

# IGB NEWS

Upcoming Events

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Image Of The Month

Research News

Department Announcements

Volume 11 Number 5

## UPCOMING EVENTS

### IGB Pioneers Seminar (IGOH)

*Rules of Engagement: Molecular Arms-Races  
Between Primate and Viral Genomes*

September 18, 2018, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Harmitt S. Malik, PhD

Fred Hutchinson Cancer Research Center

### Outpacing Antimicrobial Resistance Symposium

September 24-25, 2018

Alice Campbell Alumni Center

612 Carl R. Woese Institute for Genomic Biology

Join researchers in a two-day symposium devoted to understanding and beating antibacterial resistant microbes at the University of Illinois.

### Redrawing the Tree of Life: Carl Woese and the Revolution He Triggered

September 27, 2018, 4:00 p.m.

Knight Auditorium, Spurlock Museum

David Quammen

Author and Journalist

### IGB Seminar (CGRH)

*Multi-scale Modeling of Complex Diseases*

October 2, 2018, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Olivier Gevaert, PhD

Stanford University, Department of Medicine

### IGB Blood Drive

October 8, 2018, 9:00 a.m. - 12:30 p.m.

612 Carl R. Woese Institute for Genomic Biology

### IGB Seminar (RBTE)

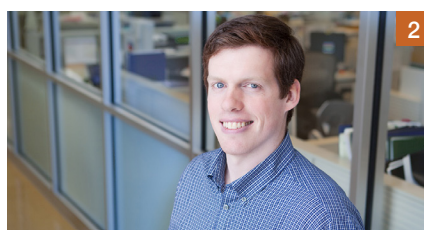
October 16, 2018, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

George J. Christ, PhD

University of Virginia, Department of Biomedical  
Engineering and Orthopedic Surgery

## FEATURED NEWS



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Researchers sequence rare  
bacteria, cause of tooth decay



