IGB NEWS

Volume 9 Number 3

UPCOMING EVENTS

IGB Pioneers Seminar (GEGC)

Role of the CBF Regulatory Pathway in Plant Freezing Tolerance

April 19, 2016, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Michael F. Thomashow, PhD

Michigan State University, Department of Plant, Soil and Microbial Sciences

Department of Microbiology and Molecular Genetics

Lunch With The Core

STED of Quantum Dots

April 27, 2016, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Lunch and learn hosted by IGB Core Facilities.

Austin Cyphersmith, PhD

Research Specialist in Life Sciences

IGB Core Facilities

Art of Science 6.0

Opening Reception April 28, 2016, 6:00 p.m.

Gallery 217 (formerly Indo go Gallery)

9 E. University Avenue, Champaign

The Art of Science celebrates its sixth year of common ground between science and art and a meeting place between the University of Illinois and the community.

2016 Fellows Symposium

May 5, 2016, 8:30 a.m. - 3:30 p.m.

612 Carl R. Woese Institute for Genomic Biology

Hear about current research, connect with other students, and submit a poster for the poster session. Registration is free, lunch provided:

http://conferences.igb.illinois.edu/fellows/

Keynote by Joan Strassmann

Charles Rebstock Professor of Biology

Washington University in St. Louis

"Genomic approaches to social interactions in the amoeba Dictyostelium discoideum*"*

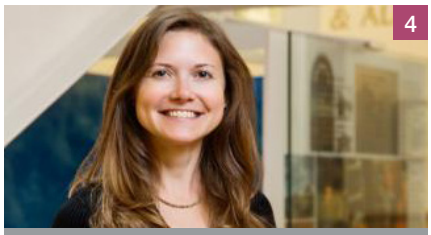
FEATURED NEWS

2

CompGen Team Builds Ancestral Trees to Identify Genetic Variants

3

Sequence Features Accurately Predict Genome-Wide Binding *In Vivo*



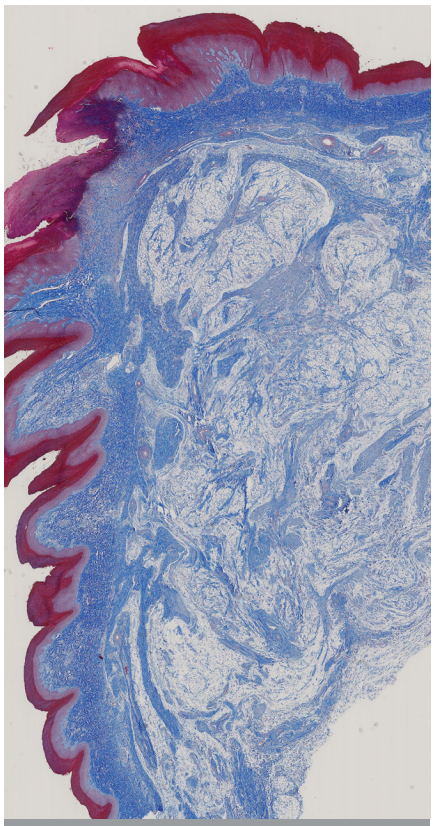
4

Profile: Megan Dailey

5

On the Grid: Happenings at IGB

IMAGE OF THE MONTH



This month's image features a chicken footpad labeled with trichrome stain imaged using the Nanozoomer. The footpad skin of chicken feet is covered with multiple reticular scales. The structure includes a thick outer layer called stratus corneum (brown) followed by epidermis (pink), dermis (blue), and subcutaneous tissue (blue and white). Footpad dermatitis (FPD) is a type of skin inflammation that causes necrotic lesions on the plantar surface of footpads. Novus International is studying the structure integrity of footpad skin and pathology of FPD.

Image courtesy of Juxing Chen, Novus International Inc., St. Charles, Missouri.

IGB News

Share your news with the IGB. Send ideas on stories, articles, and features to *nvasi@illinois.edu*.

