Vol. 21 / No. 4 / April/May 2022

ASBMB TODAY

THE MEMBER MAGAZINE OF THE AMERICAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY

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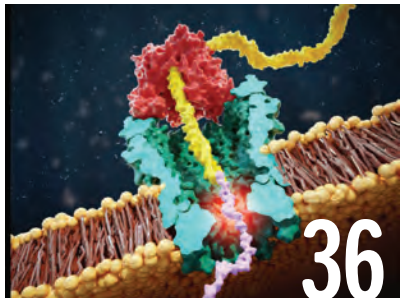

PERSPECTIVES

ASBMBTODAY
THE MEMBER MAGAZINE OF THE AMERICAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY

www.asbmb.org/asbmbtoday
PRINT ISSN 2372-0409

Good fellows

By Comfort Dorn

As a magazine, we at ASBMB Today put our work in print and online for all the world to see. So, when we get something wrong, someone tells us — usually fast. We do our best to get everything right, and we're quick to correct our mistakes. Sometimes we even learn something in the process.

That was the case after we posted the names of the 2022 American Society for Biochemistry and Molecular Biology fellows on our website in early February. The introduction referred to the fellows as "our most distinguished members," and that elicited a gentle — and educational — correction from Judith Bond, who developed the ASBMB fellows program with the society's Membership Committee, chaired by Ed Eisenstein.

"Ed and I were very careful to say 'designation as a fellow recognizes outstanding commitment to the ASBMB through participation in the Society in addition to (other) accomplishments,'" Bond wrote. "Our 'most distinguished members' would include Nobel laureates and other highly respected biochemists and molecular biologists, but if they have not participated in the Society in a meaningful way (through committees, leadership, organization of activities), they were not chosen as a fellow."

This made me stop and think. With all the logistical challenges of collecting biographies and photos for the magazine and the website, I'm not sure I'd ever considered the criteria for being a fellow. I think it blurred in my mind with being an award winner. But this focus on commitment to the society makes a wonderful kind of sense. To be a fellow, a member must be generous with time and talent — not just someone whose CV includes pages of individual BMB achievements.

And reading the essays in this issue written by four members of the inaugural 2021 class of fellows, I was struck by the joy in their generosity. Fred Guengerich, Adele Wolfson, Dan Raben and Kelly-Anne Rye have given countless hours to the ASBMB and its journals as committee members and editors and much more. Yet they make it seem like they're doing the receiving rather than the giving. They stress the rewards of spending time with other members of the society and of seeing all it can do (with their help, but they mostly don't say that).

This is probably the strongest argument we can make for getting involved — actively involved — with the ASBMB. Sure, you'll need to give some time and talent. But think of all the good you get in return.

Comfort Dorn (cdorn@asbmb.org) is the managing editor of ASBMB Today. Follow her on Twitter: @cdorn56.

CORRECTION

Five Questions with Heino Heyman in our February issue included some incorrect text. We have republished the article on page 64 of this issue.

Lieberman to chair Georgia Tech endowment fund

Raquel Lieberman, a professor in the school of chemistry and biochemistry at Georgia Tech, has been named the inaugural chair of the Kelly Sepcic Pfeil faculty endowment fund, an effort funded by alumni to increase the number of women faculty at the Georgia Institute of Technology.


LIEBERMAN

In the lab, Lieberman's research focuses on biochemical and structural details of protein misfolding. She is particularly interested in an extracellular protein that maintains pressure in the eye and, when mutated, can cause glaucoma. She also studies intramembrane proteases linked to Alzheimer's disease and the connection between Parkinson's disease and the lysosomal hydrolase acid-beta-glucosidase.

Lieberman earned her Ph.D. at Northwestern University and was a postdoctoral fellow at Harvard University's Brigham and Women's Hospital. She recently received the Gretzinger Moving Forward Award in recognition of her work to diversify tenure track faculty, create a family-friendly work environment and provide a supportive environment for early-career faculty.

Sepcic Pfeil earned her master's degree and Ph.D. in chemistry at Georgia Tech before launching a career in food and flavor science that culminated in vice president positions at Frito-Lay North America and PepsiCo before she founded a consulting company. A Georgia Tech press release about the endowment fund quoted her as saying, "Students need role models. We are building a pipeline for women in STEM, and that pipeline starts in academia."

Caltech professorship for Clemons

Bil Clemons, a professor of biochemistry at the California Institute of Technology, was selected as a named professor in 2021. He is now the Arthur and Marian Hanisch Memorial Professor of Biochemistry.

Clemons, a structural biochemist, studies membrane protein structure and biogenesis primarily using biophysical methods such as X-ray crystallography and electron microscopy. A major biological focus of his lab is the study of the biological machinery responsible for the targeting and insertion of tail-anchored membrane proteins into the endoplasmic reticulum membrane, resolving structures of many of the proteins in complex and in different conformational states. The lab also has a broader interest in membrane protein evolution and expression. For the latter, the lab developed computational tools for predicting the likelihood that a heterologous protein will express.


CLEMONS

Clemons is also interested in glycobiology with a focus on biochemical and structural studies of enzymes that catalyze the transfer of sugars to and from lipid carriers. Work in his lab has supported the development of small molecule inhibitors that might lead to useful antibiotic compounds. They also have clarified the mechanism for phage-expressed peptides that inhibit peptidoglycan biogenesis.

Clemons earned his Ph.D. in 2000 from the University of Utah while also spending time at the Laboratory of Molecular Biology in Cambridge, U.K., studying the structure of the bacterial ribosome. He conducted postdoctoral research at Harvard Medical School studying the structure of the universal protein translocation channel. He joined the faculty at Caltech in 2005. He recently was elected as an ASBMB fellow, and he chairs Caltech's president's diversity council.

Arthur Hanisch, who died in 1966, founded a pharmaceutical company in 1941 after acquiring a liquid vitamin product developed by a Caltech professor, according to a news obituary. After he underwent an aortic transplant in 1954, he and Michael DeBakey developed a synthetic knitted artery, which was distributed around the word through a foundation Hanisch formed to support heart research. He was a member of the Heart Advisory Council of the National Institutes of Health and served on a President's Commission on Heart Disease, Cancer and Stroke.

Dean elected to Virginia Academy

Dennis Dean, a distinguished professor of biochemistry and founding director of the Fralin Life Sciences Institute at Virginia Tech, has been elected a member of the Virginia Academy of Science, Engineering and Medicine.


DEAN

A member of the Virginia Tech faculty since 1985, Dean earned his Ph.D. from Purdue University

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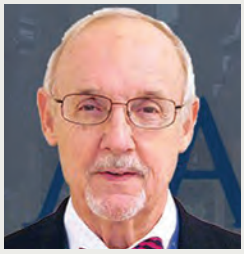
Nineteen of this year's AAAS fellows are ASBMB members

The American Association for the Advancement of Science recently announced its class of 2021 fellows. AAAS fellows are members of an honorific group elected by the AAAS Council after a lengthy review process.

Penny Beuning, a professor and chair of the department of chemistry and chemical biology at Northeastern University, was recognized for discoveries in the enzymology of DNA translesion synthesis, studying polymerases that can bypass damaged DNA, and for advancing toxicology research through studies of DNA adducts.

Charles Burant, a physician–scientist at the University of Michigan, was recognized for research combining genomic, transcriptomic, proteomic and metabolomic analysis of patient samples with behavioral and clinical studies to understand how insulin resistance, diabetes and obesity develop. He also directs a regional core facility for metabolomics studies and a clinic for weight loss studies.



James Chambers, a professor at the University of Texas at San Antonio and a member of the South Texas Center for Emerging Infectious Diseases, was recognized for his teaching and training and for his contributions to understanding the biology of the pathogenic bacteria Francisella tularensis, which causes tularemia. His lab also has worked on developing biosensors to detect F. tularensis and other emerging pathogens.

Brandt Eichman, a professor at Vanderbilt University, was recognized for his work in structural cell biology including research into how cells respond to and repair DNA damage, which has focused on DNA glycosylases that remove alkyl groups from DNA and on DNA translocases that help DNA replication machinery restart replication when it has been stalled by DNA damage.

Constance Jeffery, an associate professor at the University of Illinois Chicago, was recognized for outstanding teaching and mentoring and for her research, which uses biophysical and bioinformatic techniques to understand so-called moonlighting proteins that carry out multiple, unrelated biochemical activities. For example, one human protein in a database she runs is an enzyme in the glycolysis pathway under some cellular conditions and at other times binds to RNA to regulate translation.

Hui-Kuan Lin, a professor at Wake Forest School of Medicine, was recognized for his contributions to understanding oncogenic signaling, especially the PI3K/Akt signaling pathway. His lab discovered that ubiquitination of Akt can be oncogenic, driving kinase activation, and has worked to develop small-molecule inhibitors that may have uses as cancer therapeutics.

Aimin Liu, a professor and distinguished chair in biochemistry at the University of Texas at San Antonio, was recognized for his contributions to structural and mechanistic enzymology. His lab studies amino acid metabolism, particularly tryptophan; metalloprotein cofactor biogenesis; and metalloprotein redox reactions.

Eva Nogales, a distinguished professor at the University of California, Berkeley, a senior faculty scientist at the Lawrence Berkeley National Laboratory, a Howard Hughes Medical Institute investigator and a leader in the cryo-electron microscopy field, was recognized for her contributions to understanding the molecular function of numerous protein complexes, including microtubules and transcription initiation, polycomb and CRISPR complexes.

Melanie Ohi, a professor at the University of Michigan, was recognized for her use of structural biology techniques to understand the secretion systems that pathogenic bacteria use to puncture host cell membranes and translocate toxins into the host cell.

Kim Orth, a professor at the University of Texas Southwestern Medical Center, was recognized for her contributions to understanding how pathogenic bacteria hijack host cell signaling, ultimately offering insight into the regulation of eukaryotic signaling pathways.

Kevin Raney, a professor and chair of the department of biochemistry and molecular biology at the University of Arkansas for Medical Sciences, is recognized for studies of molecular motors on DNA and for contributions to understanding of how G-quadruplex DNA structures respond to oxidative stress.

Rajinder S. Ranu, a professor emeritus of molecular biology at Colorado State University, was recognized for his contributions to initiation of eukaryotic protein synthesis and identification of several initiation factors and for working to increase diversity in the student and faculty population at Colorado State University. He also isolated numerous genes involved in flower senescence from ornamental plants, such as roses, that might have useful biotechnology applications.

Stephen Safe, a professor at Texas A&M University, was recognized for his contributions to research that promotes safe use of chemicals in industry and for his work on safer and more effective pharmaceuticals. His lab works on mechanism-based drug development for cancer, targeting nuclear receptors and other transcription factors.

Tricia Serio, a professor and dean of the college of natural sciences at the University of Massachusetts Amherst, was recognized for contributions to protein dynamics — her lab studies cellular responses to protein misfolding, including in prion disease — and to diversity, equity and inclusion in STEM.

Nineteen of this year's AAAS fellows are ASBMB members CONTINUED

Scott Showalter, a professor at Pennsylvania State University, was recognized for developing biophysical approaches to understand intrinsically disordered or partially disordered proteins involved in gene regulation and microRNAs. His lab has found ways to use nuclear magnetic resonance spectroscopy to shed light on the structures of these flexible molecules.

David Sibley, a senior investigator at the National Institute for Neurological Disorders and Stroke, was recognized for his contributions to neuropharmacology. His research focuses on the role of G protein–coupled dopamine receptors in neuronal signaling and works to elucidate their structures, effectors and modulators. His team has identified highly selective ligands and allosteric compounds that eventually may serve as drugs for neurological or psychiatric disorders.

John Voorhees, a distinguished professor at the University of Michigan Medical School, was recognized for his contributions in skin biology, including research on psoriasis, skin aging and responses to ultraviolet radiation. The AAAS also noted his "exemplary and sustained record of leadership in dermatology"; he has served as president of five dermatology societies and volunteered in various capacities for others.

Michael Weiss, a professor and chair of the department of biochemistry and molecular biology and precision health initiative chair in chemical biology at the Indiana University School of Medicine, was recognized for contributions to molecular endocrinology, studying how conformational changes in insulin affect its signaling and how transcription controls gonad development.

Ann West, a professor, research center director and associate vice president for research and partnerships at the University of Oklahoma, was recognized both for her research, which focuses on two-component signal transduction systems in bacteria and histidine–aspartate phosphorelays in yeast, and for her contributions to the development of structural biology in Oklahoma; since 2012 she has been the principal investigator of a center of biomedical research excellence in structural biology.

CONTINUED FROM PAGE 3

College of Science in 1979 and was a predoctoral and postdoctoral fellow at the National Institutes of Health. At Virginia Tech, he has served as executive director of the Virginia Bioinformatics Institute and interim vice president for research and innovation.

Research in Dean's labs focuses on the mechanism for biological nitrogen fixation and the biological pathways for assembly of simple and complex metalloclusters. His group developed a combined biochemical–genetic approach to identify where substrates interact with nitrogenase, the biological catalyst of nitrogen fixation.

Dean is a 2022 ASBMB fellow; has served on the editorial board for the Journal of Biological Chemistry and as a member of the ASBMB Publications Committee. He is a fellow of the American Academy of Microbiology and the American Association for the Advancement of Science.

He is one of five people who

were elected to membership in the academy in fall 2021.

McCarthy takes interim chair

Pumtiwitt McCarthy, an associate professor at Morgan State University, has been appointed interim chair of the university's chemistry department.


MCCARTHY

McCarthy, a glycobiologist, studies polysaccharide synthesis in bacterial capsules. She recently landed a grant with colleague James Wachira to study substrate selection by capsule polymerases, and she also is interested in developing vaccines that target the meningitis-causing bacteria Neisseria meningitidis.

McCarthy earned her Ph.D. in biochemistry in 2009 at the University of Delaware, studying oxidative protein folding. She worked as a postdoctoral fellow at the Food and Drug Administration Laboratory of Bacterial Polysaccharides before joining Morgan State in 2013.

Permanent post for Kadakia

Madhavi Kadakia, who has been serving as interim vice provost for research and innovation at Wright State University since July 2021, has been appointed to the position permanently. She will be responsible for strategic partnerships, such as one with the nearby Wright–Patterson Air Force Base.

Wright State provides interns and jobseekers to Wright–Patterson, and the university frequently receives research grants from the federal government.


KADAKIA

Kadakia, previously chair of the department of biochemistry and molecular biology, studies the tumor suppressor protein p63. Her research has focused on an N-terminally truncated protein isoform that is expressed most highly in epithelial tissue. Kadakia's group has described microRNAs and coding transcripts that p63 affects.

Kadakia earned a Ph.D. in infectious disease and microbiology from the University of Pittsburgh. She has been on the faculty at Wright State since 2002 and was promoted to full professor in 2013.

Upcoming ASBMB events and deadlines

APRIL

2–5	**ASBMB annual meeting**
19	ESCRT biology regular registration deadline
22	Ruth Kirschstein Diversity in Science Award deadline
26	O-GlcNAc conference abstract deadline
27	Lipid Research Division monthly webinar

MAY

6	Evolution and core processes in gene expression oral abstract submission deadline
9	O-GlcNAc conference early registration deadline
16	Mass spectrometry in the health and life sciences abstract submission deadline
17–20	**ESCRT biology conference**
25	Evolution and core processes in gene expression early registration deadline
25	Evolution and core processes in gene expression poster abstract submission deadline

JUNE

1	Marion B. Sewer Scholarship deadline
6	O-GlcNAc conference regular registration deadline
20	Evolution and core processes in gene expression regular registration deadline

Tsuneo Omura

By F. Peter Guengerich, Bettie Sue S. Masters & Ken-Ichirou Morohashi

The biochemical community lost one of its pioneers with the death of Tsuneo Omura on Jan. 29. Omura discovered cytochrome P450, and his 1964 Journal of Biological Chemistry paper on this work has been cited at least 12,700 times. He was made an honorary member of the American Society for Biochemistry and Molecular Biology in 1990.

Born July 29, 1930, in Shizuoka Prefecture, Japan, Omura graduated from the University of Tokyo with a B.S. in chemistry and then worked as an instructor and lecturer at Shizuoka University. In1960 he joined Ryo Sato's laboratory at the Osaka University Institute for Protein Research as an associate professor. In 1961 he was awarded a doctorate in biochemistry from the University of Tokyo based on his work at Shizuoka University.

During the early 1960s, Omura and Sato published three major papers about the discovery of P450 (including the highly cited one in JBC), plus seven others in related areas. From 1964 to 1966, Omura was a visiting scientist at the Johnson Foundation of the University of Pennsylvania (with Ronald W. Estabrook) and then Rockefeller University (with Philip Siekevitz). He returned to Osaka and then moved in 1970 to Kyushu University as a professor of biology and molecular biology, a position he held until he assumed emeritus status in 1994. From 1995 to 1997 he was a visiting professor of biochemistry at Vanderbilt University (with Michael R. Waterman and others).

Omura's contributions to the field of P450 research included studies on the regulation of P450s and, in particular, trafficking of P450s in the endoplasmic reticulum and mitochondria. His studies with mitochondrial P450s, specifically the cholesterol side chain cleavage enzyme, led to an enhanced understanding of the regulation of these P450s by proteins such as Ad4BP/SF-1, a steroidogenic transcription factor.

Omura was a leading figure in biochemistry in Japan and around the world. Along with honorary ASBMB membership, he received the first R.T. Williams Award from the International Society for the Study of Xenobiotics in 2001, and he was honored at the 1994 International Microsomes and Drug Oxidation, or MDO, meeting. He continued to participate in meetings many years after his retirement and presented plenary lectures at the 2014 and 2018 MDO meeting. He received tributes at a special 2012 meeting in Fukuoka commemorating 50 years since his discovery of cytochrome P450.

Omura will be remembered as a humble and thoughtful man. His laboratory was open to visitors from abroad; visitors recall his joy in driving his guests all around Kyushu with stops at pottery-making artisans and notable sites including the active volcano Mt. Aso.

Students were attracted to Omura's warm personality and erudition. During his 24 years at Kyushu University, 112 undergraduate students and 42 graduate students joined his laboratory, and 33 of them earned Ph.D.s under his thoughtful and persistent guidance. Many went on to productive careers. He was always eager to help young scientists, and in his laboratory, he created an atmosphere of camaraderie and mutual respect. He was a sensei in every sense of this Japanese title of honor.

Omura was preceded in death by his wife, Yone, on Dec. 9, 2000, and is survived by their three children.

(Masahiko Negishi and Hiroshi Yamazaki contributed to this article.)

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Bettie Sue S. Masters (bettie.sue.masters@duke.edu) is an adjunct professor of biochemistry at the Duke University Medical Center and a former ASBMB president.

Ken-Ichirou Morohashi (morohashi.ken-ichirou.874@m.kyushu-u.ac.jp) is a distinguished professor of molecular biology at Kyusha University.

Carl Bernofsky

Carl Bernofsky, a former research biochemist at Tulane University and a member of the American Society for Biochemistry and Molecular Biology for 50 years, died Feb. 12, 2021, at his home in Shreveport, Louisiana, after battling lymphoma for more than 25 years. He was 87.

Born Nov. 22, 1933, in Brooklyn, New York, Bernofsky attended Brooklyn College and the University of Chicago and then worked briefly as a research assistant at the American Meat Institute Foundation before earning a Ph.D. in biochemistry at the University of Kansas in 1963. After a postdoctoral fellowship at Case Western Reserve University, he joined the faculty of the Mayo Medical School and did research at the Mayo Clinic for about eight years.

In 1975, Bernofsky moved with his wife and two daughters to New Orleans, where he took a faculty position at the Tulane University School of Medicine. There, he taught energy transduction processes for 16 years. His research interests included mechanisms of inflammatory tissue damage, spin trapping of biologically important free radicals, tumor-specific nucleases, and pyridine nucleotide chemistry and metabolism.

After he was dismissed from Tulane in 1995, Bernofsky filed a series of lawsuits against the school and others, alleging discrimination — he was Jewish — and other offenses. He detailed his legal actions on a website, tulanelink.com, and became an advocate for judicial reforms. Bernofsky's home in New Orleans was destroyed by flood waters during Hurricane Katrina. He and his wife then moved to Shreveport.

Bernofsky was an author on some 60 scientific articles. In 1998, he patented a human monocyte leukemia cell line. In addition to the ASBMB, he was a member of the American Association for the Advancement of Science, the American Chemical Society and other professional organizations. Later in his life, he became an advocate for alternative energy, specifically for replacing coal with plant-based tallowfuel.

Bernofsky is survived by his wife, Shirley Goodman Bernofsky; his daughters, Susan and Lauren Bernofsky; and his grandchildren, Nicholas and Julia Irmscher.

Maurice Bessman

Maurice Jules Bessman, professor emeritus and longtime researcher at Johns Hopkins University, died Nov. 12 from complications of pneumonia at his home in Baltimore. He was 93.

Known by peers as "Moishe" and by students as "Boss," Bessman spent his life working in biochemical enzymology.

Born in Newark, New Jersey, Bessman was elected valedictorian of Weequahic High School in 1946. He earned a bachelor's degree from Harvard University in 1949 followed by graduate research at Tufts University, where he earned a master's degree and a doctorate in 1952 and 1955, respectively.

Described by many as a gifted biochemist, Bessman was all business when it came to his work on Nudix hydrolase enzymes. His lab used bacteria to express many members of this broad enzyme family to understand better their biological role and function. His work specifically identified a core common amino acid sequence that is expressed by these proteins, allowing a broader understanding of these enzymes in their ability to cleave nucleoside diphosphates conjugated to any other moiety (x). Nudix enzymes are found in all types of organisms, acting as surveillance proteins; Bessman's work made him a pioneer in this field of study. Many of his findings were published in journals such as Nature and are cited extensively.

Bessman worked to establish a strong research program and support the growth of younger scientists, according to obituaries in the Hopkins Hub and the Baltimore Sun. Vincent Hilser, chair of the biology department, considered him "a great person." Myron Goodman, a former student, recalled that Bessman's tough love provided a turning point during his postdoc that launched his career.

Those close to him knew Bessman for his stories and sense of humor. He spent summers with his family on Cape Cod, fishing, clamming and enjoying other outdoor activities. He was an avid fan of the Blue Jays lacrosse team at Hopkins — so much so that an admiring alumnus established a Maurice Bessman lacrosse scholarship in 2016.

Bessman is survived by his wife, Zita; son, Edward; daughters Debra and Cindee; sister Marcelle; nine grandchildren; and six great-grandchildren. Another daughter, Sheri, died in 2009.