3

Sequenced fox genome hints at  
genetic basis of behavior



4

Monthly Profile:  
iGEM Team

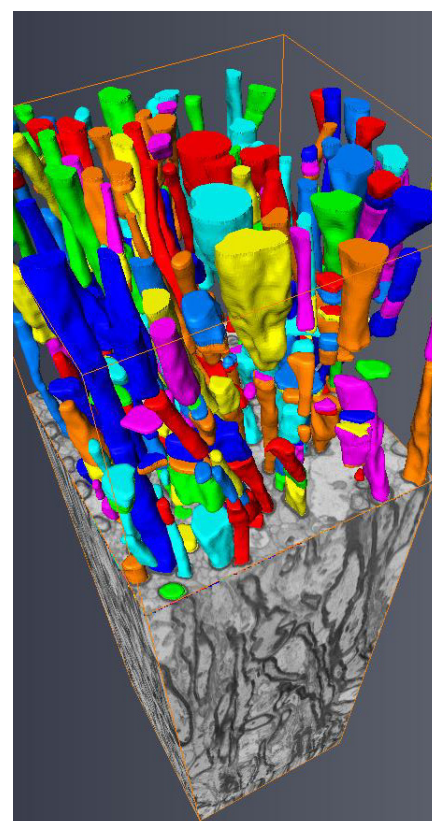
## OUTPACING ANTIMICROBIAL RESISTANCE

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SEPTEMBER 24 - 25, 2018

On the Grid:  
Happenings at IGB

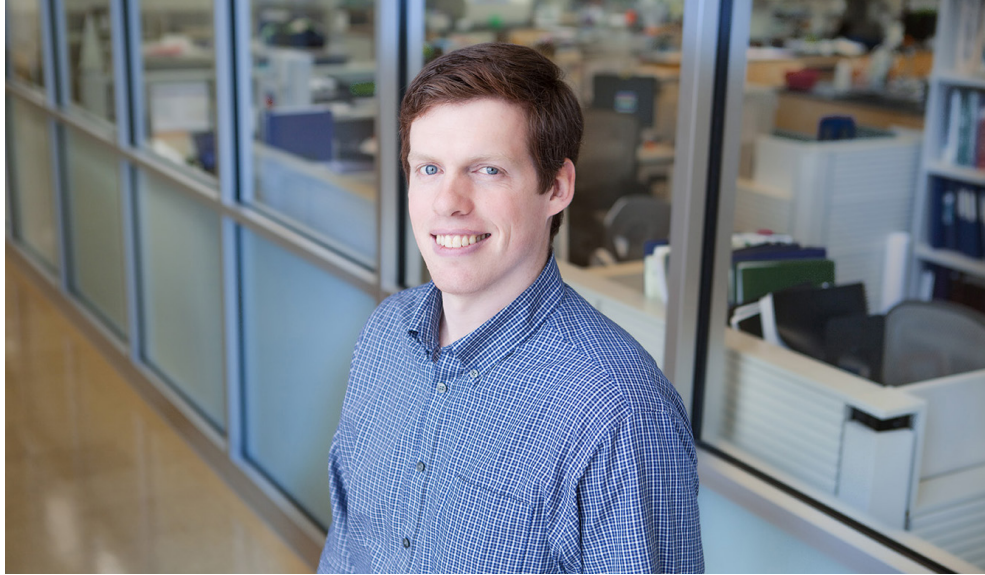
## IMAGE OF THE MONTH



This month features a section of piglet corpus callosum processed using serial block-face scanning electron microscopy. Myelinated axons are depicted by the dark circular rings. This image was acquired using the Zeiss Sigma BP 3View SBF-SEM and segmented using Amira Software by Kingsley Boateng of IGB Core Facilities; Stephen Fleming & Dr. Ryan Dilger of the Dilger Lab, and the Piglet Nutrition and Cognition Lab in the Department of Animal Sciences.

### IGB News

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



## Researchers first to sequence rare bacteria cause of rampant tooth decay

The most prevalent chronic disease in both children and adults, tooth decay occurs when the good and bad bacteria in our mouth become imbalanced. The bad bacteria, *Streptococcus mutans*, forms a bio-film (aka tartar), then takes the sugars we eat and ferments them into acid, which decalcifies our teeth and causes cavities.

Scientists know, though, that there is a second harmful bacteria called *Streptococcus sobrinus* that accelerates tooth decay in some people, but very little is known about this microbe. This will soon change because a team of Illinois Bioengineering researchers led by Assistant Professor Paul Jensen (MMG) has successfully sequenced the complete genomes of three strains of *S. sobrinus*.

According to Jensen, *S. sobrinus* is difficult to work with in the lab and it is not present in all people, so researchers have instead focused their efforts over the years on understanding the more stable and prevalent *S. mutans*, which was sequenced in 2002.

“Although it is rare, *S. sobrinus* produces acid more quickly and is associated with the poorest clinical outcomes, especially among children,” noted Jensen, a researcher in the IGB’s Mining Microbial Genomes research theme. “If *S. sobrinus* is present along with *S. mutans*, you’re at risk for rampant tooth decay, which means there’s some level of communication or synergy between the two that we don’t understand yet.”

Now that the *S. sobrinus* sequencing is complete, Jensen and his students are building computational models to better understand how the two bacteria

interact and why *S. sobrinus* can cause such potent tooth decay when combined with *S. mutans*.

Already they have confirmed, for example, that *S. sobrinus* lacks complete pathways for quorum sensing, which is the ability bacteria have to sense and react to nearby bacteria, and ultimately proliferate.

According to Jensen, *S. mutans* bacteria send out feelers in the form of a peptide to find out how many other *S. mutans* cells are nearby. Once the *S. mutans* cells reach a certain threshold, they attack and create an imbalance in a person’s mouth between good and bad bacteria, which leads to rapid cavity formation.

“*S. sobrinus* doesn’t have a complete system to do this,” said Jensen. “We’re really curious to explore this further and find out what is missing and why.”

Interestingly, the entire *S. sobrinus* genome sequencing was completed by a team of Bioengineering undergraduates and students enrolled in the one-year Master of Engineering (M.Eng.) program, rather than doctoral candidates who typically conduct this type of research over several years.

“For the *S. sobrinus* field, this is groundbreaking work because the field was plagued by a lack of information,” said Jensen. “In 2018, it is surprising that we had a whole species [of bacteria] that causes disease and no complete genome of it. Yet, an ambitious team of undergrads and M.Eng. students completed the sequencing in a year.”