FEATURE

CompGen team builds ancestral trees
to determine disease-causing genetic variants

Many of our most widespread diseases, such as diabetes, cancer, cardiovascular disease, and mental illness, are associated with variants in our genes. How do these variants in our genomes carry across generations, and how do they ultimately affect our health? University of Illinois researchers are trying to unlock the mystery.

Parsing out ancestry-related genomic variations requires some data crunching. To put it in perspective, within each human genome, there are 46 chromosomes, and a single chromosome can have 6.5 million variants. Variants can be passed down from generation to generation, creating a map of ancestral genomic history. Each of those variants may play a unique role in our health.

Using novel algorithms, researchers from CompGen, a collaborative computational genomics initiative between the Coordinated Science Laboratory and the Carl R. Woese Institute for Genomic Biology, are employing the supercomputing power of NCSA's Blue Waters to scan 2,500 genomes to determine how variants transfer through ancestral ties.

Armed with this information, they can start to understand how our ancestry makes us either susceptible or resilient to diseases.

"How our genomic variants are partitioned across geographic and ethnic diversity is really important, both for understanding human evolutionary history and patterns of migration and globalization, but also very important for understanding health and disease, which is our major focus," said Derek Wildman, a CompGen researcher, professor of molecular and integrative physiology and leader of the Computing Genomes for Reproductive Health research theme at the IGB.

Wildman, who is working with Don Armstrong, a research scientist at IGB, and Monica Uddin, an associate professor of psychology at Illinois and IGB, says past research examining ancestry and disease have relied upon self-reported ethnicity, a limiting factor.

"A lot of disease research has based ethnic categorizations along self-reported ethnicity, but genetic variation is more subtle and complex than socially constructed categories such as race," said Wildman. "We're all mixed to varying degrees with different histories, and that complexity, which we can determine using Blue Waters, likely plays a role in our health and disease."

When looking at what can causes disease, it is additionally important to disambiguate between genetic and external factors of particular ethnic groups. Wildman, for example, has found that in terms of pregnancy, African Americans are at a greater risk for pre-term birth than white Americans. The reason for this is something this team is still investigating.

"We're not sure whether that's due to environment, psycho-social factors, a history of racism and segregation, or genetics," said Wildman. "We haven't been able to tease them apart, but it seems worthwhile to examine all those aspects. Having accurate ancestral trees in relation to genetic variants is a key component."

To determine disease-causing genetic variants, the team needs to solve another genetic problem that's emerging: genomics is quickly becoming the discipline that generates the most data, surpassing other big data producers, like YouTube and Twitter, in scale. That's where Blue Waters can help.

"There are more possible phylogenetic trees from the 2,500 genomes we're analyzing than there are electrons in the universe," said Wildman. "So looking at all of those would be prohibitive, but there are approaches on Blue Waters that allow you to simulate phylogenetic trees and get an idea of what the correct ones are."

Armstrong is using algorithmic approaches called maximum likelihood and Bayesian inference to comprehensively sort through and efficiently select the likely ancestral roots of each human genome.

Once the researchers have the ancestral trees, they can map out how our ancestry affects genomic variations, and which variations are markers for disease.

"We're working to make better maps of ancestral and genomic history and to see the genetic landscape more accurately," said Wildman. "Ultimately, knowing what diseases you may be susceptible to, based on your genetics, means you can take action and make better informed decisions about your health." ■

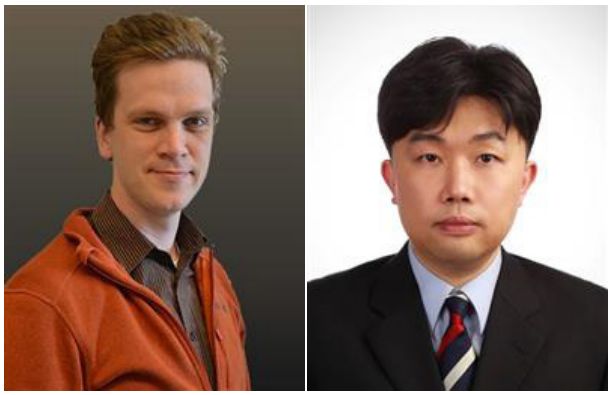
Written by August Schiess. Photo by Kathryn Faith.

