

# IGB NEWS

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Volume 7, Number 7

## UPCOMING EVENTS

### IGB Seminar

*New Techniques for Multiple Sequence Alignments with up to 1,000,000 Sequences*  
November 18, 2014, 12:00 p.m.  
612 Institute for Genomic Biology

Tandy Warnow, PhD  
University of Illinois, Urbana-Champaign  
Department of Bioengineering

### IGB Seminar (GNDP)

*Title to be announced*  
December 2, 2014, 12:00 p.m.  
612 Institute for Genomic Biology

Hagai Shpigler, PhD  
University of Illinois, Urbana-Champaign  
Institute for Genomic Biology

### IGB Seminar (GNDP)

*Title to be announced*  
December 9, 2014, 12:00 p.m.  
612 Institute for Genomic Biology

X. Shirley Liu, PhD  
Harvard University  
Dana-Farber Cancer Institute

### IGB Seminar (CDMC)

*Title to be announced*  
January 27, 2015, 12:00 p.m.  
612 Institute for Genomic Biology

Jun Song, PhD  
University of Illinois, Urbana-Champaign  
Department of Bioengineering

## FEATURED NEWS



Illinois, Mayo Clinic Collaboration  
on Genomic Data Analysis



Novel Bacterial Genome Roadmap  
Leads To New Drug Discovery

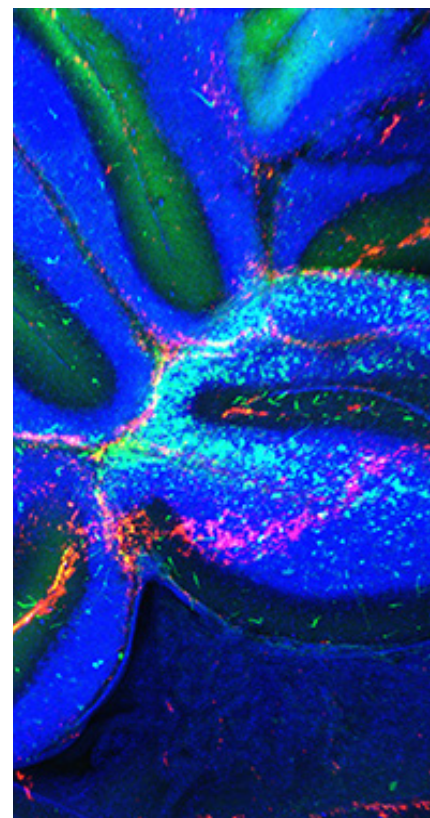


Profile:  
James Doroghazi



On the Grid:  
Happenings at IGB

## IMAGE OF THE MONTH



This month's image, provided by Xiaochen Lu of the Lisa Stubbs Lab, features an adult mouse brain cleared with the active CLARITY technique. Acrylamide and hydrogel electrophoresis were used to render the tissue transparent and optically clear. The neuronal cells were labeled with Calretinin (green), GNPY (red) antibodies counter stained with Hoechst (nuclei-blue) and mounted in RapiClear; imaged using the LSM 710 Confocal system.

### IGB News

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



## University of Illinois Collaborates with Mayo Clinic to Revolutionize Genomic Data Analysis

Today's researchers, working with the advantages of new, sophisticated laboratory technology, have unleashed a river of valuable biomedical data—much more, in fact, than many of them have the tools to properly analyze, or the capacity to store. In 2012, the National Institutes of Health created the Big Data to Knowledge (BD2K) initiative to enable efforts to harness the potential of this flood of information. As part of the first wave of BD2K funding, the University of Illinois at Urbana-Champaign and Mayo Clinic have now received a \$9.34M, 4-year award to create one of several new Centers of Excellence for Big Data Computing.

The NIH initiative encompasses a broad range of “big data” types, including collections of high-resolution research images or real-time recordings of complex biological phenomena. The Illinois-Mayo Center, to be located on the Urbana-Champaign campus, will focus on the analytical challenges posed by the rapidly growing body of genomic and transcriptomic data produced by genome-wide, high-throughput experimental technologies.

The Center's research goal is to create a revolutionary analytical tool that allows any biomedical researcher to place a gene-based data set in the context of “community knowledge,” the entire body of previously published gene-related data. This broad context for individual data sets will offer new functional insights for the genes being studied. The proposed Knowledge Engine for Genomics, or KnowEnG, will be unique in its integration of many disparate sources of gene data to increase its analyt-

ical power, as well as in its planned scalability—the tool will be designed to accommodate the continued growth of genomic community knowledge, and the increasing computational infrastructure required to work with genomic data.

