IGB NEWS

Volume 8, Number 5

IF YOU ARE NEW TO THE IGB THIS SEMESTER, WELCOME. IF YOU'VE BEEN AWAY FROM THE IGB FOR THE SUMMER, WELCOME BACK!

UPCOMING EVENTS

IGB Seminar

History and Future of Microscopy
September 29, 2015, 12:00 p.m.
612 Carl R. Woese
Institute for Genomic Biology

James A. Sharp
President
Carl Zeiss, Inc.

Lunch with the Core

Applying New NMR Techniques to Assist Structure Elucidation
October 7, 2015, 12:00 p.m.
612 Carl R. Woese
Institute for Genomic Biology

Xudong Guan, PhD
NMR Specialist, Core Facilities
University of Illinois

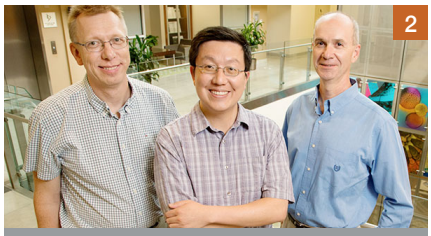
Lunch will be provided.

IGB Pioneers Seminar (GNDP)

Evolution, the Proteome, and Human Disease
October 13, 2015, 12:00 p.m.
612 Carl R. Woese
Institute for Genomic Biology

Edward M. Marcotte, PhD
Center for Systems and Synthetic Biology
Department of Molecular Biosciences
University of Texas at Austin

FEATURED NEWS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Genome Mining Effort Rapidly Discovers New Natural Products


3

Before Nature Selects, Gene Networks Set Course For Evolution


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Profile: Derek Wildman


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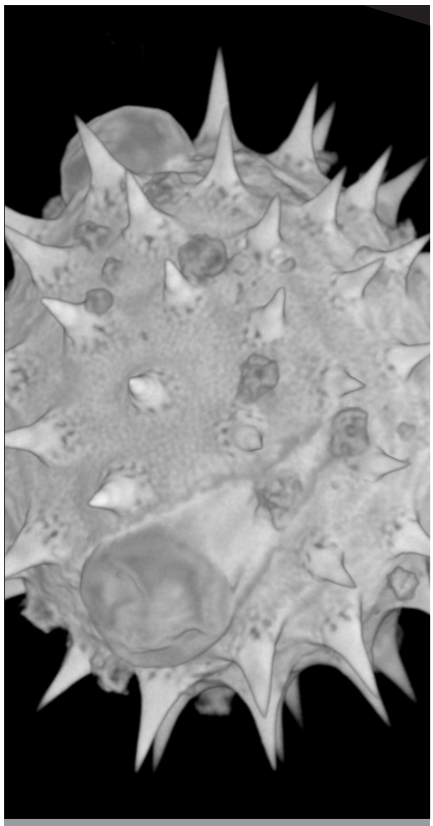
On the Grid: Happenings at IGB

IMAGE OF THE MONTH



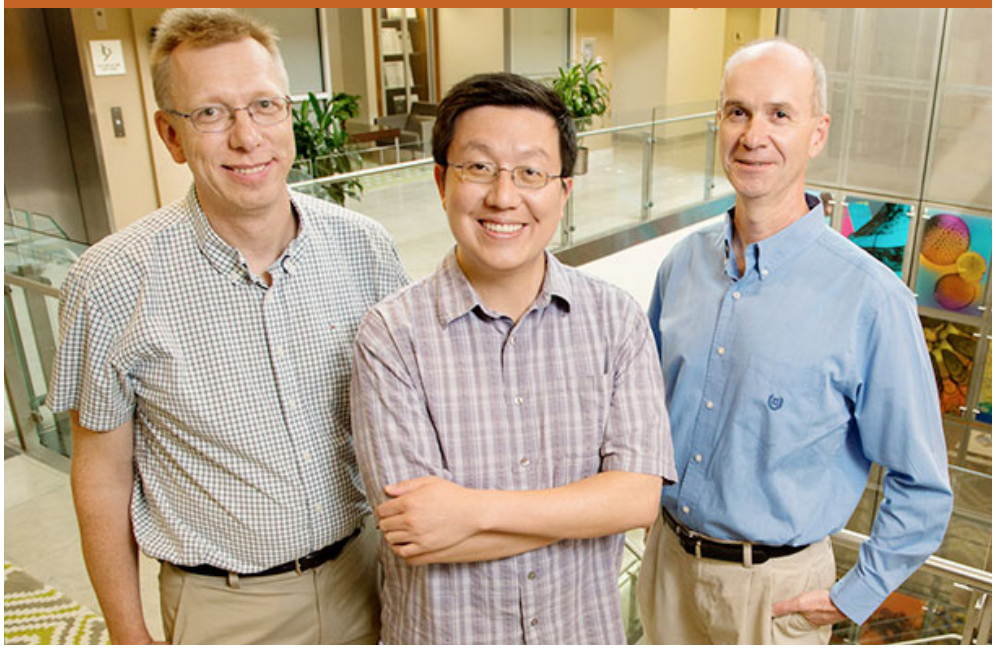
This month's image features a 3D structure of pollen using the LSM 880 Airyscan. Imaging 3D structure of pollen is important in identification of the pollen species. The spikes, surface structure, entine and exine are clearly resolved. The Sunflower (*Helianthus sp.*) pollen was labeled with Phloxine B and processed after collection (*Helianthus sp.*) from the Burlington, NC area.