Jun Song, Founder Professor of Bioengineering and of Physics, applies research in computational biology and biomedicine and leverages methodologies and tools of physics and mathematics to discover how transcription factors, chromatin structure and non-coding RNAs regulate gene expression.

Sequence features accurately predict genome-wide MeCP2 binding *in vivo*

Researchers from the University of Illinois at Urbana-Champaign and the University of California-Davis (UC Davis) are combining *in vivo* experimentation with computation for highly accurate prediction of the genome-wide binding pattern of a key protein involved in brain disorders.

"The MeCP2 gene is critical for proper brain development and expressed at near-histone levels in neurons, but the mechanism of its genomic localization remains poorly understood," explained Jun Song, a professor of bioengineering and of physics at the University of Illinois at Urbana-Champaign. "Using high-resolution MeCP2 binding data, we show that DNA sequence features alone can predict binding with 88% accuracy." Dr. Song is also a faculty member at the IGB.



Tomas Rube (left), postdoctoral researcher in Song's research group, and Wooje Lee (right), co-first author and postdoctoral fellow in the laboratory of Qizhi Gong.

Even though every cell in a person's body contains the same DNA sequence, it is possible to have hundreds of different cell types with distinct shapes and functions, because the access to genetic information encoded in DNA is regulated in a cell type-specific manner. One way of regulating the information access is through chemically modifying DNA with methylation, which is in turn recognized by various proteins that physically interact with other factors to control transcriptional activities.

According to Tomas Rube, a postdoctoral researcher in Song's research group, MeCP2 is one of the proteins previously identified to bind methylated CG dinucleotides.

"Mutations in the MeCP2 gene are directly linked to a severe brain disorder known as the Rett Syndrome, but the genome-wide binding pattern and function of MeCP2 remain poorly understood," said Rube, the lead author of the paper, "Sequence Features Accurately Predict Genome-wide MeCP2 Binding *in vivo*," appearing in *Nature Communications*.

In neurons, MeCP2 is approximately as abundant as histone octamers in the nucleus and is believed to be broadly distributed throughout chromatin. This high abundance has posed a major technical challenge in mapping the genome-wide binding sites of MeCP2 and characterizing the precise DNA sequence features that help recruit MeCP2.

The researchers showed that MeCP2 densely covers the genome in a manner that can be accurately predicted using DNA sequence features alone and that local MeCP2 binding activities can help explain the pattern of gene expression in neurons.

"These findings provide key insights into this important epigenetic regulator and highlight the complexity of understanding the relation between DNA sequence and gene regulation," stated Wooje Lee, a co-first author and a postdoctoral fellow in the laboratory of Qizhi Gong, professor of cell biology and human anatomy at the UC Davis School of Medicine and co-senior author of this study. Dr. Gong's laboratory and her colleagues at UC Davis did the experimental work, while Dr. Song's group handled the complex computation and modeling.

The research team, representing several universities in the U.S. and Korea, used new high-resolution MeCP2 ChIP-seq data from olfactory epithelium, to develop a predictive model of genome-wide MeCP2 binding pattern. Although there is strong evidence *in vitro* supporting the ability of MeCP2 to bind methyl-CpG (mCpG), MeCP2 may actually bind diverse sequences *in vivo*, as reflected in its multifaceted roles. The functional impact of MeCP2 has been previously examined by attempting to identify MeCP2 target genes in neurons. In addition to a number of genes found to be suppressed by MeCP2, multiple studies have also identified a global reduction of transcription in neurons lacking functional MeCP2, suggesting a novel activating role of MeCP2.

"Contrary to the common belief that MeCP2 can bind only methylated CG, our study shows that MeCP2 in fact has diverse modes of binding, largely attributable to the GC sequence content and often independent of the methylation status of DNA," Song said, adding that the lack of a fine-resolution genome-wide binding map has been a major bottleneck in understanding the mechanism of MeCP2 function to this point. "This study shows that MeCP2 binds distinct but numerous sites throughout the genome in a manner that can be accurately predicted using DNA sequence features alone."

