

# IGB NEWS

Upcoming Events  
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Happenings at IGB

Image Of The Month

IP @ IGB

Department Announcements

Volume 10 Number 3

## UPCOMING EVENTS

### The World of Genomics At The Field Museum

May 19-20, 2017, 10:00am - 2:00 p.m.

Field Museum

1400 S. Lake Shore Drive

Chicago, IL 60605

Explore The World of Genomics at The Field Museum during a special two-day event presented by IGB in Stanley Field Hall. Special presentations will also be available during Members' Nights on May 18 and May 19.

### IGB Seminar

*Title to be announced*

September 12, 2017, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Katherine Lyon Daniel, PhD

Associate Director for Communication

Centers for Disease Control and Prevention

### Fox Family Innovation and Entrepreneurship Lecture

*Title to be announced*

September 19, 2017, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Lucy Sanders

CEO and Co-Founder

National Center for Women and  
Information Technology

### IGB Seminar

*Title to be announced*

October 10, 2017, 12:00 p.m.

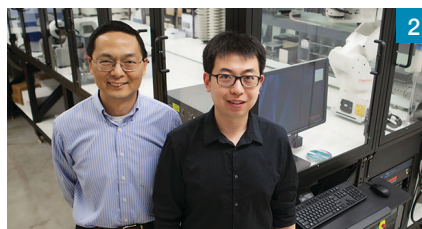
612 Carl R. Woese Institute for Genomic Biology