This image is provided courtesy of Mayandi Sivaguru, Assistant Director of Core Facilities.

IGB News

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

FEATURE



Genome Mining Effort Discovers 19 New Natural Products In Four Years

It took two postdoctoral researchers, a lab technician, four undergraduates and their faculty advisors only four years – a blink of an eye in pharmaceutical terms – to scour a collection of 10,000 bacterial strains and isolate the genes responsible for making 19 unique, previously unknown phosphonate natural products, researchers report. Each of these products is a potential new drug. One of them has already been identified as an antibiotic.

The researchers report their findings in the *Proceedings of the National Academy of Sciences*.

Phosphonates are an abundant and diverse class of natural signaling molecules that have already proved useful to medicine and agriculture, said University of Illinois microbiology professor William Metcalf, who led the research with U. of I. chemistry professor Wilfred van der Donk.

"We focused on phosphonates because we know they are strongly predisposed to have biological activity – antibiotic activity, antiviral activity, herbicidal activity," Metcalf said. Bacteria use these compounds to signal their presence to their microbial neighbors, or, at higher concentrations, to kill them, he said.

Naturally produced phosphonates have great pharmaceutical potential, the researchers said.

"Of the 20 previously known natural-product phosphonates, two are used commercially – one as a clinical antibiotic and one as an herbicide – and another one is now in clinical trials to treat malaria," van der Donk said. "This 15 percent drug-development success rate is much higher than the 0.1 percent average estimated for natural products as a whole."

Postdoctoral researcher Kou-San Ju used a technique called "genome mining" to search the genomes of 10,000 strains of actinomycete bacteria for pepM, a single gene that is required for most types of phosphonate biosynthesis. Postdoctoral researcher Jiangtao Gao then worked with Ju to purify and structurally characterize the phosphonates.

University of Illinois chemistry professor Wilfred van der Donk (left), postdoctoral researcher Kou-San Ju, microbiology professor William Metcalf and their colleagues used genome mining to discover many new natural products quickly and inexpensively.

"Genome mining has previously been used, but only with a few organisms at a time," Ju said. "We wanted to know if this approach could actually be feasibly performed on a scale that is relevant to pharmaceutical discovery."

The team identified 278 bacterial strains that had the pepM gene.

"If you have that gene, it means you're making a phosphonate natural product," Metcalf said.

The researchers then sequenced the full genomes of all 278 strains that had the gene. By examining the genes flanking pepM, the researchers could tell whether they were finding pathways to build new phosphonates or rediscovering old ones.

"In the old days, pharmaceutical companies would have done bioassays on extracts from all 10,000 species," Metcalf said. They would purify the compounds of interest, determine their structure and then try to figure out whether they had found something new, he said.

"It was very, very tedious and very expensive," he said. "That would have taken a large company with hundreds of people years, if not decades."

The new effort has yielded many novel compounds.

"We have thus far isolated 19 new phosphonates, including those with antibiotic properties and others with previously unknown structures," Ju said. "In other words, we have essentially doubled the inventory of phosphonate natural products identified to date."

