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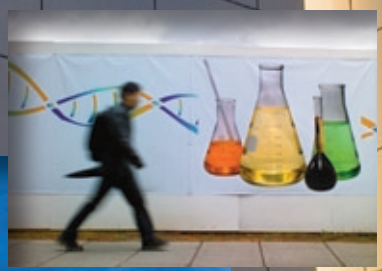
ASBMB today

Cornell University's Weill Institute

September 2008



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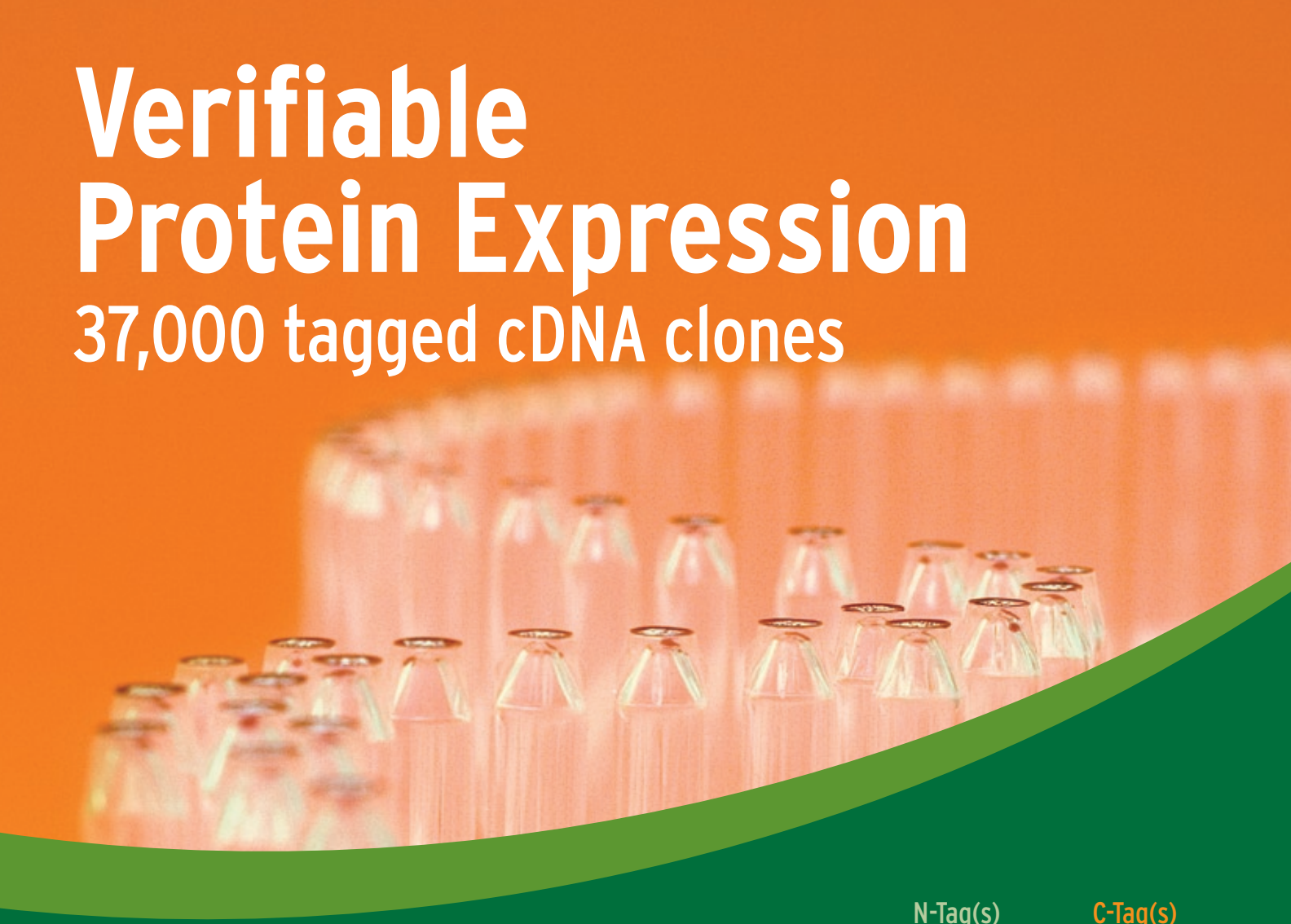

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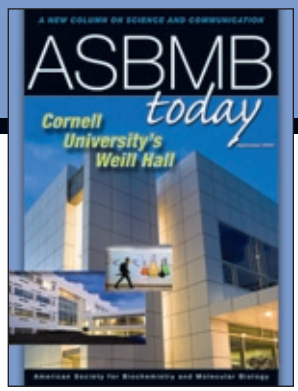

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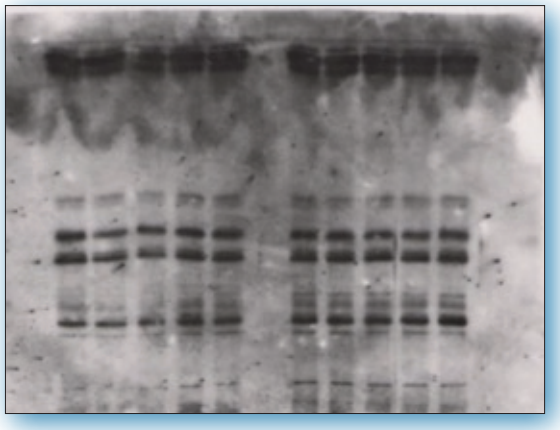

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2008 APEX AWARDS FOR PUBLICATION EXCELLENCE

president's message

Qui Tacet Consentire

BY GREGORY A. PETSKO

I get asked a lot these days what my vision is for the ASBMB. Although there are things I would like to see happen while I'm president, I have to say that I think that's the wrong question. It's certainly true that a 2-year term gives the president a chance to propose specific policies and carry them out, and that gives the ASBMB an advantage, I believe, over most other scientific societies, where a 1-year term tends to be the norm. So to that extent, yes, I think there can be strategic thinking and specific goals for this office, and I'll be writing more about them in the coming months. But I think a better question would be for YOU to ask ME how I am going to implement YOUR vision for the ASBMB.

You see, I feel strongly that for the ASBMB to have the impact on science and society that I would like it to have, it must speak, not just with the voice of its president, but with the collective voice of its 12,000 members. If scientific

Ask ME how I am going to

research is to receive the financial support it needs; if science is to regain its position of influence in American life; if we are to improve the education of our youth; and if we hope to continue to promote the acquisition of knowledge for the benefit of the human race, then we need to have a mighty voice indeed. And I believe that together we can have that.

I know that many scientists are profoundly uncomfortable with politics and policy. I know the ivory tower of the laboratory is very attractive to the sort of personality that often gravitates to science; it had that appeal for me. But we live in a world where that kind of isolation is no longer desirable, even if it were feasible. Resources on this earth are growing scarcer and the demands for public attention and public funding are ever increasing, both in number and in volume. If the voice of science is to rise above the cacophony of competing special interests, it must be loud and clear. And if it is to have credibility, it must speak on behalf of humanity, not just for its own benefit. No one person can communicate that message.

If we are to have a collective vision that deserves the backing not just of all our members but of all scientists everywhere and, I hope, of the majority of non-scientists as well, then we must climb down from the ivory tower and engage with society. That is what I am asking all of you to do. I know that part of my job is to speak out on your behalf. To be truly effective, though, we also have to get the same messages across locally, and only you can do that.

Let me try to articulate some of the things that I think we all stand for, in no particular order of importance:

1. That science is not a belief system but an evidence-based method of acquiring knowledge. The validity of scientific observations depends on reproducibility, and the validity of scientific theories depends on valid observations. Objectivity is hard to achieve, but must always be strived for.
2. That all science is undertaken for the public good. "Science" that has as its objective the fostering of terror or the killing and maiming of innocent people is an abomination. Scientific and technological progress should never be divorced from ethical considerations.
3. That the public puts us in the laboratory and trusts us to work on their behalf; therefore, we owe it to them to do just that and, whenever possible, to try to explain to them what we do for them and why it matters. We also owe it to them to speak the truth to our fellow citizens and to those in power, no matter how unpleasant or strange it may seem to be.

implement YOUR vision for the ASBMB

4. That, while we understand that policy decisions cannot usually be based solely on scientific data, we believe such data are essential to the decision-making process, and we expect that they be considered and respected, not ignored, misstated, or misused. If they are, we will speak out.
5. That, to borrow a fine phrase from West Point, we will not lie, cheat, or steal, and will not tolerate those among us who do.
6. That the education of every student requires firm grounding in basic scientific facts and principles, undistorted by religious or ethnic consideration.
7. That the earth is more than 4 billion years old; that life began on it billions of years ago and evolved to its present diversity by the process of natural selection; and that these and related facts are an essential component of every science curriculum. By the same token, religious beliefs, no matter how fervently held, have no place in that curriculum.
8. That we understand that we are human, and as individuals are just as susceptible as anyone else to the effects of ignorance, prejudice, stubbornness, blindness, and foolishness, but that our insistence as a community on reproducibility and the power of evidence makes science, ultimately, self-correcting. And that we need to explain this to non-scientists, repeatedly.
9. That our scientific priorities must be set by a combination of open, peer-reviewed competition and the needs of the public, not by bureaucratic fiat or the special interests of a sub-set of us.
10. That, in the words of the founder of the National Academy of Sciences, Abraham Lincoln, we shall endeavor to correct errors where shown to be errors, and to adopt new views as fast as they prove to be true views.

I could list more, probably, and I'm sure you could, too, but 10 seems like a nice round number for now. If you agree with me that these things are important, then we need to say so. We need to say so in our local school boards, at town meetings, in letters to our local newspapers, in the people we support for public office. Maybe more of us should run for public office, especially at the local level (the religious right figured that out a long time ago, and we have been painfully slow to respond).

There is a sense many people have that if we are silent it signifies in some way our opposition to lies, ignorance, bias, demagoguery, dogmas based on authority not on evidence, and all of the other things we claim to abhor. But, interestingly enough, that is not what the law says. The maxim of the law is, "*qui tacet consentire*": he who is silent, consents. The law assumes that if you say nothing against a statement or an action, you consent to it. And I suspect our fellow citizens may well assume the same: that if they do not hear from us, we accept what is happening.

Please, don't be silent. Tell us here at the ASBMB what matters to you. I promise you we will listen, and that even if we don't always agree with you, we will always respect and appreciate your ideas and comments. But don't just expect us to solve your problems or to be your sole voice. Speak out, become involved locally and nationally if you can, and support those who try. For silence is a vacuum into which misinformation can flow as surely as the truth.

FASEB Welcomes New President, Richard Marchase, Ph.D.

BY CARRIE D. WOLINETZ

On July 1st, Richard B. Marchase, Ph.D., took office as the 93rd FASEB president. Marchase serves as the Vice President for Research at the University of Alabama at Birmingham and professor of cell biology. "The upcoming Presidential election and the incoming administration present unique opportunities to highlight the importance of biomedical research on a national scale," said Marchase, who plans to continue to spearhead FASEB's efforts to engage voters on critical science policy issues. "It is vital that our nation's leaders recognize the value of agencies like the National Institutes of Health and the National Science Foundation."

"Between now and November," he continued, "FASEB's primary goal [regarding the election] will be to approach both political parties and attempt to reestablish scientific funding and a respect for science as important parts of their platforms. We've already submitted testimony to both the Democratic Party and the Republican Party that we hope to get included in the platforms. We are participating with various groups that are seeking direct contact with the leadership of the two campaigns to make sure that we do get our message across. We would love to have an increase in funding for NSF and NIH become something that both of these candidates are proud to bring forward in their public statements. I look forward to working with Congress and the new Administration to build a sustainable commitment for scientific research."

Marchase pointed to recent appropriations bills from Congress that include increased funding for science as evidence that research is gaining ground as a national priority. "However, as FASEB President, funding is not going to be my only focus," he said. "With public funding comes a justifiable need for accountability in how these funds are used. The challenge is in establishing systems that ensure the public trust in a manner that does not create unnecessary regulatory burdens nor unduly delay scientific progress. FASEB will be addressing these issues on a number of fronts over the next year, from biosecurity to conflict-of-interest to animal and human subjects' protection. As an example, we recently led an effort to produce a joint statement from the research community on a proposal to regulate dual use research." (To view the statement, visit: opa.faseb.org/pdf/2008/NSABB_FrameworkCommentLtr.pdf.)

Marchase has several active awards from the NIH for research infrastructure and to support his laboratory, which studies the effects of hyperglycemia on recovery from trauma. A graduate of The Johns Hopkins University (Ph.D., Biophysics), Marchase has received many honors in his career, including one of the inaugural Presidential Young Investigator Awards from the NSF. He moved to the University of Alabama at Birmingham in 1986, and from 1990 to 2000 served as chair of the Department of Cell Biology. Marchase is a member of American Association of Anatomists and has served as a member of their Public Affairs Committee and represented them at FASEB Funding Consensus Conferences prior to his joining the FASEB Board of Directors in 2002. He served as president of the Association of Anatomy, Cell Biology, and Neurobiology Chairs and as that group's representative to the National Caucus of Basic Biomedical Science Chairs.

FASEB also congratulates Mark O. Lively, Ph.D., who was voted FASEB President-Elect. Lively is a professor of biochemistry at Wake Forest University (WFU) School of Medicine and director of the WFU Biomolecular Resource Laboratory.

For more information on FASEB activities surrounding the Presidential election, please visit: sciencecures.org. In addition, FASEB invites you to visit our new Facebook page and become a fan! The page is located at: facebook.com/pages/Federation-of-American-Societies-for-Experimental-Biology/33038008112.

Carrie D. Wolinetz is Director of Scientific Affairs and Public Relations for the Office of Public Affairs at FASEB. She can be reached at cwolinetz@faseb.org.

MCP Adds Four New Associate Editors

Molecular and Cellular Proteomics (*MCP*) recently added Gerald W. Hart, Elizabeth A. Komives, Michael P. Snyder, and John T. Stults to its highly regarded group of Associate Editors bringing the total to eight, along with *MCP* co-editors Ralph A. Bradshaw and Al Burlingame, both at UCSF. Patsy Babbitt and Kevan Shokat, also of UCSF, retired this spring. Of the original group, the other four who continue to serve are Ruedi Aebersold (Swiss Federal Institute), Steve Carr (Broad Institute), Julio Celis (Danish Cancer Institute) and Ray Deshaies (Cal Tech). All four new Associate Editors have been on *MCP*'s Editorial Board since the journal was created in 2001. The following is a brief introduction to these new Associate Editors.

Gerald W. Hart, who is DeLamar Professor and Director of Biological Chemistry at The Johns Hopkins University School of Medicine, received his Ph.D. in developmental biology from Kansas State University. He currently studies the roles of cytoplasmic and nuclear glycosylation in transcription, oncogene function, neurodegenerative disease, and diabetes. In 1983, Hart and his colleagues discovered that many nuclear and cytoplasmic regulatory proteins are dynamically modified by *O*-linked *N*-acetylglucosamine (*O*-GlcNAc). *O*-GlcNAc modification of serine and threonine residues in nucleocytoplasmic proteins is both as abundant and as dynamic as protein phosphorylation. In recent years, *O*-GlcNAc has been shown to be required for life at the single cell level: it is needed to regulate both transcription and translation and to regulate signal transduction cascades in response to the nutrient status of the cell. As a result of this research, the Hart laboratory has also become a leader in the development of methods to study difficult post-translational modifications.

Elizabeth A. Komives is currently a professor in the department of Chemistry and Biochemistry at the University of California, San Diego. She received her Ph.D. in pharmaceutical chemistry from the University of California, San Francisco, studying the mechanism of p-bond oxidation by cytochrome P-450. After graduating she did a postdoctoral fellowship at Harvard University, where she looked at triose-phosphate isomerase mutants using Fourier transform infrared spectrometry and x-ray crystallography. Komives' current research focuses on the parameters that govern protein-protein recognition and the mechanisms by which these interactions contribute to biological function. Using a combination of molecular biological techniques, protein chemistry, surface plasmon resonance, multidimensional NMR, and mass spectrometry, Komives and her colleagues study the relative importance of factors such as hydrophobic effects, electrostatic interactions and dynamics. Projects in her lab include looking at how thrombomodulin converts the pro-coagulant activity of thrombin to anti-coagulant activity; studying the interactions of the low density lipoprotein receptor-related protein (LRP-1), which is responsible for clearing many ligands that are genetically linked to Alzheimer disease; and understanding the signal transduction mediated by the family of NF-κB transcription factors and their IκB inhibitors.