Gregory J. Riggins, MD, PhD

Johns Hopkins

Department of Neurosurgery

## FEATURED NEWS



New capabilities for genome-  
wide engineering of yeast



Study reveals 10,000 years  
of genetic continuity

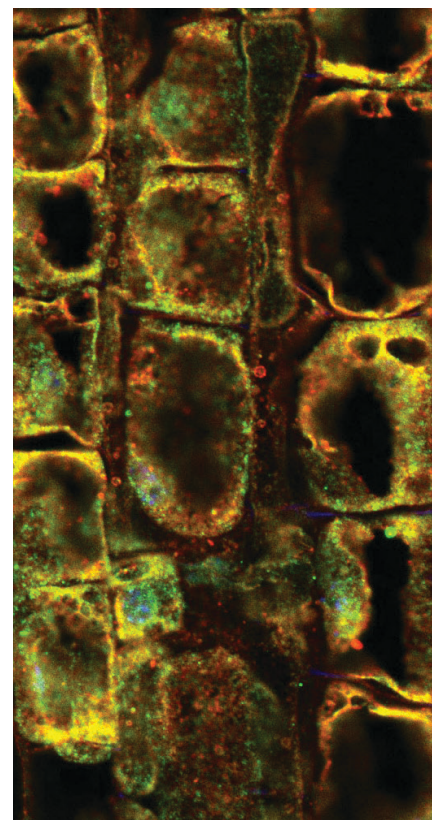


Monthly Profile: Helen Nguyen  
and Joanna Shisler



On the Grid:  
Happenings at IGB

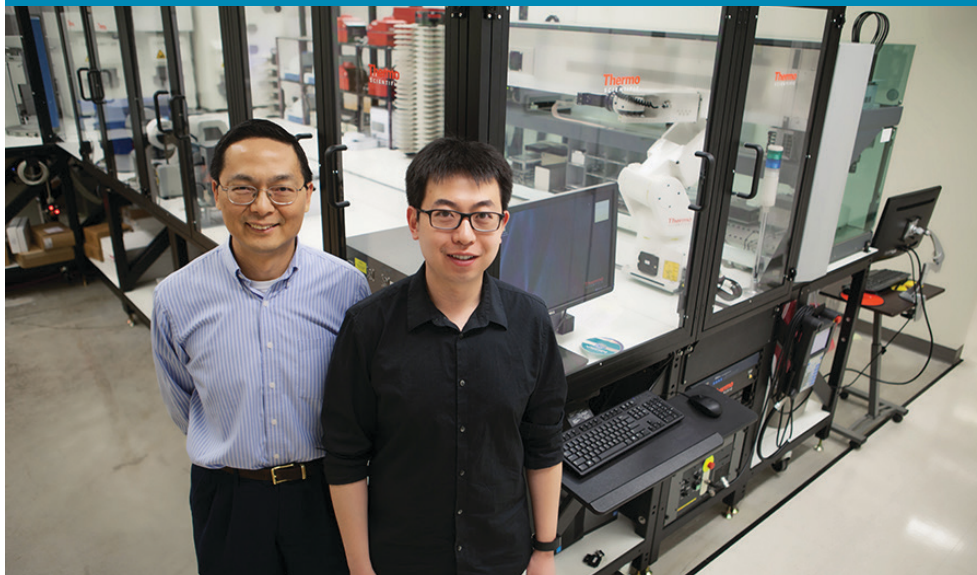
## IMAGE OF THE MONTH



This month's image features the sturdy shapes of the cells of a sorghum plant; these cells form part of the sheath that protects the growing plant shoot. This was imaged using the Zeiss LSM 880 Airyscan, and the image was provided by Dean Riechers, Rong Ma, and Yousoon Baek from the Dean Riechers Lab, and Mayandi Sivaguru, Associate Director of Core Facilities.

### IGB News

Share your news with the IGB. Send ideas on stories, articles, and features to [nvasi@illinois.edu](mailto:nvasi@illinois.edu).



## Researchers develop new capabilities for genome-wide engineering of yeast

One of humankind's oldest industrial partners is yeast, a familiar microbe that enabled early societies to brew beer and leaven bread and empowers modern ones to synthesize biofuels and conduct key biomedical research. Yeast remains a vital biological agent, yet our ability to explore and influence its genomic activity has lagged.

In a new article in *Nature Communications* ([DOI: 10.1038/NCOMMS15187](https://doi.org/10.1038/NCOMMS15187)), University of Illinois researchers describe how their successful integration of several cutting-edge technologies—creation of standardized genetic components, implementation of customizable genome editing tools, and large-scale automation of molecular biology laboratory tasks—will enhance our ability to work with yeast. The results of their new method demonstrate its potential to produce valuable novel strains of yeast for industrial use, as well as to reveal a more sophisticated understanding of the yeast genome.

“The goal of the work was really to develop a genome-scale engineering tool for yeast . . . traditional metabolic engineering focused on just a few genes and the few existing genome-scale engineering tools are only applicable to bacteria, not eukaryotic organisms like yeast,” said Steven L. Miller Chair of Chemical and Biomolecular Engineering Huimin Zhao (above left), who led the study. “A second innovation is the use of synthetic biology concepts, the modularization of the parts, and integration with a robotic system, so we can do it in high-throughput.”

The team focused on yeast in part because of its important modern-day applications; yeasts are used to convert the sugars of biomass feedstocks into biofuels such as ethanol and industrial chemicals such as lactic acid, or to break down organic pollutants. Because yeast and other fungi, like humans, are eukaryotes, organisms with a compartmentalized cellular structure

and complex mechanisms for control of their gene activity, study of yeast genome function is also a key component of biomedical research.

“In basic science, a lot of fundamental eukaryotic biology is studied in yeast,” said Tong Si (above right), a Carl R. Woese Institute for Genomic Biology Research Fellow. “People have a limited understanding of these complicated systems. Although there are approximately 6,000 genes in yeast, people probably know less than 1,000 by their functions; all the others, people do not know.”

The group took the first step toward their goal of a novel engineering strategy for yeast by creating what is known as a cDNA library: a collection of over 90% of the genes from the genome of baker's yeast (*Saccharomyces cerevisiae*), arranged within a custom segment of DNA so that each gene will be, in one version, overactive within a yeast cell, and in a second version, reduced in activity.

Zhao and colleagues examined the ability of the CRISPR-Cas system, a set of molecules borrowed from a form of immune system in bacteria (CRISPR stands for clustered regularly interspaced short palindromic repeats, describing a feature of this system in bacterial genomes). This system allowed Zhao to make precise cuts in the yeast genome, into which the standardized genetic parts from their library could insert themselves.

“The first time we did this, in 2013, there was no CRISPR . . . the best we could get was 1% of the cells modified in one run,” said Si. “We struggled a little on that, and when CRISPR came out, that worked. We got it to 70% [cells modified], so that was very important.”

With gene activity-modulating parts integrating into the genome with such high efficiency, the researchers were able to randomly generate many different strains of yeast, each with its own unique set of modifications. These strains were subjected to artificial selection pro-

cesses to identify those that had desirable traits, such as the ability to survive exposure to reagents used in the biofuel production process.