Mia Sales, who graduated with her bachelor’s degree this past May, completed the assemblies of

two of the species of *S. sobrinus*. Sales also built the computer that other team members used to do the initial genome assemblies.

Fellow undergraduate Will Herbert worked on the annotation part of the project, finding genes in the strings of approximately 2 million adenine (A), cytosine (C), guanine (G), and thymine (T) nucleotides that make up the *S. sobrinus* genomes.

Other contributors to the research include M.Eng. students Yuting Du, Amitha Sandur, and Naaman Stanley. “This work exemplifies the students’ ability to synthesize their learning experience with a completely new insight, resulting in an original research publication,” said Professor Dipanjan Pan, director of the M.Eng. program.

The Illinois team has uploaded the sequencing information to the GenBank public database so scientists worldwide will have access to the *S. sobrinus* genomic information. Their work was published in journal *Microbial Resource Announcements* under the title “Complete genomic sequences of *Streptococcus sobrinus* SL1 (ATCC 33478 = DSM 20742), NIDR 6715 (ATCC 27351 & 27352), and NCTC 10919 (ATCC 33402).”

This work was funded by a grant from the NIH National Institute of Dental and Craniofacial Research and the Illinois Master of Engineering in Bioengineering program. ■

**Written by Laura Schmitt. Photo by Kathryn Faith.**





## Sequenced fox genome hints at genetic basis of behavior

For nearly 60 years, the red fox has been teaching scientists about animal behavior. In a long-term experiment, foxes at the Russian Institute of Cytology and Genetics have been selected for tameness or aggression, recreating the process of domestication from wolves to modern dogs in real time. Today, with the first-ever publication of the fox genome, scientists will begin to understand the genetic basis of tame and aggressive behaviors, which could shed light on human behavior, as well.

“We’ve been waiting for this tool for a very, very long time,” says Anna Kukekova, Assistant Professor of Animal Sciences, member of the IGB’s Gene Networks in Neural & Developmental Plasticity research theme, and lead author of the paper. She has been studying the famous Russian foxes since 2002.

“In our previous work, we tried to identify regions of the fox genome responsible for tame and aggressive behavior, but these studies required a reference genome and all we could use was the dog genome. For us, the fox genome provides a much better resource for genetic analysis of behavior.”

After sequencing and assembling the fox genome, the team turned to the famous Russian foxes to look for genetic regions differentiating the tame, aggressive, and conventional populations – farm-raised foxes ancestral to the tame and aggressive populations but not bred for any particular behavioral trait.

The researchers sequenced the genomes of 10 individuals from each population, then compared them to the full fox genome and each other. The three populations differed in 103 genomic regions, some of which turn out to be responsible for the tame and aggressive behaviors.

“Finding genomic regions at such resolution was beyond any expectations with our previous tools. Now, for the first time, we could not only pinpoint part of a chromosome which makes foxes more tame or aggressive, but we could identify specific genes responsible for it,” Kukekova says.

The team compared the 103 genomic regions to those of other sequenced mammals and found some compelling similarities. For example, they

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*“We think this gene makes foxes more tame, but we don’t want to overemphasize it – tameness isn’t associated with a single gene.”*

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identified matches between behavior regions in foxes with regions important in domestication in dogs and with a region associated with Williams-Beuren syndrome in humans, a genetic disorder characterized by extremely outgoing, friendly behavior.

“Oddly enough, we found the Williams-Beuren region in aggressive foxes, not tame ones. We thought it would be the opposite,” Kukekova says. The mysterious finding underscores how much more research is needed before the regions are fully understood.

But the researchers dove deeper. As a test run, they honed in on a single gene, known as SorCS1, which is involved in synapse formation, functioning, and plasticity, as well as additional functions. Although

it had never before been known to contribute to social behavior, SorCS1 was clearly associated with a very specific behavior in foxes.

