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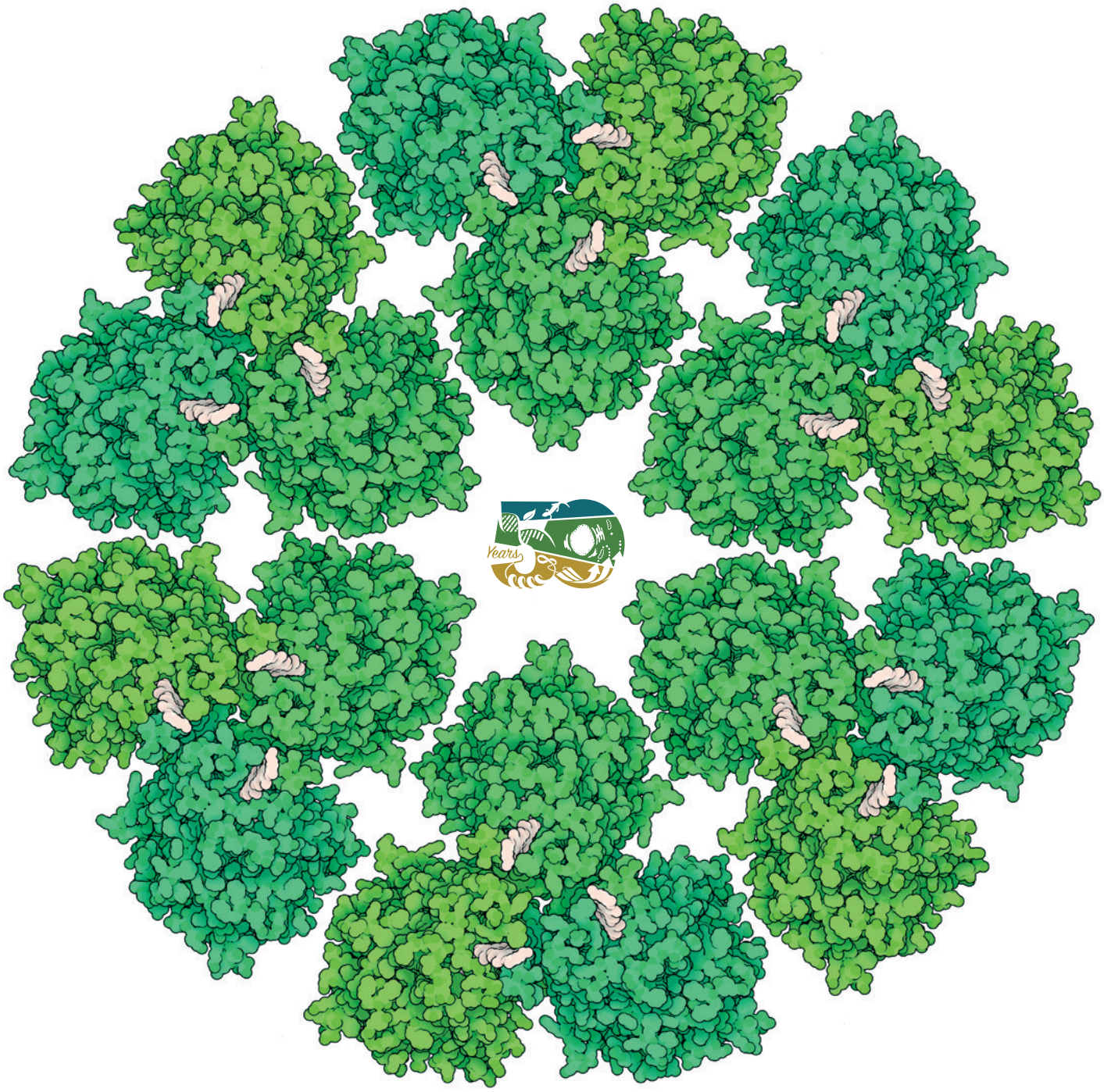
ASBMBTODAY

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



Celebrating the Protein Data Bank

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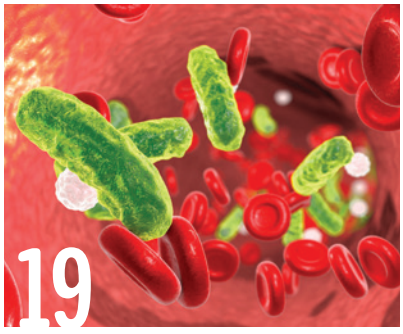

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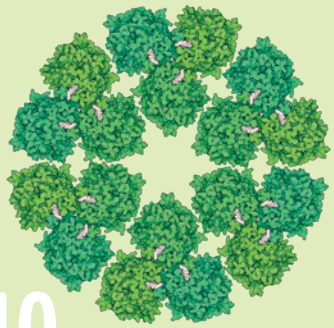

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One year later

By Comfort Dorn

The last time I ate a meal inside a restaurant was March 12, 2020. I use the word "restaurant" loosely because I was at Dulles International Airport in Virginia grabbing a sandwich and a beer before an overnight flight to Amsterdam – where I was to meet my daughter and her family for a fun trip to see friends on a Greek island.

You can guess what happened next.

Amsterdam locked down. We canceled our island trip. Daycare was closed, so I spent the next 10 days trying to keep my 2-year-old granddaughter out of her parents' hair while they attempted to do their jobs remotely, all of us crammed into their tiny Dutch house. I panicked briefly when President Trump announced that U.S. citizens who were overseas would not be allowed back home, but otherwise I had fun teaching little Penelope how to make biscuits and taking her on walks to all the nearby playgrounds. We ordered carryout food from the suddenly shuttered restaurants in their neighborhood. I learned that in seven months I was going to have a second grandchild.

That trip seems so long ago. Back then, only a few people were wearing masks or distancing at the airports. A handful of folks had donned what appeared to be disposable hazmat suits, but I dismissed them as outliers. When I returned to Dulles, a nice man took my temperature, asked me if I felt OK and told me to stay home for two weeks.

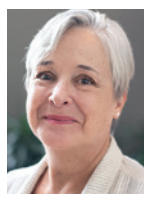
Meanwhile, the American Society for Biochemistry and Molecular Biology office closed, and the society's annual meeting was canceled. Because most of our members lacked access to their office mail, we didn't print three issues of this magazine. Shortly before the shutdown, we learned that the ASBMB's three journals would be going open access. Somehow, that had to happen with almost everyone working from home.

Since then, the way we do everything has shifted, layered with all the ordinary changes of work and life and coping. I got a new hip in July. My younger daughter got engaged in August. My mother turned 90 in September. My grandson was born in November.

The ASBMB (along with everyone else) learned to exist and thrive online, and the crowning result will be a virtual annual meeting in April. We've seen a lot of staff changes, culminating with the retirement in February of Barbara Gordon, our longtime executive director (see page 44), and the selection of Steve Miller to take on that position (see page 26).

All these changes have happened in the flat, surreal twilight of online existence. I have to wonder how different everything will feel next March when (fingers crossed) we can all be in the same room again.

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



Rylaarsdam becomes provost of Bethel University

Geneticist **Robin Rylaarsdam**, who until recently was the dean of arts and sciences at Saint Xavier University in Chicago, has been named provost of Bethel University, an evangelical Christian university in St. Paul, Minnesota, after a national search. As provost, she will oversee the education of all students and coordinate between student service offices; one provost at another university described the role as "chief academic officer."

Rylaarsdam earned her Ph.D. at Northwestern University and conducted postdoctoral research at the University of Chicago and Northwestern studying signaling through G protein–coupled receptors. She since has worked as a professor and administrator at several faith-based universities, spending five years at Trinity Christian College and 11 years at Benedictine University before accepting her most recent post at Saint Xavier Univeristy.


RYLAARSDAM

Rylaarsdam's lab studied G protein signaling, focusing on characterizing mutations to the $G_s\alpha$ protein that affect its function and can cause McCune–Albright syndrome. She also has become involved in pedagogical research, publishing on flipped classroom course designs, grading and other issues in undergraduate education.

Transition state for Lacy, Chazin at Vanderbilt

Borden Lacy, a structural biologist at Vanderbilt University Medical Center, has been promoted from associate director to director of the Vanderbilt Center for Structural Biology. She took over at the start of January.

The center for structural biology that Lacy now leads was founded in 1999. **Walter Chazin**, the founding director who led the center for 21 years, said, "The center was designed and built around what was then an avant-garde concept of integrating all structural biology techniques together."

Lacy has been a professor in Vanderbilt's departments of pathology, microbiology, immunology and biochemistry since 2006. Her laboratory studies toxins from pathogenic bacteria, focusing on transmembrane secretion systems and pore-forming multimeric toxins from gastrointestinal pathogens such as Clostridium difficile and Helicobacter pylori. They also investigate how interactions between these proteins and the host can contribute to virulence.


LACY

Lacy earned her Ph.D. at the University of California, Berkeley, and did postdoctoral research at Harvard Medical School. She is a fellow of the American Association for the Advancement of Science and of the American Academy of Microbiology.

Chazin, the chancellor's chair in medicine and a professor of biochemistry and chemistry, now will direct Vanderbilt's chemical and physical biology graduate program. His lab studies the structure of the priming engine, which synthesizes the RNA–DNA primers that DNA polymerases require for replication. The lab also works on protein complexes involved in responding to encounters with, and reversing, DNA damage as well as innate immune responses to pathogenic organisms.


CHAZIN

Chazin earned his Ph.D. at Concordia University in Montreal and did postdoctoral research at the Swiss Federal Institute of Technology in Zurich. He spent 13 years in the molecular biology department at Scripps Research before moving to Vanderbilt in 1999. He is a fellow of the American Association for the Advancement of Science and of the Biophysical Society.

Serio named associate chancellor

Tricia Serio, the dean of the University of Massachusetts Amherst College of Natural Sciences, has been named associate chancellor of strategic academic planning at the university. In the new role, she will do academic planning, working with institutional researchers to form and update college-level strategic academic plans, and also will develop cross-college educational and research initiatives.


SERIO

Serio has been a dean at UMass since 2017, prior to which she was a professor and chair of the department of molecular and cellular biology at the University of Arizona. Before that, she was an assistant and associate professor at

Brown University, a postdoctoral fellow at the University of Chicago and a Howard Hughes Medical Institute–supported graduate student at Yale University.

Serio will continue to lead a laboratory focused on the biophysics of pathological protein misfolding, using biochemical, imaging and mathematical modeling approaches to understand the initiation, accumulation and clearance of protein aggregates. Working in yeast with prion protein, her team demonstrated that aggregates can play a regulatory role in translation termination, that amyloids must reach a threshold size to be transmissible and that amyloid clearance is dependent on the size of the minimal stable aggregate; they found that post-translational modifications such as N-acetylation can modulate pathological folding activity. Her work was recognized in 2016 with a midcareer award for excellence in research from the American Society for Cell Biology.

Outside of her campus roles, Serio is an active member of the American Society for Biochemistry and Molecular Biology's Public Affairs Advisory Committee. "Tricia has been very helpful in trainee funding and in helping us identify specific needs related to sexual harassment in science," ASBMB public affairs director Benjamin Corb said.

Garcia to lead WUSTL department

Washington University in St. Louis named **Benjamin A. Garcia** the next head of its biochemistry and molecular biophysics department.

Garcia's lab at the University of Pennsylvania Perelman School of Medicine has developed novel methodologies for mass spectrometry analysis of histones for application in post-translational modifications and systems epigenetics.

In a statement, David H. Perlmutter, WUSTL's executive vice chancellor, had this to say about Garcia: "We found ourselves energized by his vision for the department to continue to be at the forefront of the field and to leverage the breadth of collaborative opportunities within our biomedical research community. His personal research program, in proteomic analysis of epigenetic regulation, supports our long-term strategic institutional goal to transition our leadership in genomics into multiomic systems medicine, which will serve as an engine producing the most imaginative approaches to personalized health care."


GARCIA

Garcia is on the editorial board of the ASBMB journal Molecular & Cellular Proteomics and will be giving a talk at the 2021 ASBMB annual meeting, which will be held virtually in April. His talk is titled "Ultra-high throughput analysis of histone modifications for cancer epigenetics."

In October, he won the Human Proteome Organization's 2020 Discovery in Proteomics Sciences Award recognizing researchers for a single discovery in the proteomics field.

His term at WUSTL as a Raymond H. Wittcoff distinguished professor begins in July. The current department chairman, John A. Cooper, also an ASBMB member, has led the department for seven years and plans to focus on his research program.

Song and Luján share TWAS prize

The World Academy of Sciences, an organization dedicated to promoting scientific research and scientists in the developing world, has announced its 2021 awards, which recognize outstanding achievements and contributions to science by scientists in the Global South. Two ASBMB members, **Erwei Song** and **Hugo Luján**, share the award in medical sciences.

Erwei Song, president of Sun Yat-Sen University Medical School in Guangzhou, China, was recognized for his studies of tumor plasticity. Song, a physician–scientist specializing in oncology, found that tumor plasticity can be regulated by pluripotency-related microRNAs and studies the effects of long noncoding RNAs on cancer metastasis and chemoresistance. He also is interested in how tumor cells and tumor-associated macrophages interact; his lab recently reported that extracellular vesicles containing long noncoding RNAs that pass from macrophages to cancer cells can regulate the tumor cells' biology.


SONG

Song trained as a surgeon at Sun Yat-Sen University. He pursued postgraduate medical training at the University of Duisburg-Essen in Germany and postdoctoral research at Harvard Medical School. He became a

CONTINUED ON PAGE 6

Academy of inventors names fellows

Six members of the American Society for Biochemistry and Molecular Biology are among the 175 individuals named as 2020 fellows of the National Academy of Inventors.

The NAI describes its fellows as academic inventors who have demonstrated a spirit of innovation in creating or facilitating outstanding inventions that have made a tangible impact on quality of life, economic development and the welfare of society.


CHAIKEN

Irwin Chaiken is a professor in the department of biochemistry and molecular biology at Drexel University. He holds a Ph.D. in biological chemistry from the University of California, Los Angeles. His lab studies molecular and structural mechanisms of protein recognition and antagonism, with a current focus on the protein machine that controls HIV-1 cell entry into host cells.


DESNICK

Robert Desnick is the dean for genetics and genomic medicine; professor and chair emeritus of genetics and genomic sciences; and a professor of pediatrics, oncological sciences and obstetrics, gynecology, and reproductive science at the Icahn School of Medicine at Mount Sinai. He holds an M.D. from the University of Minnesota Medical School. His lab works to identify variations in human genes responsible for the metabolism of drugs and studies the pathogenesis and treatment of lysosomal storage diseases and inhertited porphyrias.


GREIDER

Carol Greider is a distinguished professor of molecular, cell and developmental biology at the University of California, Santa Cruz. She holds a Ph.D. in molecular biology from the University of California, Berkeley. Her lab is focused on understanding the dynamic interaction between telomeres and telomerase that establishes the telomere length equilibrium, using telomerase-deficient mice to recapitulate age-related degenerative disease seen in families with inherited telomere syndromes.


JEWETT

Michael Jewett is the Walter P. Murphy professor of chemical and biological engineering in the McCormick School of Engineering at Northwestern University. He holds a Ph.D. in chemical engineering from Stanford University. His lab focuses on engineering biological systems involved in protein synthesis and metabolism, including glycosylation, ribosome engineering, nonstandard biopolymers and cell-free metabolic engineering.


NAGARKATT

Mitzi Nagarkatt is the SmartState endowed chair of the Center for Cancer Drug Discovery and Carolina distinguished professor and chair in the department of pathology, microbiology and immunology at the University of South Carolina. She holds a Ph.D. from the Defense Research and Development Establishment in Gwalior, India. Her lab studies inflammation as the cause of disease, using epigenomic and genomic approaches as well as in silico modeling and ex vivo cultures for determining cellular and molecular mechanisms.


SIDHU

Sachdev Sidhu is a professor in the Donnelly Centre for Cellular and Biomedical Research at the University of Toronto. He holds a Ph.D. in biochemistry from Simon Fraser University, Burnaby, British Columbia. His lab studies the relationships between protein structure and function, using phage display in conjunction with high-throughput screening and sequencing to improve library diversities and the scaffolds used for protein display.

This class of fellows will be inducted at the 10th Annual Meeting of the National Academy of Inventors to be held in June in Tampa, Florida.

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member of the Chinese Academy of Sciences in 2019.

Hugo Luján, a senior researcher in the faculty of medicine at Argentina's CONICET, or Universidad Catolica de Córdoba, studies the protozoan intestinal parasite Giardia lamblia. Luján discovered that the parasite uses RNA regulation to change its surface antigens, presenting a shifting coat that confounds the immune system. His lab found a way to weaken the protozoa for use as a vaccine by knocking out its microRNA processing machinery, which forces the parasite to express all of its antigens at once and gives the immune system a chance to recognize all of them. His lab also is studying whether variable surface proteins from giardia might be used for oral delivery of other drugs and vaccines due to their toughness.

LUJÁN

Luján received his doctorate at the Universidad Nacional de Córdoba and conducted postdoctoral research at the National Institutes of Health from 1992 to 1997. He returned to Argentina and was for 10 years a Howard Hughes Institute International research scholar. He has received numerous awards, including a Guggenheim Foundation scholarship, a research award from Argentina's Konex Foundation and the Georg–Foster prize from Germany's Alexander von Humboldt Foundation.

Regev to share inaugural James Prize

Aviv Regev, executive vice president of Genentech Research and Early Development, will share the National Academy of Sciences' James Prize in Science and Technology Integration with Harvard Medical School's **Allon Klein**. This is the first year the James Prize is being awarded; it recognizes researchers for contributions that adapt concepts and techniques from outside their own fields, integrating and applying multiple disciplines to solve important problems in science.

The pair is honored for their separate contributions to massively parallel single-cell genomics. Regev, a Howard Hughes Medical Institute investigator until last summer and faculty member at the Broad Institute and Massachusetts Institute of Technology (on leave), developed experimental and analytical tools that drew from biology, computer science and engineering to pioneer single-cell sequencing. Her research group also showed how to apply these techniques to discover cell types, understand environmental responses and develop cellular atlases that shed light on mechanisms of disease. Meanwhile, Klein also was studying single-cell transcriptomes, applying mathematical approaches to understand cell fate in tissue development and regeneration.