This selection process was greatly aided by the Illinois Biological Foundry for Advanced Biomanufacturing (iBioFAB), a robotic system that performs most of the laboratory work described above in an automated way, including selection of promising yeast strains. Use of iBioFAB greatly accelerated the work, enabling simultaneous creation and testing of many unique strains. The iBioFAB was conceived and developed by the Biosystems Design research theme at the Carl R. Woese Institute for Genomic Biology (IGB), which is led by Zhao.

With support from the High Performance Biological Computing Group at Illinois, Zhao, Si and their colleagues analyzed the modified genomes of their most promising yeast strains. They identified combinations of genes whose altered activities contributed to desirable traits; the functions of some of these genes were previously unknown, demonstrating the technique's ability to generate new biological knowledge.

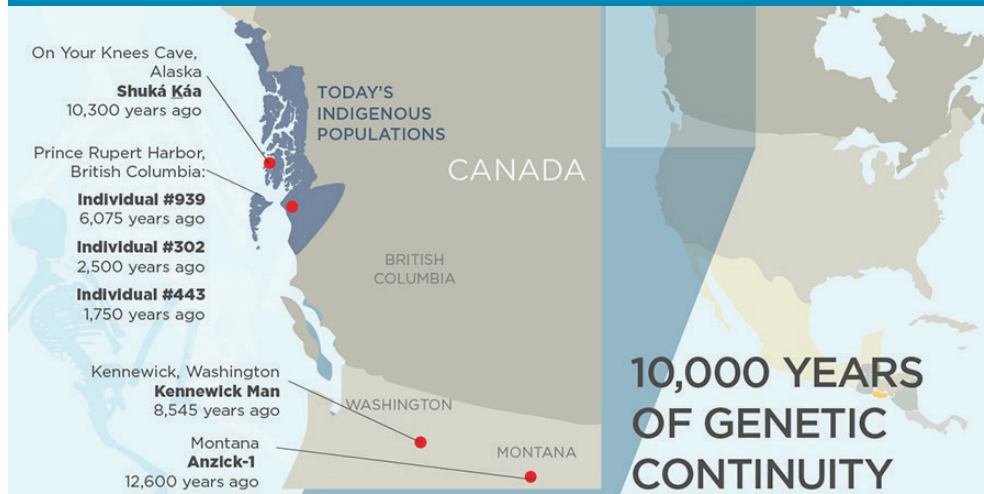
“I think the key difference between this method and the other existing metabolic engineering strategies in yeast is really the scale,” said Zhao. “The current metabolic engineering strategies are all focused on just a few genes, dozens of genes at most . . . it's very intuitive. With this we can explore all the genes, we can identify a lot of targets that cannot be intuited.”

The work, which was funded by the Roy J. Carver Charitable Trust, IGB, Defense Advanced Research Program Agency, and National Academies Keck Futures Initiative on Synthetic Biology, paves the way for similar approaches to broad-scale, automated genome engineering of other eukaryotic species. ■

Written by Claudia Lutz. Photo by Kathryn Faith.



## RESEARCH



# Study reveals 10,000 years of genetic continuity in northwest North America

A study of the DNA in ancient skeletal remains adds to the evidence that indigenous groups living today in southern Alaska and the western coast of British Columbia are descendants of the first humans to make their home in northwest North America more than 10,000 years ago.

“Our analysis suggests that this is the same population living in this part of the world over time, so we have genetic continuity from 10,000 years ago to the present,” said University of Illinois anthropology professor and IGB faculty Ripan Malhi, who led the study with University of Chicago postdoctoral researcher John Lindo; Penn State University biology professor Michael DeGiorgio; Rosita Worl, the director of the Sealaska Heritage Institute in Juneau, Alaska; and University of Oklahoma anthropology professor Brian M. Kemp.

The findings, reported in the Proceedings of the National Academy of Sciences, also suggest that these early American peoples had a complex population history, the researchers report.

The new work comes on the heels of earlier studies of ancient Americans that focused on mitochondrial DNA, which occurs outside the nucleus of cells and is passed only from mothers to their offspring.

“Mitochondrial DNA just traces the maternal line – your mother’s mother’s lineage – so, you’re missing information about all of these other ancestors,” said Lindo, the first author on the paper. “We wanted to analyze the nuclear genome so we could get a better assessment of the population history of this region.”