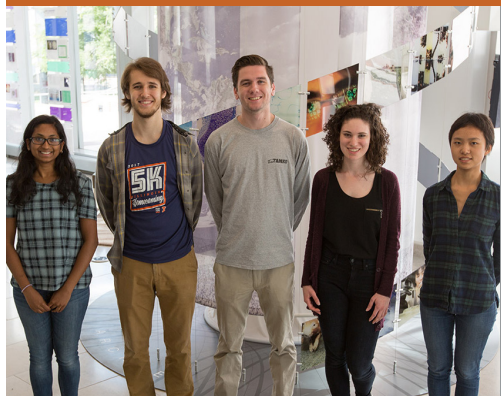
Human handlers at the Russian Institute of Cytology and Genetics interact with the foxes in a very controlled way as part of their videotaped fox behavioral assessments. Handlers stand near the enclosures for one minute, hold the door open for another minute, reach toward the fox for a third minute, then close the door, and stand near the enclosure for one final minute. The tamest foxes continue to clamor for human attention during the final minute of the assessment. It’s this group of foxes that has a version of the SorCS1 gene not found in the aggressive population.

“We think this gene makes foxes more tame, but we don’t want to overemphasize it – tameness isn’t associated with a single gene. The picture is definitely more complex,” Kukekova says.

The article, “[Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviors](#),” is published in *Nature Ecology & Evolution*. The full list of authors includes Anna Kukekova, Jennifer Johnson, Xueyan Xiang, Shaohong Feng, Shiping Liu, Halie Rando, Anastasiya Kharlamova, Yuri Herbeck, Natalya Serdyukova, Zijun Xiong, Violetta Beklemisheva, Klaus-Peter Koepfli, Rimma Gulevich, Anastasiya Vladimirova, Jessica Hekman, Polina Perelman, Aleksander Graphodatsky, Stephen O’Brien, Xu Wang, Andrew Clark, Gregory Acland, Lyudmila Trut, and Guojie Zhang. ■

**Written by Lauren Quinn. Photo by Darya Shepeleva, Russian Institute of Cytology and Genetics in Novosibirsk**

## MONTHLY PROFILE



The 2018 Illinois International Genetically Engineered Machine (iGEM) competition team, from left to right: Pranathi Karumanchi, Alexander Ruzicka, Liam Healy, Amie Bott, and Ziyu Wang.

### Illinois iGEM team takes on CABBI-funded synthetic biology project

This summer, a group of undergraduate students has teamed up with CABBI researchers to pursue an ambitious research project.

Their work is in preparation for the International Genetically Engineered Machine (iGEM) competition, which brings together undergraduate students from across the world to present their research in synthetic biology and compete for prizes.

This year's team from the University of Illinois at Urbana-Champaign is made up of five students: Pranathi Karumanchi, Ziyu Wang, Liam Healy, Amie Bott and Alexander Ruzicka.

Their project is funded by the Center for Advanced Bioenergy and Bioproducts Innovation (CABBI), a collaboration between the Institute for Sustainability, Energy, and Environment and the Carl R. Woese Institute for Genomic Biology (IGB) that aims to develop sustainable biofuels and bioproducts.

The iGEM team is mentored by graduate and post-doctoral researchers Carl Schultz, Shekhar Mishra, and Matthew Waugh, IGB Outreach Activities Manager Courtney Fenlon, CABBI Research Coordinator Elizabeth Murphy, and Associate Professor of Bioengineering and CABBI scientist Ting Lu.

The idea for the team's project came from the joint work of Ting Lu and Yong-Su Jin, a professor of food science and human nutrition and CABBI scientist. Lu is researching lactic acid bacteria, which is used in the production of cheese and yogurt, while Jin studies baker's yeast, which is used in baking bread. Lu and Jin want to see what a collaboration between these two organisms could achieve in the field of metabolic engineering.

Metabolic engineering involves modifying organisms to produce valuable products, such as biofuels and chemicals. Most metabolic engineering research involves working with a single species, but Lu said this has several limitations.

"When we look at microbes in nature, we know that they do not exist in a single cell or single strain," Lu said. "Instead, they always present in the form of complex communities."

Lu wants to investigate the ecosystem of lactic acid bacteria and baker's yeast and find a way to use them

*"Because there's not a lot of literature to go on, right from the early stages, this project has been one of inquiry."*

for producing valuable products. He said evidence has shown that these two organisms often coexist naturally and can even boost each other's production.