REGEV

The prize of $50,000, to be divided between Regev and Klein, will be presented in a virtual ceremony at the 158th annual meeting of the National Academy of Sciences. It is named for its donor, businessman Bob James, the former chairman and CEO of the advertising agency McCann Erickson Worldwide.

John W. Suttie

John W. Suttie, a longtime member of the American Society for Biochemistry and Molecular Biology and a former president of the Federation of American Societies for Experimental Biology, died Dec. 21 in Green Valley, Arizona. He was 86.

Suttie was an emeritus professor at the University of Wisconsin–Madison, where he earned three degrees — a bachelor's, master's and doctorate — before joining the biochemistry faculty in 1961 and beginning his studies of vitamin K; he eventually elucidated its role as a cofactor in glutamate carboxylation in prothrombin.

Suttie joined the ASBMB in 1967 and served as an editorial board member for JBC in the early 1980s. He chaired the University of Wisconsin's nutritional sciences department throughout the 1990s and was an active member of the American Society for Nutrition into the 2010s.

For the ASN, Suttie served as president of the governing council, editor of the Journal of Nutrition and later the founding editor of the journal Advances in Nutrition. It was through his ASN service that he became president of FASEB and chair of the Experimental Biology conference.

He was elected to the National Academy of Sciences in 1996.

Suttie served on many government and nonprofit boards and committees throughout his career, including the National Research Council's Board on Agriculture and Natural Resources, the Food and Drug Administration's Blood Products Advisory Committee, and the Institute of Medicine's Food and Nutrition Board.

He was particularly concerned with science policy and funding. According to a FASEB obituary, it was during his presidency that the organization decided to expand its public affairs activities and hire its first lobbyist.

Suttie was born in La Crosse, Wisconsin, to William Vilas Suttie and Emma Rindahl Suttie in 1934.

He married Leone Stenberg in 1955, and they raised their two children, Joan and Collin, in Madison.

The Sutties bought a home in Arizona before John retired in 2002, and they moved there permanently in 2017.

Prem Ponka

Prem Ponka, a researcher who made major contributions in the study of iron and heme metabolism, died Nov. 3, 2019, while at a conference in Paris, ASBMB Today learned recently.

Born in Czechoslovakia, Ponka earned an M.D. in 1964 and a Ph.D. in physiology in 1969 from Charles University, Prague, where he was an assistant professor in the pathophysiology department until 1979. He immigrated to Montreal and resumed his career at McGill University and the Lady Davis Institute at Jewish General Hospital, where he remained as a professor and senior investigator, respectively. He was an active scientist until his death.

Ponka demonstrated that iron uptake is the limiting factor for erythroid heme synthesis. He formulated the hypothesis that iron is delivered directly from endosomes to mitochondria in erythroid cells and discovered a critical role of the heme catabolic enzyme heme oxygenase in erythroid cell physiology. He also developed a new class of cell-permeable iron chelators, which are used widely by researchers in the field.

An active member of the International Society for the Study of Iron in Biology and Medicine, Ponka received that organization's Special Presidential Award for Lifetime Achievement in 2019. He was honored in his native country with the Medal for Merit to commemorate the 650th anniversary of Charles University, Prague, in 1998 and the Purkinje Medal from the Czechoslovak Medical Association of J. E. Purkinje in 1975. In 2014, he was elected as a fellow of the Czech Medical Academy, a member of the Federation of European Academies of Medicine.

In addition to an encyclopedic knowledge of the history and personalities of the bioiron field, Ponka had a broad interest in science, history, philosophy and the arts, according to a BIOIRON obituary. He was a dedicated proponent of political and intellectual freedom and tolerance, with a unique sense of humor.

He is survived by his wife, Jitka Ponka; children, David Ponka and Claire Ponka; and grandchildren.

Luis Glaser

Luis Glaser, former head of the department of biological chemistry at Washington University School of Medicine in St. Louis and former executive vice president and provost of the University of Miami, died Dec. 23 in Miami after a long illness. He was 88 years old and was a member of the American Society for Biochemistry and Molecular Biology for more than five decades.

Glaser was born March 30, 1932, in Vienna. Soon after Austria was annexed by Nazi Germany in 1939, Glaser's father, a physician, was told he no longer could practice medicine in the country. The family moved to Belgium for a year and then to Mexico City, where Glaser grew up.

After graduating from the University of Toronto, Glaser earned a Ph.D. in biochemistry at WUSTL, studying in the lab of Nobel laureates Carl and Gerty Cori. He joined the faculty as an instructor in 1956 and headed the biological chemistry department (now the department of biochemistry and molecular biophysics) from 1975 to 1986.

Carl Frieden, a professor of biochemistry and molecular biophysics at WUSTL, said of Glaser in a university obituary, "His knowledge and understanding of science were remarkable. A speed reader, he was always available to discuss any problem with faculty or students as he wandered down the hall, coffee in hand."

Glaser moved in 1986 to the University of Miami, where he was executive vice president and provost for almost two decades. He is credited with helping the university shed its image as Suntan U and become one of the nation's leading private research institutions, according to a UM obituary. He also co-taught a cross-disciplinary course called Ethics and Genetics with an emeritus professor of religious studies.

Glaser spoke four languages: English, German, Spanish and Yiddish. During Hurricanes football games, according to the MU obituary, he sometimes would be interviewed on Spanish-language radio stations at halftime.

He is survived by his wife of 59 years, Ruth; his daughters, Miriam Lipsky and Nicole Glaser; and five granddaughters.

Roland Schauer

Roland Schauer, a researcher fondly known as "Mr. Sialic Acid," headed the Institute of Biochemistry at the Christian–Albrechts Universität Kiel in Germany for 25 years, from 1976 to 2001, and, according to colleagues, continued his research until the last days of his life. Schauer died in October 2019 at the age of 83, ASBMB Today learned recently.

Born April 8, 1936, in Stuttgart, Schauer earned a medical degree and was one of the first five students to study a newly introduced biochemistry curriculum at the University of Tübingen. He began his sialic acid research as a postdoctoral fellow at the newly founded Ruhr University in Bochum, where he served as an associate professor of chemistry before moving to Kiel as a full professor of biochemistry.

Schauer was fascinated by mechanisms that show the complex relations between sialic acid molecules and living organisms, according to an obituary in the Glycoconjugate Journal. Jellyfish react with their stinging cells to the presence of sialic acids on the skin surfaces of predators and prey. The clown fish has no sialic acid molecules present on its skin, enabling it to hide in and be protected by sea anemones, which are related to jellyfish. In one of Schauer's last papers, "he and his colleagues were able to analyze this mechanism in detail and discuss possible applications and adaptations to the field of nanomedicine," the obituary states.

In 2002, Schauer received the Lifetime Achievements in Sialoglycoscience Award from Griffith University, Australia, and in 2009 the Rosalind Kornfeld Award for Lifetime Achievements in Glycobiology from the American Society for Glycobiology. He was founder and chair of the Sialic Acids Society at Kiel and served on the editorial boards of Glycoconjugate Journal and Trends in Glycoscience and Glycotechnology.

In addition to his two decades as a member of the American Society for Biochemistry and Molecular Biology, he belonged to numerous other organizations, including the Consortium for Functional Glycomics, Real Academia Nacional de Farmacia, Gesellschaft für Biochemie und Molekularbiologie, Group de Glucides, the Society for Glycobiology, and the Glycosciences Forum.

Willis Avery Wood

Willis Avery Wood, a microbiologist who studied enzymes of bacteria and metabolism of sugars and amino acids and a member of the American Society for Biochemistry and Molecular Biology for more than 60 years, died Jan. 17. He was 99.

Born in Johnson City, New York, in 1921, Wood was an Eagle Scout and a first lieutenant in the Quartermaster Corps during World War II. After earning a bachelor's in bacteriology from Cornell University in 1947, he followed his faculty advisor Irwin C. Gunsalus to Indiana University, where he received a Ph.D. in microbiology.

In 1950, Wood joined the dairy science department at the University of Illinois. In 1955, he received the Eli Lilly Award in Microbiology and Immunology. At Michigan State University, Wood helped form the biochemistry department and served as its chair from 1968 to 1974.

Wood studied microbial metabolic enzymes that use the molecule pyridoxal phosphate as a coenzyme. His lab characterized the structure and activity of enzymes involved in amino acid metabolism that use pyridoxal phosphate, from numerous bacterial and fungal strains. They also notably found that an E. coli threonine dehydratase required both the pyridoxal coenzyme and a dimerization-promoting adenosine monophosphate ligand to reach peak activity. It was the first known example of ligand-induced oligomerization activating an enzyme.

Wood developed a recording spectrophotometer with photomultiplier feedback loop and an automatic cuvette changer. This system, which could follow and record up to four enzyme-catalyzed reactions simultaneously, was used widely in enzyme research.

Wood was a founder and first president of the Neogen Corporation. In 1982, he became director of microbiology for Salk Institute Biotechnology Industrial Associates, researching microbial enhanced oil. In 1990 he joined the Agouron Institute as principal scientist and vice president.

Wood is survived by a son, two daughters, four grandchildren, and four great-grandchildren.

Hiroyuki Sorimachi

Hiroyuki Sorimachi, a Japanese researcher and biochemistry educator, died Oct. 1, 2019, ASBMB Today learned recently.

Sorimachi was born April 24, 1963, in Yokohama City, Japan, the son of Yoichi and Michiko Sorimachi. He received a Master of Science in 1988 and a Doctor of Philosophy in 1992, both from the University of Tokyo.

He was head of the department of advanced science for biomolecules and project leader on calpains at the Tokyo Metropolitan Institute of Medical Science. He had been an assistant professor at the Institute of Molecular and Cellular Biosciences at the University of Tokyo from 1992 to 1997 and an associate professor at the university's department of applied life sciences from 1997 to 2004.

His interests included enzymology, the molecular bases of disease, and protein synthesis and degradation. He focused on studying the structure and functions of calpains, and his last paper as a co-author, published posthumously, was on developing a fluorescence sensor probe to capture an activated muscle-specific calpain in living muscle cells.

Sorimachi received the Japanese Biochemical Society Young Investigator Award in 1999, a staff award from the Tokyo Metropolitan Organization for Medical Research in 2007 and a Lifetime Achievement Award from the Federation of American Societies for Experimental Biology Summer Research Conference on the biology of calpain in health and disease in July 2016, where he hosted a session, "Bioinformatics of Calpain Substrates and Measuring Activity."

Married to Noriko Toyama since February 1991, Sorimachi enjoyed playing and watching baseball, computers, driving, beer and musicals.

Celebrating the Protein Data Bank

Two-day virtual event will highlight the science preserved within and enabled by the resource over the past 50 years

By Angela Hopp

The Protein Data Bank has supported and transformed structural biology and structure-based drug design since its founding in 1971.

"PDB has consistently provided the three-dimensional coordinates of biological molecules to students, academic researchers and drug designers alike," said PDB co-founder Helen M. Berman. "Indeed, the current public health crisis caused by the SARS-CoV-2 virus highlights the critical importance of structural biology. Several hundred new entries have been deposited in the PDB in the quest to find therapeutics for SARS-CoV-2 and abate the COVID-19 pandemic."

Over the past five decades, the number of structures stored within the PDB has grown from the initial seven to more than 170,000.

In May, the structural biology community will celebrate the PDB with a virtual symposium called PDB50 hosted by the Worldwide PDB and the American Society for Biochemistry and Molecular Biology.

"The symposium will recognize the impact of structural biology and the PDB on fundamental biology, biomedicine, bioenergy and biotechnology," said Berman, a distinguished professor emerita at Rutgers, The State University of New Jersey.

Berman has been with the archive since the beginning. In the late 1990s, the PDB moved from Brookhaven National Laboratory to the Research Collaboratory for Structural Bioinformatics, a consortium that Berman led. Later, she helped establish the Worldwide PDB, partnering organizations in the U.S., Europe and Japan to maintain the global archive collectively.

In recognition of her contributions to the field, Berman has received many awards, including the 2013 DeLano Award for Computational Biosciences from the ASBMB.

In the interview below, Berman describes how the PDB has both shaped and been shaped by the work being done by structural biologists. It has been edited for length, style and clarity.

COURTESY OF HELEN BERMAN

Protein Data Bank co-founder Helen Berman won the 2013 DeLano Award for Computational Biosciences from the ASBMB.

How has PDB — its very existence — shaped the field?

PDB began more than 50 years ago as a very small archive of a few structures, and it's grown to more than 170,000 structures.

From my point of view, what's important about the PDB is what's *in* the PDB. Deposition of structures in the PDB is a requirement of most journals and funding agencies, ensuring a level of quality control and accessibility of structural biology data. From very, very small, very well-determined structures to structures that are huge and studied by combinations of methods, the PDB is a treasure trove for research from drug discovery to artificial intelligence. The PDB ensures no structure is lost, whether the structures are determined by X-ray crystallography, nuclear magnetic resonance or cryo-electron microscopy.

In fact, these structures greatly enhance future structure determination by providing the initial models for molecular replacement and initial fittings into a

density map. These structures are also essential in the development of integrative models of large macromolecular machines, where the structures and data come from multiple experimental and computational methods, ranging from proteomics to small-angle scattering.

The PDB plays a seminal role in structure-based drug design, a mainstay of many of our current therapeutics. And the existence of the PDB has given rise to the entire field of structural bioinformatics.

How does the PDB adapt to change in structural biology?

The PDB is constantly evolving to accommodate new structure-determination methods. Initially, all the structures were determined by X-ray crystallography, then NMR and cryo-EM. The current challenge is accommodating more complex integrative models.

Stewardship of the data is critical, with community task forces guiding the specific validation methodologies. While initial validation checks focused on geometry and nomenclature, now the structures are checked against the appropriate experimental data.

In addition, the information technology (IT) infrastructure used to manage new data must continually evolve to support the ever-growing archive.

What themes will be highlighted in PDB50?

An international panel of speakers was chosen. (They) are leaders in each of the major structure-determination methodologies. These include the quickly evolving fields of X-ray crystallography, biological NMR, cryo-EM and integrative modeling of macromolecular assemblies.

Speakers will also provide historical perspective on this critical field while describing a diverse range of structures of proteins, nucleic acids and a variety of complexes.

In the panel speakers' presentations, we touch on many critical aspects of biology, including the current COVID-19 pandemic caused by SARS-CoV-2.

The abstract deadline is coming up in March. What kinds of submissions are you expecting?

All fields relating to structural biology are welcome. We are hoping that the poster presenters will reflect the broad range of research fields that are impacted by the PDB. These range from structure determination to structural bioinformatics, from structure-based drug design to new integrative methods.

Our hope is that PDB50 will not only be an opportunity to highlight the leading experts in the field but also, in the poster session, an opportunity for new students becoming our future leaders to participate.

Basically, the sky is the limit because the PDB has so many different structural stories.

Important dates

March 15: Abstract deadline and early registration deadline

May 1: Regular registration deadline

Visit the event website:
asbmb.org/meetings-events/pdb50

About the Worldwide PDB

The Worldwide PDB was formed in 2003 to manage the global archive. Berman said it is committed to ensuring the quality and availability of the structures.

The current members are:

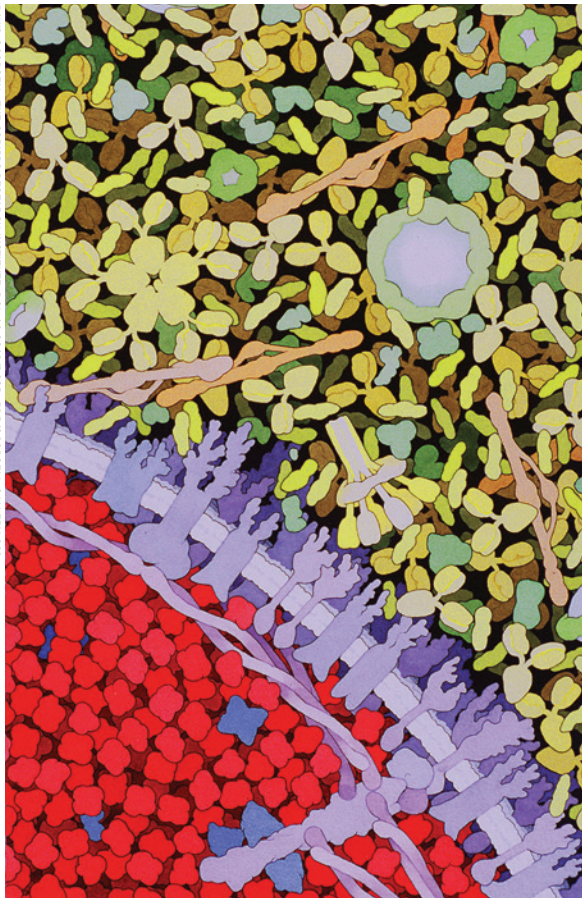
- Research Collaboratory for Structural Bioinformatics (RCSB PDB).
- Protein Data Bank Europe (PDBe).
- Protein Data Bank Japan (PDBj).
- BioMagResBank (BMRB).

This will be a virtual meeting, so it'll be more accessible. How did the virtual format affect your planning?

One advantage of having a virtual meeting is that people from around the world will be able to participate. One of the reasons that the meeting is split into two days is that we want participation throughout the worldwide time zones. We're trying to make it so that people will have the maximum chance of being able to participate.

The event will be recorded and made available to registered participants after the meeting.

After the PDB50 international meeting, regional meetings in the US, Europe and Asia will promote the broadest possible participation.



DAVID GOODSELL, THE SCRIPPS RESEARCH INSTITUTE. DOI: 10.2210/RCSB_PDB/GOODSELL-GALLERY-003

Angela Hopp (ahopp@asbmb.org) is executive editor of ASBMB Today and communications director for the ASBMB. Follow her on Twitter @angelahopp.