Michael P. Snyder is the Lewis B. Cullman Professor of Molecular, Cellular and Developmental Biology at Yale University as well as a professor of molecular biophysics and biochemistry at Yale and director of the Yale Center for Genomics and Proteomics. He is best known for his pioneering research in the area of genomics and proteomics. His laboratory laid the groundwork for large-scale characterization of genes and gene interactions, and his ongoing research in the area of functional genomics involves analyzing thousands of genes or proteins at once to discover their interrelationships. This work is the foundation for what many now call "systems biology." Some of Snyder's current areas of research include the following: control of cell division and cell morphology in yeast; characterization of proteomes; analysis of regulatory circuits in yeast; characterization of the human genome; and sex-specific gene expression in mammals. Snyder received his Ph.D. in biology from the California Institute of Technology. He was recently awarded the 2007 Connecticut Medal of Science, the state's highest honor for scientific achievement and is immediate Past-president of U.S. HUPO.

John T. Stults is Director of Protein Analytical Chemistry at Genentech, Inc. He obtained his Ph.D. in analytical chemistry from Michigan State University. Stults is widely recognized for his contributions to mass spectrometry and proteomics. His research interests encompass the development and application of new mass spectrometry techniques for protein and peptide characterization. A current focus of his research is using proteomics to determine protein expression and modification differences that correlate with disease state, development stage, or drug treatment. He has developed methods for peptide sequencing, disulfide determination, glycosylation and phosphorylation analysis, and two-dimensional gel electrophoresis. He was co-recipient of the 2002 ASMS Distinguished Contribution Award for his pioneering work in protein identification from gels by mass spectrometry.

High Gas Prices Keep NIH Funding in Limbo

BY PETER FARNHAM

The political ramifications of $4 a gallon gasoline have begun to have an impact on American life in ways other than vacations, car prices, and commuting as Congress left town for its August vacation having made no progress on most appropriations bills, including the Labor/HHS bill that funds NIH. The reason for the lack of progress? Unwillingness to confront the unpalatable political choices associated with energy prices this close to an election.

The cost of gas and other associated issues began to have an impact in June, when House Appropriations Chairman Dave Obey (D-WI) abruptly and angrily canceled a committee markup because Republican members wanted to offer an amendment to repeal the 1980s-era ban on offshore oil drilling. Obey then announced that there would be no more progress on appropriations for the remainder of the year. Instead, the government would be funded through a series of short-term continuing resolutions until after the new year (and the presidential and congressional elections) when presumably a Congress more to Obey's liking would be in place, the GOP not being expected to do well this year.

However, as the price of gasoline began to climb this spring, public opinion began to shift in favor of repealing the ban on offshore drilling. Thus, Republicans have begun pushing the issue relentlessly in recent weeks.

But, so far, the Democratic leadership has been adamant that it will not allow a vote to take place on the repeal. They do not want to put rank and file Democrats in the position of having to vote against the repeal in this political climate, to be sure; but it is also likely that many Democrats would vote *for* the repeal and so the party is afraid of losing. So far, Republicans show no signs of letting go of the issue; it is one of the few issues working in their favor this election.

Against this background, the turmoil has now spread to the Senate. Consider the fate of an "emergency stand-alone supplemental funding bill" that appeared—and disappeared—within days in mid-July.

How $5B Became $0.5B

On July 16, Senators Tom Harkin (D-IA) and Arlen Specter (R-PA), NIH's best two friends in the Senate, announced that they were going to introduce a supplemental funding bill that would boost NIH funding by $5.2 billion, the amount they said was needed to restore NIH to the funding level it enjoyed at the end of the doubling period in 2003 after inflation is taken into account. Of course this exceeded the president's request for NIH and the HHS as a whole, and so the bill very likely would have provoked a veto, except that it disappeared from consideration within days with neither a markup or a hearing—so quickly, in fact, that the usually very agile biomedical research community did not have time to get fully mobilized.

By July 21, this bill had been replaced by a second 2008 supplemental funding package with a total of $500 million for NIH—*a full order of magnitude below the level in the earlier bill*—included in an overall package totaling some $50 billion. Senate staff asked senior members of the biomedical lobbying community to make this bill their top priority. The unspoken message was to forget about the earlier $5 billion stand-alone bill. Markup was supposed to occur on July 24. Unfortunately, this markup never occurred either.

Second Supplemental in Limbo as Well

After a week or so of little news (but lots of rumors) about the fate of the "second supp," Appropriations Committee Chair Robert Byrd (D-WV) announced on July 30 that he had decided to pull the bill from consideration until at least September (Congress adjourned on July 31 until after Labor Day). The total of the bill had also been trimmed from $50 billion to about $24 billion.

In pulling the bill, Byrd announced that "…It is my desire to provide funding for critically needed investments in our infrastructure, for energy and economic recovery, and to alleviate the effects of natural disasters" through the second supplemental bill.

"Unfortunately," he continued, "it became clear that an attempt to add language to the supplemental, repealing the 2-decade-old ban on offshore oil and gas drilling *would be successful,* [emphasis added—

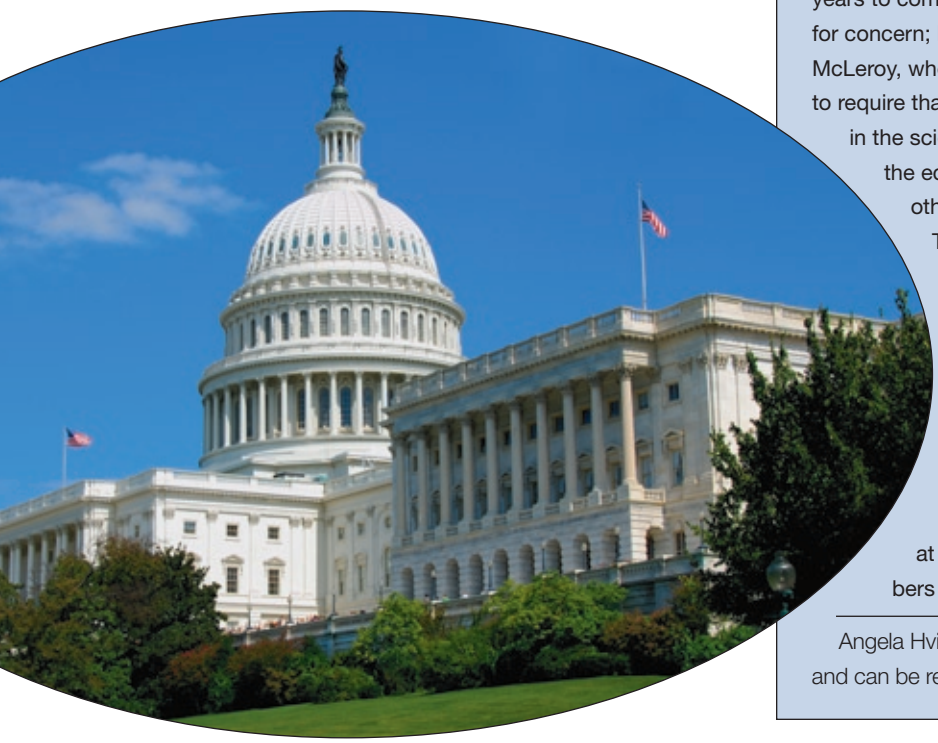
ed.] resulting in the necessity of having to produce 60 votes on the Senate floor to strip the repeal."

Thus oil prices worked their mischief in the Senate as well as the House.

The bill provides $10 billion for infrastructure, energy, and economic recovery programs; $10.1 billion for alleviating natural disasters like Hurricane Katrina; and about $4 billion for "other" programs. It is in the "other" category where one finds NIH. According to Byrd's office:

"Even with the $150 million included in the first supplemental bill, NIH funding failed to keep up with biomedical inflation in FY08 for the 5th year in a row, a trend that has discouraged many young scientists from this field and puts the Nation at risk of losing a generation of talented investigators. The second supplemental includes $500 million to restore some of the purchasing power of NIH that was lost because of inflation in the past 5 years and allow NIH to award at least 700 new research project grants that could lead to cures and treatments for cancer, Alzheimer, heart disease, and many other devastating diseases."

However, the bill has a very difficult road ahead. First, it will not be considered in the Senate until after Labor Day. Second, Congress is estimated to have at most about 20 legislative days left before it adjourns for good in advance of the upcoming elections, so unless this bill becomes top priority, work on it is unlikely to be completed. Furthermore, even if it passes the Senate, it very likely will not be brought up in the House because of Obey's earlier decree. Finally, even if by some miracle the bill did pass the House and was presented to the president for his signature, there is absolutely no indication he would sign it.



A Final Footnote…

In a further sign that energy issues are probably going to be the number one issue in these last several months before the election (and possibly beyond), House Republicans refused to go into recess and were, in early August, holding the House floor to issue denunciations of the Democratic leadership for failing to deal with the energy issue before adjourning.

The election cannot come too soon for this writer.

Peter Farnham CAE is public affairs officer of the Society. He can be reached at pfarnham@asbmb.org.

Evolution Watch

BY ANGELA HVITVED

With many still focused on the new science education law in Louisiana (see the August 2008 issue of ASBMB Today), Texas has once again made its presence known in the evolution "debate." The Texas State Board of Education is currently reviewing the state's science curriculum standards to make recommendations that will affect science education in Texas for years to come. Revising curriculum is not automatically cause for concern; however, the current Board is chaired by Don McLeroy, who is open about his creationist views and his desire to require that children be taught "the weaknesses" of evolution in the science classroom. This would be unfortunate for the education of children in Texas and potentially many others because, as the second most populous state, Texas wields a great amount of influence over the textbook market. The Board is still in the early stages of its review, but several organizations are closely watching the situation. The Texas Freedom Network (www.tfn.org) has a "Stand Up for Science" campaign through which interested Texans can sign a petition and learn how to get involved. There will be public hearings pertaining to curriculum development announced at a later date and we encourage our Texas members to attend.

Angela Hvitved is currently the ASBMB science policy fellow and can be reached at ahvitved@asbmb.org.

asbmb member spotlight

Jordan Honored by Two Professional Societies

V. Craig Jordan, Vice President and Research Director for Medical Sciences and the Alfred G. Knudson Chair of Cancer Research at the Fox Chase Cancer Center, Philadelphia, PA, has received two honorary awards from professional societies that recognize his pivotal role in the development of the selective estrogen receptor modulators (SERMs), tamoxifen and raloxifene. Jordan has been elected as an Honorary Member of the Royal Pharmaceutical Society of Great Britain and has also received what is considered to be the highest honor in medicine in the United Kingdom, an Honorary Fellowship of the Royal Society of Medicine.

Jordan was the first to recognize that tamoxifen and raloxifene are selective estrogen receptor modulators, *i.e.* they stimulated or blocked estrogen target tissues around the body. He took these laboratory data and collaborated with the clinical community to complete the appropriate clinical testing. For 20 years, tamoxifen was the gold standard for the treatment and prevention of breast cancer, and raloxifene is used to prevent osteoporosis and breast cancer.

Appella Receives the 2008 Edman Award

Ettore Appella, of the Laboratory of Cell Biology in the National Cancer Institute at the National Institutes of Health, was honored with the 2008 International Association for Protein Structure Analysis and Proteomics/ Methods in Protein Structure Analysis Pehr Edman Award at the 2008 MPSA meeting in Sapporo, Japan this past August.

In 1979, Appella and his colleagues identified the p53 tumor suppressor protein, and they have continued p53 studies since that time. For more than 15 years they have contributed to deciphering the code through which post-translational modifications to p53 modulate p53 activity and stability in response to cellular stresses, including DNA damage induced by ionizing radiation, UV light, or chemical agents used in cancer chemotherapy.

Appella's recent work includes analysis of the functional effects of single or multiple knock-in mutations at sites of post-translational modifications, especially in those tissues that show increased tumor development.

The Pehr Edman Award is given to individuals whose efforts have significantly advanced the fields of protein chemistry, protein structure analysis, or proteomics. The award honors and commemorates the work of Pehr Edman, the Swedish chemist principally responsible for developing the chemistry for sequencing proteins by removing amino acids from the amino terminus one at a time.

Berg Receives American Institute of Chemists Gold Medal

Paul Berg, Robert W. & Vivian K. Cahill Professor of Cancer Research, emeritus, at Stanford University, was awarded the American Institute of Chemists Gold Medal. Berg, along with Walter Gilbert, was given the award for his service to the science of chemistry and to the profession of chemistry in the United States. They received their medals this past May at Chemical Heritage Day in conjunction with the American Institute of Chemists National Meeting.

Berg and Gilbert shared the 1980 Nobel Prize in Chemistry with Frederick Sanger. Berg was recognized for his research on recombinant DNA, and Gilbert and Sanger were noted for their work on base sequences in nucleic acids.

Berg's Nobel Prize winning work included developing methods that make it possible to analyze the structure and function of DNA and its role in the development of genetic engineering. He has also played a preeminent role in studying risks and rewards for genetic and recombinant DNA research. He chaired the first Science Advisory Committee of the Human Genome Project, and came out in support of therapeutic cloning to produce stem cells for research and therapeutic purposes.

German Honored with David Rumbough Award

Michael German, the Justine K. Schreyer Endowed Chair in Diabetes Research and associate director and clinical director of the University of California, San Francisco Diabetes Center, recently received the 2008 David Rumbough Award for Scientific Excellence from the Juvenile Diabetes Research Foundation (JDRF).

The David Rumbough Award was established in 1974 by the actress Dina Merrill, in honor of her late son David. It is the highest honor the Juvenile Diabetes Research Foundation awards, and is presented annually to researchers for outstanding achievement and commitment to diabetes research and for their service to the foundation. German shared the award with Michael Brownlee.

A professor of medicine at UCSF, German is also director of the Hillblom Islet Genesis Network and the UCSF Diabetes and Endocrinology Research Center, and a principal investigator in the Hormone Research Institute. His research focuses on understanding the structure and development of pancreatic beta cells. He is interested in the genes that control the development of the beta cells from stem cells, as well as where these processes break down in diabetes.

Roizman Gets Lifetime Achievement Award

Bernard Roizman, Joseph Regenstein Distinguished Service Professor of Virology at the University of Chicago, was selected to receive the 2008 American Society for Microbiology (ASM) Abbott-ASM Lifetime Achievement Award. Sponsored by Abbott Laboratories, this is ASM's premier award for sustained, remarkable contributions to the microbiological sciences.

Roizman has been a leader in the field of virology for nearly half a century. In the 1960s, he was a pioneering investigator in the field of herpes simplex virus (HSV) biology, and he is widely recognized as the leading authority in nearly every area of HSV research. One of Roizman's most important early contributions was the identification of a viral gene that is responsible for HSV neurovirulence. In addition, he was one of the very first investigators to apply molecular tools to the epidemiological studies of a pathogen, and he continues to lead the way in elucidating molecular mechanisms underlying the virus-host cell interaction.

The Abbott-ASM Lifetime Achievement Award was presented to Roizman during the 108th General Meeting of the American Society for Microbiology (ASM), this past June.

Snyder Wins CT Medal of Science

Michael P. Snyder, the Lewis B. Cullman Professor of Molecular, Cellular and Developmental Biology at Yale University, has been awarded the 2007 Connecticut Medal of Science, the state's highest honor for scientific achievement.

The award, given by the Board of Governors for Higher Education of Connecticut, was presented this past spring at the annual dinner of the Connecticut Academy of Science and Engineering.

Snyder, who recently became an Associate Editor for *Molecular and Cellular Proteomics*, is also a professor of molecular biophysics and biochemistry at Yale and director of the Yale Center for Genomics and Proteomics. He is best known for his pioneering research in the area of genomics and proteomics. His laboratory laid the groundwork for large-scale characterization of genes and gene interactions, and his ongoing research in the area of functional genomics involves analyzing thousands of genes or proteins at once to discover their interrelationships. This work is the foundation for what many now call "systems biology."

"From his cutting-edge lab research to his popular university courses to teaching kindergarten, Dr. Snyder is dedicated to advancing a broader understanding of science and the joy of pursuing curiosity," said Frank W. Ridley, chair of the Board of Governors for Higher Education of Connecticut.

Rich Wins Welch Award

Alexander Rich, the William Thompson Sedgwick Professor of Biophysics at the Massachusetts Institute of Technology, has won the 2008 Welch Award in Chemistry. The $300,000 award is given annually by Houston's Welch Foundation to foster and encourage basic chemical research that benefits humankind.