— Connor O'Hara

Sadaaki Iwanaga

Sadaaki Iwanaga, an honorary member of the American Society for Biochemistry and Molecular Biology since 1989 and a pioneer in the study of blood clotting, died June 21, 2020, the ASBMB learned recently.

Born in Tokyo on Jan. 5, 1933, Iwanaga was a high school baseball player before turning his attention to science. He earned a Ph.D. in pharmaceutical sciences in 1960.

In the 1960s and '70s, Iwanaga held positions at Kyoto and Osaka universities and the Institute for Protein Research in Japan and spent several years with Birger Blombäck at the Karolinska Institute studying the chemical structure of fibrinogen, a protein that helps blood clots to form. He went to Kyushu University as a professor of biology in 1978 and stayed until his retirement in 1996.

Blood clotting and coagulation are relevant to human health, and this focus allowed Iwanaga to explore exotic biofluids such as snake venom and horseshoe crab hemolymph.

In horseshoe crabs, hemolymph coagulates in response to bacterial lipopolysaccharides or foreign polysaccharides and triggers a defensive response. (This response has been used historically to test the sterility of pharmaceutical products.) Iwanaga's lab investigated the protease cascade that kicks off hemolymph coagulation: One protease cleaves another from its inactive to active form, and that protease then activates a third enzyme. The cascade includes four proteases and a clotting protein. The lab also investigated protease inhibitors called serpins, which prevent runaway coagulation, along with LPS-binding proteins and antimicrobial peptides.

Iwanaga also studied clotting in human blood, which, as in horseshoe crabs, is activated through a cascading system of proteases. He developed protease substrates that fluoresce when cleaved, which can be used to monitor protease activity. He studied kallikrein, a protease that affects blood pressure by cleaving and activating peptide hormones called kinins. He also studied snake venom, interested in how its proteins prevent clotting.

"He was a hard-working scientist," several of Iwanaga's mentees wrote in a memorial article in the Journal of Thrombosis and Haemostasis. "He made it a custom to come to work before everyone else and go home after everyone else, even over the weekends and during holidays. He was a sharp observer of the field and this helped him to be ahead of the curve."

Iwanaga and his wife, Mihiko, loved to travel. He was also a fan of sumo wrestling, according to the article, and would bring visiting scientists to the Kyushu Grand Sumo Tournament "where Mihiko would book large box seats for the group."

Pivoting to transform a pandemic classroom

By Nicole Lynn

Shana Stoddard grew up no stranger to science. The daughter of a physician and a former dietician (now a lawyer), she heard frequent discussions of chemistry and biology around the house and at the dinner table.

"We (once) asked our dad if food goes down a person's throat because of muscles or gravity," she said. "He took my youngest sister, turned her upside down, and we gave her some food, asking, 'Did it go down? Then it can't be gravity!'"

Stoddard's passion for scientific research was ignited before her senior year of high school. During a summer research fellowship at the National Institute of Diabetes and Digestive and Kidney Diseases, she got to work side-by-side with leading researchers and physicians, eventually presenting her research to peers and scientists in Washington.

"I loved talking about science," Stoddard said. "When they flew me out to D.C. to do the research presentation … it was like, wow, I could actually do this research thing."

In 2013, Stoddard received her Ph.D. in chemistry from the University of Mississippi, and after a short postdoc with St. Jude Children's Research Hospital, she joined Rhodes College in 2015 as a William Randolph Hearst teaching fellow. Two years later, she became an assistant professor in the chemistry department.

SHANA STODDARD/ RHODES COLLEGE

Shana Stoddard in the classroom, teaching biochemistry and structural biology to undergraduates at Rhodes College.

Research in Stoddard's lab is diverse due to her numerous passions, ranging from protein structure modeling and analysis to developing novel therapies for autoimmune disorders such as primary membranous nephritis, or PMN, an incurable, kidney-specific condition that can lead to end-stage renal disease. The PMN research is of personal importance; Stoddard's mother has this disease.

SHANA STODDARD/ RHODES COLLEGE

In the lab, Shana Stoddard and undergraduate student Darius Swift work on an experiment together.

"Watching her struggle, and wanting to fix it, became the driver of my overall research," she said. "It has taken my research to different directions — learning more about the kidneys and trying to find new ways to approach autoimmune disease treatment.

Stoddard's lab combines engineering, biochemistry and computational methods to profile the structure–function relationships of proteins in PMN with the goal of developing immunotherapeutics, she said. "We're trying to find a way to trick the immune system

into thinking the disease doesn't exist, rather than trying to induce tolerance."

The lab was able to predict where the immune system targets the PMN protein THSD7a using computational homology modeling. This project led to their focus on the thrombospondin superfamily of proteins, of which THSD7a is a member.

When the pandemic threw up roadblocks to her work starting in March 2020, Stoddard used her knowledge of bioinformatics and molecular biology to transform her courses and take her students through the process of drug design and molecular modeling.

"I didn't want my students to have to sit and watch videos of lab work," she said. "I decided we'd do bioinformatics (using) the available data on COVID-19 receptors."

Her students' work on the SARS-Cov-2 virus resulted in publication of a paper in the journal Viruses. After the success of her virtual teaching design, Stoddard began to incorporate bioinformatics research into her biochemistry and advanced biochemistry courses, giving students an opportunity to see how the science in their books can and does translate to the real world. This has resulted in students designing peptide-based antivirals for COVID-19 infections and having their work published in the journal Biophysica.

A champion of diversity and inclusion, Stoddard started an unofficial STEM mentoring program in 2017 at Rhodes College that focuses on students from underprivileged and diverse backgrounds. This program has grown significantly; starting with one student, it now has served 125 students. In 2021, Rhodes officially translated the program from an individual faculty initiative to an institutionally supported program called the STEM Cohort Mentoring Program.

Stoddard has created a structured method to train mentees, including the concept of a mentoring roadmap. At Rhodes she is facilitating faculty development around mentoring as the inaugural director for student mentoring; in some of her work, she and her colleagues or students work together to promote healthy lab culture and learning.

SHANA STODDARD

Shana Stoddard and members of her research team gather on the steps of their building at Rhodes College.

"I know that my purpose is to draw out people's potential," she said. "In every moment and in every interaction, that is what I am trying to do."

Stoddard received the 2021 Council on Undergraduate Research Health Sciences Division Mentor Award, which recognizes transformative mentoring by faculty, as the early-career awardee. She uses mentoring in all aspects of her life, including research, teaching and outreach.

"Mentoring is a mindset," she said. "How can we choose to pour into people so they can be the best they can be. I'm not a 'meet you in the middle' because that implies an even playing field on both sides — I will meet you where you are."

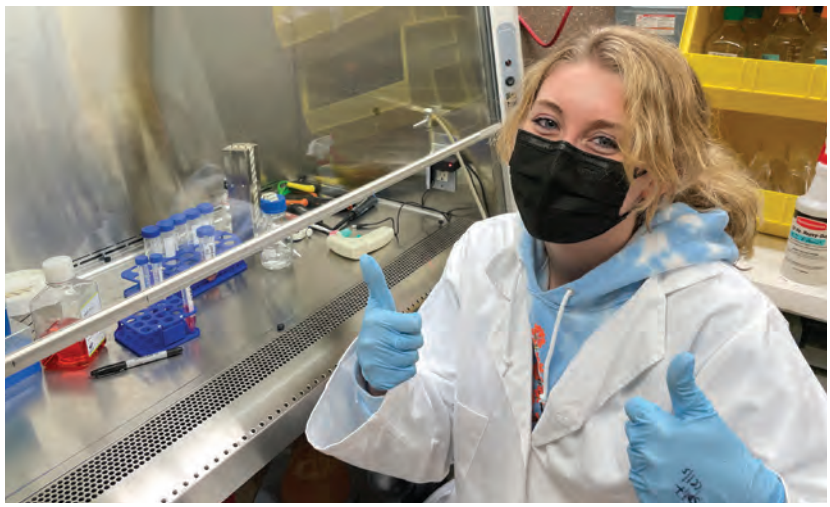
SHANA STODDARD

Stoddard, at left, celebrates with the first graduates of the STEM Cohort Mentoring Program she spearheaded in 2017.

Nicole Lynn (nalynn@ucla.edu) is a Ph.D. candidate at UCLA and a volunteer writer for ASBMB Today.

Chapter member aims for the moon, lands on astrobiology

By Heather Masson–Forsythe



LOGAN STODDARD

Hailey Kerns is a senior biomedical sciences major at Saint Leo University, an ASBMB Student Chapter member, and recipient of a 2021 ASBMB Undergraduate Research Award.

Hailey Kerns had little formal exposure to the sciences prior to beginning her undergraduate studies at Saint Leo University, but, she said, "It's always been science for me. I made my parents get me all the books and encyclopedias on animals."

She maintained a love of nature and science throughout her childhood, she said; she and her dad "would always talk about life beyond … our planet."

These conversations led to her interest in astrobiology. Now a senior majoring in biomedical sciences and a member of the American Society for Biochemistry and Molecular Biology Student Chapter at Saint Leo and president of their TriBeta Biological Honor Society, Kerns has applied for the University of Florida's microbiology and cell sciences Ph.D. program. Her ultimate goal is to study astrobiology and work with NASA or another space company on the search for extraterrestrial life.

Since identifying her interests early on, Kerns has been consistent in her commitment to astrobiology. In high school she started looking at NASA's career path suggestions page and has used it as a guide throughout her undergraduate career, which includes numerous research experiences, publications, presentations, awards and community engagement initiatives.

As a first-year undergrad, Kerns reached out to Jamie Foster, a professor in the Space Life Science Lab at the University of Florida, and has stayed in contact. This networking led to an internship at UF funded through the Florida Space Grant Consortium. Working with microbiologist Kelly Rice, Kerns studied the effects of simulated microgravity on the physiology of the bacterium Streptococcus mutans, which causes tooth decay.

Kerns' favorite research experience has been taking part in the SEA-PHAGES program headed by Iain Duffy at Saint Leo. She joined the program in her first year and since has contributed to the discovery and isolation of more than 23 bacteriophages and the publication of their complete annotated genomes in GenBank. This was her introduction to research.

"Being able to see a visual effect from something so tiny, realizing there's so much we don't see or understand yet and so much for us to learn, that's what excited me."

Hailey received an ASBMB Undergraduate Research Award to work with biomedical researcher Sergiy Borysov at Saint Leo in summer 2021. Her lab mates were scheduled to present this research on "Cytotoxic Effect of Synthetic Peptides on Normal and Cancerous Cells" at the recent 2022 ASBMB annual meeting in Philadelphia.

From parents to teachers, professors and coworkers, a long list of people make up Kerns' support network. "I send my gratitude to every person I've come across in my academic career," she said, "as each of them has contributed to shaping me into the person and scientist I am today."

Heather Masson–Forsythe (heather.forsythe1@gmail.com) completed her Ph.D. in biochemistry and biophysics at Oregon State University. She is passionate about communicating science through writing and dance. Follow her on Twitter and TikTok: @heycurlytop.

ASBMB weighs in on PREVENT Pandemics Act

The public affairs team in February submitted to a U.S. Senate committee three recommendations for legislation aiming to improve U.S. preparedness. The society recommended (1) establishing the Advanced Research Projects Agency for Health as an autonomous agency, (2) allocating funds to ensure that institutions are adequately preparing those earning STEM doctorates for diverse career paths and providing experiential learning, and (3) investing in research infrastructure at federal facilities, minority-serving institutions and emerging research institutions. Read the full comments at asbmb.org/advocacy/letters.

Send us your news!

Have you recently been promoted or honored? Do you have good news to share with your fellow ASBMB members? Email it to us at asbmbtoday@asbmb.org and include a photo!

New data integrity team members

The ASBMB Publications Committee welcomed two new data integrity team members earlier this year.

Elena Gaidamakova became the society's data integrity manager in January. She has a Ph.D. in biology from the Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences. She spent two decades as a researcher at the Uniformed Services University of the Health Sciences and before that was at the National Institutes of Health.

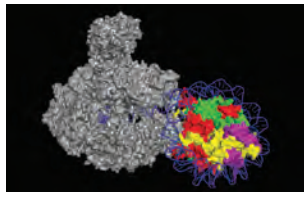
Jessica Goldsmith is an image analyst who joined the society in November. She earned her bachelor's in graphic design from the University of Maryland Baltimore County in 2007. Since then, she has worked for multiple government agencies, including the U.S. Department of Homeland Security and the Department of Transportation. She is an award-winning photographer.

New meetings coordinator

The ASBMB Meetings Committee welcomed **Megan Reder** to the team earlier this year. Reder has a hospitality management degree from the University of Alabama with a concentration in meeting and event marketing. She is assisting with the ASBMB annual meeting and the many conferences and webinars the society offers. You can reach her at mreder@asbmb.org.

July 14: Oral abstracts due for transcriptional regulation meeting

This in-person meeting will be held Sept. 29–Oct. 2 in Snowbird, Utah. Sessions will cover recent advances and new technologies in RNA polymerase II regulation, including the contributions of noncoding RNAs, enhancers and promoters, chromatin structure and post-translational modifications, molecular condensates, and other factors that regulate gene expression. The oral presentation abstract deadline is July 14. The poster abstract deadline is Aug. 18. Learn more at asbmb.org/meetings-events/transcriptional-regulation.



ASBMB responds to NIH's strategic plan for diversity

The public affairs team submitted a letter in February to the National Institutes of Health office for scientific workforce diversity with recommendations to improve the agency's draft strategic plan for fiscal years 2022–2026. The recommendations focused on mitigating gender harassment in the NIH intramural program, supporting minority-serving institutions, and supporting LGBTQAI+ scientists and scientists with disabilities. Read the full comments at asbmb.org/advocacy/letters.

May 25: Poster abstracts due for gene expression meeting

This in-person meeting will be held July 21–24 in Kansas City, Missouri. It will showcase the most recent insights into the cis-regulatory code; how cis-regulatory information is read out by transcription factors, signaling pathways and other proteins; how cellular diversity is created during development; and how we can study this problem using cutting-edge genomics technology and computational methods. May 25 is the poster abstract deadline and the registration deadline. Learn more at asbmb.org/meetings-events/gene-expression-2022.

ASBMB statement on Eric Lander's resignation

The public affairs team wrote a statement in response to Eric Lander's resignation from the White House Office of Science and Technology Policy. Lander was the president's top science adviser and resigned Feb. 7 after acknowledging that he had demeaned and disrespected his colleagues at the OSTP. The ASBMB urged the Biden administration to fill the OSTP director spot swiftly and ensure that this key Cabinet-level position is filled with a candidate who is diverse and reflective of the scientific community as a whole. Read the full statement at asbmb.org/advocacy/position-statements.

New public affairs staff members

The American Society for Biochemistry and Molecular Biology Public Affairs Advisory Committee welcomed two new science policy managers earlier this year.

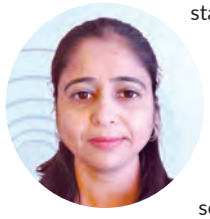
Raechel McKinley recently earned her Ph.D. in anatomy at Howard University and was an advocate for students and science policy at her university and at the Union of Concerned Scientists.

Mallory Smith earned her Ph.D. in biochemistry and molecular biology from the University of Kansas Medical Center and did a postdoc at the National Institutes of Health while simultaneously leading science advocacy efforts at the local, state and national levels. She also is vice-chair of the National Postdoctoral Association's Advocacy Committee.

New finance team members

The ASBMB accounting department has two new staffers.

Brandon Wieland became the ASBMB's finance director in October. Wieland is a certified public accountant and financial planner who spent the first 15 years of his career working in the public accounting industry, primarily with nonprofits, for which he conducted financial statement audits and regulatory and compliance tax filings and served as a consultant for accounting systems and operations. Wieland earned his B.A. in accounting from the University of Maryland and is a member of the American Institute of Certified Public Accountants and the Maryland Association of Certified Public Accountants.



Rajni Gupta is a new senior accountant who started in November. She earned her bachelor's degree in accounting at the University of Maryland in 2008. In the years since, she has worked at United States Pharmacopeia, Centrus Energy and a financial services company.

Take over the JLR Twitter account for a day

Would you like to take over the Journal of Lipid Research Twitter feed for a day? If you are a graduate student, postdoc or early-career investigator interested in hosting a #LipidTakeover, fill out the JLR #LipidTakeover application at https://bit.ly/JLRLipidTakeover.

Save the date: Meeting on epigenetic regulation and genome stability

Most meetings on epigenetics and chromatin focus on transcription, while most meetings on genome integrity include little attention to epigenetics and chromatin. This conference — to be held Sept. 28–Oct. 2 in Seattle — will bridge this gap to link researchers who are interested in epigenetic regulations and chromatin with those who are interested in genome integrity. Stay tuned for abstract and registration deadlines at asbmb.org/meetings-events/epigenetic-regulation-and-genome-stability.

Connect with colleagues at an ASBMB meeting

The ASBMB organizes virtual and in-person events that cover scientific research, educational best practices, the funding environment and more.

Upcoming ASBMB conferences

O-GlcNAc regulation of cellular physiology and pathophysiology
July 7–10, 2022 | Athens, Ga.

Evolution and core processes in gene expression
July 21–24, 2022 | Kansas City, Mo.

Mass spectrometry in the health and life sciences
Aug. 14–18, 2022 | Cambridge, Mass.

The interplay between epigenetic regulation and genome stability
Sept. 28–Oct. 2, 2022 | Seattle, Wash.

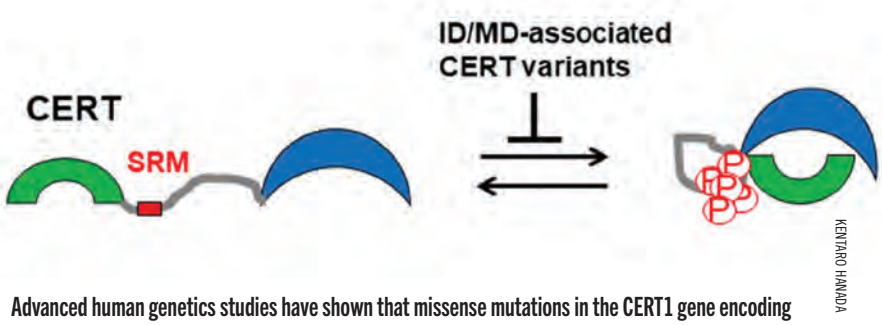
Transcriptional regulation: Chromatin and RNA polymerase II
Sept. 29–Oct. 2, 2022 | Snowbird, Utah

Explore all upcoming events at asbmb.org/meetings-events.

ASBMB
American Society for Biochemistry and Molecular Biology

Dysregulation of a lipid transfer protein linked to brain disorders

By Kentaro Hanada



KENTARO HANADA

Advanced human genetics studies have shown that missense mutations in the CERT1 gene encoding the ceramide transport protein CERT are associated with certain intellectual disabilities and mental development disorders. Recent studies in the Hanada lab showed that ID/MD-associated CERT variants are defective in serine-repeat motif phosphorylation-dependent repression. In this diagram, for simplicity, CERT is illustrated as a monomer, although it forms oligomers in cells.

Advanced studies of human genetics are a big wave in the medical sciences. Collaborative teams of clinical geneticists and bioinformaticians are surfing this wave, rapidly discovering genomic variations associated with specific human disorders. This trend is providing scientific bases for personalized medicines but also new, important questions linked to the basic biochemistry field.

Ceramide transport protein, or CERT, moves the waxy lipids known as ceramides in cells for the synthesis of sphingomyelin, a membrane lipid that is ubiquitous in mammalian cells. In 2007, researchers found that CERT is functionally repressed by multiple phosphorylations of a serine-repeat motif, or SRM, in CERT. At the time, scientists regarded this finding as pure biochemistry of a protein.

However, a decade later, large-scale human genetic studies on intellectual disabilities and mental development disorders, or ID/MD, showed that missense mutations in or near the CERT SRM-encoding regions are associated with a type of autosomal dominant hereditary ID/MD. The dominant inheritance was in line with a prediction from the previous biochemical study that loss of hyperphosphorylation of the SRM renders CERT abnormally active.

Our recent collaborative study confirmed this prediction by demonstrating that substitution of a serine residue in the SRM with other residues similar to variants found in ID/MD patients results in dysregulation of CERT in cultured cells. Nonetheless, several ID/MD-associated missense mutations that occurred in the CERT gene CERT1 also are mapped outside the SRM. This riddle was answered by another recent study showing that a non-SRM variant also compromises the SRM hyperphosphorylation, thereby abnormally activating CERT.

Moreover, cell biological analysis showed that abnormally activated CERT mutants exhibit an aberrant punctate distribution in cells, suggesting that the subcellular distribution pattern is applicable as a diagnostic tool to assess whether a CERT1 variant is an abnormally activated type that may cause ID/MD, although the precise identity of the puncta structure remains undetermined.

Kentaro Hanada (hanak@nih.go.jp) is a senior researcher in the quality assurance, radiation safety and information management department of the National Institute of Infectious Diseases in Japan, where he is also former director of the biochemistry and cell biology department and an emeritus officer.

Unveiling a microbial enzyme

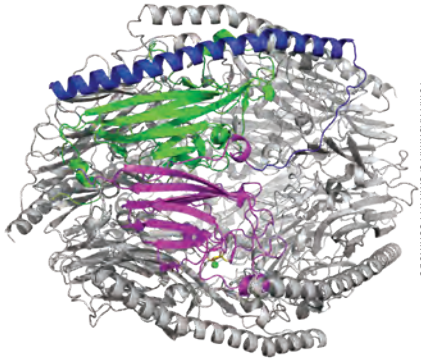
By Christian McDonald

In the 1980s, scientists isolated a novel protein from the common airborne fungus Aspergillus fumigatus. Initial studies described this enzyme's functions, but the gene encoding it remained unknown for 40 years until it recently was identified by researchers at the University of Tokyo. Graduate student Toma Kashima and collaborators published this work in the **Journal of Biological Chemistry**, providing an extensive biochemical characterization of this enzyme.

Prebiotics are nondigestible substances that can help shape specific microbial populations within the digestive tract. They are frequently dietary fibers from plant food sources but can include other compounds. Because mammals lack the enzymes required to break down the bonds within prebiotics, we rely on the bacteria that reside in our gut to do this work. Specifically, a group of enzymes in bacteria known as glycoside hydrolases, or GHs, play a significant role in this process. The University of Tokyo researchers became interested in these GH enzymes within the genome of Bifidobacterium dentium, a bacterium that colonizes the human intestine and oral cavity.