To create KnowEnG, the Center will combine the expertise of many units across the U of I campus, including the Institute for Genomic Biology (IGB), the Department of Computer Science, the Coordinated Science Laboratory, the College of Engineering, and the National Center for Supercomputing Applications (NCSA). As a leader of biomedical research and structured data collection, Mayo Clinic will play a vital role in design, testing, and refinement.

The Center will be led by computer scientist and IGB affiliate Jiawei Han, who will serve as Program Director. Other Principal Investigators are computer scientist and IGB member Saurabh Sinha; physicist, bioengineer and IGB member Jun Song; and Richard Weinshilboum, M.D., interim director of the Mayo Clinic Center for Individualized Medicine and director of the center's Pharmacogenomics Translational Program. IGB and NCSA Director of Bioinformatics and Director of the High-Performance Biological Computing Group, C. Victor Jongeneel, will function as Executive Director.

The Center's transcendence of disciplinary boundaries will be key to its success. Insights drawn from many areas of computer science will strengthen KnowEnG's design.

“By integrating multiple analytical methods derived from the most advanced data mining and machine learning research, KnowEnG will transform the way biomedical researchers analyze their genome-wide data,” said Han. “The Center will leverage the latest computational techniques used to mine corporate or Internet data to enable the intuitive analysis and exploration of biomedical Big Data.”

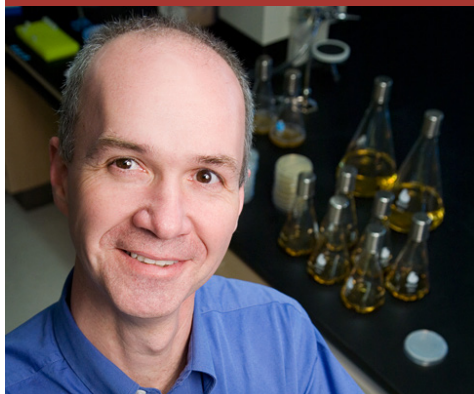
The Center will also rely on communication between interface design experts at Illinois and biomedical researchers at Mayo Clinic, who represent KnowEnG's intended users. Feedback among these Center members will ensure that the developed tool is valuable, intuitive, and customizable for use in a broad array of experimental contexts.

Describing his excitement for the project, co-PI Sinha explained, “This is [a project] that's bigger than all of us . . . what I'm most excited about is the actual possibility that this could be a tool which everybody uses in the world.”

In addition to development of KnowEnG, the Center will develop a training framework that empowers researchers to use the new tool and engage in bioinformatics research, regardless of their prior computational knowledge. The Center will also participate in a planned nation-wide consortium, composed of all the BD2K Centers of Excellence established by the NIH initiative, to exchange insights, contribute to standards for tool development, and help set broad goals for the future of work on Big Data. ■

*Written by Claudia Lutz.*

## RESEARCH



William Metcalf is the G. William Arends Professor in Molecular and Cellular Biology and Professor of Microbiology. His research centers on investigating microbial metabolic processes which may hold important biomedical, biotechnological and environmental ramifications.

# A Novel Roadmap Through Bacterial Genomes Leads the Way to New Drug Discovery

For millennia, bacteria and other microbes have engaged in intense battles of chemical warfare, attempting to edge each other out of comfortable ecological niches. Doctors fight pathogens with an arsenal of weapons—antibiotics—co-opted from these microbial wars, but their efforts are frustrated by the development of drug resistance that outpaces drug discovery. Researchers at the University of Illinois at Urbana-Champaign and Northwestern University have now innovated and demonstrated the value of an algorithm to analyze microbial genomic data and speed discovery of new therapeutic drugs.

A large proportion of the medications used today were discovered by screening bacteria and other organisms for their ability to produce natural products, biologically useful compounds. In recent years, pharmaceutical companies have largely abandoned this strategy in favor of screening synthetically created chemicals for useful properties, an area of research which has yielded a tiny number of new antibiotics.

Microbiologist and molecular and cellular biologist Bill Metcalf, a leading investigator in the new study, described the reason for pharmacological research's shift away from the exploration of natural products. "There was a reason why they gave up . . . they kept discovering the same things over and over and over again," he said. "They were getting very diminishing returns."