Rich was given the award for his pioneering work on nucleic acids, which includes his discovery of left-handed DNA, which he and his colleagues named Z-DNA for its zigzag backbone. Since then, Rich's research has focused on Z-DNA's importance in biological systems. In addition, Rich discovered and solved the three-dimensional structure of the RNA double helix. He was the first scientist to carry out DNA-RNA hybridization and to discover DNA's presence in organelles. He also discovered polyribosomes, which are a cluster of ribosomes attached to mRNA; determined the three-dimensional structure of tRNA; and revealed a novel mechanism in viral diseases such as smallpox.

"Dr. Rich is one of the towering intellects in science of the 20th and 21st centuries," said James L. Kinsey, chair of the Welch Scientific Advisory Board. "His numerous contributions have provided such important fundamental insights that virtually every important area of biochemistry or molecular biology today has Dr. Rich's fingerprints on it."

The Welch Foundation, based in Houston, is one of the nation's oldest and largest sources of private funding for basic research in chemistry. It will present the $300,000 award and gold medallion to Rich at a banquet in his honor in October.

Jeang Elected to Academia Sinica

Kuan-Teh Jeang, Chief of the Molecular Virology Section, National Institute of Allergy and Infectious Diseases at the National Institutes of Health, was recently elected to the Academia Sinica, along with 18 other new members.

Academia Sinica is the preeminent academic institution in Taiwan, similar to the National Academy of Sciences in the United States. It was first founded in 1928 in China to promote and undertake scholarly research in the sciences and humanities. Election to Academia Sinica is regarded as a high recognition of distinguished and continuing achievements in original research. Current membership in Academia Sinica consists of 226 members, including six Nobel laureates, five of whom are physicists and one who is a chemist.

Jeang's current research focuses on the gene regulation of the human immunodeficiency virus (HIV) and on how the human T-cell leukemia virus (HTLV) causes cancer. He was a recent councilor for ASBMB and is serving his third 5-year term on the editorial board of the *Journal of Biological Chemistry*.

Enzymology: Membrane Proteins, Enzymes, and Drug Design

BY RICHARD ARMSTRONG AND BRIAN CRANE

Armstrong

Crane

The cutting edge of enzymology, one of the pillars of biochemistry and molecular biology, continues to change with new and more difficult challenges. The Enzymology theme will present four symposia that highlight important areas of protein structure, function, and mechanism research.

The first symposium, "Structure and Enzymology of Membrane Proteins," is directed at emerging areas of research in membrane proteins and membrane-associated enzymes. Understanding membrane protein folding presents unique analytical challenges. James Bowie (University of California, Los Angeles), in his lecture, will discuss the latest analytical techniques and their consequences for understanding protein folding and structure in a membrane environment. The processing of membrane-associated proteins often occurs by the action of integral membrane proteases. Intramembrane proteolysis is involved in many crucial cellular processes. These reactions are catalyzed by highly specialized integral membrane proteins. Ya Ha (Yale University) will describe the mechanistic features that appear to be common among these membrane-bound enzymes. The outer membrane protein, PorB, of *Neisseria meningitidis*, a bacterium that causes 170,000 deaths by meningitis annually, triggers the activation of the innate immune system, suggesting that it is recognized by Toll-like receptors. Tina Iverson (Vanderbilt University) will discuss new studies that reveal the determinants of PorB recognition by the innate immune system.

The second symposium, "Prediction of Protein Function," focuses on the elucidation of the roles of proteins in biology that have yet to be assigned a specific function. Richard Armstrong (Vanderbilt University) will discuss experimental approaches to determining the unknown roles of several members of the glutathione transferase superfamily in *Escherichia coli* with a specific focus on the underlying biochemistry and structural biology. In contrast, Matthew Jacobson (University of California, San Francisco) will present a computational approach to aid the assignment of enzymatic function based on *in silico* docking of potential substrates to the active sites of homology models. This approach leverages the rapidly growing data bases of protein sequences and structures to help identify protein functions, including functions that have not been previously characterized. The mechanism of the intrinsic hydrolysis in the Ras GTPase and its relationship to the effect of oncogenic mutations will be discussed by Carla Mattos (North Carolina State University). The talk will focus on the conformational nuances of Ras and its mutants near the catalytic center that refine the catalytic mechanism of intrinsic GTP hydrolysis in Ras and further elucidate the role of Q61 in catalysis.

The third and fourth symposia concern how protein conformational change couples to chemistry in the production and sensing of penetrating, reactive effectors, namely nitric oxide and light. The "Nitric Oxide Generation and Response" symposium will focus on the enzymatic generation and detection of nitric oxide, one of the most potent, reactive, and widely used signaling molecules. Elizabeth Getzoff (Scripps Research Institute) will deliver a talk on nitric-oxide synthase (NOS), the complex redox enzyme responsible for the oxidation of arginine to nitric oxide, titled "Structure, Regulation and Dynamics of Mammalian Nitric-oxide Synthase." Brian Crane (Cornell University) will then discuss how bacterial homologs of the mammalian NOSs have disclosed new insights into the chemistry of NO synthesis in his talk "Mechanistic Studies of Bacterial Nitric-oxide Synthase." Finally, William Monfort (University of Arizona) will expand on the enzymology of NO delivery and detection in his talk "Nitric Oxide Signaling in Insects and Humans." Monfort will also describe how the NO-sensing soluble guanylate cyclase can be tricked by small molecules into responses

Enzymology: Membrane Proteins, Enzymes, and Drug Design

Symposium: Structure and Enzymology of Membrane Proteins

- *Determinants of Membrane Protein Structure,* **James U. Bowie**
- *The Mechanism of Intramembrane Proteolysis,* **Ya Ha**
- *Immunological Recognition of Membrane Proteins,* **Tina M. Iverson**

Symposium: Prediction of Protein Function

- *Approaches to Assigning Protein Function in Escherichia coli,* **Richard N. Armstrong**
- *The Role of Homology Models in Assigning Enzyme Function,* **Matthew P. Jacobson**
- *Probing Protein-binding Sites with Multiple Solvent Crystal Structures,* **Carla Mattos**

Symposium: Nitric Oxide Generation and Response

- *Structure, Regulation and Dynamics of Mammalian Nitric-oxide Synthase (NOS),* **Elizabeth Getzoff**
- *Mechanistic Studies of Bacterial Nitric-oxide Synthase,* **Brian R. Crane**
- *Nitric Oxide Signaling Mechanisms in Insects and Humans,* **William R. Monfort**

Symposium: Structure and Mechanism of Photochemical Sensors

- *Blue Light Photosensors: Examples of Environmentally Regulated Protein/Protein Interactions,* **Kevin Gardner**
- *Structure and Mechanism of Phytochrome,* **Katrina Forest**
- *Microbial Rhodopsins: Receptors, Channels, and Pumps from a Single Design,* **John Spudich**

that could aid treatment of cardiovascular disease.

In the final session, the speakers will collectively relate recent advances in our understanding of three major classes of photoreceptors: the flavin-containing LOV domains, the biliverdin-containing phytochromes, and the opsin-containing rhodopsins. In "Blue Light Photosensors: Examples of Environmentally Regulated Protein/Protein Interactions," Kevin Gardner (University of Texas Southwestern Medical Center) will discuss several examples of how blue light receptors convert energy into cellular signals and show how the conserved underlying principles shed light on key issues in photochemistry and allosteric control. Katrina Forest (University of Wisconsin-Madison) will develop these themes in the context of the phytochromes, the plant red light receptors that have been studied for more than 50 years. In her talk "Structure and Mechanism of Phytochrome," she will show how the study of microbial phytochromes have allowed great strides in understanding the molecular nature of these tetrapyrrole-containing light sensors. Finally, in his talk "Microbial Rhodopsins: Receptors, Channels, and Pumps from a Single Design," John Spudich (University of Texas Health Science Center) will reveal how evolution has tailored the remarkable rhodopsins for functions that involve not only sensing but the generation of membrane channels and pumps.

***Abstract Submission Deadline:* November 5, 2008**

Travel Award Application Deadline:* November 12, 2008

**A successfully submitted abstract submission to an ASBMB topic category is required by the November 5, 2008, submission deadline in order to apply for an ASBMB travel award.*

See www.asbmb.org/page.aspx?id=146 for more information.

New Insights into Protein Folding, Aggregation, and Chaperones

BY JUDITH FRYDMAN AND ROBERT TYCKO

Frydman

Tycko

The mechanisms by which proteins aggregate and the molecular basis of misfolded protein toxicity are still poorly understood. Through a variety of biochemical and biophysical approaches, it has been shown that protein and peptide aggregates can have highly ordered structures, such as amyloid fibril structures and specific prefibrillar oligomeric structures, and that formation of these structures is a nearly generic property of polypeptide chains. Understanding amyloid formation is still at an early stage, but it clearly depends on improved characterization of both intermolecular and intramolecular interactions at the most fundamental level. The inherent insolubility and noncrystallinity of aggregates requires the development of new experimental approaches to high-resolution molecular structure determination. The size of protein aggregates and the relatively slow kinetics of aggregation require the development of new theoretical and computational tools. Another major challenge is to understand why aggregates are toxic, and why the chaperone networks that control protein homeostasis decline during aging, leading to late-onset aggregation diseases. For these and many other reasons, the field of molecular chaperones, protein misfolding, and aggregation is extremely multidisciplinary, attracting the interest of scientists whose backgrounds range from pure physics and physical chemistry to molecular and cell biology. The wide range of questions and emerging insights in this exciting field will be covered in the four sessions comprising the "Protein Folding, Aggregation, and Chaperones" theme.

The "Fundamental Principles of Protein Aggregation" session will include talks by Ben Schuler (University of Zurich), Regina Murphy (University of Wisconsin), and Devarajan Thirumalai (University of Maryland) that primarily address biophysical aspects of aggregation. Schuler and co-workers have used single molecule fluorescence spectroscopy techniques to investigate the conformational distributions and dynamics in unfolded peptide chains and the influence of chaperone cages on these properties. Murphy and co-workers have studied the kinetics and pathways of peptide aggregation that lead to amyloid fibrils, and have developed compounds that inhibit these pathways. Thirumalai and co-workers have used theoretical and computational techniques, both in all-atom simulations and in simplified representations of polypeptides, to study the initial stages of aggregation and the general thermodynamic properties of aggregating systems.

The "Chaperone Machines and Cellular Protein Folding" session will focus on the cellular chaperone networks that promote protein folding and prevent aggregation. In this session, Bernd Bukau (ZMBH, Heidelberg, Germany) will discuss his seminal work characterizing how aggregation of misfolded proteins arises from an imbalance in protein homeostasis during stress. Bukau and co-workers have obtained important insights into the cellular organization of protein aggregates and the mechanisms by which molecular chaperones act upon such aggregates. Ulrich Hartl (MPI for Biochemistry, Martinsried, Germany) will discuss his fundamental contributions to our understanding of the mechanism and function of cytoplasmic chaperones and their role in cellular folding. Hartl's group has employed a wide range of approaches ranging from cell biology to single molecule spectroscopy to define how cytoplasmic chaperones, including the ring-shaped chaperonins, promote folding and disfavor aggregation. Judith Frydman (Stanford University) will discuss how different classes of chaperones cooperate to control protein homeostasis. Frydman and co-workers identified two major cellular chaperone networks: a network linked to protein synthesis, which assists folding of newly made proteins, and a stress-inducible network, which promotes quality control of misfolded proteins. How these chaperone networks maintain normal protein homeostasis and facilitate degradation of misfolded proteins will have important implications for understanding protein folding diseases.

The "Protein Folding and Aggregation Diseases" will cover the connection between protein misfolding and a

growing list of aging and neurodegenerative aggregation diseases. In this session, Christopher Dobson (Cambridge University, UK) will describe his work that ranges from theoretical contributions, including understanding how polypeptide sequence is linked to aggregation propensity through biophysical analysis of the aggregation process, to his work in animal models linking aggregation propensity of the Alzheimer Aβ peptide to cellular toxicity. Susan Liebman (University of Illinois at Chicago) will discuss her work using yeast to elucidate factors that influence the *de novo* appearance and inheritance of traits that are encoded by aggregation of specific prion proteins, such as the [PSI$^+$], [PIN$^+$], and [URE3] traits. Surprisingly, her findings reveal that cross-talk between different prions is important in these processes. Rick Morimoto (Northwestern University) will discuss how protein aggregation leads to cellular toxicity and disease. Morimoto and co-workers use *Caenorhabditis elegans* to model Huntington, Parkinson, and Lou Gehrig diseases, leading to important insights into the relationship of aggregation and toxicity with both aging and the cellular stress response.

And finally, the "Molecular Structure of Amyloid Fibrils" session will focus on experimental and theoretical studies of fibril structure and fibril formation. David Eisenberg (UCLA) will present contributions to our fundamental understanding of amyloid structure derived from crystallographic studies of domain-swapped protein oligomers, which highlight the role of domain swapping as a mechanism for aggregation by proteins that also possess globular monomeric structural states, and from extensive studies of amyloid-like cross-β structures in crystalline states of amyloid-forming peptides. These crystallographic studies reveal the high-resolution details of intermolecular interactions in cross-β structures, which are the same interactions that stabilize amyloid fibrils. Teresa Head-Gordon (University of California at Berkeley) will describe computational studies that examine the mechanisms of peptide aggregation, fibril nucleation, and fibril growth, using novel coarse-grained representations of polypeptides. These computational approaches overcome the limitations on molecular simulations that are otherwise imposed by large systems and slow kinetics, and reveal molecular level mechanistic details that cannot be observed directly in any experiments. Robert Tycko (National Institutes of Health) will describe experimental approaches to the characterization of amyloid structures and intermolecular interactions in amyloid fibrils, based primarily on state-of-the-art solid state nuclear magnetic resonance (NMR) techniques. His studies have demonstrated that disease-associated amyloid fibrils have well defined molecular structures with certain universal features but are also polymorphic at the molecular level. Amyloid polymorphism is tightly linked to the phenomenon of strains in mammalian prion diseases and yeast prions, and may have implications for amyloid diseases such as Alzheimer disease as well.

Altogether, the four sessions in this theme will comprise a tour of cutting-edge knowledge on many aspects of the biology, biochemistry, and biophysics of protein misfolding and aggregation. Hopefully, these sessions will promote new interactions among scientists with diverse backgrounds, leading to future progress toward understanding the basic phenomena and preventing their adverse biomedical effects.

Protein Folding, Aggregation, and Chaperones

Symposium: Fundamental Principles of Protein Aggregation

- *Single Molecule Spectroscopy of Non-Native States of Proteins,* **Ben Schuler**
- *Kinetics of Peptide Aggregation in Neurodegenerative Disease,* **Regina Murphy**
- *Theory of Protein Aggregation,* **Devarajan Thirumalai**

Symposium: Chaperone Machines and Cellular Protein Folding

- *Mechanism of Disaggregation Machines,* **Bernd Bukau**
- *Chaperonin Mechanism and Function,* **Ulrich Hartl**
- *Cytosolic Chaperone Networks,* **Judith Frydman**

Symposium: Protein Folding and Aggregation Diseases

- *Protein Misfolding Diseases from the Test Tube to the Cell,* **Christopher Dobson**
- *Prion: Prion Interactions in Yeast,* **Susan Liebman**
- *Restoring Proteostasis via Chaperone Networks in Aging and Neurodegenerative Disease,* **Rick Morimoto**

Symposium: Molecular Structure of Amyloid Fibrils

- *Structural Studies of Protein Aggregates,* **David Eisenberg**
- *Simulations of β-Amyloid Aggregation,* **Teresa Head-Gordon**
- *Molecular Structure of Amyloid and Prion Fibrils,* **Robert Tycko**

Proteins: Birth and Death

BY ADA YONATH AND CHRISTOPHER P. HILL

Hill

Yonath

The vast array of proteins that mediate the biochemistry of life are synthesized in a process that is highly regulated and performed on remarkable assemblies called ribosomes. Our understanding of ribosome mechanisms is advancing rapidly through the application of multiple experimental approaches that reveal dynamic as well as structural function. Additionally, the ribosome is associated with early steps of protein folding *in vivo* and targeting proteins to their appropriate physiological compartment. The cell's protein inventory is highly dynamic because protein molecules are generally removed, often by proteasome degradation, as quickly as they are manufactured by the ribosome. This throughput allows for quality control, effective response to stresses and damage, and highly regulated cellular transitions such as cell cycle progression. Proteasome activity is therefore regulated as tightly as protein synthesis, with much proteasomal targeting being performed by the elaborate protein tagging process of ubiquitylation. The overarching topic of the "Protein Synthesis and Turnover" theme is the mechanism of protein biogenesis and demise, with an emphasis on molecular regulation at the level of the ribosome and the proteasome.