"We first noticed a hypothetical gene next to a GH32 protein and predicted this unknown gene must have a similar function," said Shinya Fushinobu, corresponding author of this paper.

To begin teasing out the function of this region of the bacterial genome, Fushinobu's team isolated the protein product of this gene and



TOMA KASHIMA & SHINYA FUSHINOBU

Researchers determined that αFFase1 possesses a hexameric shape. This ribbon structure displays a tetramer, demarcated by three distinct colors, which features unique sites on αFFase1.

tested what substances it reacts with using thin-layer chromatography, a method that identifies components of a mixture and follows the progression of a reaction.

"The result was very surprising … with a specific shift in one spot that we did not expect to be there," Fushinobu said.

The team discovered that this protein had two distinct enzymatic activities, acting as both an alpha-D-fructofuranosidase and an alpha-D-arabinofuranosidase. These two activities break down specific bonds in sugars, the former targeting bonds found only in cooked substances, such as sucrose caramel. Previously studied GH proteins break down β-linked molecules (which hold sugars together), but the researchers found that these two activities acted on α-linked sugars, an area that is not well understood.

"This activity was unexpected because α-bonds and β-bonds are totally different, and cleavage of α-D-fructofuranoside bonds by a GH protein is new," Fushinobu said.

Following these initial findings and 40 years after its initial discovery, the researchers designated the protein isolated from Bifidobacterium as αFFase1.

Fushinobu's team advanced their investigation by determining that αFFase1 has a hexameric structure. They proceeded to mutagenize specific sites within the protein that were revealed to be responsible for binding and reacting with substrates. Collectively, the team assembled their data and proposed a mechanism for how αFFase1 converts particular sugars in foods we consume.

Although there are over 160 recognized GH families, Bifidobacterium's αFFase1 does not resemble any known amino acid sequence. Its unique features have prompted the creation of a new glycoside hydrolase family, GH172. After elucidating αFFase1's role in breaking down distinct α-linked bonds within sugars, this research team will explore further the metabolic systems in B. dentium that exploit αFFase1.

"We unexpectedly revisited a very old enzyme discovered by Japanese researchers in the 1980s and found very surprising results," Fushinobu said. "We believe this new gene will be involved in important degradation systems that can be broadly used in commercial products and give us insights for our health and the bacterial communities in the human gut."

DOI:10.1016/j.jbc.2021.101324

Christian McDonald (cmcdonald@miami.edu) is a Ph.D. candidate in microbiology and immunology at the University of Miami Miller School of Medicine. Follow him on Twitter: @cmdonaldd.

Chronic pain shows up in urine

Researchers distinguish urinary pelvic pain from healthy controls — and from other chronic pain diseases

By Renae Crossing

Chronic pain diseases are underresearched — particularly for women, particularly with pelvic pain. Almost certainly, someone you know suffers from this. For people with urinary chronic pelvic pain syndrome, or UCPPS, the need to urinate is particularly frequent or urgent, or pelvic pain is prominent, or both. It's often simply a diagnosis of exclusion, and there is a lack of effective treatments.

Using protein signatures in urine, researchers have been able to distinguish UCPPS from other chronic pain diseases, including myalgic encephalomyelitis/chronic fatigue syndrome, or ME/CFS, as well as fibromyalgia and irritable bowel syndrome.

According to a recent article in the journal **Molecular & Cellular Proteomics**, lurking in urine all along were pronounced differences in the proteins related to chronic pain for different sexes — and leads for diagnosis and treatment.

We often think of pain in terms of blunt force, but the workings of chronic pain are more like pulling thousands of tiny strings in the theater of a cell. To develop new treatments and diagnostics, we need to know which proteins are pulling strings and which are playing parts.

Finding those proteins is the most powerful aspect of this study, according to first author John Froehlich, professor of surgery at Harvard Medical School. He said his team is "measuring the real things that carry out functions," along with the upstream bosses of those things.

Why not a blood test? Urine is close to the pelvis and can be more sensitive than blood (or not as good at homeostasis). Also, patients are happy: one less jab for a blood draw.

In a coordinated national effort, the scientists received 244 urine samples from the masses, labeled them "for the masses" (that is, for the technique called mass spectrometry), blasted them to smithereens — smithereens ordered by mass and charge, for identification — and loaded the data onto the Proteome Discoverer version 2.2.

What did they find?

The levels of nine proteins were different between people with UCPPS and healthy controls.

There were parts of the scaffold between cells, and proteins were involved in inflammation. The researchers found proteins known for increasing bleeding (previously implicated in UCPPS), for reducing the migration of immune cells, and for the development of epithelial tissue — the lining around blood vessels and organs or their cavities. They also found proteins that work in the postal service of cells, the Golgi.

But what if these protein patterns were due to chronic pain generally, not uniquely UCPPS?

The scientists ran comparisons with people with other chronic pain diseases, and three proteins stood out uniquely in UCPPS. Next, the team wants to conduct a larger study to see if these unconventional fingerprints correlate with disease severity or duration.

Froehlich said he would be "tickled" if other researchers mined the open data to help people with chronic pain diseases. The growing global burden of ME/CFS includes an estimated 46% of people with long COVID-19 who meet criteria for the disease.

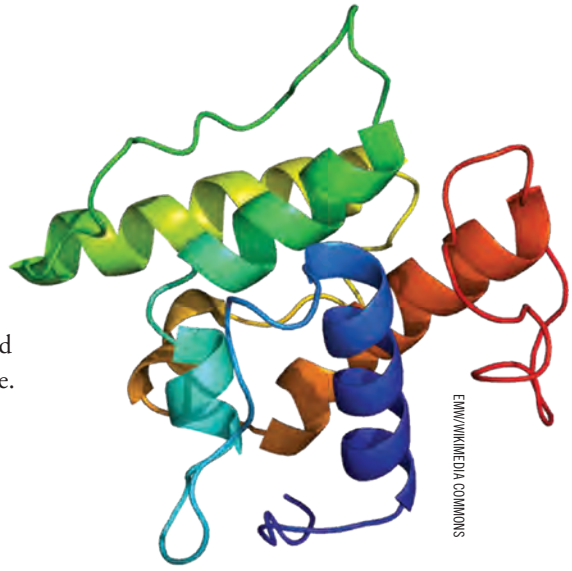
Froehlich calls corresponding author Marsha Moses a "powerhouse" behind this research.

He also credits his mother. After completing a Ph.D. on proteins in breast milk ("My mom was a midwife"), Froehlich pivoted to a fluid with its own sort of richness. He simply changed streams.

Renae Crossing (renaecrossing@gmail.com) is a writer and former teacher. She holds a first-class master's degree in life science from the Hong Kong University of Science and Technology and a first-class master's in teaching from the University of Melbourne. Follow her on Twitter: @renaecrossing.

Identifying a new lipid metabolism gene

By Nivedita Uday Hegdekar



EMW/WIKIMEDIA COMMONS

People with familial hypercholesterolemia, or FH, have very high levels of low-density lipoprotein cholesterol circulating in their blood due to aberrant LDL uptake by cells. With LDL levels elevated for prolonged periods, these patients are at increased risk for atherosclerotic cardiovascular disease.

"Mutations in several genes have been identified as contributors of FH," Diego Lucero, a research fellow at the National Institutes of Health, explained. "However, a genetic link is still unidentified in about 20% to 40% of FH patients. This makes diagnosis and drug therapy design more challenging."

Working in Alan T. Remaley's lab, which focuses on understanding lipid metabolism and developing therapies to treat cardiovascular diseases, Lucero became interested in identifying other genes that contribute to aberrant LDL metabolism.

Through genomewide CRISPR–Cas9 screening, Lucero used 76,441 sgRNAs to knock out 19,114 genes in Cas9-expressing HepG2 liver cells. sgRNA-transduced cells were incubated with fluorescently labeled LDL and sorted for LDL uptake through flow cytometry. He collected cells with 5% or lower LDL uptake and deep sequenced them to determine sgRNA representation.

"If a gene influenced LDL uptake, its sgRNAs would feature among the most enriched in the deep sequencing," Lucero said.

By studying sgRNA enrichment in his cell populations, Lucero identified 15 genes that influenced LDL uptake. He then generated HepG2 cell lines with these 15 candidate genes removed, and he remeasured LDL uptake in these cells.

"Knockout of the LDLR gene showed the most robust reduction (about 80%) in cellular LDL uptake," said Lucero. "We also observed consistent reductions in LDL uptake in three other novel genes."

One of the three was transgelin.

Lucero worked with collaborators at the Mayo Clinic to validate the gene hits through the Global Lipids Genetics Consortium and lipid-related phenotypes available in UK Biobank. They found that differences in transgelin expression in human populations were associated strongly with elevated plasma lipids (triglycerides, total cholesterol and LDL cholesterol), making transgelin a target for further investigation. However, transgelin is an actin-binding protein that promotes motility in cells. What role does it play in lipid metabolism?

"In transgelin knockout cells, we found a universal 30% reduction in uptake of LDL, very low-density lipoprotein and transferrin," Lucero said. "This led us to believe that transgelin affects something common between these cargos."

When LDL binds to the LDL receptor, the latter is internalized, facilitating transport of LDL into the cell through clathrin-mediated endocytosis. And actin filament reorganization is a necessary step during clathrin-mediated endocytosis.

"Our microscopy experiments showed that transgelin plays a vital role during LDLR internalization, most likely by binding to actin filaments during endocytosis," Lucero said. "This facilitates LDL uptake and consequently affects cellular cholesterol homeostasis."

These findings recently were published in the **Journal of Lipid Research**. Lucero plans to continue this project using mice that are genetically modified to lack transgelin.

"We are also studying other proteins besides transgelin that might be involved in the uptake of LDL," he said. "While this study focused on genes that reduce LDL uptake, we have also identified those that increase LDL uptake. This is an exciting direction because these might be therapeutic targets that could reduce cholesterol in blood."

DOI:10.1016/j.jlr.2021.100160

Nivedita Uday Hegdekar (nivedita.hegdekar@gmail.com) is a graduate student at the University of Maryland working toward a Ph.D. in biochemistry and molecular biology and an M.S. in patent law. Follow her on Twitter: @NiveditaHegdek1.

From the journals

By Ankita Arora, Isabel Casas & Latavia Hill

We offer summaries of interesting papers on a variety of topics recently published in the **Journal of Biological Chemistry,** the **Journal of Lipid Research** and **Molecular & Cellular Proteomics**.

Standardizing immunopeptidome data sets

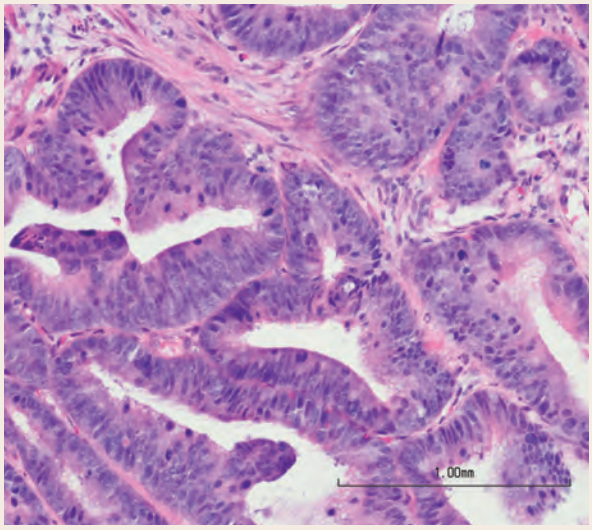
Most cells cut their own proteins into fragments called immunopeptides and present these fragments to T cells — like evidence offered to a detective. The T cells determine if the evidence, the immunopeptides, are self or foreign and, if the latter, trigger an immune response to neutralize the threat. Cancer cells and infectious pathogens generate foreign immunopeptides that mark them for destruction and hence have great potential for highly specific therapeutic approaches. With the development of high-sensitivity mass spectrometry–based proteomics, scientists have discovered new cancer-specific antigens. However, standards to assess the quality of immunopeptidomic data generated by mass spec largely are falling behind the pace of discovery.

In a recent paper published in the journal **Molecular & Cellular Proteomics**, Kevin A. Kovalchik of CHU Sainte-Justine Research Center and a Canada-based team created the first user friendly quality control software tool, named MhcVizPipe, or MVP, that enables rapid and simultaneous assessment of large immunopeptidomic data sets. The authors showed that MVP, when compared to manual approaches, accelerates the analysis and data generation process about 22-fold on average. Thus, MVP serves as a great starting point for

Adapting to nutrient starvation in cancer

Cancer cells feed on amino acids, and the amino acid serine is needed for sphingolipid synthesis, a major process in cell survival, as well as apoptosis and inflammation. The enzyme serine palmitoyltransferase mediates sphingolipid synthesis and also can use the amino acids alanine and glycine to form deoxysphinganine, or dSA, in the absence of serine.

Work by Jean-Philip Truman of the State University of New York at Stony Brook and a team from institutions around the U.S., recently published in the **Journal of Lipid Research**, focused on the molecular mechanism of dSA in cell responses. The researchers first determined that serine starvation increased dSA levels in three cancer cell lines. Next, they showed that dSA interacts with sphingosine kinase 1, or SK1, causing SK1 proteolysis and increasing the levels of SK1 substrate, sphingosine, in cancer cells. The researchers further determined that increased sphingosine, or Sph, modifies the serine synthesis pathway by elevating reactive oxygen species. Finally, they showed that dietary restriction of both serine and glycine induced SK1 loss and increases in dSA and Sph levels in tumor xenografts in immunocompromised mice.



The research team concluded this study by postulating that in response to serine starvation, dSA directly acts on SK1, which signals Sph to modulate downstream cellular processes and ultimately stimulates cancer cell growth. All this new information can be applied to understanding the role of dSA in cancer cell metabolism.

DOI: 10.1016/j.jlr.2021.100154

— Latavia Hill

nonexperts to delve into immunopeptidomics and will foster greater accessibility and expansion of the field.
DOI: 10.1016/j.mcpro.2021.100178

A sulfur trafficking pathway in plants

Sulfur is an essential nutrient for plant development, present in the amino acids cysteine and methionine and in many molecules including lipids, vitamins and cofactors. Both the cysteine desulfurase, or CD, and rhodanese, or Rhd, domain-containing protein families participate in the trafficking of sulfur for various metabolic pathways in bacteria and humans; however, researchers still do not fully understand their connection in plants.

In a recent **Journal of Biological Chemistry** article, Benjamin Selles, Anna Moseler, Damien Caubrière and collaborators in France and Germany report the biochemical relationships between an Rhd domain–containing protein, the sulfurtransferase 18, or STR18, and a CD isoform referred to as ABA3, from Arabidopsis thaliana.

Using in vitro assays and mass spectrometry, the authors determined that STR18 stimulates the CD activity of ABA3 by reducing the intermediate persulfide on its catalytic cysteine, thereby accelerating the overall transfer reaction. The researchers showed that both proteins interact in plants and form an efficient sulfur relay system whereby STR18 catalyzes transpersulfidation reactions from ABA3 to the model acceptor protein roGFP2. The authors conclude that ABA3-STR18 belongs to a novel yet uncharacterized pathway of sulfur trafficking in plant cells.
DOI: 10.1016/j.jbc.2022.101749

Enzyme flexibility for bioenergy

Lignin is one of the most abundant polymers, and converting it to fuels is quite a challenging process due to its heterogeneous composition and recalcitrance to extraction. Modifying lignin structure to facilitate this conversion in plant feed stocks has long been a goal for bioenergy production.

The cereal grass sorghum is used as a dedicated bioenergy source because its water and fertilizer requirements are lower than other grasses such as corn. There is, however, a concern about reducing lignin content and its effects on plant fitness. A clearer understanding of the enzymes involved in lignin biosynthesis, including plant nicotinamide adenine dinucleotide phosphate– dependent cytochrome P450 reductase, or CPR, can improve the tailoring of cell wall composition.

CHRIS LIGHTWIKIMEDIA COMMONS

Sorghum, like this growing in Jasper County, Indiana, is already used as a dedicated bioenergy source, but there are concerns about reducing its lignin content.

CPR is a multidomain enzyme that donates electrons for hydroxylation reactions catalyzed by the Class II cytochrome P450 monooxygenases. CPR is involved in synthesis of lignol monomers, and alterations in its activity could change lignin composition.

To better understand the structure and function of the three CPR subunits from sorghum, Bixia Zhang and collaborators from Washington State University in Pullman describe in a recent **Journal of Biological Chemistry** article how they expressed three recombinant subunits, or SbCPR2s, and performed X-ray crystallography and kinetic assays to achieve this goal.

The authors determined that all three SbCPR2s supported oxidation reactions by two sorghum cytochrome p450 enzymes. They then compared the structure of one subunit, SbCPR2b, to mammalian counterparts and identified important amino acid residues. The researchers found that the interaction between CPR and a partner P450 enzyme requires a conformational change, from a closed to an open state, which is essential for electron transfer.

The authors concluded that SbCPR2's hinge region within the connecting domain is a potential target to alter biomass composition for bioenergy and forage sorghums through protein engineering.
DOI:10.1016/j.jbc.2022.101761

— Isabel Casas

Mimetic peptide treats systemic inflammation

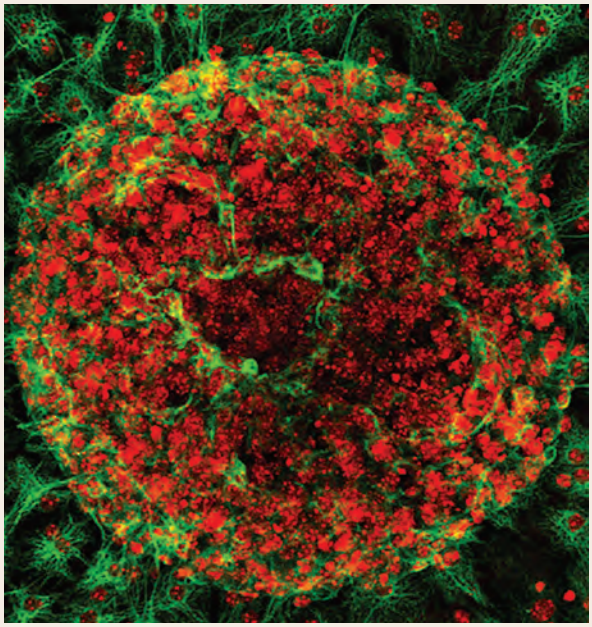
Elevated levels of low-density lipoprotein, or LDL, have been associated with the development of atherosclerosis. Studies have determined that an exogenous peptide known as apolipoprotein A-I mimetic peptide 6F Tg6F binds to oxidized lipids with high affinity. Researchers have hypothesized that Tg6F targets the intestine to reduce systemic inflammation; however, they still do not know the exact mechanism of this action. Work in the **Journal of Lipid Research** by Pallavi Mukherjee of UCLA and a team of researchers based in California focused on learning more about that mechanism of Tg6F.

First, the researchers determined that a Western diet altered the intestinal microbiome and altered the expression of genes involved in regulating the interactions between bacteria and intestinal cells in mice that had been genetically altered to remove LDL receptors. The team then did experiments to determine increased gut permeability, increased presence of reactive oxygen species and increased oxidized phospholipids in the small intestine of mice fed a Western, or high-fat, diet.

The study showed that a Western diet decreased the gene expression of three cytokines responsible for antimicrobial activity and decreased the expression of two genes respon-

Uncovering a rare disease's brain proteome

Alexander disease, or AxD, is one in a group of ultra-rare nervous disorders called leukodystrophies. In these disorders, sometimes called "white-matter diseases," myelin — the white fatty insulating layer that surrounds the nerves and promotes the rapid transmission of nerve impulses — is destroyed. This hinders nerve impulses and nervous system functions. AxD also is characterized by abnormal protein aggregates called Rosenthal fibers within brain cells known as astrocytes. AxD is caused by gain-of-function mutations in the gene encoding glial fibrillary acidic protein, or GFAP.



NATIONAL INSTITUTE OF CHILD HEALTH AND HUMAN DEVELOPMENT/NIH FLICKR

Astrocytes (green), seen here in a mouse, are star-shaped cells in the brain and spinal cord.

To understand the disease at a molecular level, researchers use mice that have been altered genetically to mimic AxD symptoms. One such mouse contains a disease-causing heterozygous point mutation at R236H in mouse Gfap and a human transgenic GFAP, leading to increased levels of GFAP in astrocytes. In a recent study published in the journal **Molecular & Cellular Proteomics**, Michael R. Heaven of Vulcan Biosciences and a team from around the U.S. compared whole-brain proteomes of altered and unaltered mice and identified pathways and proteins that are differentially expressed in the AxD mice.

Using liquid chromatography with tandem mass spectrometry–based proteomics, the team found that two pathways, namely glutathione metabolism and the peroxisome proliferator-activated receptor, or PPAR, signaling pathway, are upregulated, suggesting a role in neuroprotection. They also noted that levels of UDP-galactose-ceramide galactosyltransferase, or Ugt8, a regulator of myelin membrane synthesis, were decreased and that mice that were altered genetically to remove Ugt8 shared phenotypic characteristics of the AxD mice. Lastly, a fatty acid binding protein that activates the NF-B inflammatory response and thereby decreases the neuroprotective effects of the PPAR pathway was upregulated in both AxD mice and human patients.

This study exemplifies the use of high-resolution mass spectrometry–based proteomics to investigate whole-brain tissue in animal disease models when it is not possible to obtain sufficient patient tissues.

DOI: 10.1016/j.mcpro.2021.100180

— Ankita Arora

sible for forming intestinal cells that secrete antimicrobial peptides. The researchers determined that a diet that contained Tg6F reduces intestinal dysbiosis and proposed a model wherein Tg6F protects against the increase in reactive oxygen species and oxidized phospholipids that are hallmarks of systemic inflammation associated with a Western diet.
DOI: 10.1016/j.jlr.2021.100153

Matrigel — a necessary evil for organoids?

Researchers have been shifting recently toward growing and dividing cells in three-dimensional instead of two-dimensional cultures in petri dishes. These 3D cell cultures, called organoids, simulate microscopic and molecular features of original tissues. Hence, organoids are more clinically relevant and have tremendous therapeutic potential. Proteomic profiling of organoids could be valuable to test treatment regimens and find novel biomarkers.