The team looked at genomic data from Shuká Káa (Tlingit for “Man Before Us”), an ancient individual whose remains – found in a cave in southeastern Alaska – date to about 10,300 years ago. They also analyzed the genomes of three more individuals from the nearby coast of British Columbia whose remains date to between 6,075 and 1,750 years ago.

*Researchers are analyzing DNA from ancient individuals found in southeast Alaska, coastal British Columbia, Washington state and Montana. A new genetic analysis of some of these human remains finds that many of today’s indigenous peoples living in the same regions are descendants of ancient individuals dating to at least 10,300 years ago.*

“Interestingly, the mitochondrial type that Shuká Káa belonged to was also observed from another ancient skeleton dated to about 6,000 years ago,” Kemp said. “It seems to disappear after that. The nuclear DNA suggests that this is probably not about population replacement, but rather chance occurrence through time. If a female has no children or only sons, the mitochondrial DNA is not passed to the next generation. As a male, Shuká Káa could not have passed on his own mitochondrial DNA; he must have had some maternal relatives that did so.”

The researchers turned their attention to nuclear DNA, which offers a more comprehensive record of a person’s ancestry.

“DNA from the mitochondria and Y chromosome provide unique yet sometimes conflicting stories, but the nuclear genome provides a more comprehensive view of past events,” DeGiorgio said.

“The data suggest that there were multiple genetic lineages in the Americas from at least 10,300 years ago,” Malhi said.

The descendants of some of those lineages are still living in the same region today, and a few are co-authors on the new study. Their participation is the result of a long-term collaboration between the scientists and several native groups who are embracing genomic studies as a way to learn from their ancestors, said Worl, who is Tlingit, Ch’áak’ (Eagle) moiety of the Shangukeidí (Thunderbird) Clan from the Kawdliyaayi Hit (House Lowered From the Sun) in Klukwan, Alaska.

“We supported DNA testing of Shuká Káa because we believed science ultimately would agree with what our oral traditions have always said – that we have lived in southeast Alaska since time immemorial. The initial analysis showed the young man was native, and now further studies are showing that our ancestral lineage stems from the first initial peopling of the region,” said Worl, who also is an anthropologist. “Science is corroborating our oral histories.” ■

**Written by Diana Yates. Photo by L. Brian Stauffer. Graphic by Julie McMahon.**



*Anthropology professor Ripan Malhi works with Native Americans and First Nations groups to analyze their DNA and that of their ancestors.*

## MONTHLY PROFILE



### Helen Nguyen and Joanna Shisler

#### Engineering and Microbiology Join Forces Against Waterborne Pathogens

Access to safe and clean drinking water is a gift that is often taken for granted. Many communities in developing nations don't have the technology nor the infrastructure to consistently provide safe water, and as a result many people suffer from illness caused by waterborne bacteria, viruses, and protozoa. In the war against these tiny terrors, University of Illinois researchers Joanna Shisler and Helen Nguyen are on the front line. Nguyen, an environmental engineer, and Shisler, a virologist, work together to better understand how waterborne pathogens operate, how best to inactivate them, and how to then distribute clean, safe water to affected communities.

Dr. Joanna Shisler, Associate Professor of Microbiology, explores how viruses evade the human immune response and how they spread and persist in the environment. "Depending on the virus and depending on the host cell and host tissue it's targeting; it will have its own little arsenal of weapons," explains Shisler. "Some viruses will target innate immunity, some viruses will target specific immunity like T-cells and B-cells. For virus-host interactions, we mostly focus on pox-viruses like monkey-pox virus and the vaccinia virus. For viruses in the environment, most of the work I've been doing with Helen has been with rotaviruses and adenoviruses."

Associate Professor of Civil and Environmental Engineering Dr. Helen Nguyen also studies waterborne pathogens. "With Joanna, we mostly work with rotavirus, which is the primary diarrhea-causing virus. We look at different aspects of it, the transport of the virus in the environment and disinfection, how to control it. A lot of work has been under the general topic of water-reuse

and food safety, for that virus." The duo combines the knowledge in their respective fields to address the startling inaccessibility to clean drinking water experienced by communities located in Nepal and Kenya, among others.