The 19 new structures are among 78 newly discovered groups of phosphonates produced from the 278 actinomycetes with the pepM gene. One of the 19, which the team named argolaphos, was found to be most potent against three types of bacteria that cause illness: *Salmonella typhimurium*, *Escherichia coli* and *Staphylococcus aureus*, the researchers report.

The researchers describe the new findings as a proof of concept that genome mining can be used on a scale that will speed the process of drug discovery,

cont. on page 4

Karen Sears, Associate Professor at the School of Integrative Biology and IGB faculty member, coauthored the new study.

Before Nature Selects,
Gene Networks Steer A Course For Evolution

Natural selection is a race to reproduce, a competition between individuals with varying traits that helps direct the evolution of a species. As scientists begin to explore the complex networks of genes that shape the form and function of each individual, they can ask a new question about evolution: How do the structures of these gene networks determine which individuals appear on the starting line, silently influencing evolution before competition has even begun?

University of Illinois researchers Karen Sears and Zoi Rapti, along with collaborators at Illinois and four other institutions, have addressed this question by exploring the gene network that guides limb development in mammals.

They found that during early development, when limbs are first forming, gene activity in this network varies little; later, when detailed limb structure is beginning to emerge, the network changes in structure, and gene activity varies more widely. This pattern may make it easier for evolution to tweak, rather than remodel, limb structure.

"When we look at the evolutionary record of animals, we find that there are some forms that have evolved repeatedly, and some that have never evolved," Sears said. "I want to know the role that development has in generating these patterns."

Sears, an associate professor of animal biology, and Rapti, an associate professor of mathematics, led the study, which was published in PLOS Genetics (DOI: 10.1371/journal.pgen.1005398). Sears is a member of the Carl R. Woese Institute for Genomic Biology (IGB).

Many genes encode proteins that influence or regulate each other's activity. These functional connections, and the genes that participate in them, can be imagined as the threads and intersections of a spider's web. Some of these interactions are stronger or weaker than others, and in the network they comprise, some genes have more connections than others. Computational models can mathematically describe this network structure.

Sears, Rapti, and colleagues wanted to know what happens when a chance event, like a mutation, changes the activity of one gene. How much will the whole network, and the resulting course of development, be affected?

Using published data on developmental gene interactions, they created a model of how genes interact during early and late stages of limb development. The model allowed them to pluck at the spider web of genes, and watch how much the rest of the web is disrupted.

The researchers found that in early limb development, the network resists the spread of change; even when one gene's activity is altered, the network as a whole continues to function almost as usual. Later in limb development, however, the architecture of the network is different, and a change in one gene's activity has a more widespread impact.

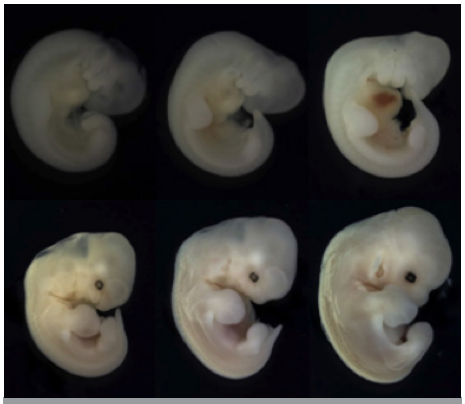
In addition, an empirical investigation of gene activity during limb develop in four different mammals—mice, bats, opossums, and pigs—showed that activity of developmental genes differs more in late development than in early development. This is true when comparing individuals of the same species, and also when comparing gene activity across species.

Together, these theoretical and empirical findings supported Sears' strongest initial hypothesis, that genomic mechanisms restrict the degree to which early limb development can vary in mammals. From an evolutionary perspective, this makes sense.

"If early development is disrupted, limb development will be severely disrupted, and it is very unlikely that the resulting limb structure will be selectively advantageous, said Sears. "Later development, which doesn't have as many downstream impacts, might be expected to be more free to vary because the consequences of that variation would be less dire."

Sears, Rapti, and coauthors were brought together by the Illinois BioMathematics Program, an NSF-funded project that promotes research collaboration among biology and mathematics undergraduates and faculty members. The BioMath Program has led to a variety of innovative research efforts. Sears is a member of the Regenerative Biology & Tissue Engineering research theme and an affiliate of the Gene Networks in Neural & Developmental Plasticity research theme at the IGB. ■

Written by Claudia Lutz. Photos by Kathryn Coulter and Karen Sears



Embryonic development of the buffy flower bat, Erophylla sezekorni, *showing the progressive growth and formation of the wings.*

focusing on naturally produced compounds, which are among the most promising new drug leads.