Most organoids are grown in the solubilized basement membrane matrix Matrigel, which serves as a scaffold and provides mechanical properties and signaling cues for cell attachment and survival. However, Matrigel is complex and poorly defined, making it difficult to identify specific ingredients necessary for organoid function. Furthermore, thousands of identical peptides are shared between Matrigel and organoids, and insufficiently dissolved Matrigel could influence proteomic analysis of organoids.

In a recent article published in the journal **Molecular & Cellular Proteomics**, Man Wang, Huan Yu and colleagues at Peking University compared three Matrigel dissolving methods (cell recovery solution, dispase, and phosphate buffered saline–ethylenediaminetetraacetic acid buffer) and studied the effect of undissolved Matrigel proteins on proteomic profiles of organoids. They found that dispase digestion was the best method, with the highest peptide yield and highest incorporation ratio of stable isotopes. Further, 312 high-confidence Matrigel contaminants were identified, and they found that exclusion of the contaminants minimized Matrigel interference.
DOI: 10.1016/j.mcpro.2021.100181

Blocking germination of a crop parasite

Parasitic weeds cause considerable economic loss and threaten food security in Africa. In particular, the plant parasite striga, or witchweed, infests a broad range of crops. Striga germinates only in the presence of a host plant; it senses the small molecule strigolactone, or SL, secreted by the host roots. While researchers know of several SL receptors, their functions are hard to determine because these parasites are difficult to grow under laboratory conditions. Furthermore, many striga species are not amenable to genetic analysis.

In a recent **Journal of Biological Chemistry** article, Amir Arellano–Saab and collaborators at the universities of Toronto and Sydney combined phenotypic screening, structural information and drug discovery methods to identify a potential inhibitor, dormirazine.

The authors found that dormirazine blocks the hormone's access to its receptor, and it reduces protein–protein interaction flexibility that affects downstream signaling. They determined that timing of the application of this inhibitor during host seed germination is critical to potentially preventing infection. In addition to revealing the novel function of a strigalactone receptor in seed conditioning, the authors state, this information could help growers prevent future striga infestations and determine timing of antagonist application to prevent parasitic plant invasions.
DOI: 10.1016/j.jbc.2022.101734

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Latavia Hill (lataviahill@ku.edu) is a graduate student studying microbiology at the University of Kansas.

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ASBMB American Society for Biochemistry and Molecular Biology

MCP MOLECULAR & CELLULAR PROTEOMICS

2022 ASBMB FELLOWS NAMED

The American Society for Biochemistry and Molecular Biology has named 28 members fellows of the society.

Designation as a fellow recognizes outstanding commitment to the ASBMB through participation in the society in addition to accomplishments in research, education, mentorship, diversity and inclusion, advocacy, and service to the scientific community.

This is the second year the society has named fellows. The program began in 2021 with an open call for nominations; 30 people were selected that year.

Judith S. Bond, a former ASBMB president, is a member of the Membership Committee, which developed the fellows program.

"Many congratulations to our 2022 fellows!" Bond said. "You make our society strong, provided leadership, contributed to the core missions of the society, and honor us by your participation in society activities."

Edward Eisenstein, who leads the Membership Committee, added that the selected fellows displayed a broad range of experiences, accomplishments and service to the ASBMB.

"The new fellows include a past president, council members, committee members and editors, as well as a previous executive director of the society," said Eisenstein, an associate professor at the University of Maryland.

Recognition of the fellows was scheduled to take place at the 2022 ASBMB Annual Meeting.

Vahe Bandarian

Vahe Bandarian is a professor at the University of Utah. His lab studies the biosynthesis of complex natural products. The lab reconstituted key steps in the biosynthesis of the highly modified transfer RNA base queuosine, which often is used as a tRNA wobble base. They are also interested in the microbial enzymes that modify peptides to produce a large class of natural products that can have antimicrobial or cytotoxic effects.

He is a member of the ASBMB Minority Affairs Committee, the Women in Biochemistry and Molecular Biology Committee, and a member of the advisory board for the society's Maximizing Opportunities for Scientific and Academic Independent Careers, or MOSAIC, program. He serves on the editorial board of the Journal of Biological Chemistry. Catherine Drennan, who nominated Bandarian, wrote, "His CV has example after example of newly discovered chemistry, newly discovered enzymes and biochemical mysteries solved."

Jeffrey Benovic

Jeffrey Benovic is a professor at Thomas Jefferson University. His research focuses on the mechanisms that regulate G protein–coupled receptor signaling, with a particular emphasis on the role of GPCR kinases and arrestins. His lab discovered a mechanism for GPCR internalization, a key regulator of receptor signaling.

Benovic is a past member of the ASBMB Publications Committee, Finance Committee and Council. He's also a past member of the Journal of Biological Chemistry editorial board. He was nominated as an ASBMB fellow by colleague Steven McMahon, who wrote, "Dr. Benovic's investigations opened up an entire new field of study … (and) his contributions to biochemistry extend well beyond his own scientific discoveries."

Ralph Bradshaw

Ralph Bradshaw is a professor emeritus at the University of California, Irvine, and professor of pharmacology at the University of California, San Diego. His research focused on nerve growth factor, fibroblast growth factor and their receptors, using proteomics and phosphoproteomics to understand growth factor signaling. Some of his scientific contributions were captured in a Journal of Biological Chemistry "Classic" article marking the journal's centennial.

He was the first editor-in-chief of the ASBMB journal Molecular & Cellular Proteomics and served on the editorial board and as an associate editor of JBC for nearly 30 years. He also served on many ASBMB committees, including what was then known as the Committee on Equal Opportunities for Minority Groups, the Nominating Committee, the Membership Committee and the Public Affairs Advisory Committee. In addition, he served on the Council and as the society's treasurer and historian, producing a history of the ASBMB in 2009. Bradshaw was nominated as an ASBMB fellow by 2021 fellows Dan Raben and William Merrick and former ASBMB President Gerald Hart. Merrick wrote, "I can think of no one who has devoted more time and energy to the ASBMB in his almost 60 years as a researcher."

David Brautigan

David Brautigan is a professor emeritus at the University of Virginia, where he studies the biochemistry of signal transduction by protein kinases and phosphatases. His lab has investigated multiple serine/threonine phosphatases, the actions of different inhibitor proteins and how phosphorylation affects protein phosphatase activity.

He has served the ASBMB in many roles, including terms as a Council member and Journal of Biological

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Chemistry editorial board member. He also served on committees for human resources, educational affairs and public affairs. He has represented the ASBMB on a committee for the International Union for Biochemistry and Molecular Biology and on the board of the Federation of American Societies for Experimental Biology, for which he was elected vice president for science policy. He is a fellow of the American Association for the Advancement of Science. Brautigan was nominated as a fellow by colleague John Lazo.

Alma Burlingame

Al Burlingame is a professor at the University of California, San Francisco, where he directs the mass spectrometry facility. His research team uses proteomic techniques to study diverse protein-level challenges, including the role of post-translational protein modifications in signaling and the regulation dynamics of protein assemblies and machines.

He was a co-founder of the ASBMB journal Molecular & Cellular Proteomics, of which he now serves as editor-in-chief; he is an elected fellow of the AAAS and organizes two annual ASBMB symposia in proteomics. Deputy editor Steven Carr, who nominated Burlingame as an ASBMB fellow, wrote, "He has worked tirelessly on behalf of biological mass spectrometry and proteomics community. … Al has been a strong and passionate spokesman for our field."

William Clemons

William Clemons is a professor at the California Institute of Technology who studies post-translational processing of membrane proteins. His lab focuses on membrane targeting and translocation of tail-anchored proteins, which use a different membrane insertion system than the typical signal recognition particle; Clemons' lab studies the alternative machinery that inserts protein tails into the membrane. A second line of research focuses on optimizing membrane protein expression, which makes the proteins easier to study; his lab observed that insertion into the membrane governs the efficiency of expression of variant proteins and developed a prediction tool to help others select targets to study that are expressed efficiently in E. coli.

Clemons is a member of the Journal of Biological Chemistry editorial board and has served on the ASBMB annual meeting organizing committee. Douglas Rees, a fellow Caltech professor and Howard Hughes Medical Institute investigator, nominated him for fellowship in the ASBMB, praising his "fearlessness in tackling significant biological hurdles" and his commitment to advocating for diversity, equity and inclusion in science.

Anita Corbett

Anita Corbett is a professor at Emory University, where she studies the function of evolutionarily conserved RNA binding proteins such as the RNA exosome complex and poly(A) RNA binding proteins. Her research explores the role of these proteins in gene expression and development. She was the inaugural winner of the ASBMB Mid-Career Leadership Award, which is administered by the society's Women in Biochemistry and Molecular Biology Committee. She currently serves on the Public Affairs Advisory Committee and as a member of the Journal of Biological Chemistry editorial board and sponsors Emory's Student Chapter of the ASBMB.

Corbett was nominated by Emory colleague Christine Dunham, who also became a fellow this year, and who praised her advocacy for colleagues, especially junior scientists and women in science.

Paul Craig

Paul Craig is a professor at the Rochester Institute of Technology. His research focuses on education: He develops educational software to simulate and help visualize laboratory experiments such as electrophoresis and mass spectrometry. He is a founder of BASIL, the biochemistry authentic scientific inquiry lab, a course-based undergraduate research experience focused on doing authentic research. For this work, Craig received the ASBMB Award for Exemplary Contributions to Education in 2018. He is a member of the ASBMB Today editorial advisory board, previously served on the

Education and Professional Development Committee, and regularly has volunteered for the undergraduate poster competition at the ASBMB's annual meeting.

"Paul is the epitome of an outstanding teacher–scholar," wrote colleague Lea Vacca Michel in a nomination letter.

Dennis Dean

Dennis Dean is a distinguished professor and was the founding director of the Fralin Life Science Institute at Virginia Tech. His lab studies the mechanism for biological nitrogen fixation and the biological pathways for assembly of simple and complex metalloclusters. Their research focuses on the enzymes that produce iron–sulfur clusters, a co-factor that is important for many redox reactions including nitrogen fixation, photosynthesis and respiration. Squire Booker, who nominated Dean, wrote that "it can be argued that he is the father of the field of iron–sulfur cluster biogenesis." He is a former member of the Journal of Biological Chemistry editorial board and the ASBMB Publications Committee.

Christine Dunham

Christine Dunham is a professor at Emory University. Her lab studies how regulation of protein synthesis alters critical aspects of cellular function in ways that are essential for life. Her current research focuses on how RNA modifications, bacterial toxins and antibiotics affect gene expression. Dunham is a member of the editorial board of the Journal of Biological Chemistry and was elected to the ASBMB Publications Committee in 2020. She was a Pew Biomedical Scholar, a Burroughs Wellcome Investigator and a recipient of an National Science Foundation CAREER Award. Dunham has received awards from the American Crystallographic Association and the National Academy of Sciences, and won the ASBMB Young Investigator Award in 2019.

She was nominated by Emory colleague Anita Corbett, who wrote, "In her research group, Dr. Dunham has tackled critical scientific questions that are key ... to addressing one of the most pressing clinical challenges of the day in antibiotic resistance."

Barbara Gordon

Barbara Gordon is the former executive director of the ASBMB. She began working for the Journal of Biological Chemistry in 1972 and went on to manage the society's meetings and its journals before being appointed executive director in 2003. During her tenure, she oversaw the journals' transition to online publishing and, most recently, their transition to open access. She also oversaw the formation of new committees, such as the Women in Biochemistry and Molecular Biology committee, and programs, such as the IMAGE grant-writing workshop, the new MOSAIC program for diverse young investigators, and the undergraduate degree-accreditation program, certification exam and poster competition. She retired in 2021. Gordon was nominated by S. Gaylen Bradley, the emeritus dean of basic health sciences at Virginia Commonwealth University, who wrote, "Barbara Gordon has made exceptional contributions to the Society and its programs over and above her role as an employee."

Susanna Greer

Susanna Fletcher Greer is the senior director for clinical cancer research and immunology at the American Cancer Society. Prior to taking that post, she was a tenured professor at Georgia State University, studying major histocompatibility complex signaling in cancer. She was a member of the ASBMB Science Outreach and Communication Committee from 2013 to 2020 and led the committee from 2016 to 2019. In addition, she has been an instructor and course developer for the society's Art of Science Communication course. She is also a member of the ASBMB's Council and Finance Committee.

Greer was nominated by Nicole Woitowich and Matt Koci, who have served with her on the ASBMB's Science Outreach and Communication Committee. They wrote, "She is a champion for broader representation among scientists, and making science more accessible to the public and stakeholders."

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J. Silvio Gutkind

J. Silvio Gutkind is a professor and chair of the pharmacology department at the University of California, San Diego, School of Medicine. He also is associate director of basic science at Moores Cancer Center. Gutkind studies G proteins and their receptors. His lab found that G protein and GPCR mutations can be oncogenic, and his studies revealed the protein–protein interaction networks that connect GPCRs to intracellular signaling cascades, such as MAP kinases, Ras and Rho GTPases and the PI3K-mTor and Hippo-YAP pathways. For many years, he was the chief of a cancer branch at the National Institutes of Health; since moving to UCSD, he has continued to pursue a research interest in oral cancers and their mechanisms, with emphasis on precision and immune therapies.

Gutkind is an elected member of the National Academy of Medicine and twice has served as an editorial board member for the ASBMB's Journal of Biological Chemistry. He was nominated by 2021 ASBMB fellow Sarah Spiegel, who praised both his scientific achievements and his commitment to mentoring and developing scientists from diverse backgrounds, adding, "Silvio is a scientific superstar and one of the preeminent biomedical scientists active in the U.S., indeed in the world."

Yusuf Hannun

Yusuf Hannun is director of the Stony Brook Cancer Center and vice dean for cancer medicine at Stony Brook University. As a postdoc, he discovered a biological activity for the lipid sphingosine, and he has spent the rest of his career investigating the roles of sphingolipids in cell signaling, programmed cell death and carcinogenesis.

Hannun was a co-founder of the ASBMB's Lipid Research Division and has served on the Journal of Biological Chemistry editorial board and the ASBMB Annual Meeting Program Planning Committee. He won the 2011 ASBMB Avanti Award in Lipids. He was nominated as an ASBMB fellow by a remarkable group of 31 colleagues, who wrote, "He brings honor and recognition to the fields of biochemistry and molecular biology."

Gerald Hart

Gerald Hart is a professor at the University of Georgia and a member of the Complex Carbohydrate Research Center there. Hart co-discovered glycosylation of proteins in the nucleus and cytoplasm at a time when experts thought glycosylation only occurred on secreted proteins. Later, he found that O-linked N-acetylglucosamine, or O-GlcNAc, can be added to serine and threonine phosphorylation sites and acts as a competing signal. His lab continues to explore O-GlcNAc signaling and its interaction with other cellular signals.

He is an associate editor for two of the society's journals: the Journal of Biological Chemistry and Molecular & Cellular Proteomics. He is also a past society president and former member of the ASBMB Today editorial advisory board. He received the society's Herbert Tabor Research Award in 2018.

He was nominated by colleagues Christopher West and Michael Tiemeyer, who wrote, "Jerry is broadly recognized and appreciated as an excellent citizen, always willing to do what is needed to support the group effort. He is approachable to students and faculty colleagues, unpretentious and can be counted on to offer a thoughtful and balanced opinion on wide-ranging issues."

Eric Johnson

Eric F. Johnson is a professor at Scripps Research. His work focuses on cytochrome P450 enzymes, membrane-bound enzymes that are expressed in the liver and are very important in metabolizing drugs and other molecules. In the early 2000s, Johnson and colleagues solved the first structure of a microsomal cytochrome P450; this and later structures helped the pharmaceutical industry to design drugs that are less likely to cause drug–drug interactions.

Johnson was nominated by F. Peter Guengerich, who became an ASBMB fellow in 2021 and who called him "a steady colleague to many in the field of drug metabolism, who can always be trusted." Johnson served five terms as a Journal of Biological Chemistry editorial board member and also served as head and interim head of the Scripps biochemistry division. Guengerich added, "Throughout

Eric's career, one of the hallmarks of his research is the very high quality of his work, regardless of the scientific area he works in."

Daniel Leahy

Daniel Leahy is a professor and former (founding) chair of the molecular biosciences department at the University of Texas at Austin. His lab studies the molecular mechanisms of signaling in the epidermal growth factor receptor and Hedgehog signaling pathways, mutations in which can drive the development of cancer.

He served a term on the ASBMB Council and has helped to organize meeting themes and other society events. He was nominated by colleagues Jessie Zhang, Daniel Raben and Jason McLellan, who praised his leadership of a new merged department at UT Austin and his efforts on behalf of junior researchers, writing, "Dan Leahy's achievements and leadership have made tremendous impacts on the scientific society and community."

Alfred Merrill

Alfred Merrill is an emeritus professor at the Georgia Institute of Technology. His laboratory developed quantitative methods to measure sphingolipids and was a major contributor to mass spectrometry–based lipidomics consortia. Merrill helped delineate how the lipid backbones of sphingolipids are made and how they function in cell signaling and disease.

Merrill is a fellow of the American Association for the Advancement of Science and an associate editor of the Journal of Lipid Research. He was a member of the editorial board of the Journal of Biological Chemistry for 20 years. George Carman of Rutgers University, who became a fellow in 2021, nominated Merrill. Carman wrote, "Al has made impressive contributions to science through both the discoveries by his laboratory and his assistance to others through service activities."

Beronda Montgomery

Beronda Montgomery soon will begin a new role as the dean and vice president of academic affairs at Grinnell College. Prior to taking that position, she was a professor, assistant provost for faculty development in research, and assistant vice president for research and innovation at Michigan State University. Montgomery's studies focus on how photosynthetic organisms respond to their environments. In freshwater cyanobacteria, Montgomery has looked at signal transduction pathways controlling growth and development; in land plants, she is interested in how photoreceptors called phytochromes affect growth and behavior. She also has published extensive research on mentoring and academic leadership and written a book called "Lessons from Plants" for popular audiences.

She is a fellow of the American Association for the Advancement of Science, the American Society of Plant Biologists and the American Society for Microbiology. She serves on the editorial board of the Journal of Biological Chemistry and previously was on the advisory board of ASBMB Today. MSU's Thomas Sharkey, who nominated her, said, she "has worked tirelessly to achieve an exemplary record of scholarly research, mentoring, and public service through diversity initiatives ... (and) is a treasured colleague in many spheres of the scientific academy."

Kim Orth

Kim Orth is a Howard Hughes Medical Institute investigator and professor at the University of Texas Southwestern Medical Center, where she studies the complex interactions between bacterial effectors and host cells in infection, working on pathogens that cause bubonic plague, gastroenteritis and other diseases. She discovered that some bacterial effector proteins can interfere with host cell immune responses by transferring acetyl groups onto phosphorylation sites, inhibiting signaling pathways. She coined the term AMPylation after observing that adenosine monophosphate, or AMP, can be covalently attached to substrate proteins by a bacterial virulence factor; her lab studies the role of AMPylation in the integrated stress response.

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Orth serves on the ASBMB Awards, Meetings and Nominating committees and has organized numerous meeting sections and small meetings. She is a National Academy of Sciences fellow and has received the ASBMB Young Investigator Award and the ASBMB–Merck Award. Eric Olson, chair of the molecular biology department at UT Southwestern, wrote in a recommendation letter that Orth's work "represents a unique convergence of biochemistry and cellular biology with the basic mechanisms of infectious disease."

Reuben Peters

Reuben Peters is a professor at Iowa State University who studies diterpenoid natural products, both the complex reactions catalyzed in their biosynthesis and their physiological function. His group has provided enough insight into terpene synthase structure–function relationships to enable redesign of their enzymatic activity and has elucidated an array of physiological roles for the resulting natural products not only in plants, where diterpenoids are widespread, but also in plant-associated bacteria.

He serves on the editorial board of the Journal of Biological Chemistry and on the steering committee of the ASBMB IMAGE grant-writing workshop as well as acting as a mentor during the workshop. Squire Booker, a 2021 ASBMB fellow who nominated Peters and who recruited him to work on the grant-writing workshop, wrote that its "success would not have been possible" without Peters' insight.

Margaret Phillips

Margaret Phillips is chair of the biochemistry department at the University of Texas Southwestern Medical Center, where her research focuses on metabolism in protozoan parasites. Her lab studies essential enzymes controlling pyrimidine biosynthesis in the parasite that causes malaria and polyamine synthesis in the trypanosome that causes sleeping sickness. The lab used structural-guided drug design to optimize and develop pyrimidine synthesis inhibitors with potential to become antimalarial drugs.

She served on the Journal of Biological Chemistry editorial board for 10 years and chairs the selection committee for the ASBMB's Alice and C.C. Wang Award in Molecular Parasitology. Phillips, a member of the National Academy of Sciences, was nominated as an ASBMB fellow by Howard Hughes Medical Institute investigator and UTSWMC professor Kim Orth, who wrote that Phillips "exemplifies the curious, clever, efficacious, rigorous and altruistic science that her peers drive to emulate."

Mary Roberts

Mary Roberts is a professor emeritus at Boston College. Her research focused on protein–membrane interactions, for which she developed novel NMR techniques, and on how archaea respond to stress by producing osmolytes.

Roberts served as co-chair of the ASBMB Annual Meeting Program Planning Committee twice, in 2019 and 2015. She also served a term on the editorial board of the Journal of Biological Chemistry and is a fellow of the American Association for the Advancement of Science.

Lizbeth Hedstrom of Brandeis University, who nominated Roberts as an ASBMB fellow, wrote that Roberts' "plethora of scientific contributions were facilitated by her generosity, manifest in many successful, lasting collaborations." Hedstrom also praised Roberts' commitment to mentorship and her advice for junior colleagues on navigating academia and parenthood.

John Scott

John Scott chairs the pharmacology department at the University of Washington. Scott's lab studies the role of anchoring proteins in modulating kinase activity. They discovered the A kinase anchoring protein, which binds to protein kinase A and regulates its activity, and they have developed inhibitors and uncovered roles for the anchoring protein in cytoskeletal organization and synaptic transmission.

He won the ASBMB's 2008 William C. Rose Award for outstanding research and mentoring. He has served on the ASBMB Council and Journal of Biological Chemistry editorial board, and he has organized meetings and programs for the society. Alexandra Newton of the University

of California, San Diego, nominated Scott. She wrote: "John is a passionate biochemist … (and) is an outstanding citizen to the biochemistry community."

Robert Stahelin

Robert Stahelin is a professor at Purdue University. His lab studies protein–lipid interactions, focusing on the interaction between viral proteins and host cell membranes to understand viral replication and seek new drug targets.