In the session "Ribosome Structure and Function," Ada Yonath (Weizmann Institute) will describe studies that build on a foundation of structural data to illuminate the roles of ribosome dynamics and the mechanisms of nascent chain elongation and initial steps in folding the protein product. In addition to its fundamental importance for life, the ribosome is also an effective target for antibiotics. Stephen Douthwaite (University of Southern Denmark) will focus on mechanisms by which antibiotics inhibit protein synthesis, a topic that is likely to grow in importance as structural and mechanistic data can be brought to bear on the global problem of confronting drug-resistant bacterial pathogens. A hallmark of ribosome studies has been the synergistic use of multiple experimental approaches. Tsutomu Suzuki (University of Tokyo) will present genetic studies that dissect the roles of specific ribosomal components and reveal architectural flexibility in assembly and function.

In the session "Regulation of Translation and Protein Targeting," Maria Selmer (Uppsala University) will describe insights gained from crystal structures of the ribosome and complexes with partners such as mRNA, tRNA, release factors, and recycling factors. Although crystal structures are providing exquisitely detailed views of some ribosome conformations and complexes, other functionally important states have resisted crystallization but can be visualized by electron microscopy. The combination of electron microscopic reconstructions with crystal structure data has the potential to provide a comprehensive series of pseudo-atomic models. Advances using this approach will be the focus of a talk by Roland Beckmann (Universität München). Similarly, a large fraction of proteins are targeted to the secretory pathway for delivery to lysosomes, and Tom Rapoport (Harvard University) will describe studies that explain how the synthesis of proteins destined for the secretory pathway is coupled to the first step in this pathway, namely translocation of proteins across the endoplasmic reticulum membrane.

In the session "Ubiquitin Pathway and Proteolytic Regulation," Raymond Deshaies (California Institute of Technology) will discuss mechanisms by which target proteins are ubiquitylated. Saurav Misra (Cleveland Clinic) will describe how a specific ubiquitylating enzyme coordinates with chaperones to balance cellular efforts at protein refolding with those of degradation. The role of regulated proteolysis in a critical cellular process, namely exit from mitosis, will be the topic of a talk by Kathy Gould (Vanderbilt University).

In the session "Proteasome Structure and Function," Tania Baker (Massachusetts Institute of Technology) will discuss strategies by which ATP-driven activators deliver substrates to proteases. Daniel Finley (Harvard University) will focus more directly on the remarkable 19S regulatory complex of eukaryotic proteasomes, which is an ATP-dependent activator that delivers ubiquitylated and other substrates for degradation. Finally, Christopher Hill (University of Utah) will discuss structural and biochemical studies of other non-ATP-dependent proteasome activators.

Protein Synthesis and Turnover

Symposium: Ribosome Structure and Function

- *Ribosome Dynamics, Nascent Chain Elongation, and Initial Folding,* **Ada Yonath**
- *Antibiotic Inhibitors of Protein Synthesis on the Ribosome,* **Stephen Douthwaite**
- *Mechanistic and Architectural Analysis of E. coli Ribosomal rRNAs Using the Comprehensive Genetic Selection,* **Tsutomu Suzuki**

Symposium: Regulation of Translation and Protein Targeting

- *Crystallographic Studies of Ribosomal Complexes,* **Maria Selmer**
- *Ribosome Complexes at High Resolution by Cryo-EM,* **Roland Beckmann**
- *Protein Transport across the Endoplasmic Reticulum Membrane,* **Tom A. Rapoport**

Symposium: Ubiquitin Pathway and Targeting

- *Mechanisms of Ubiquitination,* **Raymond Deshaies**
- *Interplay between ChIP, Hsc70, and Bag2 in Protein Quality Control,* **Saurav Misra**
- *Split Decisions: The Role of Proteolysis in Mitotic Exit,* **Kathy Gould**

Symposium: Proteasome Structure and Function

- *Strategies for Substrate Recognition by the AAA+ Proteases,* **Tania Baker**
- *The Proteasome Regulatory Particle,* **Daniel Finley**
- *Proteasome Activator Complexes,* **Christopher P. Hill**

Forensic Image Analysis

The Good, the Bad, and the Poorly Adjusted

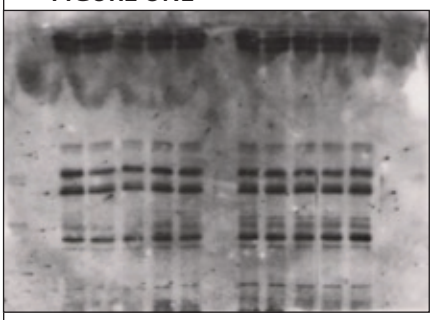
This article is seventh in a series on publishing your research in the *Journal of Biological Chemistry*. The series will address a variety of issues that authors may have when writing and submitting articles to the *JBC*. The articles are written by Cadmus Communications, a Cenveo company, which is responsible for the editing, production, and printing of *JBC* articles.

Congratulations! You have completed your research, and it's time to report the findings. This involves gathering and preparing data to truthfully present those findings.

The standards for handling and processing data are important elements of all scientific research. Some of the data may be represented by photographs, scans, x-rays, micrographs, and other continuous tone images. To maintain the integrity of the data, preparation and assembly of these images require special care.

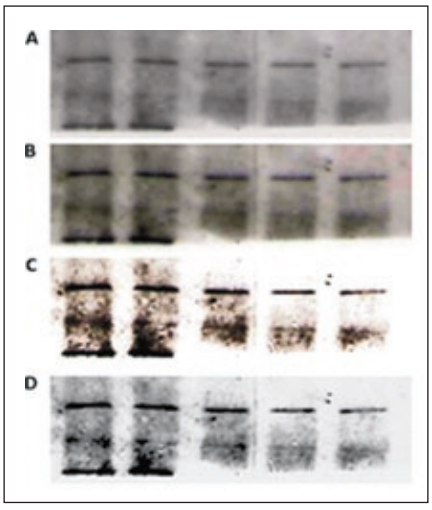
In recent years, isolated (but much publicized) incidents have raised the consciousness of the entire scientific community. Trust of scientific research has become a very serious issue. At the very least, the perception of less than truthful reporting could lead to questions of integrity. In a worst case, it could lead to charges of research misconduct.

FIGURE ONE



Representation of a first-generation source file.

FIGURE TWO



Cropped image (*A*) with different adjustments to contrast and brightness (*B*, *C*, and *D*).

Preparing Figures

Typically, digital art has been manipulated a lot by the time it is submitted for publication. Often, the selected image was part of a larger piece—the "first-generation source file" (Fig. 1)—so it has been cropped (Fig. 2*A*). If the image appears too dark or too pale, an adjustment to brightness or contrast is not uncommon (Fig. 2, *B-D*).

Frequently, digital art may be sized disproportionately and then arranged with other images and graphics to compose the final figure for submission (Fig. 3).

Most often, adjustment and layout are performed using whatever software is available. As a result, figures are prepared with applications never intended to produce publication-ready graphics (*e.g.* PowerPoint, GraphPad, Prism, Canvas, etc.). Although these programs may be popular, user-friendly, or suitable for other purposes, each of them adds its own properties to the manipulation.

Your graphic skills may further compound the issue. A figure created in a non-standard format may need to be converted into a TIF file to meet the submission requirements of a journal.

Each time an image is adjusted and that adjustment is saved, some of the original image data are lost. The degree of loss depends on what was done, the settings and defaults of the application used, and the format of the saved file, particularly if the format changed during the process (Fig. 4).

What Is Acceptable?

As a general rule, global adjustments to an image are considered acceptable if they are not done to an extreme. For example, overall brightening or contrast enhancement is acceptable as long as the adjustment does not completely blow out or obliterate the lightest or darkest parts of the image (Fig. 2*C*).

If one area of the image is adjusted independently from the rest of the image,

FIGURE THREE

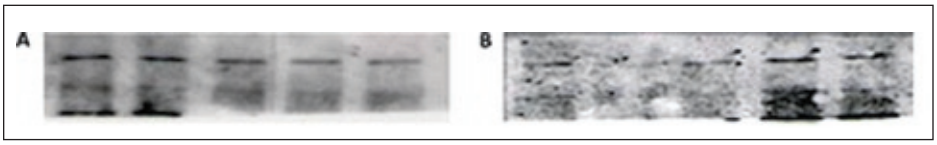


Image elements with vertical-only sizing to make them align for figure layout.

it is not a global adjustment and therefore not considered acceptable (Fig. 5*B*).

Cropping an image to focus attention to a specific feature is acceptable unless the cropping is a deliberate attempt to conceal an element that would be relevant to the science.

Bringing together images from different events or sources is acceptable only if there is a clear delineation—known as "tooling"—between the elements (Fig. 5, *C* and *D*).

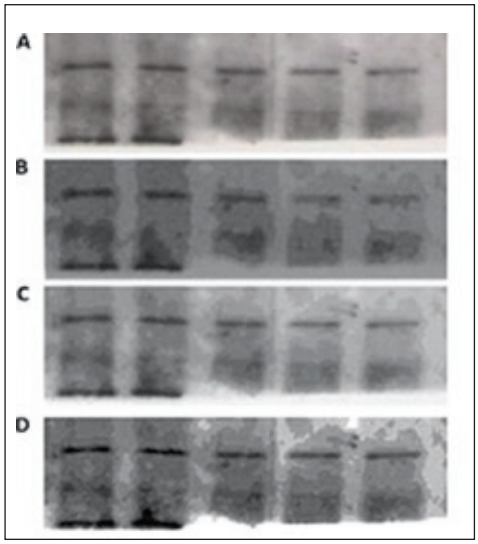
Source Files

A "first-generation source file" is the image that was originally captured and saved to become a digital file. This would be the image (i) BEFORE it was cropped, sized, or scaled; (ii) BEFORE any lines, arrows, or text elements were added; and (iii) BEFORE its properties (*e.g.* contrast, brightness, saturation, hue, etc.) were adjusted in any way. This would be the image in its original format when it was first digitized BEFORE it was converted to some other format. Depending on the image capture method, a "first-generation source file" is often a JPG, a RAW, or a TIF file.

History

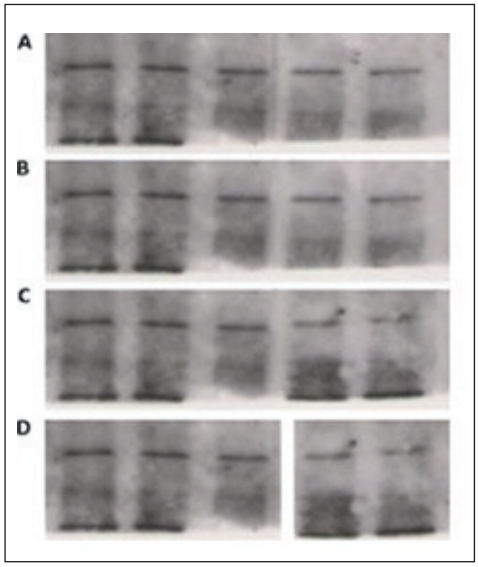
Before the digital age, image manipulation was expensive, time-consuming, and required special skills—think of airbrushing. Today, the once elaborate effects—and many new ones—are available to anyone with the software and the ability to click a mouse. Until recently, technology to reveal modifications was not keeping up with the digital tools that created them.

FIGURE FOUR



Original image (*A*) with different properties and formats, such as JPG or GIF (*B*, *C*, and *D*).

FIGURE FIVE



Original image (*A*); blemishes removed (*B*); *lanes 4* and *5* replaced with *lanes 4* and *5* from another image (*C*); *lanes 1-3* from one image and *lanes 4* and *5* from another image but with proper tooling between elements to indicate they are not one original image (*D*).

For years, limited software tools and a "good eye" were used to (hopefully) spot areas of concern concealed within digital art. Once again, the process was expensive and time-consuming and required special skills. Early software detection methods required enormous computing power to perform limited analyses… and it was slow (12-24 hours per image). Results were difficult to interpret, and the software was limited to a narrow range of image formats.

Forensic Image Analysis

Because of the concern about possible research misconduct, special methods and software (such as Rigour™ from Suprock Technologies) are now used to analyze digital art. The purpose of this forensic image analysis is to reveal evidence of tampering or inappropriate manipulations. Visual inspection of images has always been a part of the review process. The new software adds another dimension to this review and inspects images down to the random pixel arrays contained within all digital art. This software solution quickly analyzes images, performs multiple analyses, and can be integrated into a high volume production workflow. The inspection does not determine (nor make a judgment of) the intent of the image's producer.

What Is Analyzed?

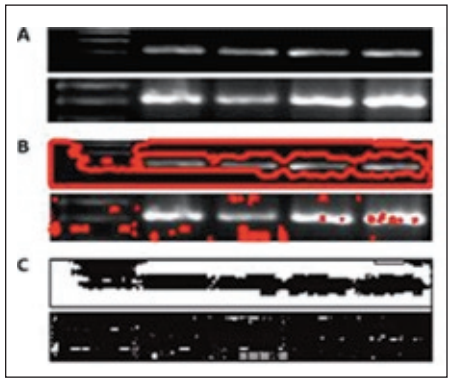
Analysis is reserved for digital art where information is stored as arrays of pixel values. This is distinct from deliberately manufactured images such as charts or graphs containing only text or line elements.

Pixels

A pixel (short for picture element) is the smallest element in a digital image. It contains values of brightness (intensity), hue, saturation, and color depth. A lot of data is stored in a pixel and can be analyzed with mathematic algorithms.

For example, the bits per pixel (BPP) determine its number of colors calculated as 2 to the power of the BPP. A typical TIF file is capable of representing 24 BPP, or 224 = 16,777,216 colors. On the other hand, a GIF file is limited to 8 BPP, or 28 = 256 colors.

FIGURE SIX



Original 2-row image as submitted (*A*); areas of blowout revealed and highlighted by two different analyses that are part of the Rigour process (*row 1* of *B* and *C*, as indicated with *arrows*). Other highlighted elements in row 2 are attributed to random noise caused by JPG compression (*B* and *C*).

Pixels and Images

Pixels per inch (PPI)—or dots per inch (DPI)—determine an image's resolution; the BPP determine color depth; and the quality of image is determined by the combination of these variables. A typical image may contain hundreds of thousands or even millions of pixels.

An important note about pixels: the normal arrangement of pixel arrays within an unaltered image is highly randomized. Groups of pixels with similar properties may appear near each other, but the arrangement of those groupings is unique.

The Basics

For the purpose of this discussion, the descriptions of images and pixels are highly simplified.

The basic concepts are as follows: images are made of pixels, pixels contain data, and unaltered arrays of pixels are random.

What Is Revealed?

Tools used to manipulate an image leave behind a unique fingerprint characteristic of that particular tool. Forensic image analysis is designed to recognize and identify those fingerprints within the pixel arrays. The analyses generate visual references to focus further review by a digital art specialist.

One Example: Blowout Detection

Blowout is probably the most common anomaly that is detected in figures. This condition occurs when the normally random pattern of pixels is replaced with a solid field of a single pixel type or where pixels are lost altogether.

When the brightness or contrast of an image is adjusted too far, it will cause blowout. This type of adjustment could be the result of an effort to enhance the appearance of an image for publication. The reason that this is a concern is because it could also be an attempt to mask the removal or addition of elements within the image (Fig. 6).

Other Detections

In addition to blowout detection, the Rigour software runs several other algorithms that will reveal many types of image manipulation.

For example, in an image-editing program like Photoshop, the blur tool is used to blend or blur the hard edges of an area that has been altered. In some cases, someone may use the blur tool to smooth out a cluttered part of the image so that focus is directed to a specific area. This can be a concern because it could also be an attempt to smooth out the edges of a meaningful added (or deleted) element.

Other analyses inspect any alterations within the texture of the pixel array. Clone or copy tools (among others) create a new texture within an image. These altered arrays appear as clumps that stand out from the typical random "noise" found in an unaltered image.

The Digital Art Specialist

After the Rigour software processes the images, the results are reviewed by a digital art specialist. Each analysis category creates a visual output similar to the images shown in Fig. 6. These images are viewed in context so that an isolated element from one analysis may show up as the same isolated element in another analysis. The context review alerts the digital art specialist when they see the same detection element appearing in multiple analyses.