Invited speakers

Eddy Arnold, Rutgers, The State University of New Jersey

Helen M. Berman, Rutgers, The State University of New Jersey and University of Southern California

Thomas L. Blundell, University of Cambridge

Alexandre M. J. J. Bonvin, Utrecht University

Stephen K. Burley, Rutgers, The State University of New Jersey and University of California, San Diego

Wah Chiu, Stanford University

Johann Deisenhofer, University of Texas Southwestern Medical Center

Juli Feigon, University of California, Los Angeles

Angela Gronenborn, University of Pittsburgh

Jennifer L. Martin, University of Wollongong

Stephen L. Mayo, California Institute of Technology

Zihe Rao, ShanghaiTech University and Tsinghua University

Hao Wu, Harvard Medical School and Boston Children's Hospital

Event organizers

Celia A. Schiffer, University of Massachusetts Medical School

Helen M. Berman, Rutgers, The State University of New Jersey; RCSB PDB

Stephen K. Burley, Rutgers, The State University of New Jersey; RCSB PDB

Jeffrey C. Hoch, University of Connecticut; BMRB

Gerard J. Kleywegt, European Bioinformatics Institute; PDBe

Genji Kurisu, Osaka University; PDBj

John L. Markley, University of Wisconsin–Madison; BMRB

Sameer Velankar, European Bioinformatics Institute; PDBe

Christine Zardecki, Rutgers, The State University of New Jersey; RCSB PDB

Meet our inaugural MOSAIC scholars

These K99/R00 awardees will receive individualized coaching and networking and presentation opportunities tailored to their needs

By Angela Hopp

The American Society for Biochemistry and Molecular Biology is pleased to present the five postdoctoral scholars in the society's inaugural cohort for the Maximizing Opportunities for Scientific and Academic Independent Careers, or MOSAIC, program.

In August, the society received a cooperative agreement with the National Institutes of Health's National Institute of General Medical Sciences to develop and execute a program that will support postdoctoral fellows and new investigators from diverse backgrounds embarking on careers at research-intensive institutions.

"I am excited to welcome our MOSAIC scholars to the ASBMB fold and looking forward to meeting and working with them soon," said Ruma Banerjee of the University of Michigan, the co-investigator for the ASBMB's MOSAIC grant.

Learn about the first ASBMB MOSAIC scholars below.

Lillian J. Brady

Lillian J. Brady is a postdoctoral scholar in the lab of Erin Calipari at Vanderbilt University, where she is studying the sex differences in cholinergic regulation of dopamine release and their impacts on behavior. A native of Jackson, Mississippi, she earned her bachelor's degree in chemistry and a master's degree in biotechnology from Alcorn State University and her Ph.D. with a focus on neurobiology from the University of Alabama at Birmingham.

"The NIH MOSAIC award will be instrumental in my career development and will provide the proper foundation I need to be able to reach my career goals of mentoring diverse scientific minds and becoming a successful independent investigator in the Neuroscience field," she said. Her research project is titled "Sex differences in cholinergic regulation of nicotinic acetylcholine receptor modulation of local nucleus accumbens circuitry underlying motivation."

John R. Jimah

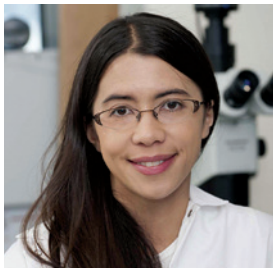
John R. Jimah is a postdoctoral fellow in the lab of Jenny Hinshaw at the National Institute of Diabetes and Digestive and Kidney Diseases. He is studying the structural basis of dynamin-mediated membrane fission and actin bundling. He earned his bachelor's degree from Colgate University and his Ph.D. from Washington University in St. Louis. Raised in Ghana, Jimah was a member of the group of trainees at the NIDDK that started the seminar series known as TREaDS, short for Trainees Recognizing Excellence and Diversity in Science.

Through the MOSAIC program, Jimah said, "I will get training in effective mentoring for budding young scientists from all backgrounds and experiences in order to help them develop into brilliant scientists who will address current and future biological and biomedical questions. I also look forward to knowing my fellow MOSAIC scholars and supporting each other for success in our careers as scientists and mentors." His research project is titled "Structural basis of dynamin-mediated membrane fission, actin bundling and interaction with binding partners."


Elias Picazo

Elias Picazo is a postdoctoral fellow in the lab of Eric Jacobsen at Harvard University, where he is developing new organocatalytic reactions. A native of California's Central Valley, Picazo earned his bachelor's degree from the University of California, Santa Barbara, and then his Ph.D. from the University of California, Los Angeles, where he studied the total synthesis of complex natural products.

"I am excited to continue my research endeavors as an independent researcher at a research-intensive university upon completing my postdoctoral training at Harvard. I will also use this opportunity to connect with a network of professionals seriously committed to increasing minority representation in science," Picazo said. His research project is titled "Strategic molecular activations for the selective synthesis of 2-deoxy-beta-glycosides, and for the synthesis of novel donor–acceptor Stenhouse adducts."


Elizabeth V. Wasmuth

Elizabeth V. Wasmuth is a postdoctoral fellow at the Memorial Sloan Kettering in the lab of Charles Sawyers and at The Rockefeller University with Sebastian Klinge. During her joint fellowship, she is defining key molecular interactions that influence prostate cancer progression. Raised in New Jersey, Wasmuth earned her bachelor's from Cornell University and her Ph.D. from the Gerstner Sloan Kettering Graduate School of Biomedical Sciences. As an undergrad, she studied both animal science and development sociology with a focus on inequalities and has since mentored and conducted outreach to vulnerable populations.

"Growing up surrounded by ethnic and socioeconomic diversity, I have witnessed firsthand how different backgrounds fuel innovative thinking. I am excited to leverage the extensive resources and network provided by the MOSAIC program to bolster my success as an independent investigator, and, importantly, to apply this knowledge to increase diversity in STEM at my home and future institutes," she said. Her reserach project is titled "Biochemical, structural and molecular dissection of androgen receptor transcriptional activity."


Velencia J. Witherspoon

Velencia J. Witherspoon is a postdoctoral fellow in the lab of Peter Basser at the Eunice Kennedy Shriver National Institute of Child Health and Human Development, where she is developing low-field MRI methods. She earned her bachelor's degree at Florida Agricultural and Mechanical University and her Ph.D. from the University of California, Berkeley, where she studied molecular motion in adsorbent materials.Raised in Jacksonville, Florida, Witherspoon has promoted diversity in STEM through participation in the National Society for Black Engineers and the Black Graduate Engineering and Science Society and by directly mentoring undergraduates.

"The NIH MOSAIC award allows me to continue my commitment to encouraging the participation in and matriculation of diverse individuals in the biomedical and STEM workforce," she said. "I am excited to network with like-minded individuals who wish to foster inclusivity and cultural awareness through active allyship while receiving the scientific training to pursue a career as an independent investigator." Witherspoon's research project is titled "Quantitative characterization of the extracellular matrix components of connective tissue: Fingerprinting macromolecular components through low-field magnetic resonance."

Angela Hopp (ahopp@asbmb.org) is executive editor of ASBMB Today and communications director for the ASBMB. Follow her on Twitter @angelahopp.

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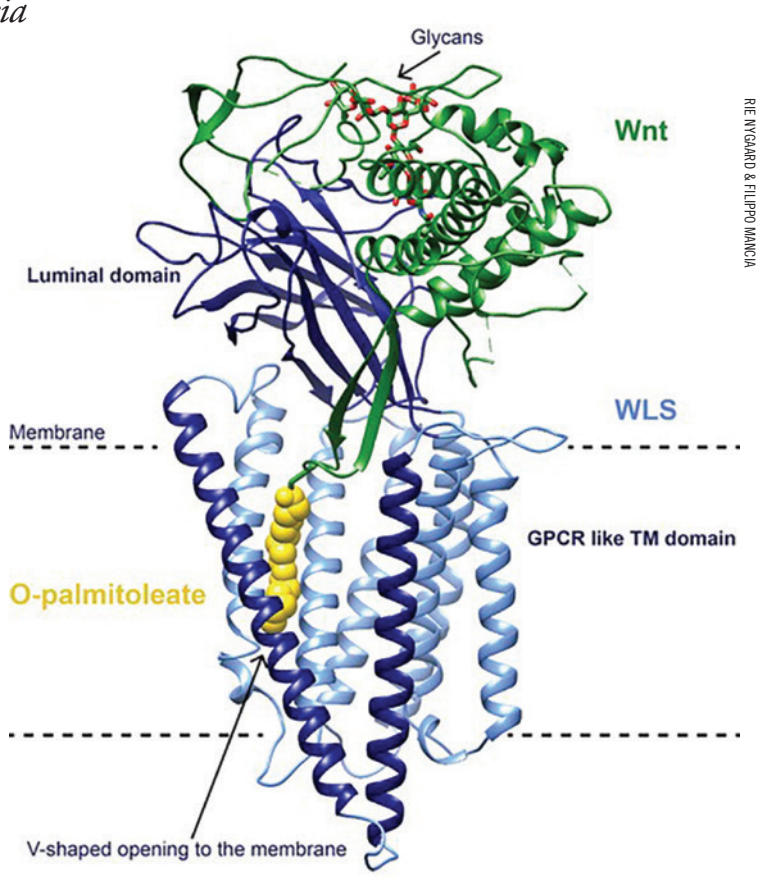
Transport of O-palmitoleated Wnts: Where does the lipid go?

By Rie Nygaard & Filippo Mancia

Wnts are evolutionarily conserved ligands that signal at short range to regulate morphogenesis, cell fate and stem cell renewal. The first and essential step in Wnts' secretion is their O-palmitoleation by the enzyme porcupine, or PORCN. This lipid modification is unique to Wnts and crucial for limiting their diffusion, restricting Wnt signaling to short range.

Modification of Wnts has been shown to be essential to their signaling capabilities. After their O-palmitoleation in the endoplastic reticulum, or ER, Wnts are loaded onto their dedicated transporter Wntless, or WLS, an integral membrane protein with a small soluble domain in the ER lumen. O-palmitoleated Wnts associated with WLS then travel to the plasma membrane, where they are transferred to receptors, such as Frizzled, on the membranes of target cells, in turn triggering the activation of signaling pathways. Structures of Wnt in complex with the cysteine-rich domain, or CRD, of Frizzled have shown how the lipid modification of Wnt is central to binding, with the O-palmitoleate buried deep in a hydrophobic groove of the CRD.

Questions remained about Wnts' transfer from the ER to target cells and the role of the O-palmitoleate: How does the transfer of the O-palmitoleated Wnt from PORCN to WLS occur? Where does the O-palmitoleate reside when Wnts are in complex with WLS, within the protein or in the membrane? How are Wnts released from WLS, and how do they travel with their water-insoluble cargo to neighboring cells?



RIE NYGAARD & FILIPPO MANCIA

The structure of human O-palmitoleated WNT8A (green) in complex with its dedicated carrier WLS (blue). The O-palmitoleate is shown as yellow spheres, and the main structural elements are labeled.

We recently reported the structure of human O-palmitoleated WNT8A in complex with WLS, determined by single-particle cryo-electron microscopy to 3.2 Å resolution. The structure shows that the WLS membrane domain has close structural homology to G protein–coupled receptors, or GPCRs, with the addition of a transmembrane helix connecting the N-terminus to its luminal domain.

Based on the structures of Wnt bound to the CRD domain of Frizzled, we expected that the O-palmitoleate would be inserted into a hydrophobic binding site within the luminal domain of WLS. Instead, the Wnt hairpin carrying the lipid as a covalent attachment inserts deeply

into a conserved hydrophobic cavity in the GPCR-like domain with the O-palmitoleate protruding between two transmembrane helices into the lipid bilayer.

We observed an extensive binding surface between Wnt and WLS, consistent with the known tight interaction between the two, while the energetically favorable environment of the membrane sheltered the hydrophobic cargo. A large opening to the bilayer within the membrane domain of WLS might be the route for shuttling the O-palmitoleate from PORCN to WLS, maintaining the lipid within the bilayer during the transfer and possibly involving a direct interaction between the enzyme and the carrier.

Comparing the structure of Wnt in complex with WLS to the structures of Wnt bound to the CRD domain of Frizzled, we observed a large conformational change on a separate Wnt hairpin, which may be important for its one-way transfer to receiving cells. For this transfer to occur, the O-palmitoleate must be extracted from the lipid bilayer and transferred to the CRD domain of Frizzled.

It's unclear if and when this involves other proteins and whether the transfer occurs in cis (the same) or trans (the opposite) membranes.

This work provides molecular-level insights into a central mechanism in animal body plan development and stem cell biology. We believe it opens up a new direction to explore membrane protein–lipid interactions.

Rie Nygaard (rn2401@cumc.columbia.edu) is an associate research scientist in Filippo Mancia's lab in the department of physiology and cellular biophysics at Columbia University Irving Medical Center. Follow her on Twitter @RieNygaard.

Filippo Mancia (fm123@cumc.columbia.edu) is an associate professor and co-director of graduate education in the department of physiology and cellular biophysics at Columbia University Irving Medical Center. Follow him on Twitter @pippomancia.

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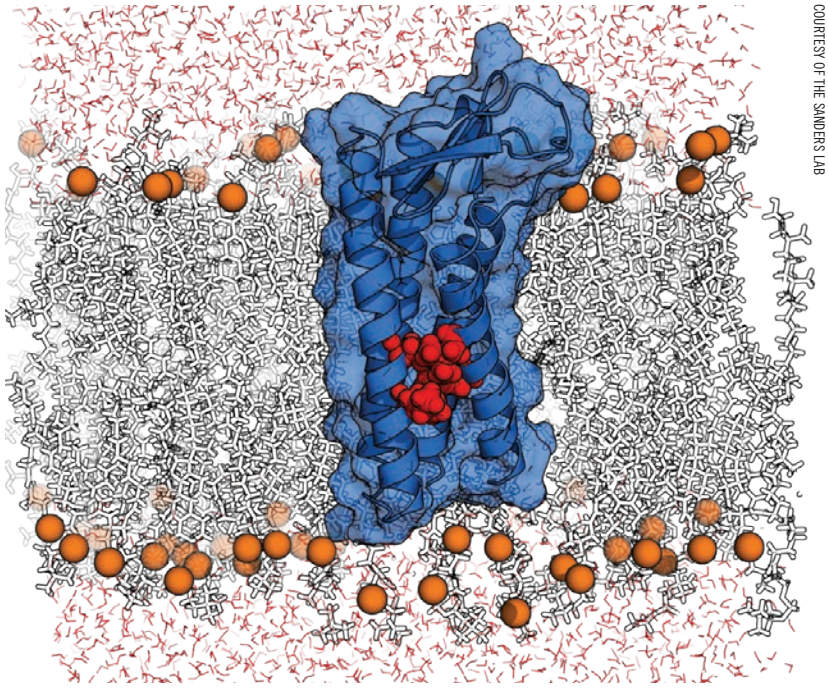
The protein defects that cause Charcot–Marie–Tooth disease

By Isha Dey



COURTESY OF THE SANDERS LAB

A molecular dynamics simulation of PMP22 in a phosphatidylcholine bilayer shows the small extracellular domain of the protein oriented at the top. The red side chains deep within PMP22 (blue) indicate a cluster of sites associated with mutations causing severe forms of Charcot–Marie–Tooth disease. The orange balls are lipid head group phosphorus atoms, and the small red molecules are water.

Looking at scientific data from different angles can broaden our understanding of a topic and sometimes opens new avenues for research. One example is a recent discovery about the mistrafficking of PMP22 protein in Charcot–Marie–Tooth, or CMT, disease, an inherited neuromuscular disorder that damages the peripheral nerves in arms and legs.

First diagnosed in the 1800s by French physician Jean Charcot, his student Pierre Marie and British neurologist Howard Tooth, CMT belongs to the cadre of diseases caused by membrane protein misfolding and affects about 150,000 people in the U.S. The type 1A phenotype, or CMT1A, is caused by an extra copy of the PMP22 gene, encoding the peripheral myelin protein 22, an integral membrane glycoprotein expressed in the myelin sheath. This leads to increased production of the protein, which triggers dysmyelination. In rodent and patient-derived cell models of CMT1A phenotype, researchers have found PMP22 aggregates that are likely cytotoxic.

Proteins expressed in a cell pass through the endoplasmic reticulum quality control system, whereby hopelessly misfolded proteins are routed to degradation pathways. Accumulation of PMP22 aggregates suggests this process is compromised in CMT. Charles Sanders' group at Vanderbilt University sought to understand the quantitative correlation between the expression and membrane trafficking of PMP22. They found that increased intracellular expression of PMP22 leads to mistrafficking of the protein, increasing the ratios of intracellularly trapped misfolded protein relative to the cell surface-localized form, which might explain the CMT1A phenotype. Their findings were published in the **Journal of Biological Chemistry.**

Sanders, a biophysicist, became interested in human membrane protein misfolding and related diseases as an assistant professor struggling with a misfolding-prone bacterial protein. "To launch into this area, I wanted to look at a protein and disease that had not been studied before," he said. "PMP22 is a small but complex protein with only 160 amino acid residues that span the membrane four times. It was an attractive candidate to study from both practical and disease perspectives."

The researchers deduced their results using a single method, a single-cell flow cytometry trafficking assay. They transfected c-Myc-tagged wild-type or disease mutant variants of PMP22 into cell models and analyzed them using this technique. For each of thousands of cells, they quantitatively analyzed the surface

membrane levels and intracellular levels of PMP22, allowing them to correlate the single-cell amounts of both correctly surface-trafficked and misfolded PMP22 with the total cellular level. This assay was developed by Ph.D. student Justin Marinko, extending earlier work by Sanders' postdoc Jonathan Schlebach, now on the faculty at Indiana University.

"One real hurdle for me was to work with mammalian cell lines," said Sanders, who had little experience in cell biology. But Schlebach and Marinko developed this line of research almost unassisted. "Having brave people in the lab and letting them do what they wanted to do was exactly what was needed for this project."

The findings in the new JBC paper resulted from reanalyzing previously acquired data from a different angle. "When labs were shut down due to the COVID pandemic, my students were looking for things to do from home," Sanders said. "So, I suggested Justin reanalyze the flow cytometry data in single-cell terms."

Going forward, in collaboration with co-author Bruce Carter, Sanders plans to test his hypothesis in human Schwann cells, the cells in which PMP22 misfolds in CMT disease. "We are also looking into understanding the molecular gatekeepers in the secretory pathway that control the trafficking of PMP22," he said.