He has served as co-director of the ASBMB Lipid Research Division and has been an editorial board member for the Journal of Lipid Research since 2017. He has served as a judge at the undergraduate poster competition at the ASBMB annual meeting and has organized multiple annual meeting workshops devoted to lipid research.

Erica Ollmann Saphire at the La Jolla Institute for Immunology nominated Stahelin as a fellow. She wrote: "Rob's service and dedication to the lipid research community (specifically the Lipid Research Division of ASBMB), ASBMB and ASBMB society journals have been nothing short of outstanding."

Alex Toker

Alex Toker is the associate director for the Cancer Research Institute at Beth Israel Deaconess Medical Center and a professor at Harvard Medical School. His research focuses on understanding how the lipid kinase PI(3)K and its downstream signaling pathways affect cancer cell behavior. He is editor-in-chief of the ASBMB's Journal of Biological Chemistry and won the society's 2022 Avanti Award in Lipids.

Lila Gierasch, a professor at the University of Massachusetts Amherst and Toker's predecessor as JBC editor-in-chief, wrote in her nomination letter that Toker "has the wonderful combination of superb research stature, generous and influential service to his profession (notably ASBMB), and compassionate and effective mentoring that position him perfectly to be selected as an ASBMB fellow."

Nathan Vanderford

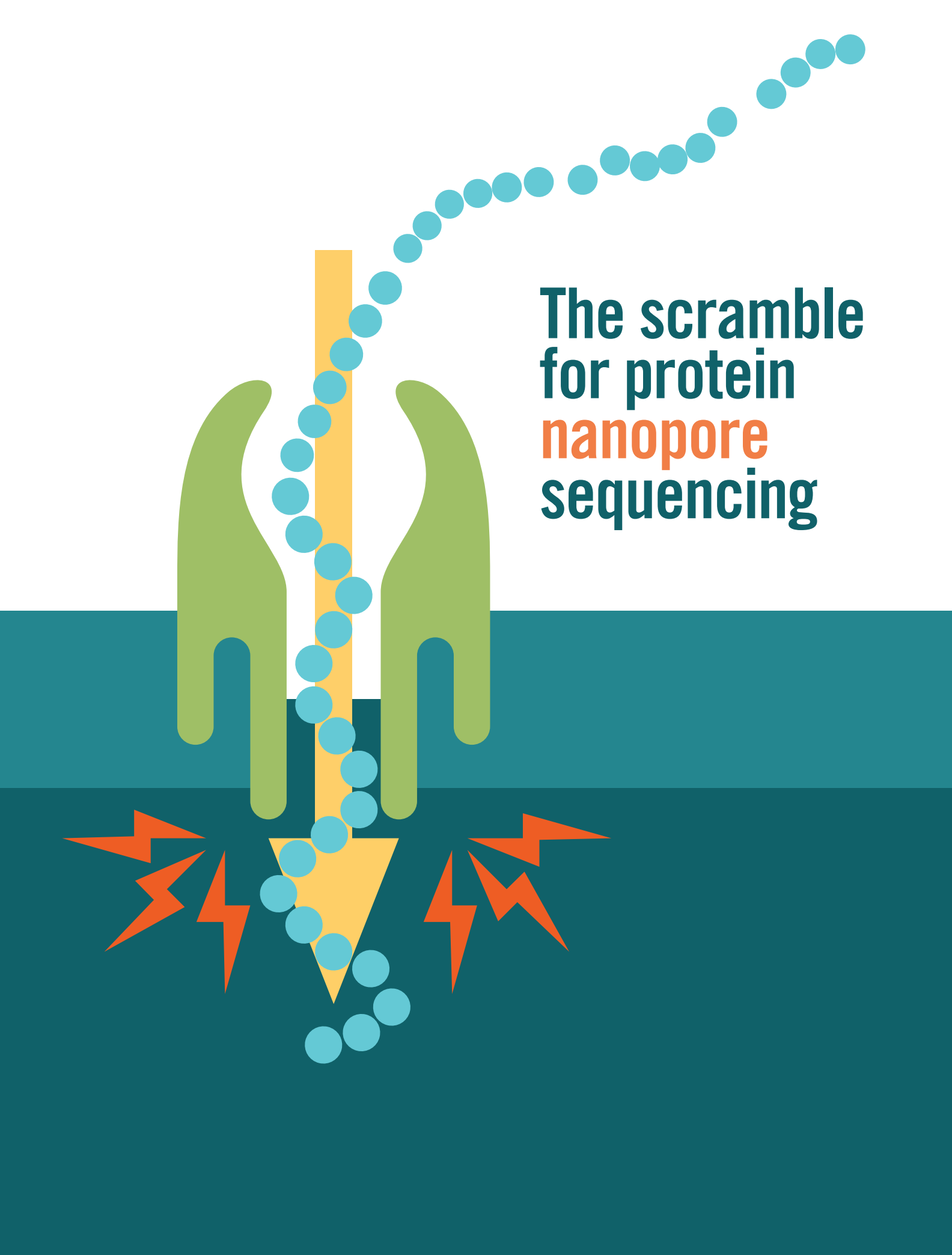
Nathan Vanderford is an associate professor at the University of Kentucky College of Medicine. He is also assistant director for education and research at the Markey Cancer Center, director of administration for the Center for Cancer and Metabolism, and director of the Appalachian Career Training in Oncology Program, or ACTION, an outreach program that he created. His research focuses on cancer disparities, health promotion, and cancer education and training. He is a member of the ASBMB Education and Professional Development Committee and has organized and been a member, twice over, of the Annual Meeting Program Planning Committee.

Vanderford was nominated as a fellow by Xiaoqi Liu, chair of UK's toxicology and cancer biology department. Liu wrote of Vanderford's work with ACTION: "Nathan has done what few faculty do in terms of creating a highly innovative and impactful program that is preparing a unique set of underserved students for graduate and professional school and ultimately for a future career in oncology."

Dennis Voelker

Dennis Voelker is a professor at National Jewish Health and the University of Colorado in Denver and former director of research in the pulmonary division of National Jewish Health. His group studies phospholipid–protein interactions, lipid metabolism, lipid transport and the important role lipids play as surfactants in the lung. He is an associate editor for the ASBMB's Journal of Biological Chemistry. He won the society's Avanti Award in Lipids in 2018, chaired the annual meeting, twice served on the Annual Meeting Program Planning Committee and held other positions of leadership relating to society events.

George Carman of Rutgers University, who nominated Voelker and who was among the society's first class of fellows, said that Voelker "has had a profound influence on our current understanding of lipid synthesis and transport and the roles lipids play in disease" and added that he "provides exemplary service to ASBMB."



The scramble for protein nanopore sequencing

As this method of sequencing DNA becomes widespread, a once-elusive goal is biophysicists' next target

By Laurel Oldach

When Jeffrey Nivala was a graduate student, his work station was a vibration-dampening table covered in electronic instruments: a patch clamp amplifier, an analog-to-digital converter, a perfusion system. All those trappings were trained on one tiny focal point: a tube roughly a nanometer in diameter and the minuscule trickle of electricity that flowed through it.

"I spent most of my Ph.D. chained to one of these things and trying to squeeze data out of it," Nivala said.

The tube, called a nanopore, was formed by a ring of proteins tunneling through a lipid membrane. After setting up an experiment, Nivala would sit and wait, hoping for a group of seven proteins to self-assemble and poke through the membrane, opening a route for ions to follow. When ions, or charged particles, move, they create an electrical current. After his equipment detected a current, Nivala would watch it intently, waiting for minute fluctuations that would indicate that a macromolecule was passing through the pore.

Nowadays, a pocket-sized device that plugs into a laptop's USB drive can deliver comparable information — from hundreds of pores at once. Nivala said, "A student in my lab now can collect more data in an afternoon than I ever did in my Ph.D."

After decades as an aspirational concept, nanopore DNA sequencing has been fully realized. Commercially available nanopore flow cells have been used to sequence DNA by astronauts on the International Space Station, biologists skiing across Iceland and geneticists piecing together the last missing fragments of the human genome.

Now, the biophysicists and engineers who developed the DNA sequencing technology are turning their attention to proteins, which are substantially more difficult to analyze with a nanopore. Researchers around the world are working to surmount the problems with proteins, hoping to make single-molecule proteomics a reality.

The biophysicists and engineers who developed the DNA sequencing technology are turning their attention to proteins, which are substantially more difficult to analyze with a nanopore. Researchers around the world are working to surmount the problems with proteins, hoping to make single-molecule proteomics a reality.

How DNA nanopore sequencing works

The engine that powers nanopore sequencing is a pair of liquid compartments separated by a membrane, with a positive charge on one side and a negative charge on the other. When a protein nanopore inserts into the membrane, it opens a path for ions to flow from one side to the other, responding to the difference in charge between them. (This difference in charge is measured

UNIVERSITY OF LEICESTER/OXFORD NANOPORE

Commercially available nanopore DNA sequencing devices, such as this MinION device from Oxford Nanopore, are small and highly portable.

in voltage; the rate of ion flow in response to a voltage difference is measured in current.)

Most of the ions that make up the current are charged single atoms such as chloride and potassium. When the pore is open, ions make the crossing easily, slipping through in nanoseconds. Larger molecules also can feel an electrical pull. The negative charge of DNA's phosphate backbone will draw it toward a positive charge, and therefore into a pore, just as the difference in charge pulls the chloride ions. But once that strand of DNA enters the pore, it takes up most of the space inside, allowing relatively few smaller ions to squeeze past and cross the membrane. That reduction in the movement of charged particles is reflected in a change in current picked up by electrodes on opposite sides of the membrane.

Each of the four DNA bases has a different chemical identity and blocks ions to a different degree. Like four different people casting distinct shadows as they pass through a door from a bright room into a dark one, the nucleotides can be identified by their signature current changes.

Left to its own devices, a linear strand of DNA would zip through the pore rapidly, although not quite as fast as the ions around it. Aleksei Aksimentiev, a biophysicst at the University of Illinois at Urbana–Champaign, said that slowing DNA down was key to the development of nanopore sequencing. "If it goes too fast, you just don't have enough ions … so you might make a huge error when you determine the average value of the current."

To measure the change in current with more confidence, researchers borrowed motors such as polymerases and helicases from cells' DNA replication machinery; these enzymes bind to the DNA and advance just one nucleotide at a time, forcing it to take measured, slow steps.

In addition to finding ways to make each fluctuation in current last a little longer, researchers also have developed algorithms to interpret the changing current and determine in real time which nucleotides are passing through the pore. The technology can collect long sequence reads from a single molecule of DNA, letting researchers draw conclusions that other technologies don't offer.

Aksimentiev is one of the many researchers who hope to apply the same principles to achieve protein sequencing. His lab has been working on the problem since transitioning from DNA sequencing in 2016. If they succeed, the work might lead to a portable device that could be used to determine the amino acid sequences and post-translational modification patterns of much longer pieces of single proteins than currently are possible using mass spectrometry, which would allow researchers to study signaling and isoform expression in greater detail than ever.

But it won't be easy, Aksimentiev said.

Biochemical challenges

"There are lots of challenges with proteins," Aksimentiev said. "In particular, they're not uniformly charged; they're not linear, most of the time they're folded; and there are 20 amino acids, plus a zoo of post-translational modifications."

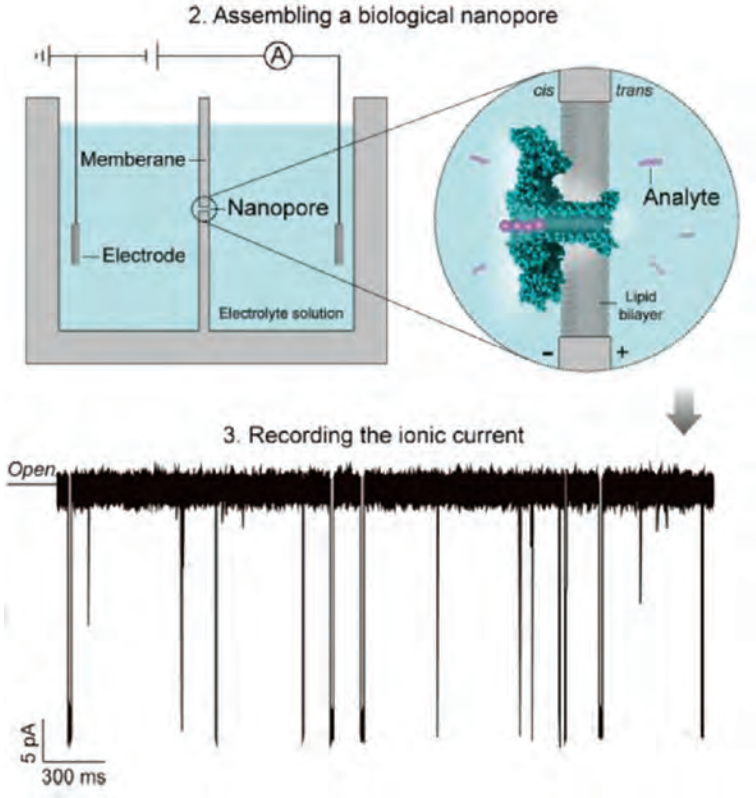
While the backbone of DNA carries a negative charge, a polypeptide backbone is neutrally charged at physiological pH, and its amino acid side chains come in a rainbow of sizes and polarities. Because of this heterogeneity, whereas DNA reliably carries a negative charge, many proteins do not.

All that heterogeneity doesn't just make it difficult to move a protein through the pore; it also may make for a more complicated analysis. Each of the four DNA bases produces a signature change in current, and it is much easier to differentiate among four signals than 20 — or, counting the possibility of post-translational modifications, many more.

Researchers have begun to show that at least a few distinct amino acid signatures exist, but they have not yet resolved all 20. In the journal Nature Biotechnology in early 2020, researchers in Abdelghani Oukhaled's lab in Cergy, France, collaborating with Aksimentiev's lab, reported that they could differentiate between the nanopore current signals from short peptides that varied by just a single amino acid. Each peptide was eight amino acids long, with seven identical negatively charged residues and one that varied. The team found a predictable interaction between the size and charge of that single variable residue and the way the current changed as the peptides passed through the pore.

When they tried to measure a mixture of all 20 peptides, the researchers found that they could pick out a few of the peptides with high confidence. According to some of their calculations, coaxing the peptides to linger longer in the pore would enable them to identify even more with confidence.

To make larger proteins pass through the pore in an orderly way, researchers must make them more linear, smoothing away secondary and tertiary structures, without damaging the structure of the proteins that make up the pore or the integrity of the lipid bilayer it is embedded in. At this point, Aksimentiev said, enough solutions are being proposed, tested and optimized that he thinks "unfolding the protein and feeding it through is probably not going to be the critical part" of achieving protein sequencing.



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A figure from a paper Yi-Tao Long's lab recently published shows a schematic diagram of the instrument used to read current through a nanopore, and an example of the ionic current such an instrument might read. The duration and amplitude of each current change (downward spike) gives researchers information about the analytes passing through the pore.

Unfolding the protein, feeding it through

As a grad student at the vibration table, Nivala, who is now a research assistant professor at the University of Washington, focused on the problem of turning a folded protein into a linear molecule that fits neatly into a pore.

"My Ph.D. was focused on showing the first proof of principle of using these motors to analyze these full-length, intact protein strands with a nanopore," Nivala said. "At that time, the writing was on the wall that the big challenges in nanopore-based DNA sequencing had been or were

Unfoldases work on proteins by tugging at one end. Like unraveling a piece of knitting, the force breaks up weaker interactions that hold the protein in its structure, rendering the protein linear.

about to be solved."

Working in the lab of University of California, Santa Cruz, biophysicist Mark Akeson, Nivala developed a way to use unfoldases — enzymes that, in their typical context in the mitochondria, unfold proteins in preparation for proteolysis — to pull proteins through an alpha-hemolysin nanopore.

The unfoldase he used, ClpX, does to a structured protein what a determined tug on a stray thread does to a sweater; it applies force to a loose end that overcomes the stabilizing power of internal interactions within the protein.

Nivala developed a C terminal protein tag that combined a highly charged stretch of amino acids and a protein motif recognized by ClpX. Because of the charged residues, a voltage difference would attract the end of the protein through the pore just far enough to encounter ClpX stationed on the opposite side. Then, Nivala said, the enzyme "would grab on to the tail and start pulling."

The motor protein would do the rest, tugging along the peptide backbone with enough force to unravel the structure on the other side of the membrane and pull the protein through. While this solved the problem of moving a noncharged protein through the pore, it also illuminated some challenges. For one thing, the pore that Nivala used was long and narrow; the portion of its tube that was the tightest squeeze, where current was determined, had space for as many as 30 amino acids at a time. Each of them could contribute to the overall flow of ions. Instead of trying to identify a single silhouette against a lighted door, imagine working with a shadow formed by a line of dozens of figures. Nivala said, "It ends up being a very intractable problem to deconvolve that into amino acid sequences."

Scientists had solved a similar challenge in DNA sequencing, but it was less complex because nucleotides are larger in size and smaller in number. They also had assistance from the stepwise work of the enzyme motors, which changed the signal by exactly one base every time. Although ClpX pulled its target proteins in regular steps of about a nanometer, one nanometer of protein backbone can include anywhere from five to eight amino acids. Nivala detected changes in current that showed some features of the test protein he was using, but he was unable to translate those changes back into a sequence of amino acids.

Cees Dekker, a physicist at Delft University of Technology, called the work "a very elegant idea … that faces some technical challenges."

In the years since, researchers have experimented with many other approaches to linearize proteins. Nivala's lab is examining unfoldases that

might meet sequencing needs better. In Nature Chemistry, in November 2021, Giovanni Maglia's lab at the University of Groningen reported that they had engineered a 42-protein complex that resembled an inverted soda bottle with its neck forming the pore in the membrane. The molecular machine, which combines a proteasome with a nanopore, uses motors from the proteasome component to drive an analyte protein into the pore.

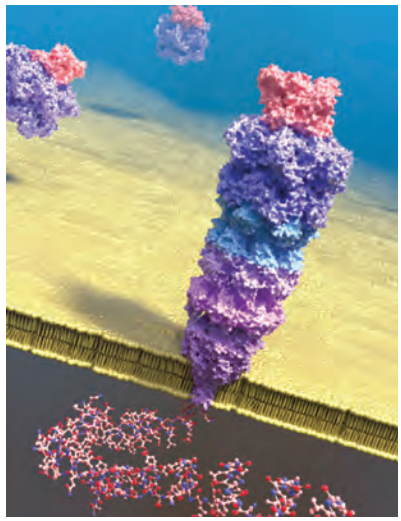
Some researchers are working on alternative motors, enzymes that act on DNA instead of proteins. Dekker's lab has worked for decades on what he calls "creative ways to get sequence information from DNA." Perhaps that familiarity is what gave them the idea to use DNA to get sequence information from proteins. Late in 2021 in the journal Science, the team reported an approach that used a DNA helicase to draw a chunk of protein through a nanopore complex called MspA, which previously had been used for DNA sequencing.

Conjugating a strand of DNA to a negatively charged short peptide, they applied voltage to make the conjugated molecule translocate through the pore. Then they added DNA helicase that would pull in the opposite direction, dragging the protein–DNA conjugate backward. The helicase's steps in one direction and the pull of electricity in the other added up to a seesaw that put tension on the linear molecule, holding it in the pore as ions whizzed by. That gave the electrode measuring current enough time to get a reliable reading at each step.

Because the helicase pulls harder than the electrical force but falls off of the DNA-protein hybrid molecule when it comes to the protein, most strands pass through the pore repeatedly. If enough helicase is in the mix, the lab showed, a new helicase can replace the first, and researchers can collect many readings from the same molecule. The first read, Dekker said, is enough to identify a peptide from a small group with about 85% accuracy; subsequent reads make the likelihood of misidentification vanishingly small.

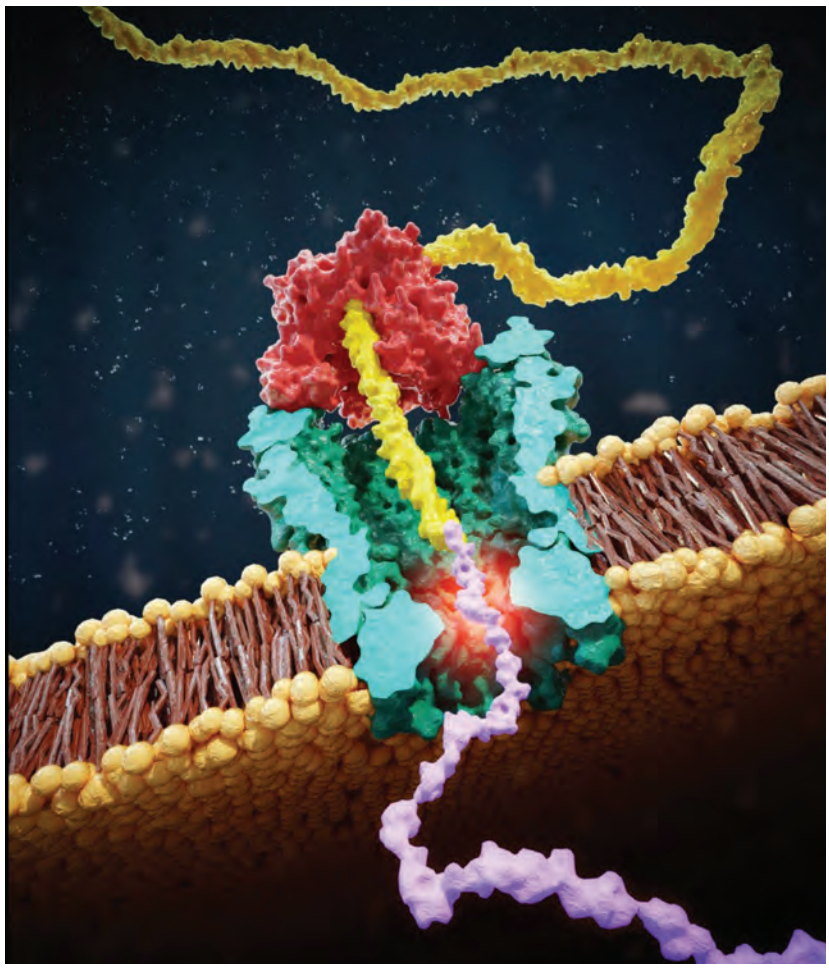
"What we have established is an identification tool that can identify certain proteins with great confidence; even single amino acid mutations can be very well resolved," Dekker said. "What we have not achieved yet is a de novo sequencing tool."