The Good, the Bad, and the Poorly Adjusted

Consider the consequences of your actions as you prepare and adjust your images. Imagine friends, family, and colleagues learning of your actions through headlines in the news. If you are making good choices, you should feel comfortable with this scenario. And finally, keep accurate and detailed records of your data so you can demonstrate they are valid and represented accurately.

Moving toward a Biochemistry Concept Inventory

BY DUANE SEARS

The 33rd FEBS/11th IUBMB Conference held in Athens this summer featured a timely symposium entitled "Concept Inventories in Molecular Life Sciences Education," organized by Susan Hamilton and Tony Wright from the University of Queensland, Australia. This symposium brought together life scientists and science educators from various disciplines who are actively pursuing the development of concept inventories (CIs). Hamilton's introduction to open this symposium reminded us that the ultimate purpose of CIs is to evaluate the nature and quality of student understanding so as to inform instructors of their classroom practices and the possible need for curricular changes, improved teaching strategies, and remediation of students' conceptual or reasoning difficulties[1].

What Are CIs?

For the uninitiated, CIs, including those geared toward biology[2], are usually modeled after the physics Force Concept Inventory[3], which has resulted in significant curricular reform[4] since it was introduced to probe physics students' conceptual understanding of the Newtonian laws of motion. In a nutshell, CIs are assessment "instruments" crafted with a series of multiple choice questions, each presenting students with one correct choice and several incorrect choices that typically embody commonly held student misconceptions–so-called "distractors"–as uncovered through actual research into student thinking, as opposed to having "experts" make assumptions about what students think[5]. This approach helps "circumvent students' test-taking strategies"[6] that depend more on factual recall or intelligent guessing instead of true conceptual understanding.

CIs are neither standardized tests that rank students according to performance nor do they assess every topic that might be covered in a course or in a textbook chapter devoted to a given subject. Rather, CIs are designed to assess students' understanding of testable concepts that collectively define overarching ideas, or the so-called "Big Ideas," that coherently integrate, underpin, or unify fundamental understanding of the targeted discipline[7]. In biology for example, the "Big Ideas" stem from how organisms function at all levels, how they evolve, how they interact with their environments, etc.

The types of questions developed for CI assessments can be content-specific where students are assessed on their mastery of specific content areas, or the questions can be more "content-neutral" in the sense that highly specialized knowledge in specific areas is not required to answer the questions. For example, questions about diffusion and random movement, two very fundamental concepts that transect all of biology, can be formulated in many different ways. In biochemistry, a student's understanding of these concepts can be probed by asking them about how enzyme-substrate complexes form without requiring more specific knowledge about how enzymes catalyze their reactions[6,8].

Ultimately, CIs aim to assess students' understanding of concepts before or in response to instruction, or both. Unlike most other testing formats, however, CIs are usually administered as low risk (ungraded) activities where students might not even be given specific feedback on their performance so that the same assessments can be administered multiple times for the purpose of measuring performance gains in response to instruction. For example, the same CI assessment might be administered for comparative analysis before and after a particular concept is introduced during instruction, or it might be administered to students in different classes, perhaps with different instructors.

Developing CIs

The next two symposium speakers, Susan Elrod (California Polytechnic State University) and Mike Klymkowsky (University of Colorado, Boulder), described their NSF-funded initiatives aimed at developing CIs in genetics[9] and basic biology[6,8], respectively. They also summarized two recent NSF-funded Concept Assessment in Biology workshops, CAB I[10] and CAB II[11], where biologists and educational researchers from many fields convened to discuss assessment methods for biological CIs.

Next, Joel Michael (Rush Medical College, Chicago) presented an overview of the difficult process of developing and testing CI questions, making the following key points: 1) "Big Ideas" constitute ideal starting points for developing CIs in biology, although the identification

of "Big Ideas" is a nontrivial process; 2) "Big Ideas"–for example, homeostasis[12], need to be "unpacked" into simpler underlying fundamental concepts, *e.g.* diffusion, etc., that are individually more amenable to rigorous concept assessment; 3) A systems approach to CI question development is likely to produce meaningful measures of student learning and understanding considering that biological processes are almost always defined by interacting systems of molecules, cells, and/or organs. Thus, when a student is asked to predict the consequences of perturbing a given system in some specific way, one is effectively probing their ability to reason scientifically[13], which is a primary goal of science education in my opinion.

Rounding out the first half of the symposium, this writer (Duane Sears, University of California, Santa Barbara) briefly reviewed ASBMB's initiatives for biochemistry curricular reform, particularly the activities supported by a Teagle grant[14]. I emphasized that CIs need to be developed to support these efforts, much like the molecular life sciences CI (MLS CI) that is currently under development with funding by the Carrick Institute for Learning and Teaching in Higher Education[15]. As outlined by Wright in the next presentation, nine "Big Ideas" are being targeted by the "Carrick Project," including: 1) Molecular Evolution; 2) Self-Assembly; 3) Compartmentalization; 4) Information and Communication; 5) Regulation; 6) Catalysis; 7) Energy and Organization; 8) Complexity of Molecular Structure; and 9) Aqueous Environment of the Cell. He also described the CI assessment instrument, which is based on an "adaptive testing method" where students are presented with a series of branching questions of graded difficulty, with question branching being dictated by the particular responses a student makes to questions in a series.

Some Sample CIs

Next, Susan Howitt (Australian National University), another Carrick project team member, described some sample questions and preliminary results from MLS CI assessments that have been administered thus far. A typical set of questions on one topic are shown below where a brief narrative is followed by three true/false questions that also include a "don't know" option to minimize guessing:

Narrative:

Myoglobin plays an important role in oxygen storage in muscle. Under physiological conditions the equilibrium between Mb and MbO_2 is reached very rapidly.

Instructions:

For each of the following statements choose a response: **true**, **false,** or **don't know**.

Questions:

a) Myoglobin binds oxygen (O_2) and is able to release it chemically unchanged.

b) Each oxygen molecule remains bound to a myoglobin molecule until it is needed.

c) Oxygen is released more easily from MbO_2 when the concentration of oxygen is low because the oxygen is bound more weakly to the Mb.

Other CI questions that were discussed at the meeting included visual representations in the form of enzyme-catalyzed reaction schemes and/or plots of catalytic data. As pointed out in the ensuing discussion of these questions, the inclusion of visual representations may complicate the analysis of student responses because a student's ability to formulate their answers may rest not only on their conceptual understanding but also on their ability to interpret and make inferences from the symbolism used in the accompanying reactions schemes or graphs. Obviously, other types of visual representations, such as diagrams or visual models used to represent chemical structures[16], are equally problematic for the same reasons. In any event, questions that depend on such interpretive reasoning skills can produce misleading assessments of a student's conceptual understanding if the student has not yet mastered the requisite skills needed to interpret the visual information included with the questions. Thus, student responses to CI questions with visual representations need to be parsed in such a way to distinguish incorrect responses that reflect conceptual misunderstanding from incorrect responses that simply reflect deficiencies in certain reasoning skills that students need in order to formulate answers to the questions. Similarly, student responses to some questions may also need to be parsed according to a student's mastery of certain basic chemical and biological concepts that instructors often tend to assume (sometimes erroneously) that students have previously mastered in course work completed prior to formal biochemistry instruction[17].

Such matters and others were taken up in the presentation by Trevor Anderson (University of KwaZulu-Natal, South Africa), another Carrick project team member. He discussed the use of students' alternative conceptions[18] to design CI assessments and considered issues with assessment validation. Anderson also presented an illustrative example of how CI assessments can actually be utilized for effective remediation of student misconceptions.

The final speaker and Carrick project team member, Manuel Costa (University of Minho, Portugal), summarized much of what has already been discussed here, and he also proposed that those of us who are involved in CI development

work collaboratively under some yet to be defined framework since the two worlds of science and science education are now clearly being brought together in ways where advances in one area potentiate advances in the other. His provocative idea that a CONCEPTBANK–like the GenBank™–might revolutionize science education worldwide was a fitting footnote to this symposium, which, after all, was held in the city that gave birth to the Socratic method of rational inquiry, a crucial feature of CI development.

In the spirit of Costa's remarks and the IUBMB Executive Committee's vision for education[19], I propose that ASBMB work together with IUBMB in terms of taking active leadership roles to foster international collaborations between the community of scientists and educators who are at the forefront of developing CIs in areas closely allied with biochemistry and molecular biology. One particularly interesting idea currently being floated among some ASBMB members is that the Society create an online "encyclopedia" of relevant educational resources, something that could easily be used as a virtual repository for the types of educational tools discussed here.

Please contact me or any of the other symposium participants if you are interested in participating in the future efforts to create a robust biochemistry CI.

Duane Sears is a professor in the Department of Molecular, Cellular, and Developmental Biology at the University of California, Santa Barbara. He can be reached at sears@lifesci.ucsb.edu.

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Turning a Society into a Community

BY SARAH CRESPI

Science and technology go hand and hand, right? Not always. Although there's no doubt that many denizens of the lab went out and bought themselves an iPhone this year and do most of their communicating via texting, email, and cell phone, many others are happy to stick with land lines and handwritten letters.

Communication tools seem to be the fastest changing technologies. Think about how much our lives have changed in the past decade with the advent of email and cell phones. Power Point has made everyone an adept public speaker.

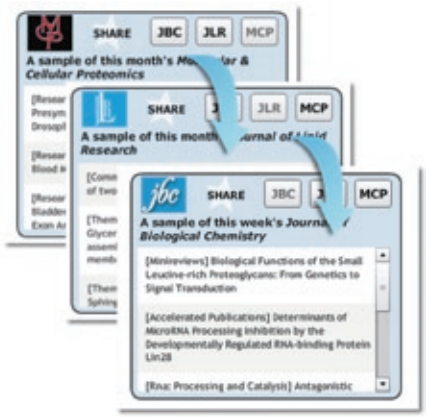
Many of the new communication methods like blogging and text messaging tend to be used as avenues for letting others know where and how we are, minute by minute. But they've also proved themselves important for communicating science both among scientists and between scientists and the public. This column will try to cover the interesting intersection of science communication and communication technology.

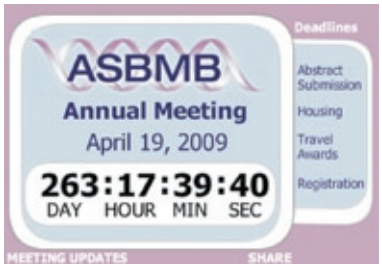
This month we will talk about how the ASBMB is keeping up with communication innovation by adding new features to our journal websites and home page.

Widgets and RSS Feeds

We've added quite a few new features to our websites that provide new paths to our content. Many readers may have noticed the addition of RSS feeds to our journal sites. RSS stands for Really Simple Syndication and for good reason. Content producers like the ASBMB journals add new items to their feeds, which users can sign up to receive. Feed receivers have a choice of how they want to stay connected: feeds can be added to the browser tool bar in Firefox or to an account at an online feed reader site like Bloglines.com or iGoogle.com. Online feed readers have the advantage of being accessible from any internet connection. Browser-based readers are convenient because they appear like bookmarks or favorites in the toolbar, no sign-in required. Some email programs' inboxes offer a third reader option. Yahoo's online email and Microsoft's Outlook 2007 both house RSS feed readers in their mail folders section.

To make things even simpler, we've now combined all our current issue RSS feeds into one easy-to-use "widget." The widget displays the current table of contents for ASBMB's three journals and can be replicated on personal homepages or iGoogle pages through the push of a button (click of a mouse).





On our widget mania page, we've created a countdown clock for the annual meeting in April 2009, which includes deadline reminders and links to meeting updates. And for fun, we've added an easy to use lab timer that can be set for up to 3 minutes. Both widgets can be also exported to iGoogle.com, Facebook.com, or your personal webpage by clicking on the "share" button.

Social Bookmarking

Little collections of symbols are popping up everywhere, at the end of news stories, on blogs, and now alongside scientific articles, always inviting readers to "share." Some are so tiny you can barely make out their implication: they're

harbingers of Web 2.0. These icons link web surfers to their preferred social bookmarking site.

Now, articles from the *Journal of Biological Chemistry*, the *Journal of Lipid Research*, and *Molecular and Cellular Proteomics* can be easily added to a multitude of social and academic bookmarking services.

In a nutshell, social bookmarking allows web users to create an online repository for their favorite pages. Descriptive tags added by the bookmarker help members of the community find others with common interests and compare favorite pages or articles. Unlike RSS feeds, where content is chosen by the publisher, social bookmarking allows content users to aggregate diverse, self-selected content into one spot. Social bookmarking accounts are accessible from any wired computer and allows users to port vast literature lists without packing a single piece of paper.

ASBMB's journals offer "add buttons" for general news sites like Digg.com and Del.icio.us and more specialized services like Connotea.org and CiteULike.org that are targeted at physical and social scientists. These sites create communities of similarly focused researchers, connected through descriptive tags. The tags allow users to maintain their own running list of studies and to find lists generated by others. Connotea, created by Nature Publishing Group, also offers the option of exporting bookmarked articles to desktop citation managers.

Faculty of 1000

The ASBMB's journals are the first High Wire online journals to link to reviews from the Faculty of 1000 Biology and the Faculty of 1000 Medicine. The Faculty's purple and blue logos will appear in the web editions in the table of contents and in the header of articles and link to F1000 reviews.

The Faculty of 1000 is actually a group of over 2,300 researchers who review recent studies in their fields and rate them and rank them in terms of their importance. Having links to F1000 in the journals serves as a guide to high impact content for our readers, and the reviews help put articles in context. This is an especially useful tool for keeping up on important research in distant fields because the short reviews provide perspective from someone on the inside.

As an additional perk, ASBMB members get a discounted subscription to F1000 if their institution is not already a member.

Of course, like everything else on the web these days, once you have an F1000 account, it can be tailored to search out specific interests and start up automated email alerts.

ASBMB on Facebook

We're on the bandwagon. The society has started its own Facebook group and invites all members with Facebook accounts to "friend" us! Joining the group allows you to track society events from inside Facebook and comment on group activities. If you're not a Facebook member, signing up is free. ASBMB's Facebook group offers an opportunity to network with researchers from all over the world. Go visit the site and check out our widgets, podcasts, and society news alerts.

Help Us Help You

The ASBMB is doing a lot more behind the scenes to improve how we communicate scientific results. In the near future, all the journal websites will be getting facelifts. We will also be introducing a society blog, *Chiral Comments*, that will cover new studies, what the society's president is up to, meeting minutiae, and the politics of science. It is our hope that the blog will stimulate discussion among members and that commenters will use our blog and Facebook page to make connections with one another. Think of them as virtual scientific meeting places. (Look for more on virtual meetings in upcoming columns.)

But this column will not only let our readers know what the ASBMB is doing to get an online community going. It's also our goal to inform readers of new ways to collaborate using advancing communication technologies such as web video, wikis, and more.

Let us know about the kinds of communication tech that have invaded your lab. Is Skype your favorite method of talking with your research partners? Does your lab have a Facebook page or communal Google document? Email us at tekkie@asbmb.org and we'll spread the word. And by the way, if you're wondering about the Sci.Comm logo, I choose a hair cell (the sensory cell of the hearing and vestibular system) for the logo because it's the cell type I did research on for my undergraduate thesis and because I see it as representing communication.

Sarah Crespi is an intern at ASBMB. She can be reached at screspi@asbmb.org.

MAC: Developing Scientists, Raising Awareness, and Promoting Change

BY PHILLIP A. ORTIZ

Modern medicine has led to a greatly improved life span and quality of life, but despite these gains Americans do not share the benefits equally. Although there have been tremendous gains in basic and applied research, diagnosis, and treatment, many minority populations suffer disproportionately. African Americans, Hispanics, Native Americans, and Asian/Pacific Islanders experience striking health disparities, including shorter life expectancy and higher rates of diabetes, cancer, heart disease, stroke, and infant mortality. As Jerome C. Nwachukwu explained in his Minority Affairs article last month, the National Institutes of Health has been stepping up its efforts to address this problem.

In parallel with the leadership of NIH, we at the ASBMB Minority Affairs Committee (MAC) have also enhanced our efforts in this area. As recently as 2003, the MAC would organize only a single symposium at the national meeting, and that session typically focused on the unique issues faced by minority scientists in their education and careers. Recently, we have expanded our offerings to four symposia: we have kept the issues-based session, and the three additional symposia have been used for addressing scientific topics in minority health disparities. Our intention is not only to raise awareness of overlooked problems but also to promote the scientific process of solving them. In recent years the MAC has covered several topics each year—HIV/AIDS, breast cancer, heart disease, sickle cell disease, diabetes, and drug addition, to name a few. Although these sessions were used to present cutting edge science and often led to interesting and engaging conversation among the attendees and presenters, the MAC recognized that multidisciplinary, integrated approaches to problem solving are often most successful. Thus, we decided to apply this principle by unifying each year's scientific sessions under a common theme.