Study was made possible by important contributions from other co-authors Miroslav Hejna (University of Illinois); Huaiyang Chen, Dag H. Yasui, John F. Hess, and Janine M. LaSalle (University of California-Davis School of Medicine). ■

Written by Rick Kubetz. Photos courtesy of Jun Song lab.

Megan Dailey is an Assistant Professor in the Department of Animal Sciences and a member of the Neuroscience Program. Her research explores the biological signaling systems that link what an animal eats with how its cells proliferate and how they act, in the digestive system and in the brain.

Megan Dailey:
Finding the connections between what we eat and who we are

Megan Dailey (RBTE) is a difficult person to categorize. An animal scientist who began her scientific career with a degree in Psychology? A neuroscientist who studies the digestive system? She is able to weave all the different threads of her work together into a seamless fabric by anchoring them to the most basic principles of life.

"All of our genes, everything, all of it meant to do two things. Survive, reproduce. Survive, reproduce. Whenever I teach a class, my students get so sick of it," Dailey said with a smile. "It's all about nutrient availability, and then can I make some offspring ... and that's it."

Of course, uncovering the complicated story of how cells use the resources in their environment to fulfill these basic drives will take Dailey and countless other researchers years of work. Dailey is interested in how nutrients affect the function of a cell, whether that cell is in the brain or in the intestine; she wants to know how what we and other animals eat changes how our bodies work.

Dailey's career in science actually grew out of a curiosity about how the structure and function of the brain influences an animal's perception of its environment. During her graduate studies at Georgia State University, she studied how different diets—high fat, high protein, high sugar—change the gene expression and signaling activity of neurons and, as a result, the feeding behavior of the animal. As she began her postdoctoral work at the Johns Hopkins University School of Medicine, she found that her questions about nutrients and the brain were outpacing the technology available at the time to help answer them.

"There's so little known about the blood-brain barrier [the layer of cells lining capillaries in the brain that strictly control what nutrients and other chemicals can enter the brain] but there's even less known about how to properly study the blood-brain barrier," Dailey said. "I decided to look a little more at how the nutrients that we eat affect cellular function within the intestine ... I was using the same exact knowledge, the same processes that I was exploring in the brain, I was just doing it in a different type of cell."

"I decided to look a little more at how the nutrients that we eat affect cellular function within the intestine ... I was using the same exact knowledge, the same processes that I was exploring in the brain, I was just doing it in a different type of cell."

Instead of examining a tissue that is affected by nutrition indirectly, through many layers of filtering and signaling, Dailey was now looking at tissues that make physical contact with nutrients as they enter the body and move into the bloodstream. Accordingly, the results were dramatic. She found that high fat diets induced growth of the epithelial lining of the intestine; this growth was stimulated by contact with the food, whether it was eaten or infused directly into the gut.

The phenomenon appears to be a unifying one across many animal taxa, including mammals, fruit flies, hydra, and roundworms. Dailey turned her attention to examining the communication that must occur between the cells that line the villi, the microscopic projections of the intestinal wall, and the stem cells that are nestled in the glands called crypts that lie in between.

Dailey's recent findings suggest that the amount of food and the type of diet are detected and signaled to the stem cells via different systems, respectively influencing the rate of cell division and types of cells produced. She is interested in how high fat diets eventually lead to chronic signaling differences in obese animals.

The connection to stem cell biology is leading Dailey back to her long-standing interest in nutrition and the brain. A neuroscience graduate student in Dailey's laboratory, Elizabeth Davis, is investigating how the autonomic nervous system influences intestinal stem cell proliferation. Dailey also hopes to explore whether the same signaling mechanisms that connect nutrient intake with cell division in the intestine also impact the rate at which new neurons are produced in the adult brain.

Through all the twists and turns of her research career, Dailey stays close to the most basic questions that drive her work, and she feels at home in the interdisciplinary environments she has discovered in the School of Integrative Biology, the Neuroscience Program, and the IGB since moving to Illinois in 2013.