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

Upcoming ASBMB events and deadlines

MARCH	MARCH	**Women's History Month**
		Brain Injury Awareness Month
	15	Abstract deadline for PDB50: A special symposium celebrating the 50th anniversary of the Protein Data Bank
	15	Early registration deadline for PDB50: A special symposium celebrating the 50th anniversary of the Protein Data Bank
APRIL	APRIL	
	12	Advanced registration deadline for the 2021 ASBMB Annual Meeting
	14	**World Chagas Disease Day**
	25	**DNA Day**
	27–30	2021 ASBMB Annual Meeting
MAY	MAY	**Asian American and Pacific Islander Heritage Month**
		National Stroke Awareness Month
	4–5	A special symposium celebrating the 50th anniversary of the Protein Data Bank
	5	Deadline to apply or submit a nomination for ASBMB Annual Awards
	9	**National Women's Health Week**
	10	**National Lipid Day**
	15	**Dementia Awareness Week**
	23	**World Melanoma Day**

A novel approach to septic shock

By Caleigh Findley

The human body responds to infection by activating its innate immune system. Sepsis occurs when that triggered immune response spins out of control and becomes life-threatening. Doctors administer antibiotics and other supportive care but are unable to prevent death in about 40% of sepsis patients. The Centers for Disease Control and Prevention estimates that some 270,000 patients in the United States die from sepsis each year.

When antibiotics are not enough, clinicians need another line of treatment to improve patient outcomes. A recent publication in the **Journal of Lipid Research** by Auguste Dargent of the Centre Hospitalier de Lyon in France and colleagues details their efforts in response to failed clinical trials investigating a toxin removal method for sepsis treatment.

Septic shock most commonly is caused by bacterial infections. Bacteria express certain toxins that provoke the immune system during sepsis, including lipopolysaccharides, or LPS. The researchers thought lowering the level of LPS in the blood could treat septic shock more effectively than antibiotics alone.

As Kenneth Feingold, a JLR associate editor, explained, "LPS is a part of gram-negative bacteria, which is the etiology of most sepsis … If one can bind up the LPS that comes off this bacteria, then this can potentially reduce the number of deaths from sepsis."

The body already has molecules in charge of clearing out LPS called lipoproteins. High-density lipoproteins grab onto LPS in the blood and pass them over to low-density lipoproteins, or LDLs, which take them to the liver for degradation.

However, as the research team previously had discovered, this built-in protection fails in septic patients with decreased lipoprotein levels. They also showed that treating with a therapeutic protein that promotes LPS clearance can improve mortality rates in septic animals. These findings led them to investigate whether the same is true in humans.

To test their hypothesis, the researchers loaded blood plasma samples from healthy patients with LPS, a process called "spiking." Then they soaked spiked samples in a solution with tiny beads that grab onto LDL, a lipoprotein with an LPS attached, and remove it from the plasma.

To determine the amount of LDL left over in the plasma, the team measured the amount of 3-hydroxymyristate, an LPS lipid component. Doing so allowed for direct measurement of LPS plasma levels, whether bound to a lipoprotein or circulating freely. With this, they saw a decrease in free LPS and LDL levels in treated samples — inspiring researchers to look further into cholesterol disorders.

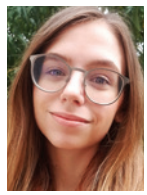
Patients with familial hypercholesterolemia have high levels of LDLc in their blood. Researchers examined serum samples from hypercholesterolemia patients undergoing treatment with the same or similar microbead-removal methods. These patients also saw a significant drop in their LDLc and LPS levels after treatment.

These results prompted the researchers to examine their strategy in serum samples collected from septic patients. They remained successful in removing circulating LPS from plasma samples using microbeads — a promising result for this team to build on moving forward.

"The key is that this is the first step," Feingold said. He emphasized that studies in animal models are needed to determine whether this therapeutic approach can be developed as treatment for sepsis. "If successful, this could be a major advance. But we have to see if this actually works."

DOI: 10.1194/jlr.RA120001132

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

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From the journals

By Kian Kamgar–Parsi, Anand Rao & Anna Tancredi

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

Chemomechanical oddities of kinesin-3

Molecular motors are a class of proteins that hydrolyze adenosine 5'-triphosphate, or ATP, to create the kinetic energy necessary to execute their many biological functions. Unique among these proteins is kinesin-3, which displays the fastest and longest bouts of movement of all kinesins but remains poorly understood.

Using stopped-flow fluorescence spectroscopy and single-molecule motility assays, Taylor Zaniewski of Pennsylvania State University and colleagues uncovered the molecular and biophysical details underpinning kinesin-3's distinctive attributes. The researchers found that hydrolysis of ATP, and not ATP binding, stimulated the forward step of kinesin-3. Their findings showed that the motor protein follows the same chemomechanical cycle as established for kinesin-1 and -2. However, the researchers showed that kinesin-3 differs from kinesin-1 and -2 in three areas: It has a rear-head detachment rate that's an order of magnitude faster than other kinesin family members; its tethered-head attachment transition is rate-limiting; and it has a relatively slow dissociation from the low-affinity, post-hydrolysis state.

These data, published in a recent paper in the **Journal of Biological Chemistry**, detail the attributes that contribute to kinesin-3's fast and long bouts of movement along microtubules.
DOI: 10.1074/jbc.RA120.014961

"Shepherd" guides understanding of protein modification

While the role of proteins in biology is quite familiar, scientists know less about the importance of post-translational modifications, or PTMs. These PTMs involve the addition of different molecular groups to the protein amino acid chain and are crucial for protein function. However, with 20 types of amino acids and dozens of PTMs, identifying PTMs in complex mixtures remains a major scientific challenge.

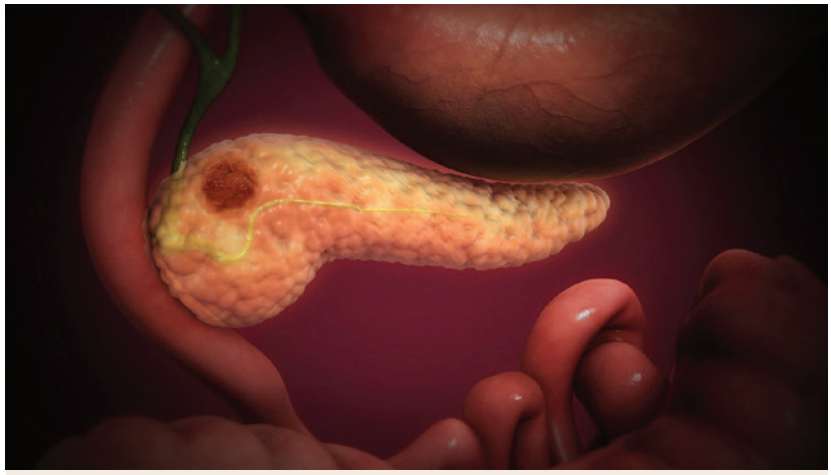
Open searching, a methodology to identify PTMs in complex mixtures without prior knowledge of which may be present, is a valuable approach in proteomics. Daniel Geiszler and a team from the University of Michigan have developed a new tool, PTM-Shepherd, to optimize and improve on this methodology.

As described in a paper published in **Molecular & Cellular Proteomics**, PTM-Shepherd was able to use small protein mass shifts detected by mass spectrometry to identify PTMs, distinguishing modifications differing in mass by as little as 1/400th of a carbon atom. Using the PTM-Shepherd tool, researchers could identify artifacts in protein synthesis and detect differences in presumably identical proteins based on the source lab. PTM-Shepherd could be a strong new tool both for protein synthesis quality control and for identifying rare/novel PTMs in biological research.
DOI: 10.1074/mcp.TIR120.002216

Expressing CETP slows endotoxin clearance in mice

When Gram-negative bacteria enter the bloodstream, they release lipopolysaccharides, or LPSs, which activate the innate immune system. LPS is not metabolized in the body and must be disaggregated and excreted in bile through a pathway known as the reverse LPS transport, or RLT, pathway. Increasing our knowledge of the RLT pathway could help with detection and treatment of sepsis, a life-threatening inflammatory immune response to infection that affects over 1.7 million adults in America each year.

Aloïs Dusuel and colleagues at the University of Burgundy recently published findings in the **Journal of Lipid Research** that a protein tightly related to key players of the RLT pathway, cholesteryl ester transfer protein, or CETP, does not contribute to the binding and transfer of LPS in plasma. However, when the researchers injected purified LPS into mice to simulate infection, the mice that were genetically altered to express CETP cleared endotoxins at a slower rate than mice who expressed no CETP. The CETP-expressing mice also had worse sepsis outcomes. The researchers suggest looking into the inflammatory response over time to better understand the role CETP plays in the inflammatory process and, possibly, in sepsis.
DOI: 10.1194/jlr.ILR120000704



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With pancreatic cancer a leading cause of death and hard to detect, an acute need exists for better early biomarkers of disease.

Turning to sugars to help detect pancreatic cancer

With nearly 50,000 deaths each year in the U.S. and only a 9% five-year survival rate, pancreatic cancer has one of the worst prognoses of all cancers. At the heart of this is the difficulty in detecting pancreatic cancer early; most patients are diagnosed after the disease is already advanced. The carbohydrate-associated molecules CA19-9 and sTRA have shown value in tracking disease progression but cannot be used to identify pancreatic cancer early or specifically, highlighting the need for other biomarkers.

Recently, researchers have found that, while historically understudied, the coating of carbohydrates on the surface of cells (called the glycocalyx), and particularly a family of these carbohydrates called N-glycans, are associated with pancreatic cancer. New data from Colin McDowell and collaborators at the Medical University of South Carolina and the Van Andel Research Institute, published in **Molecular & Cellular Proteomics**, provide early insights into the promise of these N-glycans as a potential new biomarker. McDowell and his colleagues used mass spectrometry to detect and differentiate N-glycans. Their research shows that N-glycans have increases in several modifications, including sialylation, poly-LacNAc extensions and branching, that vary in healthy, necrotic and tumor tissue.

The range and complexity of N-glycan modifications likely will preclude any one species from serving as a definitive biomarker of pancreatic cancer; an N-glycan signature is likely the key. The current study also is limited, with some N-glycan species too large to be identified. Despite these drawbacks, the complementarity of this N-glycan evaluation to CA19-9 and sTRA evaluations could improve confidence in tumor detection. The researchers are working to characterize further the role of N-glycans in pancreatic cancer. With an increased understanding of their relation to tumor formation, N-glycans could provide an important diagnostic tool in improving pancreatic cancer detection and, ultimately, saving lives.
DOI: 10.1074/mcp.RA120.002256

— Kian Kamgar–Parsi

Antigens, epitopes and NMR

When epitopes, antibody binding sites present on antigens, are discontinuous, the sequences are recognized only when the protein is folded in a particular conformation. Identification of these epitopes is crucial to understanding immunological mechanisms. However, the characterization of discontinuous antigenic epitopes, such as the lipid transfer polyproteins, or LTPs, in pollen allergens, remains a technical challenge.

In a recent study published in the **Journal of Biological Chemistry**, Martina Di Muzio and colleagues at the University of Salzburg reported a new approach for studying LTPs, involving a modified nuclear magnetic resonance–exchange measurement that detects sub-stoichiometric complexes. In this method, called hydrogen/deuterium exchange memory NMR, a gradual exchange occurs between the invisible antigen–antibody complex and the free ^{15}N-labeled antigen. Using this method, the researchers found three structural epitopes of Art v 3, a pollen LTP from mugwort: two partially cross-reactive regions around α-helices 2 and 4 as well as a novel Art v 3–specific epitope at the C terminus. This new development will be applicable for the study of a wide range of macromolecular interactions.
DOI: 10.1074/jbc.RA120.014243

Proteomic evaluation of PTX3 behavior in sepsis

Sepsis is a deadly condition brought on in response to infection, with 270,000 yearly deaths associated with the complication in the

Muscles, myosin and a mechanism mystery

Whether it's the movement of limbs (skeletal muscle), digestion of food (smooth muscle) or the pumping of blood for oxygen delivery (heart muscle), the reliable contraction of muscles is crucial for the physiological processes that support life. Myosins, motor proteins that interact with muscle fibers and generate the forces that drive muscle contraction, must precisely coordinate their mechanical and chemical cycles to execute their biological function properly.

Myosin was first described by Wilhelm Kühne in 1864. Yet, despite over 150 years of studying myosin biology and the mechanisms driving myosin-meditated processes, researchers do not know how myosin converts energy, in the form of adenosine 5'-triphosphate, or ATP, into mechanical work.

To answer this longstanding question, Laura Gunther of Pennsylvania State College of Medicine and a team of biochemists and biophysicists combined single-molecule optical trapping and fluorescence resonance energy transfer, or FRET, technologies. By doing so, the researchers were able to study myosin-related events with near minute-level temporal resolution and observe myosin-related events with unprecedented clarity.

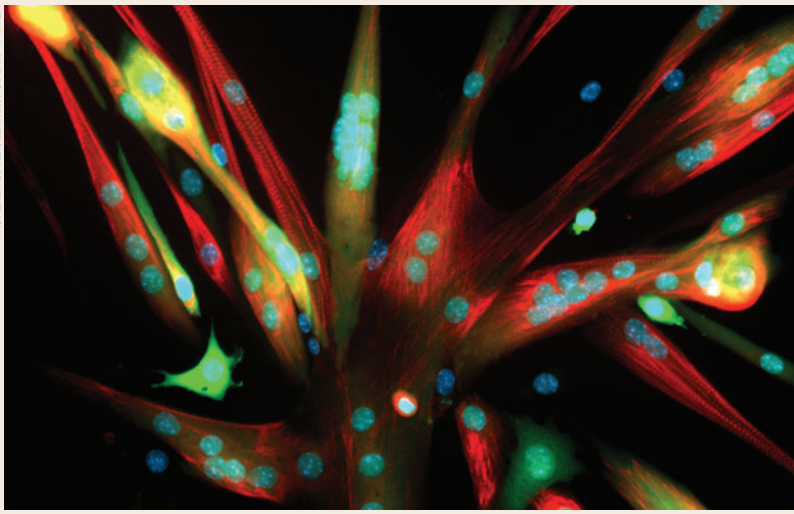
The team found that the myosin's power stroke, the force-generating step when myosin initially interacts with a muscle filament, occurs rapidly, while key biochemical events occur subsequently and more slowly. Using site-directed mutagenesis, they then showed for the first time how communication between actin- and nucleotide-binding regions of myosin is key to coordinating and producing those myosin power strokes.

The researchers present this work in a recent paper in the **Journal of Biological Chemistry**. Comprehensive knowledge about these processes one day could help scientists produce new treatments for cardiovascular diseases, musculoskeletal disorders and more.
DOI: 10.1074/jbc.RA120.015632

— Anand Rao

Mouse skeletal muscle stem cells form myotubes (green), which form muscle filaments. Red myotubes contain a protein involved in muscle contraction, myosin heavy chain, and are characteristic of mature muscle fibers.

KEVIN A. MURACH/UNIVERSITY OF KENTUCKY



United States alone. Researchers have found that formation of pentraxin-related protein PTX3 multimers (particles composed of multiple copies of a single PTX3 protein) is associated with mortality in sepsis; however, they do not understand fully yet how these multimers are formed. Now new research by Sean Burnap at King's College London and an international team provides novel insights into the role of PTX3 in sepsis.

As published in **Molecular & Cellular Proteomics**, human and mouse models along with mass spectrometry were used to interrogate the effect of lipopolysaccharide, or LPS (an endotoxin that can cause sepsis), on PTX3 behavior. As expected, higher levels of PTX3 multimers were seen after introduction of LPS, with this increase correlating with increases in proteins derived from neutrophils (white blood cells). In fact, mice without key neutrophil enzymes still showed an increase in PTX3 multimers in response to LPS. Instead of being synthesized in response to LPS, PTX3 multimers appear to be stored in neutrophils and deposited on aortic vessel walls. This improved understanding of PTX3 behavior could provide insights toward development of new treatments for acute sepsis.
DOI: 10.1074/mcp.RA120.002305

A look at atherosclerotic lesions in diabetes

Atherosclerosis is a progressive condition that increases risk of heart disease. Jenny Kanter and Karin Bornfeldt of the University of Washington School of Medicine have shown previously that the low insulin

levels characteristic of diabetes lead to increased levels of apolipoprotein C3, or APOC3, and triglyceride-rich lipoproteins, or TRLs, as well as accelerated atherosclerosis.

Kanter and Bornfeldt recently published fluorescence microscopy images of atherosclerotic lesions in a mouse with induced Type 1 diabetes in the **Journal of Lipid Research**. Their experiment focuses on two apolipoproteins: APOB, which is the primary apolipoprotein of low-density lipoprotein, very low-density lipoprotein, chylomicrons and remnant lipoproteins; and APOC3, which slows the clearance of triglyceride-rich lipoproteins and their remnant lipoprotein particles, or RLPs, lipids that have been linked previously to cardiovascular disease.

The researchers found that APOC3 and APOB colocalize in atherosclerotic lesions of the aorta, supporting their hypothesis that the lipoprotein particles containing APOC3 could be these TRLs and RLPs. Their images also show that APOC3 and APOB are localized near lesional macrophages. Accumulation of these TRLs and RLPs can lead to increased accumulation of lesional macrophages, thereby worsening atherosclerosis and increasing cardiovascular disease risk.
DOI: 10.1194/jlr.ILR120001217

Furin as a metabolic deactivator of PCSK9

The enzyme proprotein convertase subtilisin/kexin type 9, or PCSK9, regulates cholesterol metabolism by binding and chaperoning the low-density lipoprotein, or LDL, receptor to be degraded. That receptor clears LDL from circulation, making PCSK9 an appealing drug target: Blocking PCSK9 lowers blood LDL concentration, thereby reducing risk for cardiovascular disease.

PCSK9 has two known active forms: a mature form and a less understood furin-cleaved form, PCSK9_55. Carlota Oleaga and colleagues at the Oregon Health & Science University recently published the results of their studies to characterize this less known form in the **Journal of Lipid Research**.

First, Oleaga's team transfected a line of human embryonic kidney cells with the mature form of PCSK9 and furin vectors to test where PCSK9_55 was formed. As expected, the mature form was furin-cleaved to form PCSK9_55, with greater amounts of PCSK9_55 found in the extracellular space and only moderate amounts within cells. Adding a furin inhibitor that could cross the cell membrane decreased this extracellular formation.

The researchers engineered the embryonic kidney cells to express a recombinant PCSK9_55. Lacking a prodomain sequence that is essential to PCSK9 secretion, this form's abundant intracellular expression and retention were unsurprising. However, no change in secretion was detected when the recombinant PCSK9_55 was expressed with a prodomain or a prodomain donor. These results suggest that PCSK9_55 is not secreted into the extracellular space because it is markedly altered from the uncleaved parent.