The theme for the 2009 meeting to be held in New Orleans as part of Experimental Biology is a revisiting of HIV/AIDS. We made this decision because, although a great deal of progress has been made on this topic since it was last addressed, it remains a scourge. Three symposia will be centered around this theme, each chaired by a member of MAC and focusing on one aspect of the problem. Each of the session chairs have invited three distinguished scientists as presenters, and in addition, each chair will review the submitted abstracts and select additional presenters. In this way each complementary session will itself have three aspects united by a common sub-theme, and each will include an introduction and overview provided by the session chair, invited scientists, as well as newly emerging research. The MAC very enthusiastically encourages all researchers (*i.e.* not just "the usual suspects"!) to submit their work for inclusion in the symposia, and we are looking forward to reviewing the submitted abstracts.

The first of the MAC's four symposia is "issues-based" and will be led by MAC member Thomas Landefeld of California State University, Dominguez Hills. The symposium is titled "The Development and Advancement of Minority Scientists in Academia." Unlike the other three symposia, which are "science-based," this symposium will address topics that may be particularly relevant to young scientists as they develop their careers. The themes being addressed by the speakers may also be relevant to non-minority scientists, so we encourage every meeting attendee to join us for this session. The session will include the following three presentations:

The Trials and Tribulations of Attaining Tenure for Minority Scientists, **Luis S. Haro, University of Texas-San Antonio**

Importance of the Recruitment and Retention of Minority Scientists to the Future of Biomedical Research, **John Alderete, Washington State University**

Minority Faculty Decisions: From Teaching to Administration to Moving Outside of Academia, **Tuajuanda C. Jordan, Howard Hughes Medical Institute**

The remaining three symposia center on the general scientific theme of HIV/AIDS. The MAC chairperson, George C. Hill of Vanderbilt University, will be leading the first of these, and his symposium is titled "The Role

of Basic Scientists in Addressing Global Health Issues." This session will include the following three presentations, along with one or more presentations yet to be selected from the submitted abstracts:

Preventing HIV in Developing Countries: Emerging Biomedical Interventions, **Sten Vermund, Vanderbilt University**

Role of Lipid Rafts and Adhesion Molecules in Addressing the Biology of HIV and the Global AIDS Crisis, **James Hildreth, Meharry Medical College**

Stopping HIV: Cellular Defenses and Antiretroviral Therapy, **Richard T. D'Aquila, Vanderbilt University School of Medicine**

The second of the three scientific symposia on HIV/AIDS is titled "HIV: Activation and Antagonism of Host Defense" and will be led by MAC member Craig E. Cameron of Pennsylvania State University. This session will include the following three presentations, along with one or more presentations yet to be selected from the submitted abstracts:

Insights into Novel Host Factors Required for HIV-1 Replication in Human Cells, **Kuan-Teh Jeang, National Institutes of Health**

Co-option of T Cell Signaling by HIV for Viral Transcription, **Avery August, Pennsylvania State University**

In Vivo Analysis of Host Defense Mechanisms to Control HIV Disease, **J. Victor Garcia-Martinez, University of Texas Southwestern Medical Center**

The final session on HIV/AIDS is titled "Clinical and Pharmacogenomic Aspects of HIV and AIDS" and will be led by Garry D. Dotson of the University of Michigan College of Pharmacy. This session will include the following three presentations, along with one or more presentations yet to be selected from the submitted abstracts:

RNase H Activity and Drug Resistance to Nucleoside and Non-nucleoside Reverse Transcriptase Inhibitors, **Vinay Pathak, National Cancer Institute, NCI-Frederick**

Monitoring HIV Drug Resistance in the New Era of Multiple Antiretroviral Targets, **Miguel E. Quinones-Mateu, Diagnostic HYBRIDS**

HIV-1 nef Signature Sequences and Pulmonary Arterial Hypertension: Structure-Function Relationships to Pathogenesis, **Sonia C. Flores, University of Colorado**

In closing, the MAC wishes to encourage submissions of abstracts for our symposia as we intend to incorporate several of them into the sessions. We enthusiastically look forward to the 2009 meeting as an opportunity for the exchange of ideas and insights, and we encourage the entire membership of ASBMB to attend the four symposia we are organizing.

Phillip A. Ortiz is a member of ASBMB's Minority Affairs Committee. He can be reached at phillip.ortiz@esc.edu.

The ASBMB Annual Meeting Abstract Submission site is now open!

For more info go to
www.asbmb.org/page.aspx?id=146

And don't forget...
the deadline for abstract submission is
November 5, 2008

Translating Scientific Discoveries into Tangible Public Benefits

BY NICOLE MAHONEY*

I have always been interested in the practical applications of science, so when I saw a poster advertising the American Association for the Advancement of Science (AAAS) policy fellowship for scientists and engineers in my lab break room, I knew I had to apply! At that point, I was approaching the five-year mark of a challenging postdoctoral fellowship at the University of California, San Francisco, and with over a decade of basic science research experience behind me, the prospect of applying my science know-how to important policy questions seemed very exciting. After making it through the lengthy fellowship selection process and finding a host office, I finished up my experiments, packed my bags, and headed off to Washington, D.C.

I spent much of the next 2 years at the National Science Foundation and National Institutes of Health writing reports, press releases, and newsletters to communicate federally funded research results to legislators and the public. Most importantly, I learned how the government operates, sets budgets, and funds science—things they (surprisingly!) don't teach you in graduate school but are critical to the scientific enterprise in this country. And I sought out answers to some of the big-picture science policy questions I'd been curious about throughout my career such as: How are scientific discoveries translated into tangible public benefits? Part of the answer to this question, I discovered, is through technology transfer.

What Is Technology Transfer?

I had heard the term "technology transfer" while I was still working at the bench, and I knew the university had an office dedicated to it, but I wasn't quite sure exactly what technology transfer entailed. I now know that practitioners in this growing field basically do what the name implies—they transfer technologies and scientific discoveries from one place (often an academic lab) to another (another academic lab or a company). The ultimate goal of technology transfer is to ensure that the full potential of laboratory discoveries—and by extension the return on taxpayer investment—is realized. In many cases, this involves patenting and licensing technologies to the private sector for commercialization.

So what is the connection between science policy and technology transfer? Let me provide some background to clarify the link.

The technology transfer field was spawned by the 1980 Bayh-Dole Act—legislation designed to spur the development and practical application of federally funded research discoveries. Among other things, this act allowed universities and small businesses to patent inventions that were funded with federal dollars and license them to the private sector for commercialization. Because the point of this legislation was to spark innovation and increase U.S. technological competitiveness, it also provided incentives for researchers to exploit their ideas by allowing them to collect royalties on licensing income. Before the Bayh-Dole Act, the government owned patent rights to discoveries it funded, and only a tiny fraction of these inventions were ever licensed. However, most universities have established technology transfer offices since 1980, and many credit the Bayh-Dole Act with helping fuel the biotechnology industry's impressive growth over the last two decades.

Considering its impact on the biotechnology industry (my field), technology transfer represented an opportunity to implement science policy on the practical level I was searching for. Finally, I had identified a viable career path for

Mahoney

Nicole Mahoney joined the Office of Technology Development at the National Institute for Allergy and Infectious Diseases, NIH, in October 2006. Prior to this, she spent 2 years as an American Association for the Advancement of Science (AAAS) Policy Fellow working in the National Heart, Lung, and Blood Institute's Office of Science and Technology (2005-2006) and the Office of Legislative and Public Affairs at the National Science Foundation (2004-2006). Nicole was a Damon Runyon Cancer Research Fellow at the University of California at San Francisco (UCSF), where she studied microtubule motor proteins, centrosomes, and mitosis. She graduated from the Albert Einstein College of Medicine with a Ph.D. in Biochemistry.

myself and commenced the job hunt! I quickly learned everything I could about technology transfer opportunities through my fellowship network (do not underestimate the value of your professional contacts). I was informed that tech transfer is really an apprenticeship, and you best learn the skills you need through experience. I also learned that federal labs, like universities, are subject to the Bayh-Dole Act and employ a substantial number of technology transfer professionals. I applied for several positions at NIH, and landed a job in the Office of Technology Development at the National Institute of Allergy and Infectious Diseases (NIAID).

What I Do

So what do I do as a technology development associate at NIAID? My colleagues and I work directly with NIAID labs to determine whether or not their discoveries have commercial value—this part of the job is a team effort. NIAID often seeks patent protection for commercially relevant technologies. The reason behind this is that drug discovery is extremely expensive, and no matter how great a scientific discovery is, companies have little incentive to develop it further without intellectual property protection that provides market exclusivity or competitive advantage. As part of the decision whether or not to patent a new discovery, we help define a market and advertise it—through publications, poster presentations, and talks—to attract potential licensees. If the technology is not developed enough to draw investment, we help our investigators define a research path that could help make it more marketable.

Of course, most research is never directly commercialized and is instead transferred through publications and collaborations. Not surprisingly, I spend the majority of my time working one-on-one with investigators to secure the resources—equipment, plasmids, proteins, cells, you name it—they need to conduct experiments and move their research forward. On the flip side, I also help them disseminate the research tools developed at NIAID, and this is in fact a large part of the institute's mission. I also spend a considerable amount of time establishing research collaborations between NIAID investigators and outside scientists from academic, non-profit, government, and industry labs. All of these activities are guided by written agreements that I draft and negotiate with my counterparts on the other side. One of my main objectives is to make sure that such agreements are clearly written and conform to legal and policy requirements of NIAID. Although many scientists think collaboration and material transfer agreements are unnecessary (or even unseemly!), I've found that by clarifying ownership of materials, addressing data sharing and publishing issues, and spelling out the expectations of both parties, agreements go a long way toward avoiding conflicts—and can actually foster better long-term collaborations.

I truly enjoy many aspects of my job. Every day I work closely with accomplished researchers and get to learn about cutting-edge science far beyond my field of scientific expertise. Keeping up with the science is challenging, so I read the literature and attend seminars regularly. I even give seminars, except now the topics I cover relate to technology transfer and the business of science instead of primary research. In addition to law, I have developed business acumen too. Through my interactions with companies, I now have a much better understanding of what makes a scientific discovery marketable and the enormous amount of effort (and money!) it takes to bring a drug or medical device to market. Although technology transfer requires an understanding of very different disciplines—science, business, and law—I rely heavily on the valuable skills I developed during my tenure as a grad student and postdoc.

For example, I often have to learn and synthesize new information quickly, so being able to research different topics and ask the "right" questions comes in handy! Because my work is driven by what is happening in my investigator's labs, no two days are alike, and I have to juggle projects and prioritize. Basically, the investigators go wherever the research takes them, and I am along for the ride. Along the way I have strengthened skills that are helpful but not always emphasized in the lab setting—communication, negotiation, diplomacy, and tact.

Breaking into the Field

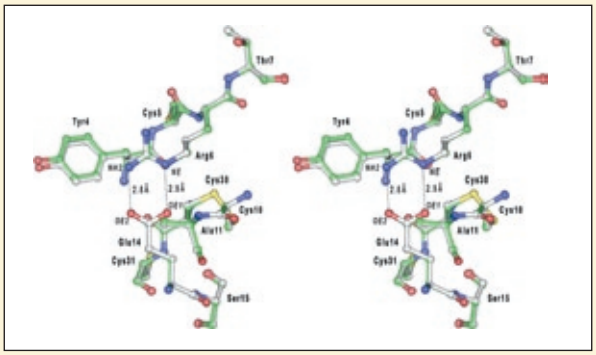
If technology transfer intrigues you, there are many ways to learn to break into the field. My first suggestion is this: pay a visit to your technology transfer office! If you are still in the lab, why not consider the practical applications of your own research and use this as a starting point for a conversation? While you are there, ask about internships and volunteer opportunities. Many universities and professional organizations offer classes in technology transfer, business development, and intellectual property. This is a great way to explore the field and meet potential colleagues or even your future boss.

Technology transfer gives me an opportunity to help develop great ideas into something tangible that could benefit people. To me, this is very rewarding. If you are a practical-minded scientist and find yourself looking for the direct links between science and society, you may find it rewarding too.

*NICOLE CONTRIBUTED TO THIS ARTICLE IN A PERSONAL CAPACITY. HER VIEWS DO NOT NECESSARILY REPRESENT THOSE OF THE NATIONAL INSTITUTES OF HEALTH OR THE UNITED STATES GOVERNMENT.

A Bridge Not Too Far

α- and β-defensins are antimicrobial peptides that play important roles in immunity. Although generally diverse overall, α-defensins do contain a few highly conserved elements, such as six invariant cysteine residues that form disulfide bonds and an arginine-glutamate pair that forms a salt bridge across a protruding loop. In this article, the authors investigated the structural and functional roles of this conserved



A region of HD5 highlighting the Arg[6]–Glu[14] salt bridge (image shown as two structures superimposed).

salt bridge in human α-defensin 5 (HD5). They synthesized normal HD5 and its precursor proHD5 as well as analog peptides (E14Q-HD5 and E57Q-proHD5) that could not stabilize the salt bridge. They discovered that although trypsin correctly processed proHD5, it spontaneously degraded E57Q-proHD5; in addition, E14Q-HD5 was susceptible to trypsin, whereas HD5 was resistant. Although the change did not affect the folding or activity of the proproteins, it did greatly reduce the folding efficiency of mature HD5, as well as enhance the killing of *Escherichia coli*. These findings confirm that the HD5 salt bridge ensures the correct processing of the prodomain and subsequent stability of the mature protein.

The Conserved Salt Bridge in Human α-Defensin 5 Is Required for Its Precursor Processing and Proteolytic Stability

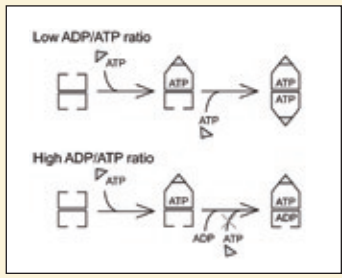
Mohsen Rajabi, Erik de Leeuw, Marzena Pazgier, Jing Li, Jacek Lubkowski, and Wuyuan Lu

J. Biol. Chem. 2008 **283**, 21509-21518

jbc

Good News for Football Fans

The *Escherichia coli* chaperonin proteins GroEL and GroES have been extensively characterized to understand how they facilitate protein folding. The current model suggests that the cylindrical GroEL protein binds a substrate in one of its two cavities and is then capped by GroES; upon ATP hydrolysis, the first substrate is released while a second becomes capped in the opposite cavity. Thus, GroEL-GroES continually form an asymmetric and alternating "bullet-shaped" complex. Some electron microscope and cross-linking studies have detailed double-capped "football-shaped" complexes, but these might just be artifacts. In a pair of closely related studies, researchers have found evidence that the football-shaped complex may be genuine. First, fluorescence resonance energy transfer was used to monitor GroEL-GroES interactions, revealing that the complex exists as bullet and football forms in roughly equal amounts. The authors of the second study further confirmed the symmetrical football complex through a series of enzyme turnover experiments with both wild-type and ATPase-deficient (D398A) GroEL.



Schematic model for the reaction mechanism of GroEL and GroES in the presence of low or high ADP.

Revisiting the GroEL-GroES Reaction Cycle via the Symmetrical Intermediate Implied by Novel Aspects of the GroEL (D398A) Mutant

Ayumi Koike-Takeshita, Masasuke Yoshida, and Hideki Taguchi

J. Biol. Chem. 2008 **283**, 23765–23773

Football- and Bullet-shaped GroEL-GroES Complexes Coexist during the Reaction Cycle

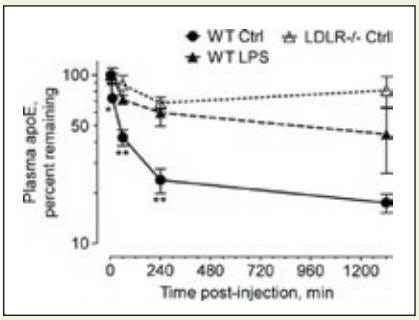
Tomoya Sameshima, Taro Ueno, Ryo Iizuka, Noriyuki Ishii, Naofumi Terada, Kohki Okabe, and Takashi Funatsu

J. Biol. Chem. 2008 **283**, 23774–23781

jbc

The ApoE Inflammation Paradox

Apolipoprotein E (apoE) plays important roles in lipid balance, anti-inflammation, and host defense. Surprisingly, although tissue mRNA levels of apoE have been reported to decrease during inflammatory responses, other studies have found that plasma apoE levels are elevated during septic infections in both humans and mice. This study aims to solve this apparent paradox. The researchers found that in mice apoE associated principally with high density lipoprotein and that apoE was cleared from plasma circulation principally via low density lipoprotein (LDL) receptors. An acute inflammatory response decreased LDL receptor expression in the liver and therefore significantly reduced the rate of apoE clearance. At the same time, inflammation increased LDL receptor expression in macrophages. These findings suggest a mechanism whereby diminished hepatic LDL receptor expression and elevated macrophage LDL receptor expression cooperate to facilitate the forward transport of apoE to these key defense cells during inflammation, maintaining high circulating levels despite a decrease in production.