While some engineers focus on the application of their research, Dr. Nguyen takes a different approach to her work on water treatment and deliv-

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*If you don't understand the fundamentals of what's going on, then we will never be able to have an effective engineering strategy. And that is why I work with Joanna, she helps us understand the mechanism of virus survival, and virus disinfection and inactivation.*

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ery. "My philosophy of engineering research is to not just do applied work," said Nguyen, "because then you don't understand what we will face next week, next year, next decade. If you don't understand the fundamentals of what's going on, then we will never be able to have an effective engineering strategy. And that is why I work with Joanna, she helps us understand the mechanism of virus survival, and virus disinfection and inactivation."

Drs. Shisler and Nguyen are affiliates of the IGB's Computing Genomes for Reproductive Health

(CGRH) theme, a relationship they both have found to be key to the expansion of their tandem research. "After we both joined the IGB," said Nguyen, "we began looking at not just lab work, but more complex environments, when we have not just one virus but a whole microbiome of viruses along with many different bacteria. Joanna and I now have a project looking at the effect of extreme events, both weather events and geological events (like earthquakes) upon the microbiome and how it then affects water quality and also how that then influences infectious disease outbreaks."

"One of the great things about joining the IGB," said Shisler, "is getting to meet a diverse set of scientists who we really wouldn't meet on campus otherwise, with broad interests different than our own. I think that's what is making us move towards thinking about environmental microbiology and ecology, I think the more you interact with people, the more you realize that you're working on a small sliver of a project and you start seeing how you can connect different ideas together in a transdisciplinary manner that would be unique, in a way that no one has thought about before."

Ultimately, the teamwork of Dr. Shisler and Dr. Nguyen highlights the effectiveness of interdisciplinary work, the epitome of the adage 'two heads are better than one.' "Working with Helen," said Shisler, "I've gotten to see how working on virology through engineering and the environment can really help shape public health. And I think those two areas really complement each other, you have human health, and also public health and policy, and both are trying to make people's lives better." ■

*Written by Gregory Toreev.*

# ON THE GRID HAPPENINGS AT THE IGB

## NEW ARRIVALS



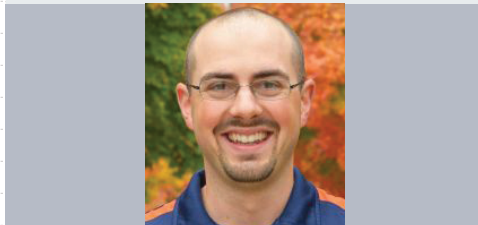
### GIRISH CHOWDHARY

Professor Girish Chowdhary has joined the IGB as an affiliate member in the Genomic Ecology of Global Change (GEGC) Research Theme. He is a faculty member in the Department of Agricultural and Biological Engineering. He is also the director of the Distributed Autonomous Systems Laboratory, which conducts research in autonomous decision making to enable the next generation of robotic systems. He received his Ph.D. from the Georgia Institute of Technology, and was a postdoctoral research associate at the Massachusetts Institute of Technology. Prior to joining the University of Illinois, he was on the faculty at Oklahoma State University.



### DAVID MILLER

Professor David Miller has joined the IGB as an affiliate member in the Computing Genomes for Reproductive Health (CGRH) Research Theme. He is a faculty member in the Department of Animal Sciences. The Miller lab studies the cell adhesion and signaling mechanisms of sperm storage in the oviduct and fertilization.



### ANTHONY STUDER

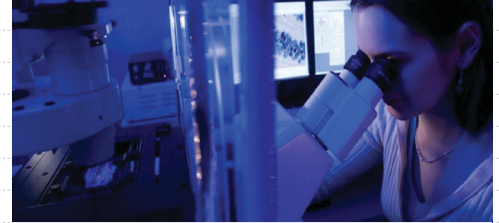
Professor Anthony Studer has joined the IGB as an affiliate member in the Genomic Ecology of Global Change (GEGC) Research Theme. He is a faculty member in the Department of Crop Sciences. He received his Ph.D. in Genetics from the University of Wisconsin, Madison. His research interests focus in the areas of evolution, regulation and function of the carbon concentrating mechanism employed by plants for C4 photosynthesis.



### HEIDEMARIE LAURENT

Professor Heidemarie Laurent has joined the IGB as an affiliate member in the Computing Genomes for Reproductive Health (CGRH) Research Theme. She is a faculty member in the Department of Psychology. She received her Ph.D. from the University of Massachusetts at Amherst. Her research interests focus in the areas of stress regulation, mindfulness, depression and close relationships.