EMW/WIKIMEDIA COMMONS

The enzyme PCSK9 protein regulates cholesterol metabolism by degrading the low-density lipoprotein receptor.

Oleaga and colleagues propose that furin could act as a metabolic deactivator of PCSK9. Furin post-translationally modifies extracellular PCSK9 to form PCSK9_55, which has reduced capacity for LDL receptor degradation. When PCSK9_55 reenters the cell, it cannot be secreted back into circulation and eventually is catabolized. Further testing of this model could provide insight into drug development and treatments for cardiovascular disease.
DOI: 10.1194/jlr.RA120000964

— Anna Tancredi

AggreCounting protein aggregates

The accumulation of misfolded proteins is a pathological feature of several human diseases, including Alzheimer's, Parkinson's and Type 2 diabetes. However, researchers have no unifying method to quantify cellular aggregates.

In a recently published paper in the **Journal of Biological Chemistry**, Jacob Aaron Klickstein and colleagues at Tufts University developed an intuitive and easy-to-use macro for the image processing program ImageJ called AggreCount. This tool allows researchers to identify and quantify different types of cellular aggregates in an automated fashion, sparing scientists from the laborious and time-consuming manual counting of protein clumps. The macro, which the researchers have made freely available to all on GitHub, can be applied to multiple cell types for a variety of applications.

DOI: 10.1074/jbc.RA120.015398

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A steady hand at the helm

ASBMB's new executive director, Steve Miller, is a society veteran but eager to make his mark

By Angela Hopp

ANAND RAO/ASBMB

In late January, the American Society for Biochemistry and Molecular Biology's president announced that longtime employee Stephen F. Miller would become the organization's next executive director.

He replaces leader Barbara Gordon, who is retiring after four decades of service.

In a letter to ASBMB members, Toni Antalis of the University of Maryland School of Medicine cited Miller's "deep knowledge of and commitment to the society" and "the importance of continuity and experience with society operations" at a time when the ASBMB journals are now open access.

Lila Gierasch at the University of Massachusetts–Amherst, editor-in-chief of the Journal of Biological Chemistry, said, "Steve has guided the ASBMB financial ship so successfully. I am sure he will help lead the society in the right directions."

Miller earned his bachelor's degree in accounting from the University of Maryland in 1980. Since then, he has held leadership positions at companies of various sizes in the Washington, D.C., metro area. At the beginning of his career, he handled payroll for a hospitality management company. He later worked at a direct marketing company and two publishers before arriving at the ASBMB in 2004.

At the society, Miller, a certified public accountant, has held several positions focused primarily on finance and overall operations. He most recently was responsible for leading the finance, membership and information technology departments, which handle the financial reporting, investment funds, member data, and in-house and web technologies. He has been the deputy executive director since 2014.

In addition, Miller oversaw the society's move from the historic Beaumont House on the 11.2-acre campus of the Federation of American Societies for Experimental Biology in Bethesda, Maryland, in 2011 to its current, more modern space a few miles north. Other FASEB societies gradually followed suit, and FASEB recently sold the campus. This summer, the ASBMB will move again, this time to a nearby office building that houses many of its sister societies and that will one day house the FASEB itself.

Miller talked to ASBMB Today about the society's evolution during his years of service and about his plans for the coming years. This interview has been edited for length, clarity and style.

Q. What informs your leadership style? Who are your models, and what are your preferred approaches?

A. I can be demanding. However, I do reach out to my staff for their input. I'm a firm believer that there's always a better way of doing what we're doing. I feel staff are comfortable with approaching me with issues and, more importantly, not afraid to ask questions.

As far as my role models, my mentors, I've been blessed both ways. I had some good mentors early in my career. And then I also have had some other supervisors who taught me how not to act and how not to treat staff. I've seen both sides of the coin.

Q. How did the jobs you had before coming to the ASBMB equip you for where you are today?

A. I was put in charge of a lot of projects and was given a lot of responsibility. I worked on my own a lot, and that required me to manage my time effectively and multitask. As much as it's important to listen to what your staff thinks and the ideas they have, it's also important to let them take ownership of their work.

Q: During your time with the society, its programs have multiplied to meet the needs of members. What are some of the trends you've observed?

A. The society has really evolved a lot from when I started in 2004. Back then, we focused primarily on preparing people for careers at the bench in academia. We have expanded what we have available for undergrads and graduate students. The Student Chapters program was started with the focus on undergraduates and developing relationships with the faculty at primarily undergraduate institutions.

And now we're looking at opportunities that are nonacademic and away from the bench. We're reaching out to industry folks to get their ideas and see how we can work with them to develop tools and resources that will help our members if they're seeking careers in industry. In a way, we're starting to reinvent ourselves to match what our members really want from us.

Q. Starting in 2023, the ASBMB will hold its annual meeting independently of the Experimental Biology conference. What are your hopes for that?

A. I welcome this change. We've been limited in what we can do by meeting as part of a bigger group — in particular with regard to operations and the registration process. Also, what we're seeing in our surveys and hearing from our members is that large meetings feel impersonal. I think we're now going to be able to really zero in on the topics of interest to our members and make it more personal.

Also, for all our meetings, even the small ones, we want to have a virtual option. Offering both an in-person and virtual option will accommodate our members who don't have the money, time or desire to travel. What we've gone through this past year with the COVID-19 pandemic — this new normal — is really making us rethink how we

"What we're seeing in our surveys and hearing from our members is that large meetings feel impersonal. I think we're now going to be able to really zero in on the topics of interest to our members and make it more personal."

> “More recently, we greatly expanded our virtual meetings program. The lipids researchers have one every month, in fact.”

run our meetings and how we interact with our members.

Q. The society also now manages meetings for other groups. How did that come to be?

A. Biochemistry is so broad. And, throughout the years, we've had people in a number of areas of research spin off and form their own societies to focus on their area of research. Expanding our efforts to manage meetings for these other areas is an attempt to reconnect with these groups.

Years ago, we began managing the Deuel Conference on Lipids to meet the needs of our lipids-focused members. Deuel has its own separate board of directors, but we have a contract with them to run the meeting. Recently, we managed a mass spectrometry meeting that will run in 2022 and hopefully continue every two years after that.

More recently, we greatly expanded our virtual meetings program. The lipids researchers have one every month, in fact. We're open to other areas of research and want to offer those members a forum where they can get together and communicate their science but still be under the ASBMB umbrella.

Q. The society historically has had a core group of very loyal members, many of whom have retired or are near retirement. What is the ASBMB doing to win over subsequent generations?

A. Twenty years ago, any new Ph.D. would hear from their mentor, “Look, you need to be part of this society.” It's different now. People don't see the value of a society membership like they did. And that's why we need to reinvent ourselves. That's one question that we've put to the membership committee: What do we need to do to get back to that?

One of the things that I've been tasked with is to come up with a strategic plan. I have a lot of ideas, but I'm going to be leaning on the directors and the committees for their input. This is a really exciting time, because we're to a point where we can put our fingerprint on the direction the society takes the next couple years. It's going to be a really interesting time.

Q. You were involved in the decision to make the ASBMB journals open access and to partner with Elsevier to do it. Is there anything that you want members to know or that you feel is perhaps misunderstood?

A. Whenever a society partners with a commercial publisher, everybody's radar goes off. They think the purpose is mainly financial. And that's not the case here.

We spent three years studying this and looking at our options. We looked at where the industry is moving — it's going open access. And we looked at researchers' funding sources — and the issue of funders requiring them to publish in open-access journals.

JBC went online back in the 1990s, before most other journals, and we wanted to be ahead of the curve again, this time with open access, and take advantage of being one of the early players.

Before we considered an outside partner, we looked at trying to do it in-house. We studied our current vendors, the limitations and the volume of articles required to make it possible. After this review, we concluded we just didn't have the volume to do this in-house and didn't want to lower our standards to achieve it. So we

ASBMB

Steve Miller and Barbara Gordon, the American Society for Biochemistry and Molecular Biology's retiring executive director, at the 2006 ASBMB Annual Meeting in San Francisco. See tributes to Gordon on page 44.

knew we would need to partner with a commercial publisher to make the ASBMB journals open access.

Elsevier has a lot of tools that we lacked. Yes, they have marketing resources, but they also have the editorial tools that will help our associate editors do their jobs more efficiently. The author and reader data they have will help in planning for the future of our journals. The most important issue was that the society demanded that the journals maintain complete editorial control of the content.

Ultimately, this partnership resulted in a lower article-processing fee for our authors than before we went open access, so it's a win for authors.

Q. You're a finance guy and deserve a lot of credit for the society's solid financial footing. What do you want members to know about the society's spending?

A. When I came in back in 2004, we took a long, hard look at our spending. When JBC was in print years ago, we were sending anywhere from 400 to 500 copies of the journal to storage every week. Nobody was looking at them! These were some of the expenditures that were reduced, along with others that were reviewed for saving opportunities.

When staff or committee chairs come to me with different ideas, I ask them one question: How does it add value to the society? If they can explain the value, sure, we'll spend the money. A lot of times they'll turn around and come back later with an answer. The point is that we spend the society's funds on activities that benefit our members and support our overall mission.

We've been fortunate. We have two very good investment managers who have done quite well with our investments. So we're in a position where we can make this move to open access and feel very comfortable about the society's finances. The society is well positioned and funded to continue for decades.

I think the other thing members should know is that the society

supports many of the scholarships and awards currently offered. With the exception of $10,000 we received this year from New England Biolabs for the Sewer diversity scholarship, we've funded all these scholarships and awards. And, to be clear, even with the gift for the Sewer scholarships, we'll continue to maintain the current levels of support. The gift will help us support even more students. As we raise additional money, the goal is not to cover the society's costs but to expand on the awards and scholarships we offer.

Q. The COVID-19 pandemic has changed how people work in myriad ways. How has it informed your plans for the ASBMB of the future?

A. On the accounting side, it has really accelerated the move to a paperless environment. It gets complicated because there's a lot of internal control steps in a paper environment that now have to be duplicated in a paperless one. However, it's a move the society will have to make this year.

As far as operational, I think my big frustration has been the lack of spontaneous thinking. Now you need to schedule a Zoom meeting or call rather than just walking down the hall to meet with staff.

Q. You oversaw the society's move in 2011, and it's moving again this summer. I'm wondering what lessons learned influenced your planning this time.

A. First, we were able to capture a deal that decreases the cost to the society, and that enables us to provide more benefits to our members. The second part is that we're moving to a space where there are a lot of different amenities. There's a gym, a cafeteria, and a shuttle that picks our employees up from the front door and takes them straight to the subway. The landlord provides three conference rooms that allow for virtual meetings at no additional cost.

We're also going to be closer to our sister societies that are also located in that building. For example, the American Physiological Society, the Genetics Society of America and the Society for Developmental Biology are there. So there might be an opportunity to collaborate and do some more joint events with those folks.

Q. What's your life like outside of the ASBMB? How do you spend your free time?

A. Several years ago, we moved to the Eastern Shore, and our home is waterfront, so I spend a lot of time on the water with our boat. Being able to escape by water has helped offset the restrictions in response to COVID-19 over the past year.

Q. Is there anything else that you want to share?

A. I'm really excited about having an opportunity to develop a strategic plan with input from both the staff and the committee chairs that will leave our footprint on the direction of the society in years to come.

Angela Hopp (ahopp@asbmb.org) is executive editor of ASBMB Today and communications director for the ASBMB. Follow her on Twitter @angelahopp.

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JBC Herbert Tabor Early Career Investigator Award winners to share research

By Anand Rao

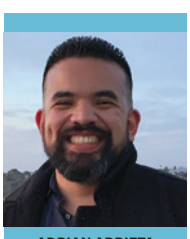
The Journal of Biological Chemistry has a longstanding mission to support the dissemination of science, enhance research visibility and promote scientific equity. As part of this mission, the journal is proud to recognize the next generation of scientists and their contributions to the field of biological chemistry. The JBC Herbert Tabor Early Career Investigator Award — named after Herb Tabor, JBC's editor-in-chief from 1971 to 2012 and a giant in his field — are awarded to early-career first authors of standout JBC papers published in the previous year. After carefully reviewing nominations from JBC readership, consulting experts in the field and evaluating the quantitative impact of the papers, a committee of JBC associate editors selected five award-winning first authors.

All five winners of the 2021 JBC Herbert Tabor Early Career Investigator Awards and one 2020 winner, who are profiled in the following pages, will give talks on their award-winning papers Friday, April 30, 11:15 a.m.–12:30 p.m. at the ASBMB Annual Meeting.

Adrian Arrieta is a graduate student at San Diego State University. His paper is titled "Mesencephalic astrocyte–derived neurotrophic factor is an ER-resident chaperone that protects against reductive stress in the heart."

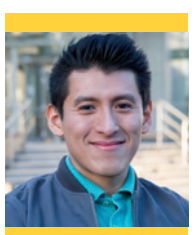
James M. Burke is a postdoctoral fellow at the University of Colorado, Boulder. His paper is titled "RNase L promotes the formation of unique ribonucleoprotein granules distinct from stress granules."

Alejandro Castillo–Kauil is a graduate student at the Center for Research and Advanced Studies of the National Polytechnic Institute. His paper is titled "Gαs directly drives PDZ-RhoGEF signaling to Cdc42."



ADRIAN ARRIETA

JAMES M. BURKE



ALEJANDRO CASTILLO–KAUIL

ANNE HARBIG

DUNCAN J. KOUNTZ

AYUMI NAGASHIMA–KASAHARA

Anne Harbig is a graduate student at Phillipps-University Marburg. Her paper is titled "Transcriptome profiling and protease inhibition experiments identify proteases that activate H3N2 influenza A and influenza B viruses in murine airways."

Duncan J. Kountz is a graduate student at Harvard University. His paper is titled "MtcB, a member of the MttB superfamily from the human gut acetogen Eubacterium limosum, is a cobalamin-dependent carnitine demethylase."

Ayumi Nagashima–Kasahara is a postdoctoral researcher at the University of Tokyo. Her paper is titled "Transcriptional regulators involved in responses to volatile organic compounds in plants."

Additional JBC Tabor Award winners, recipients from 2020 and 2019 whose recognition was disrupted by COVID-19, will give their talks Tuesday, April 27, 1:45–3 p.m. Read their previously published profiles at asbmbtoday/asbmb.org.

Anand Rao (arao@asbmb.org) is an ASBMB science communicator. Follow him on Twitter @AnandRaoPhD.

Arrieta follows the heart to find a protein function

By Leia Dwyer

When Adrian Arrieta started undergraduate studies in molecular toxicology at the University of California, Berkeley, he anticipated a career in drug development and pharmacology. However, a comparison of normal and cancerous human karyotypes in a genetics class sparked his interest in molecular mechanisms of disease.

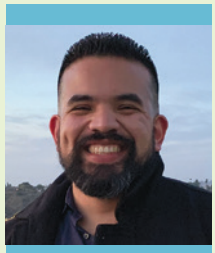
Arrieta joined Christopher Glembotski's lab at San Diego State University for his doctoral research, working on the premise that a tumor microenvironment has a high degree of protein misfolding and shares characteristics with a heart undergoing ischemia. Upregulated genes in cancer cells might provide a clue to which proteins in the heart respond protectively to stress.

Arrieta and his team's research was published in the Journal of Biological Chemistry. A collaborative environment was key to his success, he pointed out; the lab had to develop new assays and techniques. "We really had to start from the ground up," he said. "Everyone in the author block did something to make this happen."

Arrieta is now a postdoc at the David Geffen School of Medicine at UCLA in Thomas Vondriska's lab. Arrieta met Vondriska during a talk Arrietta gave at at a conference on cardiac regulatory mechanisms. The two were intrigued by each other's research, and Arrieta is now investigating protein quality control in the context of chromatin dynamics in the heart.

He's excited to be back in LA, where he grew up, because he can be with his family and enjoy home-cooked meals. "My mother told me that when I was little, I told her I was going to work at UCLA," he said. "Now, here I am — full circle."

Finding the function of an ER-resident chaperone in the heart



ADRIAN ARRIETA

After cardiac ischemia, reperfusion injury can occur when blood returns to the tissue. Ischemia/reperfusion, or I/R, disrupts protein folding and post-translational modification in the endoplasmic reticulum, causing loss of protein function and activating the ER stress response.

Mesencephalic astrocyte-derived neurotrophic factor, or MANF, is part of a gene program regulated by an ER stress response transcription factor. For more than a decade, researchers knew that MANF was upregulated in models of heart disease but didn't know its exact function. MANF bears no structural similarity to other ER proteins, and this got Adrian Arrieta wondering. "If it doesn't look like anything else that's been studied in the heart or any other tissue, it must be doing something really unique," he said. "That was the draw."

Arrieta and his colleagues in the Glembotski lab at San Diego State did experiments using a variety of techniques and specialties to deduce MANF function. They developed a knockdown mouse model to study MANF in both cells and mouse hearts. Lack of MANF expression in the heart increases cardiac damage during I/R injury, they found, and restoring MANF expression can reverse those effects. MANF also improved ER proteostasis during reperfusion injury.

The team found that MANF acts in response to reductive, not oxidative, stress during reperfusion injury and isolated its function as an ER-resident chaperone. Finally, by generating and studying a mutant version of the protein, Arrieta determined that conserved cysteine residues in the MANF molecule are required for its chaperone function. MANF's lack of structural homology remains a question for future research.

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Leia Dwyer (leia.dwyer@gmail.com) is a biotech and pharmaceutical industry professional.

JBC HERBERT TABOR EARLY CAREER INVESTIGATOR AWARD

Burke expands frontiers and maintains balance in RNA research

By Nivedita Uday Hegdekar

James Burke is an advocate for healthy work–life balance, and with good reason. Unlike most of his peers, Burke became a father while he was in grad school. Thanks to a progressive mentor and a supportive work environment, he was able to balance his doctoral research and family commitments effectively.

"Many people have asked me how I survived grad school while bringing up two children," he said. "In fact, the opposite holds true for me: I don't know how I would have survived grad school without them. They really motivated me to be more productive and efficient in my research."

Burke developed his interest in molecular biology as an undergraduate at the University of North Texas. He particularly enjoyed his research on symbiotic nitrogen fixation in Rebecca Dickstein's laboratory, and that motivated him to pursue doctoral studies at the University of Texas, Austin. There he discovered his research passion: RNA biology.

"I joined Christopher Sullivan's lab and began researching microRNAs encoded by viruses," Burke said. "I became extremely fascinated by how RNA is regulated during the innate immune response to viral infection."