This type of problem will be familiar to anyone who has ever collected trading cards. It's easy to acquire a set of the common cards, but it can be nearly impossible to find the rare ones scattered among them. A collector might wish that he or she could sneak a peek at all the cards hidden inside the wrappers, and only buy the new ones.

Genome sequence information, which is now available for an ever-increasing number of bacterial species, holds the promise to allow antibiotic hunters to do just that. Groups, or "clusters" of genes within each genome code for enzymes,

*By comparing the distribution of gene cluster families across bacterial species, researchers can now predict which species are most likely to contain novel antibiotics, and target the richest strains for study.*

*"We've got the framework, we know the number of gene clusters, we know who has them and therefore we know where to look to find new drugs. It clearly leads to discovery."*

proteins that work together to synthesize a natural product for that bacterium. Part of the vision of the Institute for Genomic Biology's Mining Microbial Genomes research group, led by Metcalf, is to use bacterial genome sequence data as an index of what products each one can produce.

If researchers could infer what type of product the bacterium is making by looking at its DNA, they wouldn't have to go through a lengthy screening process—they could just scan genomes for promising gene clusters. Unfortunately, this task is much harder than it sounds. Many clusters have some sequences or whole genes in

common, making them indistinguishable by traditional comparative methods even though they enable the production of different compounds.

Metcalf, co-lead author with former Institute for Genomic Biology Fellow James Doroghazi, and colleagues cleared this hurdle with a clever computational solution: they combined multiple comparative metrics, each with a carefully calibrated weight, to produce an algorithm that sorted 11,422 gene clusters from 830 bacterial genomes into an orderly, searchable reference. Their work was published this month in *Nature Chemical Biology* (**10.1038/nchembio.1659**)

In the database created in the study, gene clusters predicted to make very similar products are linked with each other in networks referred to as families. These predictions mesh almost perfectly with prior knowledge; gene clusters that produce similar known compounds were sorted by the new algorithm into the same family in every case but one.

The value of the new database was showcased by an experiment performed in collaboration with a group of chemists at Northwestern University, led by former University of Illinois faculty member Neil Kelleher. Kelleher's group used a high-precision analytical technique to infer the chemical composition of unknown compounds isolated from 178 different bacterial strains. The research team was then able to assign a biological function to gene cluster families by correlating their presence in the genome with the production of particular compounds.

In addition to this power to link gene cluster families to potential new antibiotics, the database is a huge step toward solving the "trading card" problem. By comparing the distribution



of gene cluster families across bacterial species, researchers can now predict which species are most likely to contain novel antibiotics, and target the richest strains for study. “We’ve got the framework, we know the number of gene clusters, we know who has them and therefore we know where to look to find new drugs,” said

Metcalf. “It clearly leads to discovery.”

In addition to Doroghazi, former Northwestern graduate student Jessica Albright was a co-first author of the study, and Neil Kelleher was a co-corresponding author. David Labeda, a microbiologist at the USDA Agricultural Research Service, shared many of the bacterial strains

that provided novel genomic sequence for the work. Funding was provided by the Institute for Genomic Biology and the NIH. The database of gene cluster families is publically available: <http://bit.ly/1rLR0O6>. ■

*Written By: Claudia Lutz. Photo by L. Brian Stauffer.*

## PROFILE



*James Doroghazi was the Mining Microbial Genomes IGB fellow, and worked closely with theme members in the study of microbially produced natural products and secondary metabolites.*

# James Doroghazi: Designing for the Next Generation

At a time when scientists and farmers are thinking about feeding several billion more people, Western corn rootworm, known as the billion-dollar pest, has been found to be resistant to multiple types of corn engineered to naturally produce pesticides.

It’s up to scientists like James Doroghazi, a former fellow at the Institute for Genomic Biology, to engineer new solutions to prevent these pests from decimating yields and risking global food security.

“We need to increase food production to meet growing world populations, and that is not going to happen without genetically modified organisms,” said Doroghazi, who recently accepted a job with Bayer CropScience. “I will be finding proteins that kill insects so that we can design the next generation of genetically modified organisms.”

Doroghazi’s experiences at the IGB, including earning the Certificate in Entrepreneurship and Management (CEM), have made him a “well-rounded” bio-informatician ready for the next stage of his career. As a member of the Mining Microbial Genomes theme, he had the opportunity to work with several labs and build an impressive publication record.