The researchers were able to analyze a small chunk of protein topping out around 25 amino acids. The peptide used in these first experiments was negatively charged, and Dekker



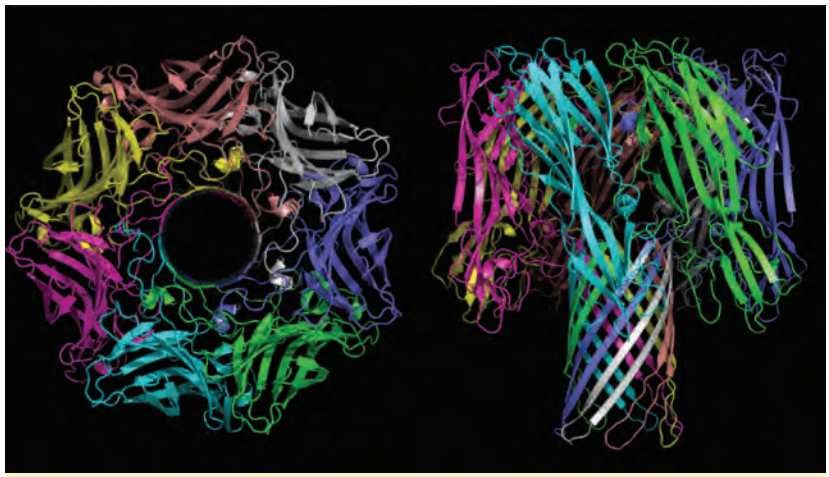
ENRIQUE SAHAGÚN/UNIVERSITY OF GRONINGEN

An artist's depiction of the Maglia lab's proteasome-attached pore complex.



CEES DEKKER LAB/SCIXEL/TU DELFT

An illustration of the nanopore reader that Dekker's lab developed shows DNA in yellow, protein in purple.



The pore-forming protein alpha-hemolysin

Many pores, many structures

The sequencing community regards pore-forming proteins as a useful biochemical tool. Another research community, one with few overlaps, studies why bacteria make the proteins, their structure and how they work.

Melanie Ohi, a structural biologist at the University of Michigan who studies the assembly of numerous protein complexes, keeps several boldly colored images of pore complexes tacked to the white board in her office. The largest depicts VacA, a pore-forming protein from the stomach pathogen Helicobacter pylori, whose structure her lab solved a few years ago. She said, "These toxins … are beautiful. They are the prettiest molecules you'll ever look at."

Beyond their pleasing aesthetics, Ohi is interested in what she called toxins' "fascinating ability to live in two very different environments."

Many bacteria, including H. pylori, secrete the subunits that make up protein pores into their environment, meaning that the toxins must be water soluble. But to function, those soluble subunits also must find one another, assemble into that pleasing symmetrical ring, and accomplish a biophysically tricky insertion into a membrane, requiring that they show a hydrophobic face. The cryo-EM revolution, Ohi said, is helping researchers to understand the many conformations these proteins can adopt at progressive stages of this attack.

Depending on its size and selectivity, the pore that eventually forms can render a membrane permeable to ions or to larger molecules. "A lot of bacteria have these types of toxins," she said. "They're used either to create a niche for the bacteria to live and grow in; or as a way for bacteria to deliver effectors into a host cell; or as bacterial warfare."

said that the DNA–peptide conjugate molecules are costly to synthesize for now.

Despite these challenges, Yi-Tao Long, a professor at Nanjing University who has worked in nanopore peptide analysis since the early 2000s, said the work has attracted significant interest to the field. "It is a milestone towards nanopore technology to directly sequence proteins."

Interactions with the pore

The Dekker lab's work also illuminated the importance of molecular modeling to understand what really happens inside a pore during a protein sequencing run. While testing whether the DNA conjugation system could help recognize a peptide that varied by just a single amino acid, Dekker's team observed that the peptide with the largest variable amino acid they tried, tryptophan, caused a peculiar signal.

"If you block part of the ion flow, you get a lower current. That's the intuition we built from," Dekker explained. But in the case of tryptophan, "You would expect, well, its volume goes up and (the current) goes down. But this saw more of a wiggling signal."

Tryptophan is bulky; it makes sense that wedging it into a small pore would block most ions from going past. The team expected that it would produce a drop in current, which they thought would recover to the baseline. The current they observed instead dropped dramatically but then went up, indicating that the pore was becoming more open.

Dekker approached Aksimentiev, a longtime collaborator, to help make sense of the strange readout.

When the structure of a pore is known at sufficient resolution, researchers can use supercomputers to

run complex, high-precision simulations of its behavior. Aksimentiev's lab specializes in this work. "Every atom of the protein, every atom of every water molecule, every ion, peptide: everything is there," Aksimentiev said. "And once we have this truly atomic-scale representation of the experimental system … just like an experiment, we can see ions moving through the pore and measure the current."

In contrast to scientists in the wet lab, though, the team can peer into the pore moment by moment to find out why the current is changing as it is. Aksimentiev's group found that tryptophan formed a hydrophobic interaction with the amino acids in the inner wall of the pore.

"The intuitive argument that if you have something bigger in the pore, that blocks the current more, is correct," he said. "It's just that once the tryptophan has passed … it sticks to the wall and brings everything to the side, actually making more space for the ions to pass."

This peculiarity gave tryptophan a highly recognizable signature, he added. "One can see how one can potentially engineer a pore to have those specific interactions and look for difficult-to-distinguish stretches."

Would this phenomenon happen when any peptide containing tryptophan crossed through this pore? Aksimentiev thinks it will depend on the peptide sequence and local chemical environment. In any case, the finding illuminates the complexity of factors affecting the current readout.

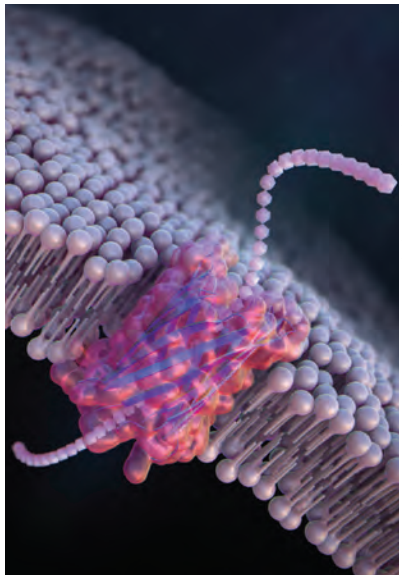
Long said that researchers are accustomed to thinking about current as only a function of volume: In other words, an amino acid's size is the most important determinant of how ions flow past. But, he said, that's probably an oversimplification. Every individual amino acid has the potential to interact with the pore, and so does every ion. These interactions may carry information, but also may increase the complexity of protein-sequencing currents dramatically. And what's more, there are many different pores to choose from.

Many pores

"A polymer is like the notes of music," Long said. "The nanopore is like a musical instrument, a keyboard."

As the polymer passes through the pore, the current is akin to a tone. The same analyte might evoke different currents from different pores, just as a melody sounds different when played on an accordion or a music box.

When, as a postdoc in 2002, Long began to analyze protein structures using a nanopore, his team initially used alpha-hemolysin, which at the time was the only pore in use for DNA sequencing. As it happened, the lab next door at the University of Saskatchewan had a convenient plasmid on hand; the PI had trained in the lab that discovered a bacterial channel toxin called aerolysin and shared it with them. Long's lab uses it to this day.



RYUJI KAWANO/TOKYO UNIVERSITY OF AGRICULTURE AND TECHNOLOGY

Researchers are increasingly able to develop pores from scratch – like this one reported in Nature Nanotechnology last year.

> "Every atom of the protein, every atom of every water molecule, every ion, peptide: everything is there. And once we have this truly atomic-scale representation of the experimental system … just like an experiment, we can see ions moving through the pore and measure the current."
>
> ALEKSEI AKSIMENTIEV

The idiosyncrasies of proteins... can give designers more room to experiment. "With 20 amino acids to play with, we can make different structures we want."

YI-TAO LONG

Hemolysin and aerolysin are just two examples of a vast protein family (see sidebar: "Many pores, many structures"). Multiple labs have published on pores borrowed from various other bacteria: hemolysin, aerolysin, fragaeceatoxin and more. These proteins have diverse characteristics. Some are barely wide enough to squeeze a polymer through the central pore, while others are broad tubes. Others are shaped like funnels that narrow to one critical sensing region.

According to Long, the complexity of how pores interact with proteins once inspired researchers in the field to try using solid-state nanopores built from carbon nanotubes or other fairly homogeneous nonbiological materials. These nanostructures have advantages; they hold up in heat, pH and detergent conditions that can linearize a protein but would destroy a biological nanopore and its lipid environment.

In addition, researchers hoped that engineered pores might yield a smoother interior surface, minimizing the potential for interactions with biomolecules. However, Long said, "That's not the case. Nobody can make an atomic structure smooth."

The idiosyncrasies of proteins, he added, can give designers more room to experiment. "With 20 amino acids to play with, we can make different structures we want."

"Nature has lots of different pores that it's using for lots of different reasons," Nivala said. "We've probably barely tapped into what nature's already built." Meanwhile, improved tools for protein design have led to researchers "starting to engineer protein nanopores from scratch that you can custom-tailor for different applications."

A spokesperson for the company Oxford Nanopore said that when working with a new bacterial pore, the company makes and tests thousands of mutants, aiming to optimize protein expression, interaction with DNA and signal clarity during sequencing.

Although Oxford Nanopore, a juggernaut in the DNA sequencing field, declined to comment on protein sequencing for this article, Nivala said that his lab works closely with the company. He said the pore currently used in Oxford Nanopore's DNA-sequencing flow cells, a secretion channel called CsgG, may not be perfect for protein sequencing. But whatever drawbacks it may have are outweighed, for now, by its ease of use.

"If we are able to do anything useful, some other lab could pretty much instantly then adopt that technology and that technique," he said. "They don't need to be nanopore experts."

Additionally, because Oxford's technology is mature, Nivala's team can focus easily on collecting and analyzing data, not on preparing nanopore wells. That's a good thing, he said. "We're going to need lots and lots of data … to develop machine learning algorithms that can make sense of these signals and decode them back into amino acid sequences."

Problems to solve

Researchers have developed software tools that reliably can identify a short test peptide from a list of options. They still have a long way to go to achieve true protein sequencing. Software that can decrypt the tiny fluctuations in current, just a millionth of an amp at a time, will be as important as choosing the proper molecular machinery.

The race is on to develop algorithms that can determine a sequence starting with no information about it. If that goal can be realized, the combination of single-molecule resolution with long reads could open a door to single-molecule studies of proteins that are currently impossible. Researchers are interested in applications such as antibody sequencing and investigating how multiple post-translational modifications on a single protein, such as a histone, could impact its function.

Instead of conclusively identifying every single amino acid, some researchers have proposed protein fingerprinting, which would pick out individual easy-to-identify amino acids that have strong signatures — such as the wiggle that Dekker's lab observed with tryptophan — and use them as landmarks to infer a protein's identity. Sample preparation that would tag individual amino acids specifically with distinctive chemical labels could help with an approach like this.

Even with their existing shortcomings, researchers say, nanopore protein sequencing systems can already be used for interesting applications such as scanning short peptides for negatively charged post-translational modifications.

And researchers are confident that more advances are just over the horizon.

"It's all coming together," Aksimentiev said. "It's a very exciting time for single-molecule protein sequencing."

Laurel Oldach (loldach@asbmb.org) is a science writer for the ASBMB. Follow her on Twitter: @LaurelOld.

Pores beyond protein sequencing

Yi-Tao Long, a professor at Nanjing University who has been working on developing protein analysis methods that use nanopores since the early 2000s, said that he does not expect pores to overtake mass spectrometry for proteomics completely.

There are uses for which mass spec has downsides, such as differentiating amino acids or modifications with identical mass, where nanopores shine. They also work fast; a researcher with a nanopore can detect biological systems in real time, "like a movie," Long said. Still, "Mass spec is a fundamental technique for protein sequences. Nanopore sequencing cannot be a replacement. It can be complementary, especially for some application environments."

In the world of DNA sequencing, by comparison, both the single-molecule long reads obtained through nanopore sequencing and the massively parallel short reads obtained through next-generation sequencing have advantages and are useful for different types of study.

Long said some of the most exciting applications for nanopores open completely new capabilities. For example, he is interested in using nanopores to make enzymatic synthesis faster at an industrial scale. Whereas chemical syntheses can use heat and stirring to increase the frequency with which reactants collide, speeding reactions, enzyme-catalyzed systems can't stand up to heat and vigorous stirring. Instead, Long said, what if researchers found ways to embed catalytic sites into the walls of a pore and then draw reactants in?

He also emphasized that while sensing specific amino acids is useful, nanopores also can be used to sense other types of analytes, such as environmental contaminants.

Structural biologist Melanie Ohi said that many basic scientists who study bacterial pores are interested in the possibility of using them for drug delivery. "A lot of these toxins are very cell-specific," she explained. Although it will take more research to determine whether their specificity comes from being released near those cells or from recognition of cell surface molecules, "It seems like it could be very powerful if you could take the bacterial toxin that is delivered to a very specific cell and re-engineer it to deliver a drug."

The gene expression conference that keeps evolving

Almost a decade since its inception, and after a brief delay caused by COVID-19, a meeting dedicated to discussing the evolution and core processes in gene expression will reemerge in Kansas City this summer

By Caleigh Findley

Later this year, the American Society for Biochemistry and Molecular Biology will host its biennial conference on evolution and core processes in gene expression. It will be held July 21–24 at the Stowers Institute for Medical Research in Kansas City, Missouri.

The in-person conference focuses on the cis-regulatory code, particularly how it is read out by the transcription machinery and how it affects everything from genetic circuitry to development and evolution. This year's event promises to delve further into the computational methods and genomics technology currently driving innovation in interpreting DNA sequence.

David Arnosti, a professor at Michigan State University and the longest-standing organizer for the conference, said, "Experimental scientists who study biological systems are sooner or later confronted with Dobzhansky's observation that nothing makes sense in biology except in the light of evolution."

Since its formal launch in 2013, said co-organizer Julia Zeitlinger, the conference has evolved constantly. A faculty investigator at Stowers, Zeitlinger said that repeat attendees can look forward to new sessions and emerging science.

Zeitlinger said she believes that the interplay between computational methods, transcription and evolutionary biology will be a fruitful topic of discussion for many attendees.

"We always knew that the substrate of evolution is DNA. We've known this for decades. And we also know that DNA ultimately controls development in a very reproducible fashion," she pointed out. "However, how exactly that information is encoded in the DNA sequence is a very complex problem. Since it is so hard, we cannot track evolutionary changes very well. Now, with deep learning, the computational methods are ripe to address that question."

Arnosti agreed that computational modeling provides exciting prospects for evolutionary biology. Researchers are "focused on individual points of deep conservation or strong divergence. In mapping the terrain … we just have a few mountains and deep valleys to shape our stories about how developmental processes evolve," he said.

Quantitative understanding of these evolutionary processes can provide exciting new frontiers for basic science and medical research.

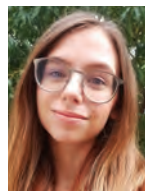
The organizers said they are eager to host the event this summer after postponing it in 2021 in light of the pandemic. All the necessary precautions and measures are in place to ensure a safe and comfortable experience for attendees, they said.

The conference will have its trademark intimate setting, providing ample opportunity for attendees to network with scientists within and outside their areas of specialty. Everyone from junior investigators to senior scientists is encouraged to attend, the organizers said.

The invited speaker list boasts a novel lineup of researchers, including "multiple people combining deep learning with experimental methods to extract cis-regulatory information out of the data," according to Zeitlinger — a unique opportunity for conference attendees.

Also featured are returning speakers, such as Nicolas Gompel of Ludwig Maximilian University of Munich, whom Arnosti characterized as a "renaissance scientist" whose talk promises to share fantastic knowledge on developmental evolution.

Caleigh Findley (cfindley68@siumed.edu) is a senior Ph.D. candidate in pharmacology and neuroscience at Southern Illinois University School of Medicine. Follow her on Twitter: @benchtopblog.



Evolution and core processes in gene expression

The focus of this meeting is to discuss the most recent insights into the cis-regulatory code; how cis-regulatory information is read out by transcription factors, signaling pathways and other proteins; how cellular diversity is created during development; and how we can study this problem using cutting-edge genomics technology and computational methods.

It will be held in person July 21–24 in Kansas City, Missouri.

DEADLINES

Talk abstracts: May 6 | Poster abstracts: May 25 | Registration: May 25

ORGANIZERS

Julia Zeitlinger, Stowers Institute for Medical Research
David Arnosti, Michigan State University
Justin Fay, University of Rochester
Nicolas Rohner, Stowers Institute for Medical Research

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SPEAKERS

Frank Albert, University of Minnesota

Courtney C. Babbitt, University of Massachusetts Amherst

Carl de Boer, University of British Columbia

Rachel Brem, University of California, Berkeley

Stirling Churchman, Harvard University

Barak Cohen, Washington University in St. Louis

Angela DePace, Harvard University

Hernan Garcia, University of California, Berkeley

Kerry Geiler–Samerotte, Arizona State University

Nicolas Gompel, Ludwig Maximilian University of Munich

Raluca Gordan, Duke University

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Tatjana Sauka–Spengler, Stowers Institute for Medical Research

Premal Shah, Rutgers University

Alex Stark, Research Institute of Molecular Pathology

Jussi Taipale, University of Cambridge

Patricia Wittkopp, University of Michigan

Emily Wong, Victor Chang Cardiac Research Institute

A hybrid symposium on mass spec

Coming to Cambridge and a computer near you this fall

By Courtney Chandler

The 14th International Symposium on Mass Spectrometry in the Health and Life Sciences will take place Aug 14–18 in Cambridge, Massachusetts, and online. Co-organizer Bernhard Küster, a professor at Technical University of Munich, talked to ASBMB Today about the symposium and what participants can expect. The interview has been edited for style and clarity.

Q: What is the goal of the meeting?

A: The purpose of the meeting is to bring together true leaders in the field, both from academia and industry, to present and discuss the latest and greatest scientific advances that are enabled by the application of mass spectrometry and related technologies.

Q: What do you think some of the themes will be?

A: People are excited about single-cell proteomics, but many improvements have to be made during sample preparation and data acquisition as well as informatics for proteomics to become practically useful.

Relatedly, proteomics informatics is continuing to be a big need as the data volumes increase and some of the informatics tools are not fully understood or validated.

Artificial intelligence also has arrived in mass spectrometry, and it will be important to learn where AI can and cannot be meaningfully applied.

Mass spectrometry–based proteomics is back on the high road in biotech and industry. The field needs not only to seize the many opportunities that this presents but also to make sure that mistakes are not repeated.

All of these and other areas require open and frank discussions, and there are no easy answers for many. Again, this meeting should be a good place to have such discussions, and these represent the true value of the meeting.

Q: What is your experience with the meeting?

A: I first heard about the meeting at very end of the 1990s, when I was a postdoc. Albeit quite a small meeting in comparison, it had already a very good reputation back then to be a forum where the top people in the field would meet and discuss the science as well as the challenges. Both are important elements of this particular meeting and are something one does often not find at larger meetings.

The first time I got to go was in 2003, when I was a group leader at the biotech firm Cellzome (now part of GlaxoSmithKline) in Heidelberg, Germany, and then again as a university professor in 2014, and I have not missed a meeting since.

Q: How did you become an organizer?

A: Up to this point, the conference had always been held in San Francisco. … In 2016, I was asked to organize a minisymposium on chemical proteomics on the day just preceding the main program. I guess I did a reasonably good job, because I was asked to co-organize the meetings in 2017 and 2019 and the current one.

The format of a minisymposium on the day before the main program turned out to be a great way to pick a nascent topic and discuss its potential but also pitfalls. This time, the topic is single-cell proteomics, an area that is in its baby years, and its direction and opportunities are just emerging. There are a lot of issues that make for great discussion material. Naturally, we aim to get the most visible players in that nascent area to present their latest results.

Q: How did you select the invited speakers?

A: For the main program, we still strive to get some of the most accomplished researchers to present. But we also complement this with selecting younger talent — of which there is, luckily, no shortage — and we keep on improving the gender balance in the program, which becomes easier to do every year as equal opportunity measures are taking more and more effect.

Q: What is the general breakdown of attendees?

A: My best guess is that the breakdown is something like 20% PIs, 50% postdocs and investigators at various levels of seniority, and 30% Ph.D. students.

Mass Spectrometry in the Health and Life Science Meeting, Aug. 14–18

ORGANIZERS

A. L. Burlingame, University of California, San Francisco
Steven Carr, Broad Institute of MIT and Harvard
Bernhard Küster, Technical University of Munich

BURLINGAME

CARR

KÜSTER

PLENARY SPEAKERS

Ivan Dikic, Goethe University Medical School
Connie Jimenez, VU University Medical Center
Ryan Kelly, Brigham Young University
Stuart Schreiber, Harvard University

DEADLINES

May 16: Abstract submission/early registration
July 1: Regular registration

SPEAKERS

Marcus Bantscheff, GlaxoSmithKline
Hannah Boekweg, Brigham Young University
Claudia Ctortecka, Broad Institute of MIT and Harvard
Katherine Donovan, Harvard University
Brad Gibson, Amgen Inc.
Albert Heck, Utrecht University
Lan Huang, University of California, Irvine
Trey Ideker, University of California, San Diego
Jeroen Krijgsveld, German Cancer Center
Fan Liu, Leibniz Research Institute of Molecular Pharmacology
Matthias Mann, Max Planck Institute of Biochemistry
Ana Martinez Del Val, University of Copenhagen
Philipp Mertins, Max Delbrück Center for Molecular Medicine
Ilaria Piazza, Max Delbrück Center for Molecular Medicine
Andreas Pichlmair, Technical University of Munich
Markus Ralser, Francis Crick Institute
Matthew Rasband, Baylor College of Medicine
Julio Saez–Rodriguez, University of Heidelberg
Yardena Samuels, Weizmann Institute of Science
Erwin Schoof, Danish Technical University
Devin Schweppe, University of Washington
Nikolai Slavov, Northeastern University
Alice Ting, Stanford University
Forest White, Massachusetts Institute of Technology
Mathias Wilhelm, Technical University of Munich
Jana Zecha, AstraZeneca
Ying Zhu, Pacific Northwest National Laboratory

Q: What do you hope participants will gain by attending?