"These biologically produced small molecules have been the source of, or inspiration for, nearly two-thirds of all human medicines, yet research in this area has dwindled in recent years due to, among other reasons, high costs and increasing rates of rediscovery," the researchers wrote. Natural products also are a much-needed source of new antibiotics.

"To this day, natural products make up 75 percent of all of our antibiotics – either the natural products themselves or derivatives thereof," van der Donk said.

"Our study shows that genome mining is not only a viable route to new natural products, but that there are a tremendous number of new compounds awaiting discovery from the genomes of microbial strains," Ju said.

Metcalf and van der Donk are IGB faculty, with Metcalf leading the Mining Microbial Genomes research theme.

The National Institute of General Medical Sciences at the National Institutes of Health supported this research.

Written by Diana Yates. Photo by L. Brian Stauffer.

PROFILE

Derek Wildman, Professor of Molecular and Integrative Physiology, is the leader of the IGB's Computing Genomes for Reproductive Health research theme. His work involves the study of mammalian evolution (primates in particular) and evolutionary mammalian genomic history, especially human pregnancy.

Derek Wildman:
Computing Genomes for Reproductive Health

More than 2 billion babies will be born over the next 35 years. As many as one in eight of these babies may be born prematurely, with increased risk for long-term problems like diabetes and mental health disorders. One researcher is working to improve their chances to reach full term—and thus their chances to lead healthier, even fuller lives.

To do that, Derek Wildman (a professor of Molecular and Integrative Physiology) founded a new research theme at the Carl R. Woese Institute for Genomic Biology (IGB) called Computing Genomes for Reproductive Health (CGRH). He is bringing together researchers from across the University of Illinois to understand problems with pregnancy that lead to pre-term birth and other complications.

These problems develop from complex interactions at many levels, from the societal issues down to intracellular interactions, and everything in between. To make sense of it all, his new research theme will use computational models.

"Think about all the things that can go wrong or right given that we have 20,000 genes and 100,000 proteins in addition to all the different organs and stuff," Wildman said. "All these multi-scale interactions play a role in whether we develop pregnancy complications or not."

But it's not just about complications. Wildman is applying his expertise in the evolution of pregnancy and reproduction to help discover the underpinnings for pregnancy risk and resilience. "What gives people good pregnancies? What are those resiliency factors?" he said. "I am interested in the other side of the coin, the health side in addition to the disease side."

> *"I am interested in interacting with the community and getting feedback about the health problems that need to be solved."*

Ultimately, he hopes to develop practical applications, like a test kit that will tell mothers if they are about to go into labor.

"I am not interested in being an ivory tower scientist that doesn't do anything of practical value for the rest of humanity," Wildman said. "I am interested in interacting with the community and getting feedback about the health problems that need to be solved."

Not surprisingly, Wildman was attracted to the land grant mission of the University of Illinois and the IGB's slogan: where science meets society. More than that, he appreciated the spirit of collaboration here. "People really know how to work together," he said. "It is not every place in the world that that happens."

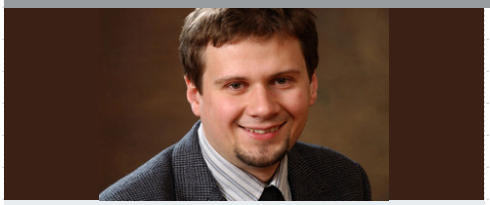
Still, it was a tough decision for Wildman and his wife, Associate Professor of Psychology Monica Uddin, to leave Detroit—where Wildman had been a postdoc and professor at Wayne State University Medical School for 15 years—and join the faculty here in 2014.

"The main thing that convinced me were the people that I met," he said. "I think there are a lot of really good people here."

Written by Claire Sturgeon. Photo by Kathryn Coulter.