The iGEM team is continuing this work; they will study how lactic acid bacteria and baker's yeast work together, testing different environments and food sources. They will then engineer the organisms to see if they are capable of creating a valuable product.

One of the biggest challenges the team faces is the lack of prior research in this area.

"We're the ones that have to figure it out," said team member Liam Healy. "We're the ones doing a lot of the failing."

The team has had to troubleshoot how to make an environment that would help the organisms grow together.

"Because there's not a lot of literature to go on, right from the early stages, this project has been one of inquiry," Mishra said.

Despite the trial and error involved in the research, their mentors said the team has been making quick progress this summer.

"They're making some discoveries that — as far as we can tell — haven't been made so far in literature, in terms of how to actually grow these two organisms together in such a way that they're both able to grow healthily," Schultz said.

Lu said the upside of the project is that any discoveries and progresses will be new to the field.

The team will present their work at this year's iGEM competition in October.

"My impression is that they're making pretty fast progress," Schultz said. "It'll be exciting to see what kind of results they're able to get by the end." ■

Written by Emily Scott. Photo by Jillian Nickell.



*CABBI is dedicated to solving the issue of providing sustainable sources of energy that meet societal needs as the population continues to grow, developing efficient ways to grow, transform, and market biofuels and other bioproducts, using genomics, synthetic biology, and computational biology to increase the value of biomass crops.*



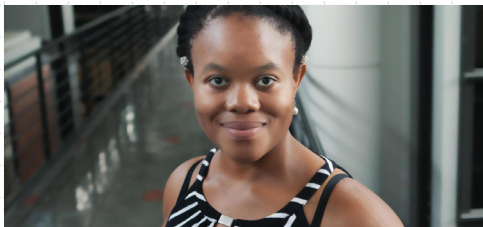
## ON THE GRID HAPPENINGS AT THE IGB

### AWARDS



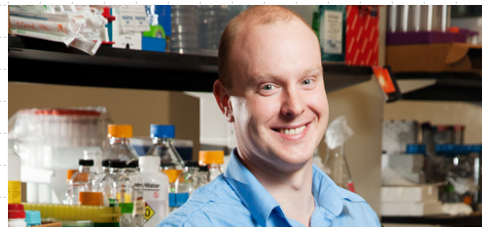
#### ALISON BELL

Alison Bell, Associate Professor of Animal Biology (GNBP) was named a University Scholar, recognizing excellence in teaching, scholarship and service.



#### PRINCESS IMOUKHUEDE

Princess Imoukhuede, Assistant Professor of Bioengineering (RBTE), received the 2018 Distinguished Leadership Award from the Illinois Mathematics and Science Academy (IMSA), which recognizes IMSA alumni for distinguished achievements or leadership contributions in their professional fields of endeavor consistent with the academy's mission.



#### DOUGLAS MITCHELL

Douglas Mitchell, Professor of Chemistry (MMG) was named Alumni Research Scholar Professor of Chemistry, as well as receiving a 2018 Campus Distinguished Promotion Award in recognition of excellence through contributions and achievements within his field.



#### BRIAN CUNNINGHAM

Brian Cunningham, Donald Biggar Willett Professor of Engineering and Professor of Electrical and Computer Engineering (ONC-PM Theme Leader/MMG) was named to the Institute of Electrical and Electronics Engineers (IEEE) Photonics Society Distinguished Lecturer Program, which honors excellent speakers who have made technical, industrial, or entrepreneurial contributions to the field of photonics.



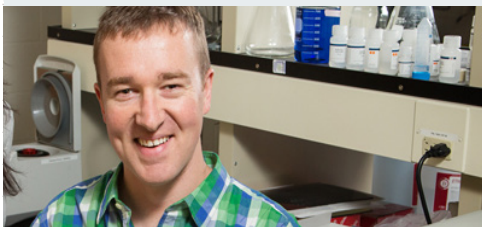
#### PAUL KENIS

Paul Kenis, William H. and Janet G. Lycan Professor and Head of Chemical & Biomolecular Engineering (RBTE), was named to the Elio Eliakim Tarika Endowed Chair in Chemical Engineering, which recognizes research excellence in honor of Illinois alumnus Elio Tarikia.



