tissues.

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