ON THE GRID
HAPPENINGS AT THE IGB

AWARDS

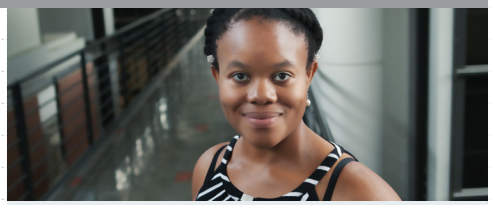


ALEKSEI AKSIMENTIEV
Aleksei Aksimentiev, Associate Professor of Physics (Cellular Decision Making in Cancer) has been selected as a 2015-16 NCSA Faculty Fellow.

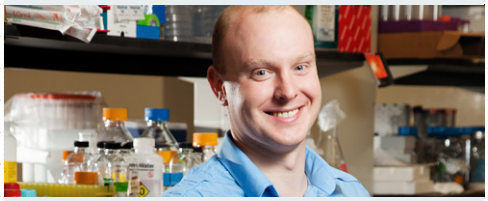
EVAN DELUCIA
Evan DeLucia, Professor of Plant Biology (Genomic Ecology of Global Change) was named a fellow of the Ecological Society of America.

LEE DEVILLE
Lee DeVille, Professor of Mathematics (Biocomplexity) received the Distinguished Teaching Award in Mathematics for Tenured Faculty from the College of Liberal Arts and Sciences.

BRENDAN HARLEY
Brendan Harley, Assistant Professor of Chemical & Biomolecular Engineering (Regenerative Biology & Tissue Engineering) received the Everitt Award for Teaching Excellence.



PRINCESS IMOUKHUEDE
Princess Imoukhuede, Assistant Professor, Department of Bioengineering (Regenerative Biology & Tissue Engineering) was named a 2015 Young Innovator of Cellular and Molecular Bioengineering.



DOUGLAS MITCHELL
Douglas Mitchell, Assistant Professor of Chemistry (Mining Microbial Genomes) received the National Fresenius Award, administered by the American Chemical Society. Mitchell also received a Camille Dreyfus Teacher-Scholar Award from the Camille & Henry Dreyfus Foundation.

JEFFREY MOORE
Jeffrey Moore, Murchison-Mallory Professor of Chemistry (Biosystems Design) has been named the 2015 recipient of the Leete Award by the American Chemical Society Division of Organic Chemistry.

EVENT

IGB POSTDOC ASSOCIATION CAREER DEVELOPMENT WORKSHOP
IGB postdocs are invited to attend a workshop in IGB 612 on November 6. Hosted by the IGB Postdoc Association, the goal of the event is to provide postdocs with the resources and expertise that are essential for preparing a Career Development Plan. The event will include a panel discussion with invited panelists from a variety of science-related professions. Following the panel, small workshops will be available in which participants can prepare and hone their Career Development Plans with direct guidance from accomplished researchers, teachers, and professionals.

For more information and to register, see **https://www.igb.illinois.edu/education/postdoctoral-association**.

GIVING

WALK OF LIFE
Walk of Life pavers are the perfect way to commemorate a special event, like graduation. For a paver to be installed, please contact Melissa McKillip at mmckilli@illinois.edu.

More information can be found at **www.igb.illinois.edu/about/giving**.

ON THE GRID
HAPPENINGS AT THE IGB

OUTREACH

GENOME DAY

The fourth annual Genome Day will be held on Saturday, November 14 from 1-5 pm at the Orpheum Children's Science Museum. As with previous years, the event will be an open house and the activities will be primarily for elementary aged children. These hands-on activities will teach children about DNA, genes, genomes, and evolution and will be free and open to the public. If you are interested in volunteering, we invite you to use the following volunteer signup form: **http://www.igb.illinois.edu/content/genome-day-volunteer-form.**

If you have any questions about volunteering or the activities, please contact your theme fellow or Courtney Cox, outreach fellow, at *Cox22@illinois.edu*.

LECTURE SERIES

ENTREPRENEURSHIP LECTURE SERIES

The entrepreneurship lecture series is an opportunity for students, academics and professionals in the life sciences, engineering and other disciplines to gain insight about entrepreneurship and innovation. The second lecture in the series will be presented by Jed Taylor from the Technology Entrepreneur Center. It will be on Tuesday, October 6 at Noon in the IGB Conference Center Room 612. Pizza will be provided. For more information, please contact Courtney Cox, outreach fellow, at *Cox22@illinois.edu*.