"I see a cell with a cell membrane, and somehow all that stuff on the outside, growth factors, nutrients, are affecting the way that that cell functions," she said. "That's also one thing that's good about Illinois, is that you have a home department that of course brings you one theme of your research, but because there's these other interdisciplinary programs, you really can highlight tangential aspects of your research."

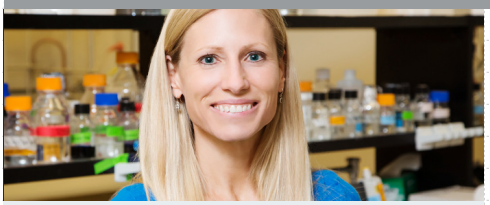
In addition, she appreciates the collegiality and genuine enthusiasm for scientific inquiry that has characterized Illinois for her since her first visit.

"It also felt like people wanted to hear about what you were doing, they wanted to try to help you, it felt very genuine," she said. "And then I came back for a second interview, and it just got better. It kept getting better every single time. Now I've been here for two and a half years, and my first impression never went away." ■

Written by Claudia Lutz. Photo courtesy of the Dailey Lab.

ON THE GRID
HAPPENINGS AT THE IGB

NEW ARRIVALS



MARNI BOPPART

Marni Boppart, Associate Professor of Kinesiology and Community Health (Regenerative Biology & Tissue Engineering) received a Campus Excellence in Undergraduate Teaching Award from the University of Illinois for her positive impact on student learning.

REX GASKINS

Rex Gaskins, Professor of Immunobiology, Departments of Animal Sciences and Pathobiology (Regenerative Biology & Tissue Engineering) has received a Distinguished Scientist Award from the Society for Experimental Biology and Medicine (SEBM), which promotes interdisciplinary investigation in the biomedical sciences.

HYUNJOON KONG

Hyunjoon Kong, Associate Professor and Centennial Scholar in Chemical and Biomolecular Engineering (Regenerative Biology & Tissue Engineering) has received the College of Engineering Dean's Award for Excellence in Research, given annually to faculty in recognition of their outstanding research.

KAREN SEARS

Karen Sears, Associate Professor of Animal Biology (Regenerative Biology & Tissue Engineering) received a Campus Excellence in Undergraduate Teaching Award from the University of Illinois for her positive impact on student learning.

ART

ART OF SCIENCE

The Art of Science is celebrating its 6th year with a gallery opening at Gallery 217 (formerly Indi Go Artist Gallery) on Thursday, April 28th. Showcasing imagery from the Core Facilities at the IGB, the Art of Science traveling art exhibit highlights cutting-edge research that is addressing significant problems in the environment, medicine, energy use and production, and fundamental research.

SUMMER CAMP

POLLEN POWER

Registration for Pollen Power summer camp at the IGB is now open! Pollen Power is a week-long day camp for girls entering 6th-8th grade to learn about the biological sciences, climate change, and research careers. Find out more and sign up at **http://pollensummercamp.illinois.edu/**.

SYMPOSIUM

IGB FELLOWS SYMPOSIUM

MAY 5, 2016

IGB FELLOWS SYMPOSIUM

Learn about IGB research, hear about current issues in the life sciences, connect with other students on campus and share your research at the popular poster session.

Registration is free and lunch will be provided: **http://conferences.igb.illinois.edu/fellows/**

Registration will close on April 29, 2016. For inclusion in the program posters must be submitted by April 28, 2016.

DONATE

IMPACT

BLOOD DRIVE

The IGB is having a blood drive on Monday, May 9, in IGB Conference Room 612 from 8:00 a.m. to 1:00 p.m. Our goal is set for 25 units of blood. Please help us meet this goal and show how great our team is.

Remember—one pint of blood can save up to 3 lives, the number one use of blood products is to help people fighting cancer. Every donor is a hero in the eyes of the person who is receiving that blood donation!