## IGB AT THE FIELD



### THE WORLD OF GENOMICS AT THE FIELD MUSEUM

Explore The World of Genomics May 18-20 at The Field Museum during a special event presented by the IGB. Meet with IGB scientists in Stanley Field Hall and take part in hands-on activities to discover the fascinating world of genomic science and its impact on our lives.

Learn about how genes affect behavior and health by examining bee brains in 3D, witness the drug discovery pipeline in action, see how scientists are learning to grow enough food for tomorrow by identifying better crops yourself and observe how life begins and adapts in our ever-changing world by interacting with samples of the earliest life on Earth. Visit <https://www.fieldmuseum.org/at-the-field/programs/world-genomics> for more info.

## ONLINE COURSE

The Coursera logo, featuring the word "coursera" in white lowercase letters on a blue background.

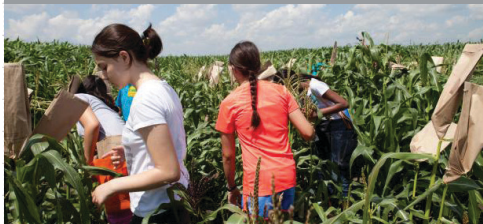
### IGB MOOC

The IGB's Massive Open Online Course (MOOC) "Genomics: Decoding the Universal Language of Life" is open for enrollment. This beginner level course contains 6 weeks of study and encompasses topics drawn from the IGB's expansive research portfolio such as how genes work, why microbes play such an important role chemically, how DNA sequencing can be used to predict risk to health and wellness, and what differences exist in genetically modified plants. There are several enrollment options available through Coursera, and more information can be found at <https://www.coursera.org/learn/genomics-research>.



# ON THE GRID HAPPENINGS AT THE IGB

## SUMMER CAMP

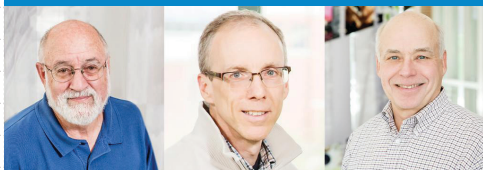


### POLLEN POWER!

Join us for Pollen Power!, our summer camp that provides an opportunity for girls to study plant responses to climate change. Small research groups led by female graduate students will use million-dollar microscopes to image pollen, giving the campers first-hand experience in a research environment with female mentors. The camp is designed for girls who are entering 6th, 7th or 8th grade in the Fall 2017, and who have an interest in plants and the environment.

Visit <http://pollensummercamp.illinois.edu/> for more info and to register.

## RECOGNITION



### THREE IGB MEMBERS ELECTED TO NATIONAL ACADEMY OF SCIENCES

The National Academy of Sciences announced the election of their 2017 members, including three from the Carl R. Woese Institute for Genomic Biology at the University of Illinois at Urbana-Champaign. The three newly elected members include John Cronan, Professor and Head of Microbiology and Professor of Biochemistry, who is a member of the Mining Microbial Genomes research theme; Donald Ort, Robert Emerson Professor of Plant Biology, USDA/ARS Photosynthesis Research Unit and Adjunct Professor of Crop Sciences who is the leader of the Genomic Ecology of Global Change research theme; and Jeffrey Moore, Murchison-Mallory Professor of Chemistry and Professor of Materials Science and Engineering, also a member of the Biosystems Design theme.

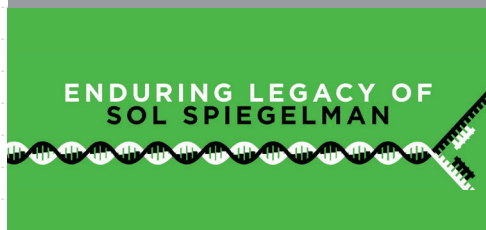
## RESEARCH



### MODIFIED SOYBEANS YIELD MORE IN FUTURE CLIMATE CONDITIONS

By 2050, we will need to feed 2 billion more people on less land. Meanwhile, carbon dioxide levels are predicted to hit 600 parts per million—a 50% increase over today's levels—and 2050 temperatures are expected to frequently match the top 5% hottest days from 1950-1979. In a three-year field study, researchers proved engineered soybeans yield more than conventional soybeans in 2050's predicted climatic conditions. [Read the full story here.](#)

## SYMPOSIUM



### THE ENDURING LEGACY OF SOL SPIEGELMAN

In honor of University of Illinois microbiologist Sol Spiegelman and his work with recombinant DNA technology, the IGB is hosting the symposium "The Enduring Legacy of Sol Spiegelman." We are featuring a public lecture and a series of plenary talks from October 20-22, 2017.