Burke's doctoral research led to what he described as "exciting and unexpected findings" in RNA biology. Eager to probe more into unanswered questions, particularly in RNA metabolism, he joined Roy Parker's lab for his postdoc in 2017.

"The University of Colorado, Boulder has some of the best researchers and facilities for basic RNA biology research," he said. "I can't talk enough about great collaborations I have been a part of."

Burke aspires to an academic research position and is enthusiastic about exploring the uncharted frontiers of RNA biology during the mammalian antiviral response.

He is also an avid guitar player. And after spending most of his life in his native Texas, he now loves living in Colorado. He and his family enjoy mountain biking, hiking and rock climbing in the wondrous Colorado outdoors.

With his experience of juggling Ph.D. research and parenthood, Burke believes more mentors should promote a healthy work–life balance for their trainees.

"My undergraduate advisor once told me 'Don't put off life for science. Just live life and do science,'" he said. "These simple words have been and will always be my guiding philosophy."

Newfound granules might play a role in RNA turnover

JAMES BURKE

Stress granules are aggregates of proteins and RNAs that form during cellular stress or innate immune system activation.

While studying how innate factors could modulate stress granule formation, James Burke noticed several previously unreported granules within cells. He and his colleagues in Roy Parker's lab at the University of Colorado, Boulder, wrote in a paper in the Journal of Biological Chemistry about finding that these granules, termed RNase L–dependent bodies, or RLBs, are distinct from conventional stress granules in terms on their synthesis, composition and interactions.

These RLBs interact extensively with complexes that are responsible for RNA formation and decay. In upcoming experiments, the researchers will address whether the RLB association makes the RNA turnover process more efficient or has differential effects on RNAs. Burke and his colleagues also hope to learn how viral infections might alter the formation and role of the RLBs.

DOI: 10.1074/jbc.RA119.011638

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Experimenting with recipes and signaling proteins

By Deboleena Guharay

When Alejandro Castillo–Kauil isn't working in the lab, you'll find him experimenting with new recipes in his kitchen. "One of my favorite places at home is the kitchen," Castillo–Kauil said. "It's like lab, and you can experiment. I love cooking, it works like a therapy."

When he perfects a recipe for a Mexican dish, he shares it with his friends and family.

Castillo–Kauil grew up in the Yucatan state of Mexico and pursued his undergraduate studies at the Autonomous University of Yucatan. In Rolffy Ortiz–Andrade's lab, he analyzed the antihyperglycemic effects of Morinda panamensis fruits on rat models. He learned how to use analytical chemistry tools and handle lab animals, and he became familiar with clinical chemistry concepts.

That lab also provided one of the teachers and mentors who triggered Castillo–Kauil's interest. "It was Dr. Ortiz–Andrade who inspired and motivated me to pursue a career in science," he said, "and then I moved to Mexico City to pursue my master's degree."

At the Centre of Research and Advanced Studies, part of Mexico's National Polytechnic Institute, Castillo–Kauil studied active constructs of guanine nucleotide exchange factor, or RhoGEFs, in Jose Vazquez–Prado's lab. He loved his research work so much that after earning his master's in pharmacology, he decided to pursue his Ph.D. in the same lab.

In addition to cooking, Castillo–Kauil enjoys cycling, watching classic and animated movies, and reading. He successfully defended his Ph.D. thesis in October and hopes to pursue postdoctoral research in the field of cell signaling.

Activation of Cdc42 by G proteins

ALEJANDRO CASTILLO–KAUIL

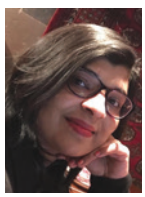
Gα proteins are an important part of the cellular membrane and are actively involved in cell-signaling processes in mammals. They help actin cytoskeleton make cell shape adjustments through activating Rho guanine nucleotide exchange factors, or RhoGEFs. RhoGEFs and the proteins with which they interact could be potential targets for molecules that might prevent the progression of cancer. A study of these cell signaling pathways is essential to develop pharmacological strategies to prevent cancer growth. Alejandro Castillo–Kauil and colleagues at the Vazquez–Prado lab in the Center of Research and Advanced Studies at Mexico's National Polytechnic Institute have tried to understand one such potential cell signaling pathway through investigating the activation of Cdc42 by G proteins.

$G\alpha_{12}$ and $G\alpha_{13}$ interact with RhoGEFs that drive RhoA activation, but researchers did not know if additional Gα proteins directly regulate these RhoGEFs. Castillo–Kauil and colleagues evaluated the morphological effects of constitutively active constructs from the subfamily of RhoGEFs activated via $G\alpha_{12}$ and $G\alpha_{13}$. All the constructs promoted cell contraction and activated RhoA, consistent with their known specificity. One of them, PRG, also induced filopodia-like cell protrusions and directly activated Cdc42, an ability that was increased by constitutive active Gαs.

Their results show that Gαs can recognize PRG as a novel effector to gain affinity for Cdc42. Further study of the involvement of this Gs/ PRG/Cdc42 pathway in cell migration could help researchers develop targets that might reduce progression of some cancers.

DOI: 10.1074/jbc.AC120.015204

Deboleena Guharay (deboleenamitra@gmail.com) earned her Ph.D. in chemistry from Virginia Commonwealth University. She is very enthusiastic and passionate about science communication.



JBC HERBERT TABOR EARLY CAREER INVESTIGATOR AWARD

Challenged by a pandemic, Harbig pursues a new approach to treating flu

By Guananí Gómez–Van Cortright

When Anne Harbig found out she had won an award for her very first authored paper, she was shocked.

"It totally caught me by surprise," Harbig said. The paper was the culmination of all of her data from her Ph.D. research in Eva Böttcher-Friebertshäuser's lab at the Marburg Institute of Virology. "I always wanted to deepen my knowledge about viruses, and I was able to have this great Ph.D. project. I'm very grateful for my supervisor."

Harbig's research takes on the challenge of finding proteases that activate specific strains of influenza, which could be targeted with drugs in order to prevent infection and treat the disease. If inhibiting proteases proves effective in halting influenza infection, these methods could be used to target other enveloped viruses as well, including coronaviruses.

Harbig's project came with all kinds of challenges — wading through piles of transcriptome data, hundreds of in vitro studies with proteases that never activated — and now, the global COVID-19 pandemic has introduced more disruptions as she continues to pursue the project as a postdoc.

"Sometimes, especially on a Friday when you have the results of the week's experiments and things are not working and everything sucks," she said, "it's good to have the weekend to take a break and have ideas for how to do it differently next week."

To stop flu infection, target host enzymes

ANNE HARBIG

Anne Harbig seeks to develop targeted treatments that prevent influenza viruses from entering potential host cells. For a flu infection to begin, the virus must have its surface protein called hemagglutinin cleaved by host enzymes known as proteases.

"A protease is a protein, an enzyme, that cleaves other proteins at specific sites," Harbig explained.

Because the virus cannot enter a cell without a protease present, Harbig and her colleagues are identifying proteases involved in activating certain flu strains so they can develop drugs that can block them.

Harbig used RNA sequencing to search for any segments of mRNA coding for proteases found in the lower respiratory system of mice. Once she identified an array of lung proteases, each one was tested individually for its ability to split apart the hemagglutinin on the surface of influenza B viruses. The proteases that were able to do so were narrowed down further to four candidates that activated influenza B infection in mouse cells.

"The idea is, if we know the protease that activates our virus, we can use protease inhibitors to prevent infection," Harbig said. "If we know all the proteases involved, we can test the inhibitors in murine models, in vivo, and if they work there, then maybe later [we can test them] in human studies."

Harbig has earned her Ph.D. and is continuing to work on the project, hoping to see it reach human clinical trials.

DOI: 10.1074/jbc.RA120.012635

Guananí Gómez–Van Cortright (guananigvc@gmail.com) is a teacher and freelance science writer.

Kountz tracks methyls in microbe metabolism

By Courtney Chandler

Duncan Kountz became interested in microbial biochemistry through a seemingly standard source: a textbook. But this wasn't a textbook assigned for class or research — he chose it himself because it seemed interesting, a habit he started in high school.

"Textbooks help me expand what I'm exposed to," Kountz said, "and I find them perfectly tolerable as long as they're on a subject I'm interested in."

The habit helped him prepare for a career in science, which he knew he wanted to pursue from the time he was in high school. Following a family legacy, he attended Ohio State University and sought research opportunities. He started out in a developmental biology lab, but that textbook, "The Physiology and Biochemistry of Prokaryotes," inspired a move to microbial metabolism. He contacted Joseph Krzycki, an OSU researcher in the field, and joined Krzycki's lab as a sophomore.

"Complexity and diversity really interest me, and I found that in microbial physiology, those are both on display," Kountz said. "Microbes may seem like they're a simple system, but they're also amenable to detailed work."

The Krzycki lab was finishing a project on an enzyme belonging to a superfamily of methyltransferases, and Kountz wanted to investigate similar enzymes in the context of the gut microbiome. He observed that a particular gut bacterium, Eubacterium limosum, encoded many of these enzymes and could utilize several unusual molecules for its growth. He focused on one in particular, carnitine, and tracked down the enzymes responsible for its metabolism.

His research shows how microbial metabolism can affect both microbial prosperity and the health of the human host, as carnitine metabolism can produce toxic byproducts. Kountz was excited about the findings, in part for this potential real-world applicability.

"I think we are really at the dawn of using microbes to solve problems," he said. "I'm excited about the idea of engineering or finding new microbes with interesting properties that we can exploit to make human life better."

Now a fourth-year Ph.D. student in Emily Balskus' lab at Harvard, Kountz said his textbook count currently exceeds 100.

Methyl-removing enzyme diverts toxin precursor

DUNCAN KOUNTZ

Gut bacteria can produce harmful compounds as a byproduct of their normal metabolism. Carnitine, a quaternary amine found abundantly in red meat, can lead to production of a toxin precursor called trimethylamine, or TMA, during digestion. TMA is converted in the liver to TMA oxide, a marker of cardiovascular disease.

Duncan Kountz and colleagues at Ohio State showed that the gut bacteria Eubacterium limosum can use carnitine as fuel, thereby potentially curbing TMA production. They also identified a new metabolite, called norcarnitine, produced by demethylation of carnitine.

Seeking to identify the enzymes involved in this metabolic transformation, Kountz noticed that E. limosum encoded many enzymes in the MttB superfamily. MttB proteins are involved in methyl transfer reactions.

Kountz characterized the enzymes involved in this pathway and identified a methyltransferase, MtcB, that demethylates carnitine and shuttles the product into pathways responsible for energy utilization and biogenesis.

The study highlights how metabolic activities in gut microbia may promote health by preventing production of toxin precursors.

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JBC HERBERT TABOR EARLY CAREER INVESTIGATOR AWARD

I smell a winner: Linking plant olfactory stimuli to genetic regulation

By Nicole Lynn

All creatures communicate through odor; the sense of smell picks up environmental cues to detect food or evade danger. Research by Ayumi Nagashima–Kasahara demonstrates that like most animals, plants also detect and respond to odorants called volatile organic compounds, or VOCs.

Nagashima–Kasahara had a unique introduction to plant science — performing research under the guidance of her high school biology teacher. "We studied seed dispersal, which for ants is driven by odorants given off by elaiosomes, which are rich in lipids and proteins," she said. "Normally, ants go straight to the elaiosome, but one day, they didn't. … The results were surprising, that ants may select efficient prey by smell."

This experience motivated her to pursue a research career. As an undergraduate at the University of Tokyo in Kazushige Touhara's lab, she studied the fate of odorants in olfactory mucus before they bind to receptors, and she later studied molecular mechanisms of plant odor perception as a grad student and postdoc. She received the 2020 JBC Herbert Tabor Early Career Investigator Award for her contributions as first author on a paper published in the Journal of Biological Chemistry. Due to maternity leave, her talk was postponed to 2021.

Outside the lab, Nagashima–Kasahara spends time with her husband and two children, ages one and five. "My children are my pride and joy," she said, "but they're little, so they don't really understand my job."

She tries to help them understand with science- and health-focused picture books and comic books called manga. In one book, the main character is a white blood cell battling pathogens; in another comic, astronauts perform crystallography in space for new ALS treatments.

Nagashima–Kasahara is interested in science, art and education and especially loves engaging with budding scientists. "Some students can't get the opportunities I did, or have good science education," she said. "I want to pay it forward and help the next generation."

She hopes one day to make her own science illustrated books or manga for young children.

Discovering a genetic element involved in plant olfaction

AYUMI NAGASHIMA–KASAHARA

Many animals gather information from their environment via volatile organic compounds, or VOCs. When plants are exposed to these odorants, their stress-related genes increase, helping them prepare for environmental changes; similarly, VOCs help parasitic plants identify suitable hosts. Until recently, researchers did not know how plants sense and convert the information from VOCs to signal genetic change.

Using TOPLESS-like proteins, or TPLs — genetic elements that repress gene expression — in tobacco, Ayumi Nagashima–Kasahara and colleagues in the Touhara lab at the University of Tokyo found that in plants, TPLs not only bind to VOCs but also act as transcriptional co-repressors, a process reminiscent of the steroid hormone recognition used by mammals to regulate gene expression.

"Some people can grow plants, others can't," Nagashima–Kasahara said. "Having 'green fingers' may mean finding out odorants your plants prefer."

This work suggests plants evolved to use transcriptional regulator proteins for odor detection, unlike animals, which use proteins in their cell membranes.

Nagashima–Kasahara continues her work on plant olfaction, hoping to identify the mechanisms and pathways involved in plant responses to VOCs. Further research could have applications in agriculture as a potential alternative to pesticides.

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Nicole Lynn (nalynn@g.ucla.edu) is a graduate student at the University of California, Los Angeles in the chemistry and biochemistry department.

JLR junior AEs to present postponed session

By George M. Carman & Robert V. Stahelin

The ASBMB 2020 Annual Meeting was canceled due to the COVID-19 pandemic, meaning the Journal of Lipid Research spotlight session featuring JLR junior associate editors now will take place Thursday, April 29, 2:15-3:30 p.m., as part of the 2021 meeting.

The JLR instituted the junior associate editors program to facilitate development of review skills and associated editorial activities. Since their appointments, the four junior AEs not only have been involved with the review process but also have organized a series of virtual issues, highlighting cutting-edge research in the JLR on lipoprotein clearance, sphingolipids, lipoprotein (a) and lipids in transcription.

The JLR's four early-career scientist associate editors are Raymond Blind of the Vanderbilt University School of Medicine, Gissette Reyes–Soffer of the Columbia University Irving Medical Center, Brandon Davies of the University of Iowa Carver College of Medicine and Rotonya Carr of the University of Pennsylvania Perelman School of Medicine. Read their previously published profiles at asbmbtoday/asbmb.org.

As co-chairs of this JLR session, we invite you to attend "Lipid Diversity and Disease: Spotlight on Journal of Lipid Research Junior Associate Editors," highlighting their lipid-based research ranging from basic to clinical studies.

George M. Carman (gcarman@rutgers.edu) is the founding director of the Rutgers Center for Lipid Research, a Journal of Lipid Research associate editor and co-director of the ASBMB Lipid Research Division.

Robert V. Stahelin (rstaheli@purdue.edu) is the Retter professor of pharmacy and a professor of medicinal chemistry and molecular pharmacology at Purdue University.

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MCP hosts early-career researcher session focused on proximity-dependent biotinylation

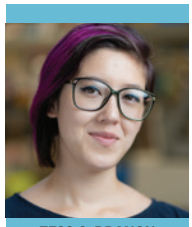
By Anne-Claude Gingras

How proteins interact with one another and with other macromolecules, their organization in cells and how these associations are modulated following perturbations long have defined an important branch of the field of functional proteomics. In the past 10 years, approaches that enable the study of these connections in the context of live cells — and now live organisms — have revolutionized the role of proteomics in cell biology.

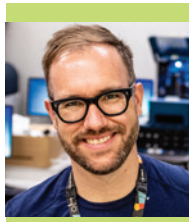
This session at the 2021 ASBMB Annual Meeting focuses on proximity-dependent labeling approaches, which allow for the covalent tagging of proteins that have come in close proximity to a bait protein (a protein of interest fused to an enzyme) in the context of living cells. Coupling of this strategy to mass spectrometric identification of the labeled proteins permits the characterization of cellular organization.

Since its first implementation to identify the components of the nuclear lamina in cultured cells, proximity-dependent biotinylation has contributed to better understanding of the composition of both membrane-bound and membraneless organelles, defined new signaling complex components, and illuminated the molecular mechanisms underlying several diseases. Proximity-dependent biotinylation methods, including APEX and BioID, still are developing, permitting new experimental modalities and answering increasingly complex questions.

The three presenters selected by the editorial leadership of Molecular & Cellular Proteomics are early-career researchers pushing the boundaries of proximity-dependent biotinylation methods and their applications. Read more about them in the following pages.



TESS C. BRANON



GEOFFREY HESKETH

ILIA DROUJININE

Tess C. Branon, a postdoctoral fellow at the University of California, Berkeley, will present her work on the directed evolution of promiscuous biotin ligases for efficient proteomic mapping in vivo.

Geoffrey Hesketh, a postdoctoral fellow at the Lunenfeld–Tanenbaum Research Institute of Mount Sinai Hospital in Toronto, will describe how he used proximity-dependent sensors to reveal new intricacies in amino acid signaling.

Ilia Droujinine, a principal investigator and Scripps fellow at Scripps Research, will introduce new work exploring protein trafficking by in vivo tissue-specific labeling in Drosophila.

Anne-Claude Gingras (gingras@lunenfeld.ca) is an investigator at the Lunenfeld–Tanenbaum Research Institute of Mount Sinai Hospital in Toronto and a deputy editor of Molecular & Cellular Proteomics.

See all the sessions scheduled for the 2021 ASBMB Annual Meeting:

asbmb.org/meetings-events/2021-annual-meeting#schedule

Branon works to break barriers in science and higher education

By Joseph Ong

When Tess Branon arrived at the Massachusetts Institute of Technology for grad school, she felt out of place in a class full of Harvard and Yale graduates. However, as Branon, a North Carolina native and graduate of Western Carolina University, progressed through her classes and research, she realized that her undergraduate education fully had prepared her to excel.

"Academia is a very exclusive institution," she said. "You have to go down a path with, yes, merit and intelligence, but also several factors that are out of your control, like where you are born or what opportunities are available to you."