“The combination of resources and fast pace of research at the IGB gave me a CV that I think is suited for applying to both academic and industry positions,” Doroghazi said. “I feel lucky that my experiences as an IGB Fellow prepared me to pursue an industry job. CEM exposed me to the business side of thinking and

*“I feel lucky that my experiences as an IGB Fellow prepared me to pursue an industry job. CEM exposed me to the business side of thinking and made me more comfortable with switching from an academic track to an industry track.”*

made me more comfortable with switching from an academic track to an industry track.”

Equally valuable are the relationships that Doroghazi formed during his time at the IGB.

Doroghazi and Scott Woolbright, also an IGB fellow, bonded during a trip to the BGI (formerly the Beijing Genomics Institute) in China. The trip sparked a collaboration to study bacterial and fungal communities in and around the roots of prairie plants, Doroghazi said. “The conversations that happen through theme hops or programs like the BGI trip extend your network in ways that wouldn’t happen if you were a postdoc isolated in one department.”

Doroghazi received his doctorate in Microbiology from Cornell University in 2010 under the direction of Dan Buckley. For his dissertation work, he studied the population genetics and evolution of *Streptomyces*. At the IGB, he worked on novel natural product genetic diversity and elucidating common themes in secondary metabolite evolution. His work was recently published in *Nature Chemical Biology* (see page 3). ■

*Written by Claire Sturgeon. Photo by Kathryn Coulter.*

# ON THE GRID HAPPENINGS AT THE IGB

## AWARDS



### MAY BERENBAUM

May Berenbaum, Professor and Head of Entomology (Genomic Ecology of Global Change) received the National Medal of Science, the nation's highest honor for achievement and leadership in advancing the fields of science and technology, administered by the National Science Foundation (NSF) and bestowed by the President of the United States.

## SERVICE AWARDS



### 15 YEAR AWARDS

The IGB is proud to recognize those academic professionals who have served on campus. We

recognized two important milestones at the Service Award luncheon held in late October. Becky Heid celebrated 15 years on campus, formerly with the EBI and the RIPE project under the Gates grant, and presently at the Department of Business Administration. Bruce Barnes also celebrated 15 years on campus, most recently with the IGB business office before moving to support the Gates grant position left by Becky! Congratulations to all.

## NEW ARRIVALS



### STEPHEN LONG

Stephen Long, Gutsell Endowed Professor of Crop Sciences and Plant Biology (Genomic Ecology of Global Change, Biosystems Design) was presented with the Thomson Reuters Highly Cited Researcher in recognition of ranking among the top 1% of researchers for most cited documents in their specific field. Long was also named one of the World's Most Influential Scientific Minds for 2014.



### KINGSLEY BOATENG

Kingsley Boateng joins the IGB as a Research Specialist at the IGB Core Facilities. He received his Ph.D. in Molecular and Cell Biology from the University of Miami, Oxford, OH in 2007. Before joining IGB, Kingsley worked as a Research Fellow (Postdoc) at the Genetic and Biochemistry Branch of The National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) of National Institute of Health (NIH), Bethesda.

### SUSAN JONGENEEL

Susan Jongeneel joins IGB as an editor and grant development specialist. Susan holds a Ph.D. in sociology from Vanderbilt University. She has worked at the University of Illinois since 2010 at ACES and in the Office of the Vice Chancellor for Research. Before coming to Illinois, she worked as a competitive intelligence advisor at the international headquarters of Nestlé in Vevey, Switzerland.



### NICHOLAS VASI

Nicholas Vasi, IGB Director of Communications, received the 2014 Communicator of the Year award from the office of Public Affairs. This Award for Communications & Marketing Excellence (ACME) is presented to an individual who exemplifies the qualities of service, innovation, and advancement.



### CHRISTINE INGLEMAN

Christine Ingleman joins the IGB Business Office as an Accounting Clerk, reconciling t-card and p-card charges as well as providing support to t-card and p-card users. Christine started at the University of Illinois in 2003 with the Fire Service Institute, and then moved to the Engineering Business Services Center. Prior to joining the University, she worked as an optician at Illini EyeCare.



### JOYCE KOEBERLEIN

Joyce Koeberlein joins the IGB as an Office Manager supporting the Cellular Decision Making in Cancer research theme and the Core Facilities. Before joining the IGB, Joyce worked for a short time in the Department of Chemical and Biomolecular Engineering providing clerical support to the Graduate Programs. Prior to that time, she worked as a Construction Management Project Assistant for the Capital Programs Department for eight years. She has worked at the University of Illinois for 15 years.