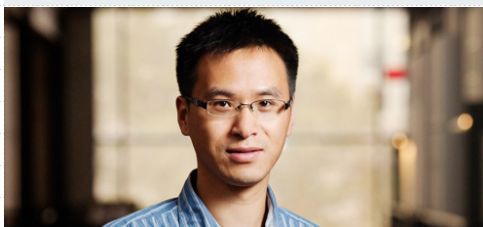
#### JEFFREY MOORE

Jeffrey Moore, Murchison-Mallory Professor of Chemistry and Professor of Materials Science and Engineering (BSD), received the U.S. Secretary of Energy's Achievement Award for his work with the Scientific and Operational Leadership team for the Joint Center for Energy Storage Research project, which is developing high-performance, low-cost energy storage technologies for transportation and the electric grid.



#### BRANDAN HARLEY

Brandon Harley, Professor, Chemical & Biomolecular Engineering (RBTE Theme Leader), received a 2018 Campus Distinguished Promotion Award in recognition of excellence through contributions and achievements within his field.



#### TING LU

Ting Lu, Associate Professor of Bioengineering (BSD/BCXT/MME) received the American Chemical Society Infectious Diseases Young Investigator Award, which recognizes outstanding early-career individuals in the field of infectious diseases.

### CALL FOR PAPERS



#### THE ANCIENT DNA REVOLUTION IN ARCHAEOLOGY

Brown University has an open call for papers for State of the Field 2019: The Ancient DNA Revolution in Archaeology conference on February 22-24, 2019. Abstracts are due by October 15th, and full information is available at the [Archeology at Brown](#) event website.

# ON THE GRID HAPPENINGS AT THE IGB

## NEW ARRIVALS



### MARY CALLAWAY

Mary Callaway has joined the IGB as the Assistant to the Director. Prior to joining the IGB, she worked in the Office of the Vice Chancellor for Diversity, Equity & Inclusion and the Office of the Chancellor. She has a Bachelor's degree from Eastern Illinois University and has worked on campus for 17 years.



### ERIN JOHNSON

Erin Johnson recently joined the IGB as a Business and Policy Specialist in the Business Office. Prior to joining the IGB, she worked as an Administrative Aide in the Department of Bioengineering. She has worked on Campus for 18 years.



### JULIA POLLACK

Julia Pollack has joined the IGB as an Creative Program Manager who will be Managing the Art of Science initiative. She has a Masters degree in Library and Information Science from Illinois, and a Masters degree in Digital Humanities from the City University of New York's Graduate Center. She previously worked as a Librarian for Bronx Community College in New York, and a User Experience designer for Pixa in Urbana. She has shown multimedia art pieces at local venues and presented work internationally. Her work seeks to visualize concepts of information transmission and knowledge production, with a specific focus on audience interaction.

## TALK



### DAVID QUAMMEN

Author David Quammen will give a talk based on his latest book *The Tangled Tree*, entitled "Redrawing the Tree of Life: Carl Woese and the Revolution He Triggered." A reception and book signing will follow the event.

Thursday, September 27, 2018  
4:00pm  
Knight Auditorium, Spurlock Museum

## CALL FOR IDEAS



### NSF 2026 IDEA MACHINE

NSF is looking for fresh ideas, large in scope and different from what the foundation already does. These ideas should address compelling challenges in science, technology, engineering and mathematics (STEM). From Aug. 31, 2018 through Oct. 26, 2018, the foundation will open the entry window for its first-ever NSF 2026 Idea Machine, a competition that gives entrants a chance to help inform the agenda for basic research, through the Nation's 250th anniversary in 2026 and beyond. Ideas should be designed for broad areas of research that would require a long-term commitment (10 years or more) and potentially transform a research area through new explorations and creative inquiry.

Full details available on the [NSF website](#). Entries will be accepted through October 26, 2018.

## SYMPOSIUM

### OUTPACING ANTIMICROBIAL RESISTANCE

SEPTEMBER 24 - 25, 2018

### OUTPACING ANTIMICROBIAL RESISTANCE

Join researchers in a two day symposium devoted to understanding and beating antibacterial resistant microbes at the University of Illinois. Experts in the fields of microbiology, immunology, infectious disease, drug development and policy will present on this critical issue.