In the middle of Branon's Ph.D., her adviser, Alice Ting, moved cross-country from MIT to Stanford. Moving to California was a difficult decision for Branon, but after finishing her Ph.D., she ended up staying in the Bay Area. Now, she's a postdoc in Greg Barton's lab at the University of California, Berkeley, studying host–microbiome interactions and how gut bacteria affect physiology and disease.

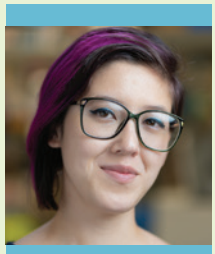
Changing from bioengineering to microbiome studies was a challenge, Branon said, and learning mouse work and immunology has been demanding but rewarding. Thinking about proximity labeling techniques from an engineering perspective was important during her Ph.D., but for her postdoc she sought to answer biological questions and understand how organisms interact to influence each other's biology at a molecular level, she said. "In my work, I want to make the quality of human life better."

After her MIT experience, Branon became passionate about mentoring the next generation of scientists and addressing equity issues in higher education. She hopes eventually to lead her own research group and dismantle barriers in academia.

At UC Berkeley, as a member of the Union for Postdocs and Academic Researchers, Branon is pushing for restructuring of academic institutions, with particular focus on community outreach, resolving racial biases, and creating more diverse and inclusive academic environments.

"Even in progressive California," she said, "diversity and equity issues are still definitely a problem."

Fast, nontoxic proximity labeling with TurboID



TESS BRANON

As a grad student, Tess Branon used directed evolution to engineer a new enzyme that addressed the shortcomings of previous proximity labeling methods. She worked on the development of TurboID to identify interacting proteins of interest.

"In multicellular organisms, old proximity labeling methods are inefficient, require toxic labeling conditions (so they can't be used in animals), or give insufficient labeling," she said.

TurboID can label cellular substrates efficiently in just 10 minutes and uses biotin, a nontoxic compound, as a chemical label. Branon and her collaborators at Stanford and Harvard used TurboID labeling in worms and flies, demonstrating its safety and efficacy in whole animals. Later experiments verified that it can be used in plants and mice.

Branon thinks the next step for proximity labeling is to study the interactors of an endogenous protein of interest without any labeling enzyme tags that might disturb the protein's natural function.

"Finding a method where we can map the interactome, where we don't have to fuse APEX or TurboID" to the protein of interest, she said, "would be really useful."

Joseph Ong (jong2@ucla.edu) is a Ph.D. student in biochemistry and molecular biology at the University of California, Los Angeles. Follow him on Twitter @p53p21rb.

MOLECULAR & CELLULAR PROTEOMICS SESSION

Decoding organ communication systems

By Alyson Smith

Like musicians in an orchestra, our organs perform highly specialized jobs yet depend on other organs to perform these jobs properly. To cooperate, organs must communicate using secreted proteins that travel through the blood. Ilia Droujinine is working to decode this communication system to understand how our organs work together to keep us healthy.

Droujinine has always enjoyed reading books about science and nature. While an undergraduate at the University of Waterloo, he completed several semester-long internships in labs around the world, studying neural stem cell migration at the University of Toronto, immune cell development at the Max Planck Institute for Immunobiology in Freiburg, Germany, and cancer biology at Brigham and Women's Hospital in Boston.

Equipped with a new appreciation for the power of experiments to reveal how living organisms work, Droujinine decided to pursue a Ph.D. at Harvard Medical School in Norbert Perrimon's group. His thesis research focused on long-distance communication between organs in the fruit fly Drosophila melanogaster.

The proteins that carry messages between organs are vastly outnumbered by other proteins in the blood such as hemoglobin. This makes them challenging to identify. Droujinine developed new tools to scan through all secreted proteins and find those that travel from one organ to another.

After completing his Ph.D., Droujinine moved to Scripps Research in California in October to start his own lab as a Scripps fellow and principal investigator. His lab will continue his work in the fruit fly and expand the tools he developed in mice to study how interorgan communication could apply to human health.

"I am very fortunate and thankful for this opportunity to develop my research program and grow into independence," Droujinine said.

When not in the lab, Droujinine enjoys reading science fiction and fantasy by such authors as Neil Stephenson and Brandon Sanderson and spending time with his wife and 3-year-old daughter.

Tracking messages between organs

ILIA DROUJININE

Our organs send messages to each other by secreting proteins that travel through the blood. This communication system allows our organs to work together to support our health: Muscles can request more energy production from fat tissue, or wounded skin can tell the bone marrow to deploy immune cells.

These interorgan communication proteins can be hard to find, because they are surrounded by thousands of other proteins in the blood and carry little information about their origins or destinations.

Ilia Droujinine and his colleagues turned to the fruit fly Drosophila melanogaster, which shares organ systems and secreted proteins with humans, to look for interorgan communicators. They developed a large-scale tracking system to tag proteins in the fat body (similar to the human liver and adipose tissue) and the muscles. Their tracking system found hundreds of proteins made by these organs that traveled to other areas of the fruit fly body.

Many of these proteins have relatives in humans and could reveal new communication networks that help our organs work together. Droujinine and his colleagues plan to continue to investigate the functions of the secreted proteins they identified and to expand their tracking system to mammals.

Alyson Smith (alysonscsmith@gmail.com) is a recent Ph.D. graduate in cell biology from Scripps Research in La Jolla, California. She now works as a scientific writer for Vala Sciences, Inc. Follow her on Twitter @cellbionerd.

Understanding cellular function to understand life

By Gabriela Contreras

When Geoffrey Hesketh was growing up in Canada, he loved sciences and math and wanted to be a medical doctor. He became curious about molecular mechanisms after he started volunteering in a biochemistry lab in his second undergraduate year at Queen's University, and he realized that his huge curiosity would be more satisfied working as a scientist than as a physician.

Since then, Hesketh has wanted to understand molecular processes, especially those that have evolved for billions of years but that we still are far from understanding, such as cellular nutrient uptake. "Experimentally unravelling a previously obscure or unknown biological function is the ultimate scientific achievement," he said.

Now a postdoctoral fellow in Anne-Claude Gingras' group at the Lunenfeld–Tanenbaum Research Institute of Mount Sinai Hospital in Toronto, Hesketh earned a Ph.D. in biological chemistry at Johns Hopkins School of Medicine in Baltimore and then did a postdoc at the Cambridge Institute for Medical Research.

Hesketh is interested in cellular membrane trafficking and signal transduction. "If you are understanding cell function at the molecular level, you understand life," he said.

Using advanced mass spectrometry and cell biology tools, he studies the molecular mechanisms by which lysosomes control cellular nutrient biology. In nutrient signaling, mechanistic target of rapamycin complex 1, or mTORC1, plays a key role.

"Life is largely driven by the flow of key elements — carbon, hydrogen, nitrogen, oxygen, phosphorus, and sulfur — in different chemical states, from organism to organism," he said.

Hesketh is fascinated by how mTORC1 is fundamental to life, participating in the sensing of the key elements, synthesis and degradation of macromolecules.

Many human diseases originate in cellular dysfunction, so Hesketh believes understanding cellular processes is the way to understand disease. Therefore, as a cellular biologist, he is pursuing his childhood interest in medicine and human diseases.

There's more than one way to activate this protein

GEOFFREY HESKETH

Amino acids, sensed by the cell, can be derived through lysosomal degradation of external proteins acquired through macropinocytosis or via amino acids acquired exogenously through cell surface transporters by macropinocytosis. Mechanistic target of rapamycin complex 1, or mTORC1, is activated by both these sources of amino acids, and mTORC1 function is regulated on the surface of lysosomal system organelles.

Exogenous amino acids are sensed by a mechanism dependent on the Rag guanosine triphosphatases, or GTPases, that control the mTORC activation. Geoffrey Hesketh and collaborators at the Lunenfeld–Tanenbaum Research Institute have demonstrated that lysosome-derived amino acids activate mTORC1 through a Rag GTPase-independent pathway. They have shown that both sources of amino acids activate mTORC1 by two different pathways. Using proximity-dependent biotinylation, known as BioID, and mass spectrometry for protein identification, they designed organelle sensors with which they showed the surface proteomes of late endosomes and lysosomes.

In highly lethal Ras-driven cancers, researchers know that macropinocytosis and lysosomal degradation of external proteins fuel cancer growth, but they do not yet know the mechanisms behind these processes. Hesketh's research results may lead to mechanistic insight into how lysosome-derived nutrients fuel the growth of Ras-driven cancers.

Gabriela Contreras (gicontrerasa@gmail.com) earned her Ph.D. in biology at Heidelberg University. Follow her on Twitter @gabiitca.

Tributes to Barbara Gordon, ASBMB executive director 2004–2021

Barbara Gordon, who worked at the American Society for Biochemistry and Molecular Biology for almost 50 years, retired in late February. Here, society members and former staff share their memories and appreciation.

COURTESY OF RALPH BRADSHAW

Ralph Bradshaw, Penny Bradshaw, Barbara Gordon and Barbara's sister Kay in Versailles, France, at the first Human Proteome Organization Congress, 2002.

The ASBMB-PB (post Barbara)

For some of us, this is a concept that is not really imaginable even though we knew that it was bound to happen someday. I really never have known the society without her presence in some role; I joined the ASBMB (in those days, the ASBC) in 1971, and she began on the staff in 1972, working on the Journal of Biological Chemistry.

Over the next nearly 50 years, as her responsibilities grew and my involvement in the society deepened, we worked, planned and schemed with various colleagues and staff on innumerable projects, committees and governance activities involving both the society and JBC — far too many to list here, but I note a few favorites: launching the online version of JBC and creating High Wire Press with Chuck Hancock, Herb Tabor, Bob Simoni, John Sack and Mike Keller; writing the 100-year history of the ASBMB and shepherding it through the publication process; and, perhaps the best, launching Molecular & Cellular Proteomics and nursing it through its growing pains, particularly during the first 10 years.

This last effort spanned the time when Barbara took over as executive director of the ASBMB. MCP really just had begun when Chuck Hancock, Barbara's predecessor, announced his retirement and the society began a serious search for a replacement. With a brand-new journal on my hands (with all the issues and problems associated with that), this decision was of crucial importance to me; I needed an executive director who understood academic publishing and could provide the support and leadership necessary to allow

it to succeed. Frighteningly, when the final interviews were scheduled, I discovered I couldn't be there in person, so I sat down and wrote probably the most impassioned letter of my career, literally begging the search committee to select Barbara. They did, and the rest is history.

Over the years, I have shared countless hours in committee meetings, dinners (both good and bad), and not just a few nightcaps with Barbara. As a result, she became not only a colleague but a friend (with my wife too), and I have enjoyed several social occasions with her and/or her husband Jerry.

Blessed with a special southern charm and innate enthusiasm, she was an indispensable part of any team (no matter who that was nor what the project or activity was), at ease in almost any setting, and able to maintain a rapport with scientists at all levels, even though she herself was not formally trained as such. When Barbara asked you to do something you didn't feel put upon, you felt good about being asked. Although I always maintained Chuck Hancock was going to be a hard act to follow, Barbara not only filled his shoes but set new standards of accomplishment that will be a challenge for future directors to match (but that is a good thing). The ASBMB has flourished under her guidance and probably will continue to do so but it won't be quite the same when she is gone.

My best wishes to Barbara for a glorious, relaxed and well-earned retirement (and Penny and I look forward to seeing her in Charleston when we visit our daughter).

Ralph Bradshaw, University of California, Irvine

COURTESY OF RALPH BRADSHAW

Barbara Gordon and Penny Bradshaw in Siena, Italy, in 2002.

Our appreciation of Barbara Gordon

We first met Barbara in 2004 (16 years ago!) at the Boston ASBMB meeting. After a session in the afternoon/evening, we went to the entrance of the convention center and discovered that it was raining cats and dogs. We were not dressed for this. However, Barbara, who is always prepared for every eventuality, was there standing in the rain with umbrellas and escorted us, and many others, to taxis. That was a very strong message that Barbara was a very special and caring person at the ASBMB.

Since that time, Barbara has helped us organize a large conference in Banff. Importantly, she also took over organization of the Deuel Conference on Lipids, which was faltering, and it is now a hugely successful annual meeting. We always have treasured our opportunities to interact with you, Barbara; thanks so much for all you have done for so many scientists over all these years.

We wish you the very best in your retirement years.

Dennis and Jean Vance, University of Alberta

Dear Barbara,

Thank you for your leadership, thoughtfulness and years of dedication to high-quality BMB education!

With best wishes and congratulations on your retirement,

Ludmila Tyler, University of Massachusetts Amherst
Educational and Professional Development Committee

Best wishes, Barbara!

Of thee we sing, Barbara —

Dear Barbara,

The two of us have known and been admirers of your commitment and outstanding service to the ASBMB and JBC for the last three and a half decades! We have worked with you on innumerable domestic committees and activities (from committees on equal opportunities for women, to Council, to associate editor meetings, to public affairs, to centennial committees and celebrations, to the Membership Committee) and international programs (Promoting Research Opportunities for Latin American Biochemists and the International Union of Biochemistry and Molecular Biology), and we have traveled the world with you.

For every one of those committees and activities, you were central to the logistics, decisions, function and successes. You have been the catalyst for promoting collegial interactions, strengthening trainee and diversity programs, and promoting international collaborations. By organizing and participating in scientific and social activities for scientists around the world, you provided the know-how to get things done. You have been THE source of information about the society and about the people involved with the society due to your long commitment. Your energy and insight have been invaluable to the society and journals and to the staff and volunteers.

As former presidents of the ASBMB, we appreciate the support and organizational skills that you provided for us as novices in that leadership position. It was clear that your heart and soul were in the society's success through appropriate management and your selection of personnel. It is hard to imagine the ASBMB and JBC without you. You deserve every minute of a full, happy retirement, and we look forward to seeing you (if only on Zooms) in afternoons and evenings, since we know you are not a morning person.

Thanks, Barbara, for all you have given us and for your warm and continuing friendship.

Judith Bond, University of North Carolina at Chapel Hill
ASBMB past president

Bettie Sue Masters, Duke University Medical Center
ASBMB past president

COURTESY OF JUDITH BOND

Pictured, from left, are Bettie Sue Masters, Barbara Gordon, Judith Bond and Debora Foguel (former president of the Brazilian Biochemical Society) at an Experimental Biology meeting in April 2011.

Barbara has been the friendly face of the ASBMB for as long as I can remember. She has moved the society through many new transitions and has shepherded its growth to the robust society it is today. Service to the ASBMB members has always been her highest priority. We certainly will miss her but wish her all the best in her well-deserved retirement.

Enjoy Charleston!

Toni Antalis, University of Maryland
ASBMB president

I still remember when I first met Barbara; it was on a walk from a meeting venue to a restaurant for a dinner celebrating the first day of the ASBMB grant writing workshop in Washington, D.C. We had struck up a conversation about our mutual interests in the intersection of science and politics. Not only was it a fascinating conversation, but Barbara remembered our conversation. After the workshop was over, she took the time to introduce me to the ASBMB staff who manage the Public Affairs Advisory Committee. My interactions with Barbara started a snowball of events that eventually led to my service on the PAAC.

Over the years, I have been able to see Barbara at PAAC meetings and Experimental Biology meetings, and every time, despite her incredibly busy schedule, she always took time to talk with me and still remembered details about my family. It was clear every time I talked with Barbara that she truly cared about how I was doing as a person. It is incredibly rare to meet someone like Barbara who is so genuine, kind, perennially happy and always incredibly generous with their time.

I am greatly appreciative of the opportunities through ASBMB, and I can trace all of these opportunities back to Barbara, to her kindness and to her incredible support. I cannot express enough how much I appreciate Barbara and her generosity and kindness. Thank you, Barbara!

Rick Page, Miami University
Public Affairs Advisory Committee

I have two memories of Barbara that stand out. First would be the times when committees would meet and we would have dinner together. Barbara often came with us and was always warm and fun to talk to. She felt like an old friend from the first time I met her. The other memory I have of Barbara would be seeing her at EB meetings. Here again Barbara always made me feel like she knew me, knew where I was from and knew my story, like an old friend. Barbara, thank you for making me feel welcome in a society and community that I've always valued. Enjoy your retirement.

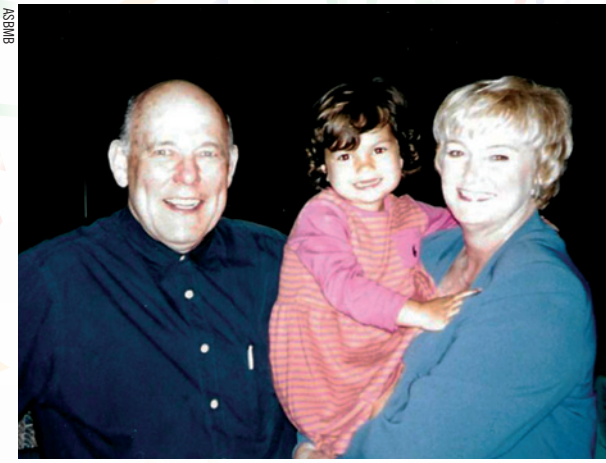
John T. Tansey, Otterbein University
Science Outreach and Communication Committee

Thanks for all you have done and made possible, Barbara.
Enjoy your new adventure and stay healthy.

All the best,

Kim Orth, University of Texas Southwestern Medical Center
Awards Committee and Nominating Committee

ASBMB



Well known for her love of babies and small children, Barbara Gordon poses here with Dick Hanson of Case Western, who served as ASBMB president and a JBC associate editor, and Sophia Gull, daughter of Kelly Gull, a former ASBMB meetings and education director.

ASBMB

Barbara Gordon has always been interested in hearing about everyone's work, family lives and interests. She's pictured here with an unidentified man, at left, and Alan Goodridge of Ohio State, a former Journal of Biological Chemistry associate editor.

Dear Barbara,

You are the spirit of the ASBMB! I have been privileged to be involved with the leadership of the ASBMB since before you became executive director and through your entire tenure. I am in awe of how you dealt with everyone with whom you came in contact. Your dedication and open embracing of ASBMB members has contributed so much to its success. Through thick and thin, you have had the most positive attitude imaginable. I had the privilege to observe close up between sessions at the last Deuel Conference how you navigated the impending COVID-19 epidemic and led FASEB to make the brave decision to cancel the 2020 annual meeting as well as the subsequent decisions in dealing with these most challenging times for the society and the journals.