The addition of inflammatory stimulant LPS decreases plasma clearance of apoE by the LDL receptor.

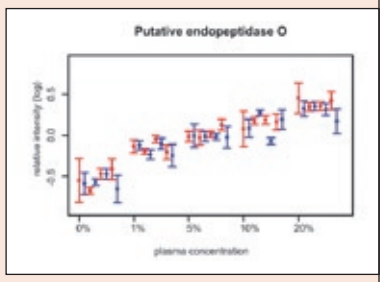
Infection Induces a Positive Acute Phase Apolipoprotein E Response from a Negative Acute Phase Gene: Role of Hepatic LDL Receptors

Li Li, Patricia A. Thompson, and Richard L. Kitchens

J. Lipid Res. 2008 **49**, 1782-1793

Achieving Proteomic Reproducibility

In systems biology, it is essential that identical protein sets are precisely quantified when comparing related samples such as a group of differentially perturbed cell states. Such a high degree of experimental reproducibility has not been achieved by classical mass spectrometry-based proteomics, but in this study the authors present a promising approach. Their method consists of three steps. First, the proteome is extensively mapped out by multidimensional fractionation and tandem mass spectrometry, and the results are assembled in a data base. Second, peptides uniquely identifying the proteins of interest are selected and undergo a process of transition selection and validation with the aid of a suite of software tools known as TIQAM. Third, the selected target protein set is quantified in multiple samples by multiple reaction monitoring. The authors successfully applied this approach to quantify low abundance virulence factors from the human pathogen *Streptococcus pyogenes* exposed to increasing amounts of plasma; the resulting protein patterns enabled them to clearly define which virulence proteins are regulated upon plasma exposure.



Changes in the expression of one *S. pyogenes* virulence factor when exposed to increased plasma amounts.

Targeted Quantitative Analysis of Streptococcus pyogenes Virulence Factors by Multiple Reaction Monitoring

Vinzenz Lange, Johan A. Malmström, John Didion, Nichole L. King, Björn P. Johansson, Juliane Schäfer, Jonathan Rameseder, Chee-Hong Wong, Eric W. Deutsch, Mi-Youn Brusniak, Peter Bühlmann, Lars Björck, Bruno Domon, and Ruedi Aebersold

Mol. Cell. Proteomics 2008 **7**, 1489-1500

Cornell's Weill Institute for Cell and Molecular Biology

BY NICK ZAGORSKI

The Cornell University campus in upstate New York offers some remarkable scenery such as towering gorges and cascading waterfalls.

Today, on a former soccer field on central campus stands an equally beautiful new building—Weill Hall, a cutting-edge research facility that will house, among other departments, Cornell's newly created Joan and Sanford I. Weill Institute for Cell and Molecular Biology (Weill Institute). Inside the modern and spacious facility, researchers will combine disciplines from biology, chemistry, biophysics, engineering, and computer science in a concerted effort to probe the fundamental processes underlying cell behavior.

With the formation of this building and institute, Cornell hopes that the basic biology research at the university will experience its own transformation and reach new heights of recognition and renown. And if the work done over the past year to prepare Weill Hall for its grand opening is any indication, the sky may be the limit.

The Insider

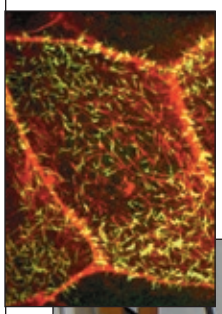
Anthony Bretscher has been a professor in Cornell's Department of Molecular Biology and Genetics since 1981, and he knows firsthand the University's long tradition of quality research in the biological sciences. Some of that quality can be evidenced in Bretscher's own outstanding studies into the role of the cytoskeleton in shaping the cell, including his discoveries of the actin-binding proteins villin and ezrin (the latter named after Ezra Cornell).

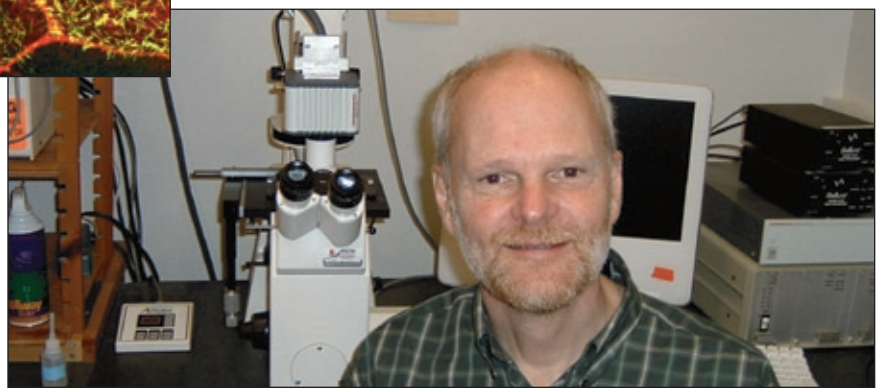
Yet for much of Cornell's recent history, Bretscher notes that the biological science programs in the University have been somewhat overshadowed by Cornell's widely recognized strengths in physics, chemistry, and engineering (having several Nobel winners among the faculty in these fields as well as luminaries like Carl Sagan can do that). So, in 2002, the University's life sciences advisory committee, a distinguished–and completely extramural–panel chaired by Nobel laureate and former NIH director Harold Varmus recommended that the life sciences needed to be significantly enhanced.

That decision led to the $750 million New Life Sciences Initiative (NLSI), an ambitious, campus-wide project that all told will result in the construction of three new buildings (including Weill Hall), the formation of several new departments, and the hiring of over 100 new faculty members. The objective of the NLSI is to both expand the life science curriculum at Cornell and raise its national profile, through efforts such as integrating biological science programs with Cornell's strong physical science presence (*e.g.* establishing departments like Biological Statistics) and creating new multidisciplinary research centers like the Weill Institute.

"For Cornell, this was a completely radical venture, creating an institute that didn't belong to any single college," Bretscher says, "but with the changing face of science, it needed to be done."

The Weill Institute hopes to be one of the premier examples of this changing face of research. The institute will employ a host of model organisms





Weill Associate Director Anthony Bretscher will bring his longstanding work on the cytoskeleton to the new Institute (inset: localization of ezrin (green) and actin (red) in the microvilli of polarized epithelial cells).

and variety of techniques, ranging from classic biochemistry, structural biology, and yeast genetics to cutting-edge, high-throughput technology–"proteomics and live cell imaging are two areas of particular interest," Bretscher says–to better understand the molecular dynamics of cells. Much like taking apart a car or a computer and studying its component parts to uncover their functions, the Weill Institute will explore subcellular topics like receptor signaling pathways, vesicle trafficking, cytoskeletal dynamics, and cell cycle regulation to piece together how a cell works.

The vision is grand, but for the Weill Institute to be a success, it needed a visionary leader. Considering the project had to be done essentially from the ground up, Cornell needed to find a director with the prominence, dedication, and energy to guide the Weill Institute in its first critical steps. "And in that regard," notes Bretscher, "I think we nailed it. We found an absolutely spectacular director."

The Director

A couple of years back, after 14 years at UCSD, Scott Emr was experiencing a desire for change. The professor of cellular and molecular medicine at the University of California, San Diego, and Howard Hughes Medical Investigator had built up an accomplished body of work into membrane trafficking and secretion–the process of how proteins move into, out of, and around cells (see sidebar)–and wanted something a little different. "After 25 years of running a lab, I was ready to go beyond supervising just my own research group and find some area where I could make a greater impact."

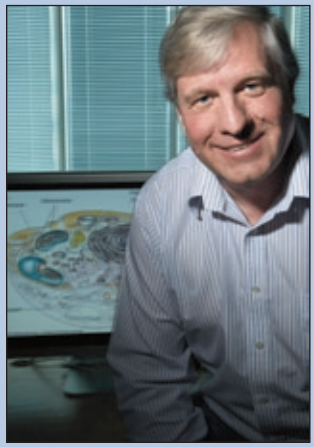
As it happened, he traveled to Ithaca to give an invited seminar at Cornell, and in talking with some of the faculty he found out about the Cornell Life Sciences Initiative and the proposed institute. "And I remember telling them how intriguing this new center sounded and how it would be

Meet Scott Emr: Frank H.T. Rhodes Class of '56 Director of the Weill Institute

Scott Emr's foray into biological research began at home, where he raised and bred fish during his youth (he even conducted a high school science project where he examined the mutagenic effects of alpha and beta emitters on fish egg development). Later, while an undergraduate at the University of Rhode Island, Emr became captivated with genetics of a different sort, when a particularly engrossing course on bacterial genetics set him on the path that he follows to this day.

He went on to graduate school at Harvard University and began studying protein secretion in bacteria with Tom Silhavy and Jon Beckwith, characterizing the first signal sequence mutants; he switched to the simple eukaryote yeast for his postdoc with Randy Schekman at UC Berkeley, but still used a genetic approach to study vesicle-mediated protein sorting and secretion.

It's a theme he has kept with him in his own laboratories—first at California Institute of Technology then UC San Diego—where his major focus has been examining the role for phosphoinositide lipids in the regulation of protein sorting in both the secretory and the endocytic pathways. His approach of using simple model systems to ask fundamental questions in cell biology has resulted in discoveries that have impacted our understanding of several human diseases.



One excellent example would be his identification of the ESCRT (endosomal sorting complex required for transport) protein machinery. This set of protein complexes is critical for down-regulating activated cell surface receptors, but also has been demonstrated to be essential for cell division and the budding of HIV. His 'basic' discoveries with ESCRTs have aided other researchers in diverse fields such as virology, neurobiology, and cancer biology. These contributions have led to his election into both the American Academy of Arts and Sciences (2004) and the National Academy of Sciences (2007).

fun, personally, to train new faculty and not just graduate students and postdocs," he says. So naturally, when he received a phone call from Cornell a few months later informing him that the faculty search committee had nominated him as institute director, Emr replied, "No."

Now, it wasn't an outright refusal. "I was interested," Emr says, "but at that time the proposal was still in its infancy, and it didn't seem tangible enough for me. So I told them, "When you break ground on a building, call me again. And, fortunately, they did."

Before arriving at Cornell in April 2007, Emr's first order of business was appointing Bretscher as his associate director; Bretscher was chosen both for his expertise in cell structure and organization–a major cog of the Weill Institute mission—and his longstanding tenure that would give Emr valuable insight into the inner workings of Cornell culture.

Then, much like the building being constructed nearby, the pair began the task of shaping the still somewhat amorphous Weill Institute into a more concrete presence, working on everything from laboratory layout to budget appropriations. "The way we approached it," notes Bretscher, "was to ask: looking into the future, what do we want to see around us? And our answer was an institute where everyone can freely talk to each other and know what everyone else was doing."

That meant designing a center that offered an "open" lab environment as well as plenty of formal (conference rooms) and informal (lounge areas) meeting spaces to encourage interaction. More importantly, it meant finding faculty that was eager to collaborate and try new avenues of research. Emr's goal was to hire 10 new faculty members over a five-year period, and he steadied himself for one of the most arduous tasks as director: recruitment.

The Recruits

When Chris Fromme was an undergraduate at Cornell University back in the 1990s, he quite literally got his eyes turned on to the wonders of structural biology while taking a course taught by crystallographer Steve Ealick. "We got to put on these special glasses and see protein structures in 3-D, which was really amazing," he says. After that course, he continued learning more about crystallography by doing some undergraduate research with Ealick, where he notes, "I was probably a drain on resources more than anything else, but I certainly had a lot of fun."

Still, after receiving his bachelor's degree in 1999, Fromme never envisioned that he would be returning to the Cornell campus. But around a year ago Fromme, then a post-doc with Randy Schekman at UC Berkeley, happened to catch a conference lecture by another Schekman protégé, Scott Emr. "And during his talk, I remember he began advertising this new institute that Cornell was putting together to study molecular and cell biology and that they were looking for faculty."

The multidisciplinary nature of the Weill Institute suited Fromme well. He initially went to graduate school at Harvard to continue studying structural biology and joined the lab of chemical biologist Greg Verdine, studying the role of DNA glycosylases in DNA repair. However, the structures he solved did not quite answer all of his biological questions. "That was my first clue that you need more than just a physical structure to really understand what's going on with a protein." Fromme therefore wanted to learn more traditional biochemical and cell biology techniques, as well as try out a new research area, and that led him to Schekman's lab at Berkeley to study vesicle budding.

"I think I have too short of an attention span to thrive in any one field," Fromme says. "I like to think that everything is possible, and the Weill Institute seemed like a place that would welcome that mentality." So when he returned to Berkeley he decided to throw his hat in the ring.

Fromme wasn't alone, though. Besides Emr's own tireless promotion efforts, the University spent a lot of resources advertising the new institute, and the campaign worked. Nearly 500 applications filtered in, more than twice the anticipated amount. About a dozen of the applicants were invited to interview in person, and five were ultimately chosen, four of whom accepted. In addition to Fromme, the Weill Institute is now home to proteomics researcher Marcus Smolka from UCSD, and from Yale University both Yuxin Mao, a structural biologist with expertise in both x-ray crystallography and NMR, and and Fenghua Hu, a neurobiologist who studies factors that regulate neuron growth (see sidebar).

Weill Hall's sterling new lab space is ready for some research.

The Future

"It's been a pretty exciting first year," says Emr, as he sits in his spacious office on the top floor of Weill Hall, which–after some delays and last-minute adjustments–is ready to begin its scientific mission (the official opening ceremony won't be until October 16th, but most of the staff and equipment has already moved in).

He and Bretscher have no time to rest on their laurels, however. Besides getting their own new labs up and running, they have to start preparing for the next cycle of faculty hiring that will aim to bring in three to four more top-level researchers into the fold. And while the first round primarily concentrated on bringing in the best and brightest scientists, regardless of area of study, Emr says that they will now start looking more closely at appointing researchers that will bring more diversity and balance to the Weill Institute family. Emr is also preparing for the Institute's first symposium, an annual event that will further showcase the outstanding work being done in this facility.

Fromme and the other new faculty won't find much time to relax and enjoy the wonderful Ithaca summer either. "I ordered all my supplies in advance, so I arrived to the sight of boxes from floor to ceiling," says Fromme, who is busying himself with unpacking and planning out his research agenda as the new semester is set to begin.

So, there is still plenty of work to be done, and more hectic times are sure to come, but the participants of Cornell's newest enterprise wouldn't want it any other way.

Nick Zagorski is a science writer for ASBMB. He can be reached at nzagorski@asbmb.org.

Meet the New Weill Institute Faculty:

Yuxin Mao *(Assistant Professor)*

Ph.D.—Baylor College of Medicine, 2001
(Advisor: Florante Quiocho)

Postdoctoral—Yale University, 2002-2008
(Advisor: Pietro de Camilli)

Yuxin uses structural biology to study phosphoinositide lipid signaling and ubiquitin-mediated endocytic membrane trafficking pathways. Structural biology is one of the key areas that the Weill Institute has targeted for development at Cornell. Yuxin is a rare breed of structural biologist, as he is accomplished in both X-ray crystallography and nuclear magnetic resonance (NMR); at Weill he will pursue exciting projects that relate to the molecular mechanisms for the inactivation of phosphoinositide signaling events within neuronal synapses.

Marcus Smolka *(Assistant Professor)*

Ph.D.—State University of Campinas, Brazil, 2002
(Advisor: José Camilo Novello)

Postdoctoral—UCSD, 2003-2008.
(Advisor: Huilin Zhou)

Marcus is an expert in proteomics, another key area targeted by Weill Institute that will impact many departments at Cornell (including Weill Medical College in New York City). A leading authority in the mass spectrometry of phospho-peptides, Marcus is working on a functional analysis of protein kinases that are key regulators of DNA damage response. He developed novel approaches for proteome-wide analysis of these key phospho-modifications that occur during the activation of DNA repair systems essential for maintaining genome stability.