A: We hope for open and frank discussions about the merits of the technology and its application in the life sciences. … As mass spec and related technologies become more and more accessible, there's a need to make sure that the basic education and understanding are kept at a high level.

Courtney Chandler (courtneyec19@gmail.com) is a biochemist and microbiologist in Baltimore, Md., and a careers columnist for ASBMB Today. Follow her on Twitter: @CourtneyCPhD.

‘I hope it turns out to be a beautiful firework’

Organizers of ASBMB conference on transcriptional regulation look forward to igniting attendees’ curiosity and passion in Snowbird, Utah

By Isha Dey

The American Society for Biochemistry and Molecular Biology is holding its popular biennial conference on transcriptional regulation Sept. 29 through Oct. 2 in Snowbird, Utah.

Since its inception in 2004, the meeting has garnered a lot of attention from what the organizers call “people of the year in the field of transcription.” The meeting is highly interactive and collaborative, with presenters and audience members from academia and industry.

ASBMB Today spoke to the organizers — Karen Arndt of the University of Pittsburgh; Dylan Taatjes of the University of Colorado, Boulder; and Yan Jessie Zhang of the University of Texas at Austin — about what makes the event special, how trainees can get involved, and what excites them most about the meeting and the field.

Q. What is unique about this meeting?

Zhang: It is a great tradition. We have a longstanding record of attendance and loyal followers. For the past 20 years or so, we have been having this in-person meeting, and exciting science is presented. With an audience size of 120 to 150, it provides a great opportunity for trainees for one-on-one interaction with professors, which helps advance their academic careers.

Taatjes: The audience is a good mix of graduate students, postdocs and faculty. So there is a lot of energy. Plus the venue is spectacular, with lots of activities, and the setting is informal, so everyone is in a good mood. The meeting provides a very supportive and collegial environment to the attendees.

Arndt: There is a lot of exchange of ideas between attendees during poster sessions because people get the time to see each and every poster. My personal favorite part is that winners from the poster session are asked to give talks on their work, and this is the only conference that does it.

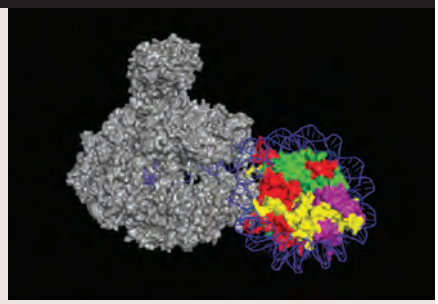
Q. Why did you decide to hold the meeting in person?

Taatjes: Considering the intimacy this meeting provides with respect to building relationships between trainees and professors, as well as academia and industry, we decided that an in-person meeting would be the best setup. Also, after the long break because of the pandemic, people are craving in-person interaction, so that was a big driving force behind our decision.

Zhang: I think an in-person meeting really benefits the trainees.

CONTINUED ON PAGE 52

Transcriptional Regulation: Chromatin and RNA Polymerase II, Sept. 29–Oct. 2



Sessions will cover recent advances and new technologies in RNA polymerase II regulation, including the contributions of noncoding RNAs, enhancers and promoters, chromatin structure and post-translational modifications, molecular condensates, and other factors that regulate gene expression.

ORGANIZERS

Karen Arndt, University of Pittsburgh
Dylan Taatjes, University of Colorado, Boulder
Yan Jessie Zhang, University of Texas at Austin

ARNDT

TAATJES

ZHANG

IMPORTANT DATES

July 14: Oral abstract deadline
Aug. 1: Early registration deadline
Aug. 18: Poster abstract deadline
Aug. 28: Regular registration deadline

SPEAKERS

KEYNOTE | **Patrick Cramer**, Max Planck Institute of Biochemistry, "Structure and Function of Transcription Regulatory Complexes"

Karen Arndt, University of Pittsburgh

Lu Bai, Penn State University

David Bentley, University of Colorado School of Medicine

Stephen Buratowski, Harvard Medical School

Stirling Churchman, Harvard Medical School

Ibrahim Cisse, Massachusetts Institute of Technology

Philip Cole, Harvard Medical School

Xavier Darzacq, University of California, Berkeley

Rani George, Dana Farber Cancer Institute

Steven Hahn, Fred Hutchinson Cancer Research Center

Cigall Kadoch, Dana Farber Cancer Institute

James Kadonaga, University of California, San Diego

Craig Kaplan, University of Pittsburgh

W. Lee Kraus, University of Texas, Southwestern

Daniel Larson, National Cancer Institute/ National Institutes of Health

Shannon Lauberth, University of California, San Diego

John Lis, Cornell University

Karolin Luger, University of Colorado, Boulder

Catherine Musselman, University of Colorado School of Medicine

Anders Näär, University of California, Berkeley

Geeta Narlikar, University of California, San Francisco

Karla Neugebauer, Yale University

Eva Nogales, University of California, Berkeley

Frank Pugh, Cornell University

Joseph Reese, Penn State University

Francois Robert, Montreal Clinical Research Institute

Ali Shilatifard, Northwestern University, Feinberg School of Medicine

Brian Strahl, University of North Carolina at Chapel Hill

Dylan Taatjes, University of Colorado, Boulder

Dong Wang, University of California, San Diego

Carl Wu, Johns Hopkins University

Ken Zaret, University of Pennsylvania

Yan Jessie Zhang, University of Texas at Austin

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Q. What opportunities are available for the trainees?

Zhang: We have two poster awards and a special session for the poster award winners where they get to give talks on their work, and the competition is very tough. We have seen in the past that these works usually are published in top journals around the globe.

Also, the industry sponsors put up their job ads right near the entrance to the conference hall, so it is a great opportunity for the trainees to seek future opportunities.

Q. What's the format?

Taatjes: The talks are short, and we allow enough time for questions and answers. The poster sessions are very lively. Our talks are grouped into various themes. We have seen that this format has been successful. It is enjoyable and productive, and that is why people attend this year after year.

We have had keynote speakers like Roger Kornberg, Steven Henikoff, Ali Shilatifard, Eva Nogales, who are stalwarts in the field. This time, we have Patrick Cramer.

Zhang: We are very proud of our meeting tradition for the past two decades, but we have tried to maintain a balance between tradition and new developments. So while we want to keep the format and timing of the conference consistent, we update the theme topics very frequently to keep up with the latest developments in the field.

In this conference, we get to learn about the latest technologies and concepts in the field from our speakers before they become breakthrough developments. We also look out for young and upcoming scientists and reach out to them to invite them to talk about their work. This helps build relationships.

Q. What are you looking forward to most?

Zhang: The biggest opportunity for a scientist is to be able to discuss their work with other scientists. In the process, you have new ideas to improve your work. In the past two years, because of COVID-19, we have been living in our own shells. We need the sparks between fellow scientists, and I am looking forward to it. I hope it turns out to be a beautiful firework.

Arndt: While the virtual meetings have allowed me to keep up with what's happening in science to some extent, I think two things have been lost: the communication and the bouncing of ideas. Also, the virtual posters are almost impossible to navigate. So an in-person communication helps make connections with people who might be your postdoc advisers or who might hire you in their companies or universities. I am looking forward to having the trainees back.

Isha Dey (ishaadey@gmail.com) is a scientist at Thermo Fisher Scientific in India.

No one better

Essays by 2021 ASBMB fellows

By Angela Hopp

If anyone knows how valuable and impactful being a member of the American Society for Biochemistry and Molecular Biology can be, it's our fellows.

They've started, served on and led our committees. They've published important papers, improved the manuscripts of others and transformed our journals. They've organized meetings and divisions, influenced pedagogy, and advocated for science locally and nationally. They've made lasting relationships that have made their lives and their work better.

I can think of no one better to provide testimony about the ASBMB member experience than this group of engaged and committed scientists.

That's why I called on them late last year to reflect on what ASBMB membership has meant to them all these years — and to invite them to write short personal essays about it for ASBMB Today in 2022.

Many fellows, true to form, were happy to volunteer. We're publishing some of their essays this month and will publish others as the year goes on.

I hope you'll take time to read about their experiences and think about what ASBMB membership has added to your professional and personal life. And, as it is graduation season, you might consider giving the gift of membership to a student or colleague so that they too can reap rewards.

Bonding over biochemistry

By F. Peter Guengerich

How did I become a biochemist? I was not one of those kids who played with a chemistry set or dissected frogs. But I did like chemistry. I spent the summer after my sophomore year of college in Harry Broquist's lab at the University of Illinois, and since then I never have wanted to be anything else.

Chemistry was so cool when applied to life. I got my Ph.D. and tried to become a complete biochemist, mastering a number of areas. After starting my own lab as an enzymologist in the biochemistry department at Vanderbilt University, I joined the American Society for Biological Chemistry (now the American Society for Biochemistry and Molecular Biology) in 1978. At that time, membership was pretty selective, but I had a couple of JBC papers published on my own and got in.

The ASBMB sponsors many activities that are important to biochemists and to the scientific community as a whole. One of the most important is scientific publishing.

The Journal of Biological Chemistry, founded in 1905, actually predates the ASBMB by a year. I was privileged to serve as a JBC editorial board member for 18 years. I remember my first day on the board — three manuscripts for review (all from different associate editors) arrived in the mail (yes, they came by mail then, always in recognizable green and white envelopes). Since 2006, I have been an associate editor, and I've served twice as interim editor-in-chief.

Why would anyone want to do these things? It has been rewarding to be a part of a journal that has published so many seminal papers and continues to be a leader in scientific publication. The emphasis is always on quality. JBC was the first journal in the field to go electronic and also has been a leader with its empha-

sis on data integrity, which I became very involved in. I still get excited about publishing my own papers in JBC (and my lab has also published in Molecular & Cellular Proteomics and the Journal of Lipid Research, the other two ASBMB journals).

I also had the honor of working with and knowing Herbert Tabor, who served as editor-in-chief of JBC for almost 40 years and gave so much to the journal and the society. Knowing biochemists like Herb is priceless.

I have gone to most of the ASBMB annual meetings. It is great to meet old friends — and make new ones. Our lab at Vanderbilt is called the Dogs — just like some athletic teams — and I always try to organize a "Dog Dinner" of our alumni who are at the meeting and those living in the area. I think of my lab as a fraternity that people spend some time in and always remember — you can check out but never really leave. Indeed, I could extend that analogy to the whole field of biochemistry.

I've been privileged to meet and work with many fine people, including the staff at the ASBMB. I doubt if many people outside the ASBMB staff know this, but about a dozen of my large landscape and nature photographs hang on the walls in their office. I am grateful that I could in some way help pay them back for all of their efforts, providing something to brighten a day now and then. If you ever get to the office, check them out.

Biochemistry is great because if you learn and understand it, you can apply it to almost any kind of science — I've done that in pharmacology, toxicology, endocrinology and other things. It all comes back to knowing biochemistry. I was elated to be named an ASBMB fellow last year, and every biochemist or other biochemically minded scientist should be an ASBMB member and be involved in its programs. It's great to bond with other biochemists.

F. Peter Guengerich (f.guengerich@vanderbilt.edu) is a professor of biochemistry at Vanderbilt University, an associate editor of the Journal of Biological Chemistry and a 2021 ASBMB fellow.

A journey with scientists

By Dan Raben

We often remember how important journeys in our lives begin. I began my journey with the American Society for Biochemistry and Molecular Biology as a graduate student at Washington University in 1976 while in the biochemistry department (now the department of biochemistry and molecular biophysics).

This department had an atmosphere of excitement and discovery among the faculty, students and postdoctoral fellows. The departmental culture encouraged the free exchange of results and ideas, and we were all excited when we had the opportunity to extend these discussions to others in our own and related fields. We had two major avenues for these exchanges: publishing our results in good journals and going to national and international meetings. The two premier platforms for such exchanges were the Journal of Biological Chemistry and the ASBMB annual meeting.

This did not change for me as a postdoctoral fellow and continued when I joined the faculty at Johns Hopkins University in 1986. The high esteem for JBC and the ASBMB annual meeting was palpable among the biochemists and molecular biologists at Hopkins. Dan Lane, director of the biological chemistry department, was elected president of the ASBMB in 1990 and championed the benefits of becoming an ASBMB member. He wasn't wrong. As I started my career, my first-choice journal was JBC, and my go-to meeting was the ASBMB annual meeting, where I met colleagues and made friends that remain in my life to this day.

In 2010, I organized a lipid-themed session for the ASBMB meeting, and I then served as a co-chair for the 2011 meeting. It was exciting for me to learn more about how the ASBMB functions and makes decisions; I was gratified to learn that the underlying motivation was to serve scientists. This applied beyond the principal mission to help scientists disseminate and discuss their results with leaders in a variety of fields

and foster new interdisciplinary collaborators. The society also has a well-oiled structure to stay abreast of important trends that affect both established investigators and trainees. These include issues such as funding, job placement and career development, minority affairs, and education.

As my career developed and my associations with the ASBMB grew, I had the opportunity to become the chair of the Meetings Committee. Not surprisingly, I saw firsthand how dedicated ASBMB members can work together to organize a great annual meeting. We had the freedom to explore new ideas and structures for the meeting, adjusting to those that worked well and jettisoning those that were less successful. While committee members held differing views on various topics, it was clear that the meeting's success was of paramount importance. It was refreshing and reaffirming to see how folks from different areas of biochemistry and molecular biology could work synergistically to put together an exciting meeting.

In addition to my work on annual meetings, I helped establish the ASBMB Lipid Research Division with Binks Wattenberg, a professor at Virginia Commonwealth University. This division, now under the direction of George Carman and Rob Stahelin, exemplifies how the ASBMB can help foster and support a field of biochemistry occupied by many society members. Its impetus came from lipid scientists who felt this diverse field lacked a platform where investigators and trainees in its subfields could form a more cohesive community and foster collaborations. The ASBMB — in particular, Barbara Gordon, then the executive director — went above and beyond any job description to help establish this division and foster a now healthy and growing community that addresses community-specific issues.

For example, many lipid investigators felt their National Institutes of Health grant proposals were placed in study sections that lacked reviewers with the lipid expertise necessary for an adequate review. This wasn't surprising, given the interdisciplinary nature of lipid research and its impact on a variety of fields. Consequently, lipid-related proposals often were assigned to study sections that were unfamiliar with the field. To address this, the ASBMB LRD collaborated with the NIH Center for Scientific Review and provided a list of qualified lipid scientists within the ASBMB, along with their specific expertise, who were willing and able to serve on study sections. This list was shared with the scientific review officers to help them find the necessary expertise. Given the LRD's success, more divisions are likely to develop in the future to serve other disciplines within the ASBMB community.

The ASBMB not only has been influential in my development as a scientist but also has been instrumental in fostering a vibrant scientific community. From what I can tell, there's a lot more excitement to come.

Dan Raben (draben@jhmi.edu) is a professor at the Johns Hopkins University School of Medicine and a 2021 ASBMB fellow.

Making a bigger footprint

By Kerry-Anne Rye

One of the first tasks on my to-do list each morning is to quickly peruse the many emails I receive overnight. You might think that getting a large number of emails during the night is strange, but I live in Australia and am therefore asleep during regular office hours in the U.S. More often than not, one or two things in this long morning list affect, and occasionally completely mess up, my plans for the rest of the day.

While skimming through an unusually long list of messages one morning in early April 2021, I noticed an email from Toni Antalis, president of the American Society for Biochemistry and Molecular Biology. Because this was unexpected, it was one of the first messages I opened that day. I was hugely surprised and delighted to read that I had been selected as an inaugural ASBMB fellow. So, rather than mess up my day, Toni's message had quite the opposite effect.

On looking through the list of fellows, I was even

more surprised to discover that I was the only one who was not from the U.S. While it could be argued that this made my election as an ASBMB fellow special, that is not how I saw it. Indeed, the first thing that occurred to me is that we need to develop a strategy to remove any notion that membership in the ASBMB only benefits people who reside in the U.S. In other words, it is really important to increase the international footprint of ASBMB membership at all levels, from the most junior postdoctoral fellow right through to senior scientist.

I have been involved with the ASBMB since the late 1980s when I was a junior postdoctoral fellow and a frequent author of submissions to the Journal of Biological Chemistry. As the years passed, my interests moved away from the biophysical chemistry that formed the foundation of my career as an independent scientist and headed toward the biology and function of lipids. This led to an invitation to become an editorial board member of the Journal of Lipid Research. After several years of reviewing manuscripts for the journal, I was appointed as an associate editor, a position I held for 10 years until assuming my current role as co-editor-in-chief in 2019.

This appointment has given me a much greater insight into the ASBMB as an organization and not just as a publisher of quality scientific research. In addition to making an invaluable contribution to the scientific community and advancing knowledge with its three journals, the ASBMB also provides numerous opportunities for its members to develop networks and initiate important, long-standing collaborations with like-minded scientists at all career stages.

The vibrant and active community that constitutes the membership of the ASBMB has contributed to many a stellar scientific career and not only serves to expand individual interests but also ensures that its members are fully informed about the most recent research advances. Membership comes with huge benefits for all of us, and it is something I value enormously.

For this reason I strongly encourage anyone reading this to join the ASBMB, to sign up for online ASBMB events, to attend ASBMB meetings — whether virtual or face-to-face — and to take advantage of the resources the society offers to build your personal and professional networks.

I have resolved to assist the society in any way I can to build its international membership profile, and this year I plan to work toward engaging with U.S.-based as well as international members in all aspects of the ASBMB's activities. I look forward to many of you joining me in this endeavour and hope to see you either virtually or face-to-face in the coming year.

Kerry-Anne Rye (k.rye@unsw.edu.au) is a research professor, head of the Lipid Research Group and deputy head of research in the University of New South Wales School of Medical Sciences, co-editor-in-chief of the Journal of Lipid Research and a 2021 ASBMB fellow.

Connecting by committee

By Adele J. Wolfson

Everyone hates committee meetings — the kind that we all say could have been an email, the kind that interrupt your flow of writing or working in the lab, the kind where someone repeats something you said five minutes ago and everyone forgets you said it first, the kind that run over and make you late to pick up your kids from daycare.

But committees and committee meetings are what have connected me to the American Society for Biochemistry and Molecular Biology over many years and influenced my career as a scientist, educator and administrator.

I clearly remember my first encounter with an ASBMB committee. The phone call asking me to serve on the Committee for Equal Opportunities for Women made me feel validated (and valued) as a new faculty member. I even remember what I wore to that meeting.

We met in the little house behind the old ASBMB headquarters in Bethesda, Maryland, and I was in awe of the group around the table — appropriately so, since

many distinguished scientists and future presidents of the society were there. It was also the first time I met Barbara Gordon, the ASBMB's former executive director, and made a connection and friendship that have endured.

Over the years, I have served on many ASBMB committees; some of them developed initiatives that have changed the annual meeting and the society overall — education satellite meetings, women's networking sessions, undergraduate poster competition, better integration of education and professional development programming into the mainstream, undergraduate program accreditation.

It was the wisdom of the committee, not that of any individual, that allowed good ideas to come to fruition.

In the course of serving on these committees, I have met members whose research overlapped with mine and who gave me guidance about research and publication, those whose suggestions led to major changes in my teaching, and those who became collaborators in education and pedagogy scholarship. I also learned how to be a constructive committee member and, eventually, an effective committee chair.

Like any big organization, the ASBMB has a large, loosely affiliated membership. Members sample what they need or find interesting from the society's publications, meetings and other offerings. But what I'd call the "back office" of those offerings is a network of committees populated with members and supported by extraordinary staff, and there is always a need for members to find their place and their way to contribute within that network.

Adele J. Wolfson (awolfson@wellesley.edu) is a professor emerita in the physical and natural sciences and professor emerita of chemistry at Wellesley College and a 2021 ASBMB fellow.

Collaborating with a librarian

For crisper class projects, make this your gDNA

By Alyssa H. Young & Christopher E. Berndsen

While today's undergraduates are at home in the digital world, many do not know how to sort through the noise to find and organize information. For example, when a student comes across a peer-reviewed article about dark DNA blackholes in PubMed, do they have the skills to evaluate it? Or do they believe it is accurate because it has the peer-reviewed stamp of approval?

We have found that some students are more accustomed to searching in Google with natural language than in a research database using keywords. They prefer to use the search function instead of creating a directory structure to organize the sources they find. How do we teach our students these information and data literacy skills?

Students face many challenges: choosing valuable and efficient resources; gaining access to articles behind paywalls; and evaluating the reliability of information from preprints, online lectures, or non–peer-reviewed sources. Along with these challenges, students have questions about the research process.

This is where a librarian comes in.

For the past several years, we (a biochemist and a librarian) have collaborated to address these obstacles in undergraduate biochemistry lecture and lab courses. We thought some science department faculty might be interested to learn how partnering with a science librarian in the classroom works.

The partnership began when the biochemist reached out to the librarian and asked if she could help his biochemistry students improve their citations in class. We set up a meeting to further discuss this request so the librarian could better understand the citation problem; she hoped this was not just a request to come to a class to teach a specific citation style. When we met, we agreed the root of the problem was that students were not finding the best sources, and therefore the information cited could be of better quality. The problem was less about citation style and more about how students found sources and evaluated information. After this meeting, we got to work.

Looking at previous class projects, we noticed that students were getting their information from popular general-use websites such as HealthLine and LiveStrong rather than journals or academic websites. We learned that students don't always know about the best resources for biochemical information, especially if they have no previous research experience in the field. Experienced scientists know how to find information and reliable sources; the challenges come in explaining the step-by-step process or the benefits of one search tool over another.

We have structured our courses as project-based classes that benefit from acquainting students with literature. However, if students do not know where to search, they have difficulty finding good resources and may lose their motivation to explore and find information.

How do we get students to search effectively? We start by defining what resources would be the most efficient and helpful to share with students while also reflecting our open science values. Open resources in biochemistry exist, but students need help gaining access to them and understanding their importance as resources for biochemical information. We teach the use of UniProt, the RCSB Protein Data Bank, PubMed, OMIM and PubChem for students to find information, while using the Open Science Framework and Zotero to aid students in managing their research activities. Several of these resources narrow down where to find information, so students are not overwhelmed. The others help streamline and organize the projects.

We make sure to incorporate these resources into the projects students work on during the course. For example, students might use PubMed to search literature while exploring the diverse scientists in the biochemical field, or they extrapolate mutation data from Uniprot to explain the molecular basis for disease.