For me, it has been a personal pleasure to work with you on everything from national meetings to the Journal of Lipid Research and council. I have especially enjoyed the numerous events, dinners and social hours we have enjoyed around the country these last couple of decades. I hope we will be able to stay in touch in the future.

I know you have been looking forward to your retirement on the beach in Charleston and your well-deserved escape from the daily challenges of a bunch of rowdy scientists! I wish you the best.

Best personal regards,

Edward A. Dennis, University of California, San Diego

Barbara has been a fantastic leader on many levels. She made the ASBMB a place where a bench scientist could excel in science policy while making the society a welcoming place for me and my family. She expertly handled the needs of members without compromising the society's mission and purpose. I have learned so much from her and wish her the very best in a well-deserved retirement.

Chris Pickett, Rescuing Biomedical Research
Former ASBMB policy fellow

Barbara,

Congratulations on your impending retirement! I am so happy for you. I look forward to seeing all the forthcoming fun pictures. That said, I am sad to see you go. I will miss you greatly. I can't tell you how much I learned from you while I was at the ASBMB. I use those lessons daily in my current job and even in my personal life. I am so grateful to you. I am sure you have touched so many other lives like this as well.

Erica Gobrogge, Van Andel Institute
Membership Committee

Barbara has been an amazing leader for the ASBMB Deuel Conference on Lipids. Barbara is one of a kind, the best administrator ever. She combines extraordinary intellect with great decision-making, patience, kindness, cheerfulness, breathtaking diligence and an amazing positive attitude. Barbara is radiant. I have so many cherished memories. I will miss her immensely, but my heart is warmed by imagining how much joy and happiness she will bring to family and friends in the years to come.

Stephen Young, UCLA
Deuel Board

ASBMB

Barbara Gordon, center, behind sign, poses with staff members at the 2015 ASBMB Annual Meeting.

Cheers and happy trails, Barbara!

I feel so lucky to have been part of the ASBMB while you were executive director. I remember back in 2008 or 2009 (or whenever it was) when Ellis Bell recruited me to serve on the EPD. I asked him about the expectations, and he said, "You will work really hard, but then Barbara treats us really well."

He could not have been more correct. Barbara did push us hard — she prompted us to challenge our assumptions and think outside the box. She played devil's advocate when warranted and cheerleader when we were on the road to getting it right. And she gave us a healthy dose of reality when our academic sensibilities started leading us down the garden path.

And after all that — after hours of making and unmaking decisions, often in one of the meeting rooms at the Marriott across from the White Flint metro — she took us out for an amazing dinner, and ordered incredible wines, and even allowed me to invite my brother and sister-in-law as my plus-one.

My favorite memory of Barbara is probably a dinner on Coronado Island when we were planning a San Diego meeting. Barbara took us to an amazing Italian restaurant that offered a panoramic view of downtown San Diego, and she introduced us — well, at least me — to Amarone. One word: Wow!

So cheers and happy trails, Barbara! You've left enormous shoes to fill. Thank you for the generous and creative spirit you've brought to the ASBMB. I look forward to hoisting a glass or two on your deck in Charleston as we watch our puppies play in the surf!

Suzanne Barbour, University of North Carolina at Chapel Hill
ASBMB Council, Minority Affairs Committee

Barbara —

Wishing you all the best on your next adventure!

With gratitude for all you have done for us biochemists,

Susan Baserga, Yale University
Women in Biochemistry and Molecular Biology Committee chair, Public Affairs Advisory Committee

COURTESY OF GEOFF HUNT

Enjoying a Chicago Bears game at Soldier Field are, from left, Geoff Hunt, Ben Corb (ASBMB director of public affairs), Barbara Gordon and her son Brian.

My favorite memories of Barbara are from when we would travel together for meetings. We'd work, do our jobs and get through the serious stuff. But once that stuff was over, I always wanted to know where Barbara was going to be, because she was the life of the party. Football games, blues clubs, the Grand Ole Opry, Bourbon Street: Wherever there was fun to be had, Barbara was smack in the middle of it.

At the office, I feel like she had to actively hold herself back from just having fun all the time. Now that she's retiring, I hope she gets to enjoy herself 24/7.

Geoff Hunt, American Society for Microbiology
Former ASBMB manager of public outreach

Barbara Gordon wasn't just the executive director of ASBMB; she also has been the Audrey Hepburn of the society. She is dignified, possesses impeccable taste, is good humored and articulate, and thus has been a persuasive and admired leader. Her impression on all of us has been indelible, and I'm particularly grateful for her trust and belief in me.

Thank you, Barbara, for all you touched. All best wishes in your next adventure.

Ed Eisenstein, University of Maryland
Membership Committee chair

It's hard to describe the impact Barbara has had on the ASBMB, much less on me personally. Most importantly, I would like Barbara to know how motivating it has been to me to see her lead the ASBMB with aspirational courage, confidence and character. I admire her leadership and decision-making and am grateful for the advice she's shared that has shaped my own professional career.

Barbara, you will be sorely missed!

Susanna Greer, American Cancer Society
ASBMB Council, Finance Committee

Dear Barbara,

Congratulations on your retirement — the ASBMB will not be the same without you at the helm! I am so appreciative of everything you have done for the society, particularly as it relates to science outreach, science policy and professional development.

As a trainee, the ASBMB provided me with experiences and opportunities that led me to my current career path and helped me build a robust network of mentors, colleagues and friends. I can say confidently that my professional success is due, in large part, to the ASBMB — and for that I am incredibly grateful.

Many thanks to you, Barbara! Cheers to an enjoyable and relaxing retirement!

My very best,

Niki Woitowich, Northwestern University
Committee on Science Outreach and Communication chair

Barbara's dedication to the ASBMB over the decades is truly amazing! Everyone knew she was the go-to person for all things related to the ASBMB. She will be sorely missed!

Kelly G. Ten Hagen, National Institutes of Health
ASBMB Council, Women in Biochemistry
and Molecular Biology Committee

Barbara Gordon has been the face of the ASBMB ever since I joined. Her warm personality and sense of humor have put a caring face on the society that will be hard to match. I will miss the chats at the PAAC dinner and the "sidebars" in the corridors at the annual meeting and particularly her big smile.

Susan Forsburg, University of Southern California
Public Affairs Advisory Committee

COURTESY OF GEOFF HUNT

Members of what was then the ASBMB Public Outreach Committee (now the Science Outreach and Communication Committee) sample Hurricanes on Bourbon Street in New Orleans. Pictured, clockwise from bottom left, are Niki Woitowich (in boa), Jeanne Garbarino, Ed Eisenstein, Geoff Hunt, Edwin Li, Teaster Baird Jr., Barbara Gordon, Teresa Evans Moore and Susanna Greer.

PERSPECTIVES

In October 2010, members of the ASBMB staff went to Charm City Cakes in Baltimore to explore the possibility of a specialty cake for an annual meeting event. The knockout mouse cake didn't make the cut, but posing during the visit are Joan Geiling, Jessica Homa (then ASBMB marketing director), baker Duff Goldman and his associate, and Barbara Gordon.

COURTESY OF JOAN GEILING

On one particular Saturday, Barbara and I thought it would be fun to bring our dogs to the office to keep us company. The memory of canine chaos as Wiggum, Turk and Zoey bounded through the halls of the historic Beaumont House has made us laugh again and again.

Thank you, Barbara, for being a generous teacher and mentor through my meeting planning career. Congrats on your well-earned retirement!

Joan Geiling
Former ASBMB meetings director

Dear Barbara,

Congratulations on your upcoming retirement! Your dedication to the ASBMB and JBC has contributed significantly to the success of all the members. I know that I am not alone when I say that I have the utmost gratitude for all you have done to help me, from everyday interactions to long-term planning. You have been a trusted colleague, and we all will miss you greatly.

Thank you for all of your hard work, and good luck in the next exciting chapter of your life.

Again, congratulations on your retirement. I wish you all the best.

Kevin Campbell, University of Iowa
Awards Committee

Dear Barbara,

I always enjoyed working with you on the organizations of the ASBMB centennial meeting, the annual and satellite meetings, and the editorial boards of the JLR and JBC. You always helped me with whatever obstacles I encountered or directed me to someone who could help. I especially enjoyed all the social events like the AE dinners and of course the awards dinners at the annual meeting. I always will value the conversations about our families.

You are No. 1 in my book; I'll miss you dearly.

George Carman, Rutgers University
Journal of Lipid Research associate editor

I'm going to miss Barbara's cheery disposition a huge amount. I really admire her "everything is doable" attitude and look back with considerable nostalgia on some of the interesting and wide-ranging conversations we have had over the years while driving back to wherever we needed to be next after attending Deuel conferences. She's going to be a hard act to follow!

Kerry-Ann Rye, University of New South Wales Sydney
Journal of Lipid Research co-editor-in-chief

As the ASBMB's executive director, Barbara embodied empathetic leadership long before it became a hot trend in business executive coaching. I learned so much about being generous, kind, fair and sensible as a leader from Barbara. I also learned from her that there is a true joy to uncorking a wine bottle and hearing the cork go pop that no boxed wine can replicate.

Rajendrani Mukhopadhyay, Chemical & Engineering News
Former ASBMB Today managing editor

Merle Olson, an ASBMB member since 1973, sent this photo of roses as a virtual tribute to mark Barbara Gordon's retirement.

Barbara,

I always have valued how much gratitude you have shown to members who volunteer their time for the many activities of the ASBMB. Our society is its members, and your support of these activities and the people who do the work is a great legacy.

Terri Kinzy, Western Michigan University
Public Affairs Advisory Committee chair

Dear Barbara,

Retirement? Let's keep this simple …

Wake up every morning and do something that makes you happy. Do everything possible to protect your health.

All the best in your next adventure.

Merle Olson, University of Texas Health Science Center

Although I only met Barbara once, she left a lasting impression! I was truly inspired by her commitment to the ASBMB and her candid and easy-going personality that made everyone feel welcome. She will be missed!

Carlos Lopez, Vanderbilt University
Minority Affairs Committee

Barbara definitely qualifies as one of the more special friends in my life. We got to know each other when the ASBMB Lipid Research Division started. She'll tell you that was an "interesting" time, but we quickly grew to respect and trust each other, which then developed into a wonderful friendship that I now cherish.

We've shared a lot of dinners together and especially share a love for Amarone wine! I have too many memories to pick a favorite, and we laugh a lot!

I sure hope our friendship continues even in her retirement.

Daniel M. Raben, Johns Hopkins University School of Medicine
Meetings Committee chair

COURTESY OF FRED GUENGERICH

Herb Tabor, Barbara Gordon and Fred Guengerich at the Tabor house at the National Institutes of Health shortly before Tabor's 101st birthday.

All ASBMB members owe Barbara Gordon enormous gratitude as she retires from her position as executive director of the society. But perhaps the most appreciative are those of us in the educational community. Barbara has helped to make scientist–educators a core constituency of the ASBMB and education a central aspect of the society's mission.

From the days when educational programming was relegated to one inconvenient time slot at the national meeting, we now find ourselves with education as one of the main themes. The society now sponsors a biennial small meeting devoted to student-centered learning, while the undergraduate poster session has grown to oversubscription. Leaders in education are honored with a society award and with the designation of ASBMB education fellow. BMB education research is emerging as an area of serious scholarship, with members beginning to understand that how students learn is even more important than what they learn. And the jewel in the crown is the accreditation program for undergraduate programs and certification of degrees.

All of these activities sprang from our members' interest and efforts, but none would have been possible without Barbara. She has provided enthusiastic support and necessary resources at every stage. She believed during those times when we wrestled with doubts. She knows everyone and could always suggest members to be recruited to committees and panels. She has been generous with funding and staff time when needed. Barbara has been a true partner in raising the profile of education within the society, and we have been privileged to work with her.

Pete Kennelly, Virginia Polytechnic Institute and State University
Membership Committee

Adele Wolfson, Wellesley College

I remember meeting Barbara in the last millennium (i.e., before 2000) when I was a member of the editorial board at JBC. She was running the operation when Herb Tabor was editor-in-chief. Later, when I was on the ASBMB Council, Barbara got the job of heading the ASBMB when Chuck Hancock retired. I recall that she stated her goal was to emphasize the members ("It's their society"), and I believe that she has done that.

Perhaps the event with Barbara I will remember most is a morning in June 2015 when I was acting as deputy editor at JBC. I had just parked my car at the airport, about to leave for a meeting in Japan. When I got out my iPhone to note my parking spot, there was a message from Barbara telling me Steve McKnight (then ASBMB president) needed to talk to me. I had a sinking feeling about what it was about. I had to take over as editor of JBC for a year, and there were a lot of interactions with Barbara. But she got publications director Nancy Rodnan back in the fold at the ASBMB!

I always got along well with Barbara, and we will miss her. All the best, Barbara, in whatever you do now!

Fred Guengerich, Vanderbilt University School of Medicine
Journal of Biological Chemistry deputy editor

"The pleasure of my life"

By Laurel Oldach

With 70 papers and patent filings to her name, Genentech senior scientific advisor Melissa Starovasnik has worked on many drug discovery projects since first being hired there as a postdoc. For 10 years, the structural biologist led departmements as a senior director and then vice president; she shared some insights into research leadership with ASBMB Today. This interview has been condensed and edited.

1 How did you get involved in leading research operations?

I had the opportunity to head research operations at Genentech while still leading our structural biology department. In that role, I was responsible for everything that wasn't the science: overseeing our budget, headcount, salaries, promotions, and interacting with the rest of our company.

I've always found that while the science I can do by myself is fun, what's really exciting is the science a group of people can do together. Clearing the path for researchers to do their science unencumbered by unnecessary distractions while continuing to lead science within my own area was very satisfying.

2 You later were vice president of protein sciences. How was that job?

Leading protein sciences and large-molecule drug discovery as part of our research leadership team has been the pleasure of my life. I spent a lot of time reviewing and guiding protein therapeutic discovery projects and weighing in on how to move forward. Most important, though, is the people part: mentoring scientists and leaders one-on-one and in teams.

3 It seems many decisions in pharma have to be made with less data than you'd like. How is that?

That's real life, I'm sad to say; we rarely have the data we wish we could have. You have to decide what to work on and what to kill, and why. But I didn't need to make decisions entirely by myself. It's about drawing not only on your own experience but on talented colleagues to overcome obstacles and come to the best outcomes.

4 A project you're especially proud to have worked on?

An antibody against a protein called BR3, which is important for B cell survival and autoimmune diseases. Leading the discovery and then the early development team was just exhilarating: a ton of work, a ton of learning.

Not everything works in drug discovery. My project ended up not moving forward, but I'm proud of the decisions we made.

5 Advice for people who want to lead drug discovery someday?

It's absolutely critical to work as a scientist first. You've got to learn, gain experience and credibility. I wouldn't have wanted to lead a whole department if I didn't have hands-on experience in various roles.

You don't need to know everything at the beginning. You just need to continue to grow and move closer to what you want to do next. Hopefully, you're also having fun and making a meaningful contribution to science. If you're doing those four things, then you're in good shape.

Melissa Starovasnik

CURRENT POSITION

Senior scientific advisor, Genentech

CAREER PATH

Ph.D., biochemistry, University of Washington, 1992

Postdoctoral research: protein NMR spectroscopy, Genentech

FAVORITE MOLECULE

BLyS Receptor 3 aka BAFF-R

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


ASBMB
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CLASSIFIEDS

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A NIH-funded postdoctoral position is immediately available to join the Scaraffia research group. Scaraffia´s lab is particularly interested in unraveling the physiological, biochemical, and molecular basis underlying the regulation of nitrogen and carbon metabolism in mosquitoes, as well as in discovering new metabolic targets that can be used for the design of better mosquito–control strategies. The successful candidate will apply traditional and modern biochemical approaches to investigate the mechanistic regulation of ammonia metabolism in Aedes aegypti mosquitoes.

Requirements

- PhD degree in biochemistry or related discipline with a strong background in protein biochemistry, and metabolic signaling
- Research experience in metabolic studies
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To apply, submit a single PDF file to mmobilliot@tulane.edu with the subject Postdoc Application and include:

(1) a cover letter describing research interests (no more than 1 page);
(2) your curriculum vitae; and
(3) contact information for three references.

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https://careers.asbmb.org/job/sales-development-representative/55942642/

Research Scientist, Downstream Process Development
DynamiCure Biotechnology

Dynamicure Biotech is seeking a Scientist/Sr Scientist for a position based at a Waltham, MA site. The individual in this role will be responsible for antibody/protein engineering and characterization in a dynamic and highly interdisciplinary environment. Familiar with Ab phage display, RNA isolation, gene construction, expression, purification and characterization using phage panning, RT-PCR SDS_PAGE, HPLC SEC, ELISA, WB, AKTA FPLC, Octet, Biacore etc. Antibody and antigen cloning and sequencing, affinity maturation and epitope binning, kinetic characterization (KD, kon and koff).

- Ability to contribute to antibody/protein characterization for pre-clinical programs is a necessary requirement.
- A breadth of knowledge and lab skills on cell biology, molecular biology and protein biochemistry is required.
- The successful candidate must have a strong foundation in Ab biology, biochemistry and protein engineering with an understanding of biological mechanisms.
- Experience with basic molecular/cell biology and biochemistry lab experiments is required.
- Familiarity with NGS approach to mAb discovery is highly desirable.

https://careers.asbmb.org/job/research-scientist-downstream-process-development/55942749/

Postdoctoral Research-Teaching
James Madison University

The Biology Department at James Madison University (JMU) is seeking applications for a Postdoctoral Research-Teaching position in the laboratory of Dr. Jonathan Monroe at James Madison University beginning Fall 2021. This position is funded in part through a Research at Undergraduate Institutions (RUI) grant from the NSF. This position is offered for one year, with the option to extend one additional year.

The research involves investigating the structure, function, and evolution of a beta-amylase in Arabidopsis using analysis of gene expression, purified proteins, T-DNA insertion mutants, and starch structure and metabolism. In addition to gaining experience in mentoring undergraduate researchers, the postdoc will also undertake some classroom and laboratory teaching in introductory and upper-level courses fitting the background of the postdoc. Travel support is available to attend the national conferences of ASPB and the Council on Undergraduate Research.

https://careers.asbmb.org/job/postdoctoral-research-teaching/55938464/

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