# ON THE GRID HAPPENINGS AT THE IGB

## IP @ IGB

### NOMINATIONS FOR INNOVATION CELEBRATION NOW OPEN

Innovation Celebration is an annual event that recognizes the entrepreneurial spirit in our community and on our campus. Awardees are recognized for contributions in several categories, including economic impact, social entrepreneurship, and student start-ups.

The Office of Technology Management is proud to partner with event organizers to host the Innovation Transfer award, which is specific to nominees from the University of Illinois. This award recognizes an individual or group from the University whose research has resulted in a discovery or a work with the potential for significant societal impact.

Past Innovation Celebration winners include: Dr. Stephen Boppart, for his work on medical imaging devices capable of delivering real-time

microscopic imaging at the point-of-care.

Dr. Yoram Bresler, for his work on innovations used in computerized tomography (CT) scans.

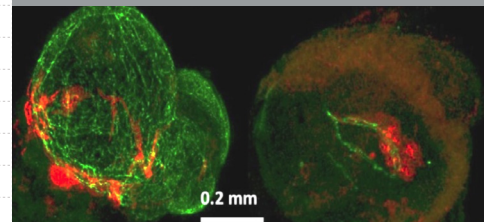
Dr. Martin Burke, for his work involving the synthesis and study of small molecules with protein-like functions.

Although Innovation Celebration is not until March, nominations are open and will be accepted through Dec. 5, 2014. Nominate yourself or a colleague today by filling out a very brief form, which can be found at [www.innovationcelebration.com](http://www.innovationcelebration.com).

The event ceremony will take place on March 2, 2015 from 5:30 to 8:30 p.m. in the Krannert Center for the Performing Arts Lobby.

Do you have questions about patenting your research? Please contact Brad Edwards ([ebeward@illinois.edu](mailto:ebeward@illinois.edu)) or Lisa Dhar ([ldhar10@illinois.edu](mailto:ldhar10@illinois.edu)) of the Office of Technology Management.

## RESEARCH



### EMBRYONIC STEM CELL-DERIVED CARDIOVASCULAR ORGANOID

Associate Professor of Chemical & Biomolecular Engineering Hyunjoon Kong (ReBTE) recently published in *PLOS One* on how stem cell clusters derived from embryonic stem cells are used to create complex tissues. Kong's study demonstrates a simple but effective strategy to promote the formation of vascularized cardiac muscle, improving our understanding of stem cell behavior in developmental and regeneration process. Read the paper: DOI: [10.1371/journal.pone.0094764](https://doi.org/10.1371/journal.pone.0094764).

## BLOOD DRIVE



### IGB BLOOD DRIVE

The next IGB blood drive will be on **January 23**, from 8 am to 1 pm in conference room 612. Our first blood drive was so successful we would like to make this a continuing event. Below are the stats from our first blood drive. The fact that we had 11 first time donors is amazing – this is very rare outside of a high school setting.

Great job IGB!

Goal	25
Donors Registered	31
Temporary Deferrals	4
First time donors	11!

## GENOME DAY



### GENOME DAY 2014

Over 300 people attended our 2014 Genome Day, with seventeen creative and interactive activities used to present to the public some of the research that takes place at IGB and across our campus.

Thank you to the 2014 co-chairs, Professor Karen Sears (ReBTE & GNDP) and Dr. Farhan Chowdhury (CDMC Fellow), Coordinator of Outreach Activities Sara Haag, Director of Development and Outreach Melissa McKillip, and the 100+ volunteers from the IGB and across campus, including the Society Devoted to Advancing Hispanics, Chicanos & Native Americans in Science (SACNAS) who provided Spanish speakers to allow for a bilingual day.

## HALLOWEEN



### IGB HALLOWEEN PARTY

A special thank you to everyone who attended the IGB Halloween party. Much fun was had by all and there was as always tremendous creativity shown in the costumes.

Our special thanks to the volunteers and to the IGB Community-Building Team for putting together such an enjoyable afternoon for all.



# ADMINISTRATIVE NEWS

## UNIVERSITY LIBRARY

### RESEARCH DATA SERVICE

The Research Data Service (RDS) (<http://researchdataservice.illinois.edu/>) is a new campus-wide service that is initially focused on ensuring campus researchers are able to meet new data management and sharing requirements from funders and publishers.. Currently, the RDS provides data management expertise through consultations and workshops, provides tools, such as the DMPTool for writing data management plans for grant proposals, and helps to identify appropriate repositories for data deposit, on and off campus.