Sign up at **www.bloodcenterimpact.org**, call Darci Edmonson at 244-2200 or email at *darci@illinois.edu.*

DEPARTMENT ANNOUNCEMENTS

BUSINESS

UNIVERSITY OF ILLINOIS TAX EXEMPT STATUS

The University of Illinois is an instrumentality of the State of Illinois, and as such it is exempt from federal income tax under Section 115 of the Internal Revenue Code. The Internal Revenue Service also recognizes the University as exempt from federal income tax under Section 501(c)(3).

In addition, the University is exempt from the following Illinois state and local taxes:

- Income Tax
- Real Property Tax
- Retailers' Occupation Tax
- Service Occupation Tax
- Use Tax and Service Use Tax

The University is not exempt from Electricity Excise Tax or Hotel Operators' Occupation Tax.

When making purchases on behalf of the University, please present suppliers with the University's sales tax exempt letter to avoid paying sales tax on purchases. The State of Illinois Tax Exempt Letter can be found at the following url: *https://www.obfs.uillinois.edu/common/pages/DisplayFile.aspx?itemId=93238*.

For additional information, see the OBFS Policies and Procedures Manual Section 18.6, Sales and Use Tax found at the following url: *https://www.obfs.uillinois.edu/bfpp/section-18-taxes/section-18-6* ■

COMMUNICATIONS

ILLINOIS RESEARCH CONNECTIONS BETA

Illinois Research Connections BETA (IRC BETA) allows members of the Illinois research community to access nearly 1,800 STEM and social science faculty profiles through an online, searchable database, updated weekly from the Scopus abstract and citation database.

For the BETA launch in fall 2015, profiles were created for all tenure-line faculty in STEM and social sciences units at the University of Illinois at Urbana-Champaign, and all researchers within OVCR institutes.

IRC BETA does not include non-tenure line researchers from most units at this time (emeritus faculty, clinical faculty, academic professions), and is investigating the most efficient ways to include non-faculty research experts from across campus.

Following the BETA launch, Illinois Research Connections will grow to include up to 2,500 public faculty and researcher profiles from all Illinois disciplines, and expand to include grants, patents, and more. Use cases include:

- Faculty, researchers, and staff can identify a potential collaborators with niche expertise on- or off-campus, identify potential reviewers with needed expertise for a grant, fellowship, P & T, and more
- Grad students, postdocs, and undergrads can identify advisors, mentors, and committee members
- General public, legislators, and potential corporate partners can view the breadth, depth, and significance of campus research in one central place

Now would be an excellent time to log in, review your profile, and update your information as needed. Simply visit **http://experts.illinois.edu** and click "Log into Pure" at the bottom of the page. Your login information is your Active Directory (AD) username and password.

IRC BETA can also be used to export a list of captured publications into several formats, including Word, PDF, RIS, BibTeX, and HTML.

An extensive FAQ list and training videos can be found at **http://publish.illinois.edu/researchconnections/?page_id=67**

Illinois Research Connections is a joint project supported by the University Library and the Office of the Vice Chancellor for Research. The service has been developed using the Elsevier Pure Experts researcher information portal. By using Elsevier Pure, Illinois Research Connections will facilitate discovery of potential collaborators on the Illinois campus as well as a larger network of more than 160,000 researcher profiles at 160+ institutions worldwide, including CIC peers Michigan, Northwestern, and Minnesota.

Questions can be sent to *irc-help@illinois.edu*. ■

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.

Muhamed I, Wu J, Sehgal P, Kong X, Tajik A, Wang N, Leckband DE. E-Cadherin-mediated force transduction signals regulate global cell mechanics. *J Cell Sci*. 2016 Mar 10. pii: jcs.185447.

Lee J, Abdeen AA, Wycislo KL, Fan TM, Kilian KA. Interfacial geometry dictates cancer cell tumorigenicity. *Nat Mater*. 2016.

Vlcková K, Gomez A, Petrželková KJ, et al. Effect of antibiotic treatment on the gastrointestinal microbiome of free-ranging western lowland gorillas (*gorilla g. gorilla). Microb Ecol*. 2016:1-12.