Our national panel of speakers, including two Nobel Laureates, encompasses diverse disciplines such as microbiology, biochemistry, cellular and development biology, neuroscience, and biomolecular engineering, and will be presenting on current and future work in their respective fields. Register now at <http://spiegelman2017.igb.illinois.edu/>.

## AWARD



### GIVING WITH PURPOSE

Mark Tracy, PhD, founder and president of Tracy BioConsulting, LLC, strives to introduce undergraduate science students to biotech industry research. By exposing students with different backgrounds to biopharma industry research, the drug development process, and the business of developing new medical products while they're still in their undergraduate years, he hopes to promote interest in solving important medical problems. [Read more about Dr. Tracy's gift to the IGB and vision for education.](#)

## SPEAKER



### GENETICIST MARY-CLAIRE KING DISTINGUISHED LECTURE

On April 17, 2017, Mary-Claire King, Professor of Genome Sciences and of Medicine at the University of Washington School of Medicine, spoke as part of the IGB Distinguished Public Lecture series. Her talk, entitled "Genetic Analysis of Inherited Breast and Ovarian Cancer: From Gene Discovery to Precision Medicine and Public Health," drew a full crowd at the Alice Campbell Alumni Center, followed by a robust Q&A session and a reception for all attendees.

Our thanks to Dr. King for a memorable and rewarding experience from a true pioneer in the sciences.

# DEPARTMENT ANNOUNCEMENTS

## BUSINESS

### FY18 BENEFIT CHOICE ENROLLMENT FOR UNIVERSITY OF ILLINOIS EMPLOYEES

The FY18 Benefit Choice period will begin on Monday, May 1, 2017 and end on Wednesday, May 31, 2017 with an effective date of July 1, 2017.

If you are eligible for State of Illinois insurance and benefits, you will no longer use NESSIE to make Benefit Choice changes. Instead, you will use the state's new CMS MyBenefits Marketplace website: <https://mybenefits.illinois.gov/account/login/choseclient>.

There are two helpful resources for using the new MyBenefits site:

- MyBenefits Tips blog post found at <https://uofi.illinois.edu/blog/view/1418/472472> is a quick-start guide for registering, logging in, and using the site.
- MyBenefits Marketplace FAQs found at [https://www.hr.uillinois.edu/benefits/mybenefits\\_fa](https://www.hr.uillinois.edu/benefits/mybenefits_fa) will help to address some common questions.

#### Questions

For assistance with your state benefit plans (health, dental, and life insurance, and flexible spending accounts) contact the MyBenefits Mar-

ketplace Service Center. Bilingual customer service representatives are available.

- Phone: 844-251-1777 or TTY 844-251-1778
- Hours: 8:00 a.m. – 6:00 p.m. CT Monday through Friday

For questions about university plans or benefit counseling, please contact University Payroll and Benefits by sending an e-mail to [benefits@uillinois.edu](mailto:benefits@uillinois.edu) or via phone at (217) 265-6363. ■

## OPERATIONS AND FACILITIES

### BLOOD DRIVE

The next IGB blood drive will be held on Monday, July 1, from 9:00am to 1:00pm in the IGB conference room near Array Cafe. Please call or email Darci Edmonson at 244-2200 or at [darci@uillinois.edu](mailto:darci@uillinois.edu) to schedule a convenient appointment time. Or, if you prefer to register online please visit [www.bloodcenterimpact.org](http://www.bloodcenterimpact.org). ■

# RECENT PUBLICATIONS

*Please include your connection to the IGB in your author byline when submitting publications, as it will greatly help track potential newsworthy items and increase the possibility of coverage.*

Barbey, A. K. (2017). Aerobic fitness, hippocampal viscoelasticity, and relational memory performance. *NeuroImage*, 179-188. DOI: 10.1016/j.neuroimage.2017.03.061