September 24th public lectures, 7:00PM  
Alice Campbell Alumni Center

September 25th Session Speakers, 8:30AM  
612 IGB Conference Room.

Register at [outpacesymposium.igb.illinois.edu](http://outpacesymposium.igb.illinois.edu).

## SCHOLAR PROGRAM



### IGB VISITING SCHOLAR PROGRAM

The IGB is seeking international partners to participate in a new Visiting Scholar Program to form partnerships with universities, foundations and government laboratories. Qualified individuals will join an existing IGB theme and receive training in team-based science. Visiting Scholars will also engage in workshops and seminars featuring experts in the science and practice of team science.

For additional information and to nominate international partners, please contact IGB-VSP coordinator Dr. Brian Allan at [ballan@illinois.edu](mailto:ballan@illinois.edu).



## ON THE GRID HAPPENINGS AT THE IGB

### OUTREACH

#### WORLD OF GENOMICS WORLD OF GENOMICS WORLD OF GENOMICS

##### WORLD OF GENOMICS

One of the IGB's most successful and comprehensive public engagement events, the World of Genomics, will be showcased for three days at the St. Louis Science Center from October 18-20, 2018. The World of Genomics will feature six interactive learning stations. At these stations, a team of Illinois volunteers from dozens of scientific fields will highlight hands-on activities and interactive demonstrations that describe the deep portfolio of IGB research in easy to understand terms.

### SPOTLIGHT



##### DONOR SPOTLIGHT: SANDRA PERRY SIGMAN

In 2009, Sandra Perry Sigman visited the University of Illinois campus with her husband David and son, Ryan. While visiting, her son's interest in genetics led them to take a tour of the IGB. They walked away impressed with the institute's interdisciplinary nature, which inspired them to become donors to the IGB.

Read Sandra's full story on the [IGB website](#).

### GRANT



##### NEW NIH GRANT

Marni Boppert (RBTE), Associate Professor in Kinesiology and Community Health, recently received an NIH R01 grant "Development of a Cell-Based Therapy to Improve Muscle Recovery Following Immobilization." Co-PIs on this grant include Wawosz Dobrucki, Assistant Professor in the Department of Bioengineering; Jonathan Sweedler (MMG), James R. Eiszner Family Endowed Chair in Chemistry; Hyun-joon Kong (RBTE), Professor, Departments of Chemical and Biomolecular Engineering, Bioengineering, & Pathobiology; and Stephen Boppert (RBTE), Professor of Electrical and Computer Engineering.

## DEPARTMENT ANNOUNCEMENTS

### BUSINESS

#### IGB COPIER ACCESS

For black and white copier machine access please fill out the "copier access form" located [here](#), indicating each floor you need access too. If you need multiple floors or access to the copiers on each side of a certain floor, please note that on this form. Once you have been added to the copier, you will receive an email letting you know you have access has been granted. In addition, the IGB will provide our users a drop box so you can receive all scanned documents on your desk top. To access the copier, you will input the last six numbers of your UIN, and this will become your log on number. Copies are charged to the CFOP you provide at .06¢ a copy, all scans are free.

If you have any questions, please contact Bobby Alexander at 217-244- 6789 [bgalexan@igb.illinois.edu](mailto:bgalexan@igb.illinois.edu). ■

### OPERATIONS AND FACILITIES

#### UPDATING YOUR IGB INFORMATION

All new members to the IGB must fill out an entry form and be properly registered. However, there are occasions when this information will need to be updated. Please email Kathy Millage, IGB Operations & Facilities Office Administrator, at [kmillage@illinois.edu](mailto:kmillage@illinois.edu) should any of the following occur:

- Your theme or status (undergrad, grad, post-doc, etc.) has changed since you originally submitted your IGB entry form. You may need to submit an updated IGB entry form.
- You are leaving IGB permanently. An IGB exit form should be completed.
- Your IGB key(s) are no longer needed. A form is required to receive your \$20.00 refundable key deposit. ■

## 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.

Ohmann, A., Li, C. Y., Maffeo, C., Al Nahas, K., Baumann, K. N., Göpflich, K., ... Aksimentiev, A. (2018). A synthetic enzyme built from DNA flips 107 lipids per second in biological membranes. *Nature Communications*, 9(1), [2426]. DOI: 10.1038/s41467-018-04821-5