The librarian provides videos on using the resources and best practices to search for biochemical information. She joins the class twice to dig deeper and discuss ways to find information and learn more about the scientific process. She is also available to meet with students throughout the semester when questions arise. Students typically ask for more help in searching PubMed or UniProt, expanding their possible keywords to use in searches, and using Zotero to its fullest potential. While these topics are taught or brought up in

the instruction sessions, one-on-one consults can lead to the student learning more than what was taught in the class session.

We work with students so they can understand better how to evaluate and synthesize information. They learn to examine critically who the authors are, where they publish and who is citing the information. We each bring our own perspective as a biochemist and librarian to these discussions; we can connect information that flows from one field into the other and, in the process, emphasize the importance of librarians and libraries during the scientific process.

As we become more comfortable with our collaboration and better understand students' interests, class discussions have evolved from the nuts and bolts of searching for information to more in-depth conversations about how scientific information is created and disseminated and how scientific research evolves. Students learn how the research they find in the literature is recorded and shared with the scientific community and beyond. They also learn about systemic issues in the research world such as gender issues in scientific publishing, challenges in responsible sharing of data, and article retractions. Students understand that science is a human process: Ideas are discovered, tested and modified. They learn that by effectively searching for information they can see this entire process.

The collaboration between a biochemist and librarian also allows the two of us to learn more about one another's roles in the scientific process, and we better understand how we can support one another. While we use many of the same search tools, we learn from one another and improve our skills based on the type of information we might be searching for. The librarian learns more about the information found within UniProt, while the biochemist learns how MeSH terms work in PubMed. We often share sources from our fields related to topics discussed in class that expand our knowledge in those areas. For example, we have found resources about open-access publishing from different sources related to our fields that we share with one another. This allows us to expand from the sources in our own fields and see shared interests from different field perspectives.

Resource	Description	URL
OMIM	Database of human genes and variants	https://www.omim.org/
RCSB Protein Data Bank	Database of 3D structures from X-ray, NMR and cryo-EM experiments	https://www.rcsb.org/
PubChem	Search interface for chemical information including chemical and physical properties, biological activities and toxicity information	https://pubchem.ncbi.nlm.nih.gov/
PubMed	Search interface for biomedical and life sciences with sources from MEDLINE, PubMed Central and Bookshelf	https://pubmed.ncbi.nlm.nih.gov/
The Open Science Framework	Online software to aid in project collaboration and dissemination of data	https://osf.io/
UniProt	Database of protein structure/function	https://www.uniprot.org/
Zotero	Tool that saves, organizes, generates, integrates and shares citations	https://www.zotero.org/

All these resources are free and open-access.

Our collaboration benefits all involved. We've had to take time away from the usual course content to add information and data literacy instruction, but there are rewards. These lessons help students understand why they are doing what they do in science courses. A previous student, Claire, said, "Although literature searches are an important aspect of science, I was not confident in my ability to successfully do so as a sophomore at JMU. Alyssa's explanations of library resources, popular STEM databases, and searching techniques made literature reviews more approachable. I have continued to use these skills outside of the biochemistry course."

Students can transfer information and data literacy skills to other courses and continue to expand on them throughout their careers.

Another student, Roma, said, "I appreciated that Alyssa would moderate discussions in class about ethics in science and considered her a very useful resource for searching through recent and relevant literature for any of my chemistry classes or labs."

So take a chance and reach out to your library; you might be surprised at how your course will change.

In 2022 and beyond, we will be hosting a series of conversations for librarians and scientists aimed at increasing collaboration between these communities to further student information literacy. Please reach out to us if you would like to be involved.

Christopher E. Berndsen (berndsce@jmu.edu) is an associate professor in the chemistry and biochemistry department at James Madison University.

Alyssa H. Young (young2ah@jmu.edu) is an assistant professor in the libraries at James Madison University and the liaison librarian to the college of science and math.

A tale of two ZIP codes

By Christopher D. Radka

Memphis is a renowned, multi-faceted gem of the Midsouth that tells its story through the cultural outpouring of diverse attractions like the National Civil Rights Museum, Sun Studio (the birthplace of rock 'n' roll, where musical legend B.B. King was discovered) and world-class barbecue. Memphis is also home to some of the worst inequity in the U.S.

April is National Minority Health Month, a time to reflect on the importance of closing racial and ethnic gaps in health disparities and consider actionable goals that can improve the quality of life across our communities.

Disparities in access to healthcare or in outcomes for different health conditions are important topics that receive substantial attention. But what comes before healthcare? Basic needs that are the right of all humans: food and air.

Disparities in access to clean air and fresh food are major predictors of the prevalence of so-called diseases of poverty (i.e., obesity, diabetes and hypertension). The lack of access to fresh food and clear air precipitates a domino effect in the predisposition to more fatal illnesses, such as cancer, stroke or compromised ability to fight infection. Although there are genetic causes to these illnesses, much of the pathology is triggered by behavior and poverty.

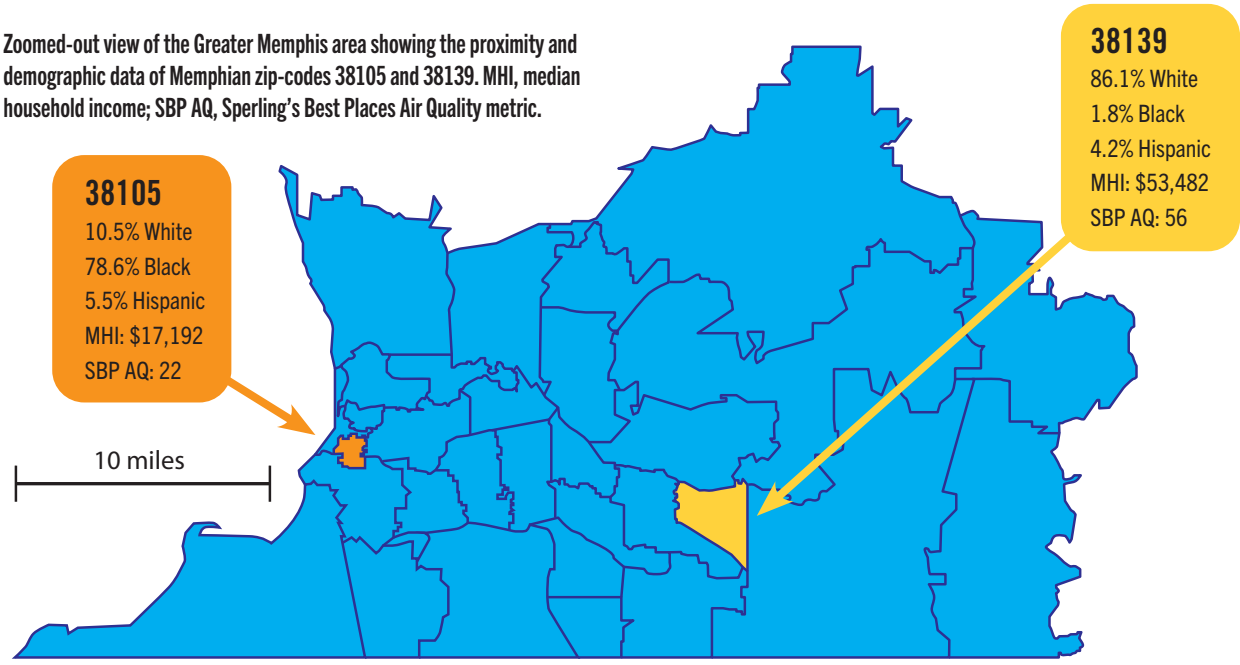
My origin motivates me to understand better the variances in lived experience between the privileged and the needy.

I think of my mom — a Honduran immigrant who came to this country for opportunity, struggled as a young mother, and is now an executive who teams with my dad to put on the largest back-to-school event in the state of Florida, which provides medical screening, school supplies, backpacks and other essentials at no cost to those in need.

Lessons from my mother have inspired my own community involvement in every place I've lived, most recently as a founding member of the St. Jude Children's Research Hospital Black Employees and Allies Resource Group. My mom taught me you don't have to belong to a particular group to recognize or act on a need.

I came to Memphis to advance my scientific training at a premier research institution, and now, as a father of two, my motivation has intensified to improve our society for the next generation.

I reflect on the poor air quality and unhealthy food many children



Zoomed-out view of the Greater Memphis area showing the proximity and demographic data of Memphian zip-codes 38105 and 38139. MHI, median household income; SBP AQ, Sperling's Best Places Air Quality metric.

consume at school, and improving these aspects of daily life would be an important step toward improving our society. My hope is that shedding light on the situation can stimulate action here and beyond.

As a contributor to ASBMB Today and writing for such an important purpose, I found someone to engage in conversation about Memphis, and the conversation went from local to global.

Local experiences, global application

Miguela Caniza is an infectious diseases expert and the director of the Infectious Diseases Program of St. Jude Global, an ambitious initiative to enhance the global quality of pediatric care by providing access to better therapies and improving the standard of care.

During her master's of public health training at the University of Memphis, Caniza studied health and environmental contamination across Memphis ZIP codes and now travels all over the world to train and equip healthcare providers in mostly developing nations.

"Memphis is an incubator, a lab for the world, because there is so much disparity in Memphis," Caniza told me. "Although markers of environmental contamination can be correlated with diseases of poverty, access to fresh water, fresh food and clean air have profound impacts on health. Thinking about Paraguay, Argentina, and Brazil, they are such beautiful countries with so many resources, but big companies have come in, misused the land, killed the biodiversity, and the overall health of the people has suffered."

Speaking with Caniza inspired me to investigate further what is going on in my community as it relates to differences in health outcomes, disparities in access to healthy food, and disparities in air quality across ZIP codes.

Proximity in location, distance in air quality

The U.S. Environmental Protection Agency performs a triennial review called the National Air Toxics Assessment, or NATA, that provides ambient measurements of 180-plus air toxics, identifies emission sources and correlates this data with health risks such as respiratory illness.

Sperling's Best Places is a market data analysis firm that analyzes NATA and other data to provide interpretable and reliable analysis down to the ZIP code level.

Using the NATA data, SBP created an air-quality index where 100 is the best air quality in the U.S., and the average ZIP code scores a 58.

St. Jude Children's Research Hospital is the premiere pediatric treatment and research facility in the United States, employs some of the world's top minds and is intrinsic to Memphis' identity. St. Jude also is located in one of Tennessee's most impoverished ZIP codes: 38105.

38105 scores a 22 on the air-quality index and has more than double the risk for respiratory illness of the state of Tennessee or the U.S. overall.

According to SBP, the 38105 population of 6,449 residents is 10.5% white, 78.6% Black and 5.5% Hispanic. It has a median household income of $17,192.

A 30-minute drive east takes you to ZIP code 38139, where SBP reports an air quality index of 56, and half the risk for respiratory illness of 38105. 38139 has a median household income of $53,482 and a population that is 86.1% white, 1.8% Black and 4.2% Hispanic.

These data show the demographic of people exposed to the highest levels of environmental contamination in Memphis.

ZIP code effect on survival

ZIP codes 38105 and 38139 are in Shelby County, and according to Shelby County Health Department statistics, the annual age-adjusted mortality rate in the county from chronic lower respiratory disease is 39.6. This rate rises to 54.2 for the downtown Memphis area and falls to 27.2 in a more affluent area.

The annual age-adjusted mortality rate in Shelby County from diabetes is 26.9. This rate rises to 32.1 in the downtown Memphis area and falls to 7.4 in the same affluent area.

These statistics seem to paint a picture that health needs wealth, and in Memphis, wealth is often white.

Another difference is access to fresh food and groceries. There are seven locations of the main grocery store chain in the region within five miles of 38139 but only two locations within five miles of 38105.

Having to travel at least five miles, depending on where in the ZIP code one may live, might not seem like a long distance, but for individuals without reliable transportation or access to public transportation, it is an exceedingly difficult task to travel just to have access to groceries.

On the other hand, fast food is readily available. There are eight locations of a major global fast-food chain within five miles of 38105 but only five locations within the same distance of 38139.

A Memphian experiment to start to affect health outcomes by changing access to clean air and fresh food could become a template for other places across the U.S. or the world to do the same.

Call to action

If Memphis is a laboratory, then why not do an experiment?

Since access to fresh food is limited, what if local masters of cuisine used their skills in the culinary arts and resources from their businesses occasionally to sponsor a school in 38105 and the downtown Memphis area to provide better food options and maybe even teach the children and their families how to cook? Schools can be great hubs to create initiatives in the community, and their partnership could help provide schools with good food and pass on employable skills.

This also could be an opportunity for schools to teach the taste buds of children who are not regularly exposed to fresh produce at home. Children who grow up learning about this might adopt better eating habits as adults.

On the other hand, local government could incentivize food companies, such as major grocery store or supermarket chains, to open more locations in low- to middle-income areas or even open miniaturized versions of the stores just to have a presence and serve these underserved communities.

Another aggressive idea might be for local government to stop enabling the opening of the same fast-food chains and lure more alternative food options so residents conveniently can access a broader menu of hopefully healthier options.

A radical idea would be to use existing resources, such as gas stations, that are readily abundant and demand they sell groceries, since gas stations are easy to get to without public transportation, especially in food desert areas.

As for the environmental contamination, a practical solution is the purposeful and intentional identification of environmental aspects that can be fixed.

Abroad, that could mean reducing the use of and reliance on plastics or not selling land to foreign investors to plant soybeans or cut trees. These changes would stimulate biodiversity and dramatically change the air quality and access to the land that is a source of living.

In Memphis, and more specifically in ZIP code 38105, that could mean creating community gardens and community-supported agriculture, educating the residents about recycling, deploying mobile units to go into underserved communities and distribute fresh food, and holding businesses accountable for their production of air pollutants.

Shelby County is the only county in Tennessee to earn a failing grade in excessive ozone pollution in the 2021 American Lung Association State of the Air report.

A Memphian experiment to start to affect health outcomes by changing access to clean air and fresh food could become a template for other places across the U.S. or the world to do the same.

These ideas and data are intended to serve as a primer for conversation and action this National Minority Health Month as we consider the differences in parallel lives separated by a 30-minute drive.

(The content of this article is solely the responsibility of the author and does not necessarily represent the official views of his employer.)

Christopher D. Radka (Christopher.Radka@STJUDE.ORG) is a postdoctoral fellow studying lipid biochemistry in the infectious diseases department of St. Jude Children's Research Hospital.

‘A different career almost every three years’

By Martina G. Efeyini

Christian Cunningham, a director and principal scientist at Genentech, talked to ASBMB Today about his career journey and offered some advice for people interested in industry careers. This interview has been condensed and edited.

1 How did you get started in science?

I did my bachelor’s at the University of California, Berkeley. I’d always wanted to be in a lab, but couldn’t get into one until my third year. Prior to that, the closest I got was working the dishwashing facility in our organic chemistry stockroom. So for two years, I washed dishes to try and get lab experience.

2 And you succeeded?

I was an undergraduate researcher in Robert Glaeser’s lab looking at membrane protein crystallography focused on a technology known as the lipidic cubic phase, which was still in its infancy back then. I worked with Glaeser for two years, and he helped me decide to continue my studies and go to graduate school.

I went to UC, San Francisco, (for my Ph.D.), and joined the lab of David Agard, a foundational mentor in my career. I was a biophysics student, and I studied the structural conformational dynamics of a protein chaperone known as HSP90, trying to understand how proteins fold. I learned skills in structural biophysics, conformational dynamics of proteins.

Christian Cunningham

CURRENT POSITION
Director and principal scientist of peptide therapeutics at Genentech

CAREER PATH
Bachelor’s at UC, Berkeley; Ph.D. in biophysics at UC San Francisco and a postdoc at Stanford University

FIRST JOB OUTSIDE OF ACADEMIA
Senior research associate, Genentech

FAVORITE MOLECULE OR PROTEIN
Cyclosporine. “Nature has figured out how to get a large molecule across the cell, and that molecule is the foundation for a majority of the research that we do.”

3 You have been at Genentech for 10 years. Tell me about your work.

I’ve had a different career almost every three years. In my first project with our neuroscience group, we discovered a new ubiquitin base associated on the mitochondria of neurons that seem to have pathologies related to Parkinson’s. This genetic screen evolved into a mechanistic profiling of that enzyme.

Then I moved to oncology, where we were interested in drugging the Hippo pathway. I was asking, can we disrupt the co-activator from turning on transcription? But this protein is lipidated in its core. I spent the next three years trying to figure out the role the lipidation played in signaling.

My group now focuses on whether peptides and peptide-based modalities can be the next broad class of modalities for drug discovery.

4 How did things change with the pandemic?

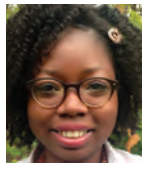
My staff worked shifted schedules, and we had to leverage a lot of international contract groups to facilitate science abroad for us when we were shut down.

At the end of 2020, we got rid of the shifting and allowed people more freedom to work on-site. Balancing the mental well-being of our staff with the constraints of our internal deliverables became a central focus. Our remedy, which was quite nice, included companywide protected time: No meetings between noon and 2 p.m. to allow people dedicated time to work.

5 What advice do you have for scientists interested in industry careers?

You have to apply for something that excites you, even if you’re not perfectly qualified. If it’s an area of science that you’re intrigued by, toss it in there. It doesn’t hurt.

Martina G. Efeyini (mefeyini@gmail.com) is a science communicator and STEM education advocate, and a career columnist for ASBMB Today. Follow her on Twitter: @mefeyini.



'A holistic view'

By Laurel Oldach

After hunting for natural products in Pretoria and helping users plan experiments near Walla Walla, Heino Heyman now works for Metabolon. He took a break from talking with potential customers to tell ASBMB Today about being a metabolomics application specialist.

1 What does an application specialist do?

We sell metabolomics analysis as a service. I join our sales team to give technical insights into our platform, consult and discuss study design. Later, I help the customer engage with their data. I talk metabolomics every day with many different people and hear about projects that they're working on: clinical trials, population health studies, process engineering for bioprocessing plants.

2 What skills do you need that you didn't need in academia?

We underestimate, as postdocs or Ph.D.s, how much communicating and teamwork we do — but because we are the experts, we usually do the talking. Industry is very much about listening, understanding the customer's questions and thinking on your feet. In an academic setting you are given plenty of time to explain your thinking, but in a commercial setting you have to get the message across very quickly. I also work very closely with the marketing team to understand the questions people are asking and what might get their attention on many different platforms.

Heino Heyman

CURRENT POSITION
Field application specialist, Metabolon

CAREER PATH
Ph.D., University of Pretoria, medicinal plant sciences
Postdoctoral research: University of Johannesburg, Pacific Northwest National Lab
First job outside of academia: Application scientist, Bruker

FAVORITE MOLECULE OR PROTEIN
Tricaffeoylquinic acid will always be close to my heart. It was a major component of my Ph.D., and a lot of sweat and tears went in. They've now discovered how it fits into the integrase enzyme of HIV.

3 What got you into metabolomics?

My first love in science was finding active ingredients within plants that can be used to treat diseases. Natural product discovery is notorious for being very long; we used metabolomics to look at different species to find an active fingerprint and speed up our isolation of a compound. That really got me excited about metabolomics.

My first postdoc took me to crop biotechnology at the University of Johannesburg. After that I went to Pacific Northwest National Laboratory for a second postdoc.

4 You worked on many projects at PNNL. Does this job feel similar?

That was actually my first exposure to many different types of metabolomics interests. PNNL has a user facility; people from all over the world can apply to run metabolomics, genomics or proteomics. I enjoyed that client-collaborative environment.

I liked being in the lab. But now where I get my energy is engaging with customers and getting them excited about metabolomics — or when we have all of these data points and those aha moments appear.

5 What's most exciting about metabolomics?

Metabolomics at its core is a comprehensive measurement of all the metabolites in a sample. It gives you a holistic, real-time view of the system that other omics do not give you. If it's in your genes, it wasn't necessarily ever transcribed. If the proteins are there, that doesn't necessarily mean they're switched on. But metabolites can give you that readout. I think it's set to become mainstream in the next five to 10 years.

(This interview has been edited and condensed. Read a longer version at asbmb.org/asbmbtoday.)

Laurel Oldach (loldach@asbmb.org) is a science writer for the ASBMB. Follow her on Twitter: @LaurelOld.

CLASSIFIEDS

Professor & Department Head
Texas A&M University

The Texas A&M College of Medicine seeks to fill a position for the Head of the Department of Molecular and Cellular Medicine (MCM) with an appointment as a tenured Professor of the College of Medicine. Reporting to the Dean of the College of Medicine, the Department Head is a member of the senior leadership team of the College working collaboratively with the central administration, fellow department heads, center and institute directors, and faculty members to support and advance the strategic goals of the University, College and Department.

https://careers.asbmb.org/job/professor-department-head/61762235/

Faculty Positions in Reproductive Sciences
Cincinnati Children's

The Center for Reproductive Sciences at Cincinnati Children's Hospital Medical Center (CCHMC) invites applications for tenure-track positions at the Assistant or Associate Professor level in all areas of male and female reproductive biology. Candidates whose research has the potential to bridge basic science discoveries with the broader translational and clinical communities at CCHMC and the University of Cincinnati Health System will receive special consideration.

https://careers.asbmb.org/job/faculty-positions-in-reproductive-sciences/61395887/

Assistant Professor of Biology
Northern State University

The applicant will develop and teach undergraduate courses in the following areas: Microbiology, Medical Microbiology, Immunology, and Cell Biology, along with introductory courses for majors and/or non-majors, depending upon the expertise of the applicant and departmental needs. The applicant will be expected to be actively involved in student recruitment and curriculum development. The applicant should have a strong commitment to undergraduate education and will be required to be involved in service activities as requested to the university (e.g., serving on committees). The applicant will be expected to develop a research program that includes undergraduate students.

https://careers.asbmb.org/job/assistant-professor-of-biology/61856845/

Post-Doctoral Associate
Jacobs School of Medicine and Biomedical Sciences

A post-doctoral position is available at the Jacobs School of Medicine and Biomedical Sciences (JSMBS) under the direction of Arthur M. Edelman, Ph.D. Of critical importance to the research which the Post-doc will undertake is the highly collaborative environment in which the research will be performed. The JSMBS is an integral part of the Buffalo Niagara Medical Campus (BNMC) a center of health care, life sciences research and medical education with all participating institutions within walking distance located on 120 acres in Buffalo, New York.

https://careers.asbmb.org/job/post-doctoral-associate/61161706/

To see a full list of jobs, please visit careers.asbmb.org

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