Jayakody LN, Ferdouse J, Hayashi N, Kitagaki H. Identification and detoxification of glycolaldehyde, an unattended bioethanol fermentation inhibitor. *Crit Rev Biotechnol*. 2016:1-13.

Zhang H, Li X, Su X, Ang EL, Zhang Y, Zhao H. Production of adipic acid from sugar beet residue by combined biological and chemical catalysis. *ChemCatChem*. 2016.

Kang S, Paul K, Hankosky ER, Cox CL, Gulley JM. D1 receptor-mediated inhibition of medial prefrontal cortex neurons is disrupted in adult rats exposed to amphetamine in adolescence. *Neuroscience*. 2016;324:40-49.

Mesquita RD, Vionette-Amaral RJ, Lowenberger C, et al. Erratum: Genome of rhodnius prolixus, an insect vector of chagas disease, reveals unique adaptations to hematophagy and parasite infection (proceedings of the national academy of sciences of the united states of america (2015) 112 (14936-14941) DOI 10.1073/pnas.1506226112). *Proc Natl Acad Sci* U S A. 2016;113(10):E1415-E1416.

Marzin S, Hanemann A, Sharma S, et al. Are pectin esterase inhibitor genes involved in mediating resistance to rhynchosporium commune in barley? *PLoS ONE*. 2016;11(3).

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Chang H-, Domier LL, Radwan O, Yendrek CR, Hudson ME, Hartman GL. Identification of multiple phytotoxins produced by *fusarium virguliforme* including a phytotoxic effector (fvnis1) associated with sudden death syndrome foliar symptoms. *Mol Plant-Microbe Interact*. 2016;29(2):96-108.

Qin H, Hejna M, Liu Y, et al. YAP induces human naive pluripotency. *Cell Rep*. 2016.

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Hortensius RA, Ebens JH, Harley BAC. Immunomodulatory effects of amniotic membrane matrix incorporated into collagen scaffolds. *J Biomed Mater Res Part A*. 2016.

Li T, Kromdijk J, Heuvelink E, van Noort FR, Kaiser E, Marcelis LFM. Effects of diffuse light on radiation use efficiency of two anthurium cultivars depend on the response of stomatal conductance to dynamic light intensity. *Front Plant Sci*. 2016;7(FEB2016).

Despres J, Forano E, Lepercq P, et al. Unraveling the pectinolytic function of bacteroides xylanisolvens using a RNA-seq approach and mutagenesis. *BMC Genomics*. 2016;17(1):147-016-2472-1.

Gomez A, Petrzelkova KJ, Burns MB, et al. Gut microbiome of coexisting BaAka pygmies and bantu reflects gradients of traditional subsistence patterns. *Cell Rep*. 2016.

Soleh MA, Tanaka Y, Nomoto Y, et al. Factors underlying genotypic differences in the induction of photosynthesis in soybean [glycine max (L.) merr.]. *Plant Cell Environ*. 2016;39(3):685-693.

Dibattista JD, Roberts MB, Bouwmeester J, et al. A review of contemporary patterns of endemism for shallow water reef fauna in the red sea. *J Biogeogr*. 2016;43(3):423-439.

Wang X, Rahil Z, Li ITS, et al. Constructing modular and universal single molecule tension sensor using protein G to study mechano-sensitive receptors. *Sci Rep*. 2016;6.

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Li X, Park A, Estrela R, Kim S-, Jin Y-, Cate JHD. Comparison of xylose fermentation by two high-performance engineered strains of *saccharomyces cerevisiae. Biotechnol Rep*. 2016;9:53-56.

Webster RJ, Driever SM, Kromdijk J, et al. High C3 photosynthetic capacity and high intrinsic water use efficiency underlies the high productivity of the bioenergy grass *arundo donax. Sci Rep*. 2016;6.

Kim T, Zheng S, Sun J, et al. Dynamic visualization of alpha-catenin reveals rapid, reversible conformation switching between tension states. *Curr Biol*. 2015;25(2):218-224. *(recently ranked as highly cited)* ■

ILLINOIS

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www.igb.illinois.edu 16.031