Chris Fromme *(Assistant Professor)*

Ph.D.—Harvard University, 2004
(Advisor: Greg Verdine)

Postdoctoral—Miller Fellow, UC Berkeley, 2004-2008
(Advisor: Randy Schekman)

Chris is a talented biochemist and structural biologist. He has combined these skills to successfully reconstitute and characterize a key vesicle-mediated membrane transport reaction using membrane and cytoplasmic extracts from mammalian cells. In addition, he has biochemically purified essential components of these membrane transport reactions and made crystals of these components for structural studies. His future plans include an interdisciplinary approach using chemistry and biology to dissect the mechanism for mammalian protein secretion.

Fenghua Hu *(Research Scientist)*

Ph.D.—Baylor College of Medicine, 2002
(Advisor: Steve Elledge)

Postdoctoral—Yale University, 2002-2008
(Advisor: Stephen Strittmatter)

During her Ph.D., Fenghua made important contributions to the study of cell cycle checkpoints. She then switched to neurobiology for her postdoctoral studies where she has undertaken a molecular analysis of the neuronal protein Nogo, a factor that inhibits axonal growth and regeneration after central nervous system injury. She plans to expand these studies to include a systematic search for additional factors that regulate axon outgrowth.

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Min. Quals.: PhD. degree with preference given to applicants with postdoctoral experience and a good publication record. A strong background in the following areas is required: molecular biology, tissue culture, protein expression and purification. Experience in protein crystallography and biophysical instrumentation is desirable. Competency in written and spoken English is mandatory.

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University of Pennsylvania School of Medicine

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Please contact: Dr. Linda E. Greenbaum, Dept. of Medicine, greenbal@mail.med.upenn.edu; or Dr. Klaus H. Kaestner, Dept. of Genetics, Kaestner@mail.med.upenn.edu at the University of Pennsylvania School of Medicine Philadelphia, PA 19104.

ASSISTANT/ASSOCIATE PROFESSOR

Department of Molecular Medicine
College of Medicine
University of South Florida, Tampa, Florida.

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The Molecular Medicine Department is comprised of a diverse faculty of Biochemists, Molecular Biologists, Microbiologists, and Immunologists with expertise in genetic mechanisms of disease, structure-function relationships, microbial genetics and pathogenesis, and cellular and molecular immunology. The Department has active teaching programs for MSc, PhD, and MD students. The Department is housed in the expanding USF Health Complex on the main campus of the University of South Florida with the core colleges of Medicine (including the schools of Physical Therapy and Biomedical Sciences), Nursing, and Public Health. Currently, the College of Medicine has over 540 full time core faculty members, over 450 medical students, and over 300 students in the biomedical graduate program.

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Successful candidates are expected to have a commitment to actively participate in medical and graduate education and to develop and maintain a competitively funded research program. Examples of suitable applicants would include those with an academic background in molecular/cell biology, metabolism, enzyme mechanisms, protein crystallography, microbiology or immunology, and a successful research record in structural biology, signal transduction, gene expression, functional genomics/proteomics or bacterial pathogenesis.

Applicants must submit a letter summarizing their qualifications, interests, and future research plans, an updated curriculum vita and the names and contact information of five professional references, all by e-mail, to **Ms. Rochelle Morris (rmorris@health.usf.edu)** by November 1, 2008 to be considered for a position. The review of materials will begin immediately and will continue until the positions are filled. Competitive start-up packages and salaries will be provided commensurate with experience.

USF Health is committed to increasing its diversity and will give individual consideration to qualified applicants for this position with experience in ethnically diverse settings, who possess varied language skills, or who have a record of research issues that support/benefit diverse communities or teaching a diverse student population. For disability accommodations, contact Rochelle Morris 813-974-8349 within 5 days of an event.

According to Florida law, search records, including applications and search committee meetings, are open to the public.

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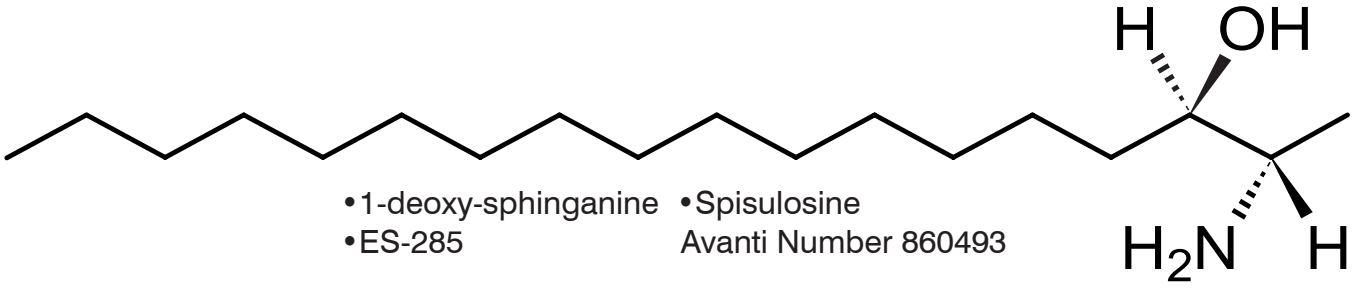

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Reference: Pruett, S.T., A. Bushnev, K. Hagedorn, M. Adiga, C.A. Haynes, M.C. Sullards, D.C. Liotta, and A.H. Merrill Jr. (2008). Thematic Review Series: Sphingolipids. Biodiversity of sphingoid bases ("sphingosines") and related amino alcohols.
J Lipid Res 49:1621-39.

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scientific meeting calendar

SEPTEMBER 2008

14th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology
SEPTEMBER 1–5, 2008
CAPE TOWN, SOUTH AFRICA
www.kuleuven.ac.be/aidslab/veme.htm

Lupus Autoimmunity: Mechanisms and Immune Regulation
SEPTEMBER 8–9, 2008
LA JOLLA, CALIFORNIA
www.biosymposia.org/content26853.html

Workshop: Biology of Signåaling in the Cardiovascular System
SEPTEMBER 11–14, 2008
HYANNIS, MA
www.navbo.org/BSCS08Workshop.html

Symposium on Extracellular and Membrane Proteases in Cell Signaling
SEPTEMBER 18–21, 2008
AMES, IA
www.bb.iastate.edu/~gfst/homepg.html

International Conference on Structural Genomics
SEPTEMBER 20–24, 2008
OXFORD, UK
www.spine2.eu/ISGO

Keystone Symposium—Metabolism and Cardiovascular Risk
SEPTEMBER 23–28, 2008
BRECKENRIDGE, CO
www.keystonesymposia.org/Meetings/ViewMeetings.cfm?MeetingID=999

World Congress on the Insulin Resistance Syndrome
SEPTEMBER 25–27, 2008
LOS ANGELES, CA
www.insulinresistance.us

13th International Congress on Hormonal Steroids and Hormones & Cancer
SEPTEMBER 27–30, 2008
QUEBEC CITY, QUEBEC
www.ichshc2008.com/

OCTOBER 2008

17th South East Lipid Research Conference
OCTOBER 3–5, 2008
PINE MOUNTAIN, GA
www.selrc.org

Mitochondrial Biology in Cardiovascular Health and Diseases
OCTOBER 6–7, 2008
BETHESDA, MD
www.mitochondrial2008.com
E-mail: jennifer@strategicresults.com
Tel.: 443-451-7254

2nd Congress of the International Society of Nutrigenetics and Nutrigenomics
OCTOBER 6–8, 2008
GENEVA, SWITZERLAND
www.symporg.com/conferences/2008/ISNN/index.html

9th International Congress on Cell Biology, ICCB 2008
OCTOBER 7–10, 2008
SEOUL, KOREA
www.iccb2008.org/

Glycobiology of Human Disorders
OCTOBER 9-13, 2008
ATLANTA, GA
Organizer: Richard D. Cummings, Emory University
www.asbmb.org/meetings.aspx

Translating Science into Health: Cytokines in Cancer and Infectious Diseases
OCTOBER 12–16, 2008
MONTREAL, QUEBEC
www.cytokines2008.org

Proteomics Europe
OCTOBER 16–17, 2008
LISBON, PORTUGAL
www.selectbiosciences.com/conferences/pe2008/index.aspx

Transcriptional Regulation by Chromatin and RNA Polymerase II
OCTOBER 16–20, 2008
GRANLIBAKKEN, LAKE TAHOE
Organizer: Ali Shilatifard, Stowers Institute for Medical Research
Plenary Lecturer: Robert G. Roeder, The Rockefeller University
www.asbmb.org/meetings.aspx

Cellular Lipid Transport-Connecting Fundamental Membrane Assembly Processes to Human Disease
OCTOBER 22–26, 2008
CANMORE, ALBERTA, CANADA
Organizers: Dennis R. Voelker, National Jewish Medical Research Center; Jean Vance, University of Alberta, Edmonton; and Todd Graham, Vanderbilt University
www.asbmb.org/meetings.aspx

Post Translational Modifications: *Detection & Physiological Evaluation*
OCTOBER 23–26, 2008
GRANLIBAKKEN, LAKE TAHOE
Organizers: Katalin F. Medzihradszky and Ralph A. Bradshaw, UCSF
www.asbmb.org/meetings.aspx

48th ICAA/IDSA 46th Annual Meeting
OCTOBER 25–28
WASHINGTON, DC
www.icaacidsa2008.org

Protein Design and Evolution for Biocatalysis
OCTOBER 25–30, 2008
SANT FELIU DE GUIXOLS, SPAIN
www.esf.org/index.php?id=4569

2008 Biophysical Society Discussions Meeting Program: Calmodulin Modulation of Ion Channels
OCTOBER 30–NOVEMBER 2, 2008
ASILOMAR, CA
www.biophysics.org/discussions/2008%20Meeting%20Program.htm

NOVEMBER 2008

2nd Latin American Protein Society Meeting
NOVEMBER 4–8, 2008
ACAPULCO, GRO. MEXICO
www.laproteinsociety.org

2008 Annual Meeting of the Society for Glycobiology
NOVEMBER 12–15, 2008
FORT WORTH, TX
www.glycobiology.org

Oils + Fats 2008
NOVEMBER 18–20, 2008
MUNICH, GERMANY
www.oils-and-fats.com
E-mail: info@oils-and-fats.com

DECEMBER 2008

The Annual Meeting of the American Society for Matrix Biology (ASMB)
DECEMBER 7–11, 2008
SAN DIEGO, CA
www.asmb.net/

The 48th American Society for Cell Biology Annual Meeting
DECEMBER 13–17, 2008
SAN FRANCISCO, CA
www.ascb.org/meetings/

The Science of Eliminating Health Disparities
DECEMBER 16–18, 2008
NATIONAL HARBOR, MD
www.blsmeetings.net/2008healthdisparitiessummit/

JANUARY 2009

2009 Glycobiology Gordon Research Conference
JANUARY 18–23, 2009
VENTURA, CA
www.grc.org/programs.aspx?year=2009&program=glycobio

Keystone Symposium–Obesity: Novel Aspects of the Regulation of Body Weight
JANUARY 20–25, 2009
BANFF, ALBERTA, CANADA
www.keystonesymposia.org/Meetings/ViewMeetings.cfm?MeetingID=997

FEBRUARY 2009

Gordon Research Conference—Plant Lipids: Structure, Metabolism, & Function
FEBRUARY 1–6, 2009
GALVESTON, TX
www.grc.org/programs.aspx?year=2009&program=plantlipid

The 14th Annual Proteomics Symposium
FEBRUARY 6–8, 2009
LORNE, AUSTRALIA
www.australasianproteomics.org

PLA 3rd Annual Scientific Forum
FEBRUARY 20–22, 2009
SALT LAKE CITY, UT
www.lipid.org

US HUPO 5th Annual Conference
FEBRUARY 22–25, 2009
SAN DIEGO, CA
www.ushupo.org
E-mail: ushupo@ushupo.org
Tel.: 505-989-4876

Keystone Symposium–Complications of Diabetes and Obesity
FEBRUARY 24–MARCH 1, 2009
VANCOUVER, BRITISH COLUMBIA
www.keystonesymposia.org/Meetings/ViewMeetings.cfm?MeetingID=998

2nd International Conference on Advanced Technologies and Treatments for Diabetes (ATTD)
FEBRUARY 25–28, 2009
ATHENS, GREECE
www.2.kenes.com/attd/Pages/home.aspx

APRIL 2009

3rd International Congress on Prediabetes and the Metabolic Syndrome—Epidemiology, Management, and Prevention of Diabetes and Cardiovascular Disease
APRIL 1–4, 2009
NICE, FRANCE
www.kenes.com/prediabetes

ASBMB Annual Meeting
APRIL 18–22, 2009
NEW ORLEANS, LA
www.asbmb.org/meetings

Keystone Symposium—Complex Lipids in Biology: Signaling, Compartmentalization, and Disease
APRIL 22–27, 2009
OLYMPIC VALLEY, CA
www.keystonesymposia.org/Meetings/ViewMeetings.cfm?MeetingID=961

2009 NLA Scientific Sessions
APRIL 30–MAY 3, 2009
MIAMI, FL
www.lipid.org

MAY 2009

57th ASMS Conference on Mass Spectrometry
MAY 31–JUNE 4, 2009
PHILADELPHIA, PA
www.asms.org
E-mail: office@asms.org
Tel.: 505-989-4517

JUNE 2009

VIII European Symposium of the Protein Society
JUNE 7–11, 2009
ZURICH, SWITZERLAND
Organizer: Andreas Plückthun (University of Zurich)
www.proteinsociety.org

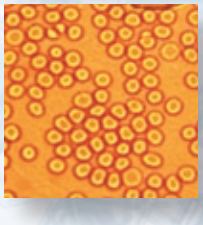
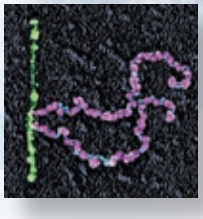
3rd EuPA Meeting—Clinical Proteomics
JUNE 14–17, 2009
STOCKHOLM SWEDEN
www.lakemedelsakademin.se/templates/LMAstandard.aspx?id=2529

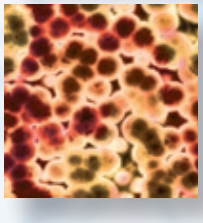
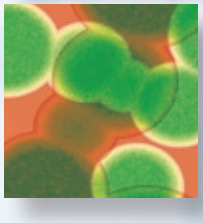
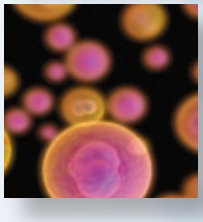
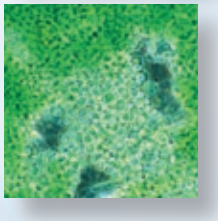
APRIL 2010

ASBMB Annual Meeting
APRIL 24–28, 2010
ANAHEIM, CA
www.asbmb.org/meetings

AUGUST 2010

14th International Congress of Immunology
AUGUST 22–27, 2010
KOBE, JAPAN
www.ici2010.org

2008 ASBMB Special Symposia Series

Glycobiology of Human Disorders

OCTOBER 9-13, 2008
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ORGANIZER: **Richard D. Cummings**, *Emory University*
ABSTRACT SUBMISSION DEADLINE: SEPTEMBER 5, 2008

Transcriptional Regulation by Chromatin and RNA Polymerase II

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Granlibakken, Lake Tahoe
ORGANIZER: **Ali Shilatifard**, *Stowers Institute for Medical Research*
PLENARY LECTURER: **Robert G. Roeder**, *The Rockefeller University*
ABSTRACT SUBMISSION DEADLINE: SEPTEMBER 5, 2008

Cellular Lipid Transport: Connecting Fundamental Membrane Assembly Processes to Human Disease

OCTOBER 22-26, 2008
Radisson Hotel & Conference Center, Canmore, Alberta, Canada
ORGANIZERS: **Dennis R. Voelker**, *National Jewish Medical Research Center,*
Jean Vance, *University of Alberta, Edmonton, and*
Todd Graham, *Vanderbilt University*
PLENARY LECTURER: **Robert Molday**, *University of British Columbia*
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Ralph A. Bradshaw, *UCSF*
PLENARY LECTURER: **M. Mann**, *Max Planck Institute of Biochemistry, Martinsried*
ABSTRACT SUBMISSION DEADLINE: SEPTEMBER 15, 2008

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