Headquartered in the University Library, the RDS is a partnership between the Library, the Office of the Provost, the Office of the Vice Chancellor for Research, the Graduate School of Library and Information Science, CITES, and NCSA. Perhaps of particular interest, the Director of the RDS is Dr. Heidi Imker, who was previously at the IGB as the Executive Director of the Enzyme Function Initiative.

If you would like more details about the RDS or if you would like data management assistance from the RDS, please contact Heidi Imker, RDS Director, at [imker@illinois.edu](mailto:imker@illinois.edu). ■

## BUSINESS

### HOLIDAY BREAK REDUCED SERVICE DAYS

Please be aware for this year there are four reduced services days for the holiday break. The IGB will be closed during the holiday break. Please start planning ahead to insure that you will have a sufficient number of vacation days/floating holidays to cover the four reduced services days listed below. Employees can choose to use their accrued vacation days and/or floating holidays to cover their time off for the four reduced service days.

Wednesday, December 24, 2014	1/2 Gift Day and 1/2 Excused Day
Thursday, December 25, 2014	Christmas Day Holiday
Friday, December 26, 2014	Day after Christmas Holiday
Monday, December 29, 2014	Reduced Service Day
Tuesday, December 30, 2014	Reduced Service Day
Wednesday, December 31, 2014	Reduced Service Day
Thursday, January 1, 2015	New Year's Day Holiday
Friday, January 2, 2015	Reduced Service Day

If you have any questions, please contact Jacinda King at 244-2276 or [jkking@illinois.edu](mailto:jkking@illinois.edu). ■

## RECENT PUBLICATIONS

Bauweraerts I, Mannaerts TBHL, Wertin TM, McGuire MA, Teskey RO, Steppe K. Elevated [CO<sub>2</sub>] and growth temperature have a small positive effect on photosynthetic thermotolerance of *pinus taeda* seedlings. *Trees-Struct Funct.* 2014;28(5):1515-1526.

Hwang H, Opresko P, Myong S. Single-molecule real-time detection of telomerase extension activity. *Sci Rep.* 2014;4:6391.

Kim HJ, Kim M-, Turner TL, et al. Pyrosequencing analysis of microbiota reveals that lactic acid bacteria are dominant in korean flat fish fermented food, gajami-sikhae. *Biosci Biotechnol Biochem.* 2014;78(9):1611-1618.

Liu H, Wang Y, Tang Q, Kong W, Chung W-, Lu T. MEP pathway-mediated isopentenol production in metabolically engineered *escherichia coli*. *Microb Cell Fact.* 2014;13:135.

Cox CL, Tietz JI, Sokolowski K, Melby JO, Doroghazi JR, Mitchell DA. Nucleophilic 1,4-additions for natural product discovery. *ACS Chem Biol.* 2014;9(9):2014-2022.

Kaiser E, Morales A, Harbinson J, Kromdijk J, Heuvelink E, Marcelis LF. Dynamic photosynthesis in different environmental conditions. *J Exp Bot.* 2014.

Lian J, Zhao H. Recent advances in biosynthesis of fatty acids derived products in *saccharomyces cerevisiae* via enhanced supply of precursor metabolites. *J Ind Microbiol Biotechnol.* 2014.

Agarwal V, Vondenhoff G, Gadakh B, Severinov K, Van Aerschot A, Nair SK. Exploring the substrate promiscuity of an antibiotic inactivating enzyme. *MedChemComm.* 2014;5(10):1567-1570.

Goicoechea N, Baslam M, Erice G, Irigoyen JJ. Increased photosynthetic acclimation in alfalfa associated with arbuscular mycorrhizal fungi (AMF) and cultivated in greenhouse under elevated CO<sub>2</sub>. *J Plant Physiol.* 2014;171(18):1774-1781.

Dong Y, Sanford RA, Locke RA,II, Cann IK, Mackie RI, Fouke BW. Fe-oxide grain coatings support bacterial Fe-reducing metabolisms in 1.7-2.0 km-deep subsurface quartz arenite sandstone reservoirs of the illinois basin (USA). *Front Microbiol.* 2014;5(SEP).

Erice G, Sanz-Sáez A, Urdiain A, Araus JL, Irigoyen JJ, Aranjuelo I. Harvest index combined with impaired N availability constrains the responsiveness of durum wheat to elevated CO<sub>2</sub> concentration and terminal water stress. *Funct Plant Biol.* 2014;41(11):1138-1147. ■



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Contact Nicholas Vasi ([nvasi@illinois.edu](mailto:nvasi@illinois.edu))  
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