Lee, M. W., Han, M., Bossa, G. V., Snell, C., Song, Z., Tang, H., ... Wong, G. C. L. (2017). Interactions between Membranes and "metaphilic" Polypeptide Architectures with Diverse Side-Chain Populations. *ACS Nano*, 11(3), 2858-2871. DOI: 10.1021/acsnano.6b07981

Bauza, V., Ocharo, R. M., Nguyen, T. H., & Guest, J. S. (2017). Soil ingestion is associated with child diarrhea in an urban slum of Nairobi, Kenya. *American Journal of Tropical Medicine and Hygiene*, 96(3), 569-575. DOI: 10.4269/ajtmh.16-0543

Huang, L., May, J., Pan, X., Ji, H., Ren, X., Han, J., ... Hendler, J. A. (2017). Liberal entity extraction: Rapid construction of fine-grained entity typing systems. *Big Data*, 5(1), 19-31. DOI: 10.1089/big.2017.0012

Comi, T. J., Do, T. D., Rubakhin, S. S., & Sweedler, J. V. (2017). Categorizing Cells on the Basis of their Chemical Profiles: Progress in Single-Cell Mass Spectrometry. *Journal of the American Chemical Society*, 139(11), 3920-3929. DOI: 10.1021/jacs.6b12822

Hoon Lee, Y., Schuh, J. K., Ewoldt, R. H., & Allison, J. T. (2017). Enhancing Full-Film Lubrication Performance Via Arbitrary Surface Texture Design. *Journal of Mechanical Design, Transactions of the ASME*, 139(5), [053401]. DOI: 10.1115/1.4036133

Lee, J. S., Yu, X., Wagoner Johnson, A. J., & Murphy, W. L. (2017). Mineral binding peptides with enhanced binding stability in serum. *Biomaterials Science*, 5(4), 663-668. DOI: 10.1039/c6bm00928j

Song, Y., Moore, E. G., Guo, Y., & Moore, J. S. (2017). Polymer-Peptide Conjugates Disassemble Amyloid  $\beta$  Fibrils in a Molecular-Weight Dependent Manner. *Journal of the American Chemical Society*, 139(12), 4298-4301. DOI: 10.1021/jacs.7b00289

Bakir, M., Bahceci, E., Meyer, J. L., Economy, J., & Jasiuk, I. (2017). Aromatic thermosetting copolyester foam core and aluminum foam face three-lay-

## RECENT PUBLICATIONS

er sandwich composite for impact energy absorption. *Materials Letters*, 196, 288-291. DOI: 10.1016/j.matlet.2017.03.116

Zeng, F., Wang, C., Zhang, G., Wei, J., Bradley, C. A., & Ming, R. (2017). Draft genome sequence of *Cercospora soja* isolate S9, a fungus causing frogeye leaf spot (FLS) disease of soybean. *Genomics Data*, 12, 79-80. DOI: 10.1016/j.gdata.2017.02.014

Nasir, A., & Caetano-Anollés, G. (2017). Identification of capsid/coat related protein folds and their utility for virus classification. *Frontiers in Microbiology*, 8(MAR), [380]. DOI: 10.3389/fmicb.2017.00380

Denisov, I. G., & Sligar, S. G. (2017). Nanodiscs in Membrane Biochemistry and Biophysics. *Chemical Reviews*, 117(6), 4669-4713. DOI: 10.1021/acs.chemrev.6b00690

Ameen, A., Hackett, L. P., Seo, S., Dar, F. K., Gartia, M. R., Goddard, L. L., & Liu, G. L. (2017). Plasmonic Sensing of Oncoproteins without Resonance Shift Using 3D Periodic Nanocavity in Nanocup Arrays. *Advanced Optical Materials*. DOI: 10.1002/adom.201601051

Mesa, K. J., Selmic, L. E., Pande, P., Monroy, G. L., Reagan, J., Samuelson, J., ... Boppart, S. A. (2017). Intraoperative optical coherence tomography for soft tissue sarcoma differentiation and margin identification. *Lasers in Surgery and Medicine*, 49(3), 240-248. DOI: 10.1002/lsm.22633

di Chiara, T., DiNunno, N., Clark, J., Bu, R. L., Cline, E. N., Rollins, M. G., ... Klein, W. L. (2017). Alzheimer's toxic amyloid beta oligomers: Unwelcome visitors to the Na/K ATPase alpha3 docking station. *Yale Journal of Biology and Medicine*, 90(1), 45-61.

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