O'Dwyer, J. P., & Cornell, S. J. (2018). Cross-scale neutral ecology and the maintenance of biodiversity. *Scientific Reports*, 8(1), [10200]. DOI: 10.1038/s41598-018-27712-7

Shen, Y., Huang, P. C., Huang, C., Sun, P., Monroy, G. L., Wu, W., ... Nguyen, T. H. (2018). Effect of divalent ions and a polyphosphate on composition, structure, and stiffness of simulated drinking water biofilms. *npj Biofilms and Microbiomes*, 4(1), [15]. DOI: 10.1038/s41522-018-0058-1

Dsouza, R., Won, J., Monroy, G. L., Hill, M. C., Porter, R. G., Novak, M. A., & Boppart, S. A. (2018). In vivo detection of nanometer-scale structural changes of the human tympanic membrane in otitis media. *Scientific Reports*, 8(1), [8777]. DOI: 10.1038/s41598-018-26514-1

Diefenbacher, M., Sun, J., & Brooke, C. B. (2018). The parts are greater than the whole: the role of semi-infectious particles in influenza A virus biology. *Current Opinion in Virology*, 33, 42-46. DOI: 10.1016/j.coviro.2018.07.002

Xu, J., Huang, C., Shi, X., Dong, S., Yuan, B., & Nguyen, T. H. (2018). Role of drinking water biofilms on residual chlorine decay and trihalomethane formation: An experimental and modeling study. *Science of the Total Environment*, 642, 516-525. DOI: 10.1016/j.scitotenv.2018.05.363

Rodriguez-Zas, S. L., Wu, C., Southey, B. R., O'Connor, J. C., Nixon, S. E., Garcia, R., ... Dantzer, R. (2018). Disruption of microglia histone acetylation and protein pathways in mice exhibiting inflammation-associated depression-like symptoms. *Psychoneuroendocrinology*, 97, 47-58. DOI: 10.1016/j.psyneuen.2018.06.024

Pangborn, H. C., Koeln, J. P., Williams, M. A., & Alleyne, A. G. (2018). Experimental validation of graph-based hierarchical control for thermal management. *Journal of Dynamic Systems, Measurement and Control, Transactions of the ASME*, 140(10), [101016]. DOI: 10.1115/1.4040211

Koeln, J. P., & Alleyne, A. G. (2018). Robust hierarchical model predictive control of graph-based power flow systems. *Automatica*, 96, 127-133. DOI: 10.1016/j.automatica.2018.06.042

Davis, J. P., Dumas, T. M., & Roberts, B. W. (2018). Adverse Childhood Experiences and Development in Emerging Adulthood. *Emerging Adulthood*, 6(4), 223-234. DOI: 10.1177/2167696817725608

Staley, J. T., & Caetano-Anollés, G. (2018). Archaea-First and the Co-Evolutionary Diversification of Domains of Life. *BioEssays*, 40(8), [1800036]. DOI: 10.1002/bies.201800036

Gaba, R. C., Mendoza-Elias, N., Regan, D. P., Garcia, K. D., Lokken, R. P., Schwind, R. M., ... Schachtschneider, K. M. (2018). Characterization of an Inducible Alcoholic Liver Fibrosis Model for Hepatocellular Carcinoma Investigation in a Transgenic Porcine Tumorigenic Platform. *Journal of Vascular and Interventional Radiology*, 29(8), 1194-1202.e1. DOI: 10.1016/j.jvir.2018.03.007

Kong, W., Meldgin, D. R., Collins, J. J., & Lu, T. (2018). Designing microbial consortia with defined social interactions. *Nature Chemical Biology*, 14(8), 821-829. DOI: 10.1038/s41589-018-0091-7

Grier, W. K., Tiffany, A. S., Ramsey, M. D., & Harley, B. A. C. (2018). Incorporating  $\beta$ -cyclodextrin into collagen scaffolds to sequester growth factors and modulate mesenchymal stem cell activity. *Acta Biomaterialia*, 76, 116-125. DOI: 10.1016/j.actbio.2018.06.033

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