NEW ARRIVALS

MEGAN DAILEY

Professor Megan Dailey has joined the IGB as an Affiliate in the Regenerative Biology and Tissue Engineering (RBTE) Research Theme. Professor Dailey is a member of the department of Animal Sciences. She received her Ph.D. in Behavioral Neurosciences from Georgia State University. Her research focuses on gaining a broader understanding of the mechanisms responsible for nutrient-driven cellular adaptation in the intestine, which could help find therapies for intestinal disorders such as Crohn's disease and irritable bowel syndrome.

AMY MARSHALL-COLON

Professor Amy Marshall-Colon has joined the IGB as an Affiliate in the Genomic Ecology of Global Change (GEGC) Research Theme. Professor Marshall-Colon is a member of the department of Plant Biology. She received her Ph.D. in 2009 from Purdue University and was a NIH-NRSA Fellow from 2010 to 2013 at New York University. Her research focuses on integrating genomics and metabolomics to investigate the regulatory cross-talk between primary and secondary metabolism.

CHENGXIANG ZHAI

Professor Chengxiang Zhai has joined the IGB as an Affiliate in the Biosystems Design (BSD) Research Theme. Professor Zhai joined the faculty in the department of Computer Science in 2002 after receiving his Ph.D. from Carnegie Mellon University. His research interests include information retrieval, text mining, natural language processing, machine learning, and bioinformatics.

JOSEPH LEIGH

Joseph Leigh has joined the IGB as a Research Programmer in the Computer and Network Resource Group. He'll be supporting the information technology needs of the IGB's faculty, staff, and students, as well as assisting with the maintenance of the computational infrastructure. Before joining the IGB, he worked for three years as a Research Programmer for the Illinois Natural History Survey, on a project for the Advancing Digitization of Biological Collections NSF program.

DEPARTMENT ANNOUNCEMENTS

BUSINESS

BUSINESS MEALS FOR EMPLOYEES AND GUESTS

Allowable for:

Recruitment - Meals or refreshments provided during meetings with non-employees or potential students, related to their possible employment at or admission to the University.

Business Meetings - University business discussions held between one or more University employees AND one or more visitors from an outside entity.

Hospitality Events - An event honoring distinguished guests who are not University employees. May include meals or receptions for faculty from other universities, members of external organizations, and/or visiting dignitaries. Dignitaries typically visit at the invitation of the University to participate in seminars, speaking engagements, and related events.

Amount Limits:

Breakfast - $25 per person
Lunch - $40 per person
Dinner - $60 per person
Refreshments and Reception - $25 per person
Alcohol - $20 per person for non-donor events

Allowable Fund Types

State (for business meetings and recruitment only); gift, institutional, service plan, or self-supporting if the event is directly related to generation of the funds revenue. Convocation or graduation events may be funded by the Chancellor's or President's Public Function funds.

How to Purchase

Do NOT purchase business meals with a University P-Card. Make the purchase using:

- T-Card
- Purchase Order
- Reimbursed personal funds – Consult Request Reimbursement for Domestic or International Employee Travel and Business Meals ■

UNIVERSITY LIBRARY

PUBLIC ACCESS TO ARTICLES AND DATA

In October 2015, several federal agencies are expected to fully implement their public access plans for publications and data resulting from grant funding. These agencies include: AHRQ, ASPR, CDC, DOE, FDA and NASA.

For publications, the mandate requires articles to be openly available, whether or not the original publication was open access. Most plans call for articles to be deposited into a central government repository, such as PubMed (AHRQ, ASPR, FDA) or CDC Stacks (CDC). The DOE plan allows for open access articles on publisher websites and articles in local institutional repositories (e.g., UIUC's IDEALS). Most agencies require publications to be deposited within a year of publication, although some agency plans state within a year of acceptance for publication.

The expectations for data are more varied. One commonality is that data management plans (DMPs) will be required for most agency grant proposals. Where and when data are expected to be deposited varies widely. Agency plans offer few specifics on where to deposit data but mention established, disciplinary repositories; data commons; and data inventories. Regarding when to deposit, most agency plans say with article publication, but some plans say within one year of collection or within a reasonable time.

Be aware that more that more agency plan implementations are on the horizon. In December 2015, NIH will complete its plan implementation, which includes a new requirement for DMPs with all grant proposals. In January 2016, NSF and USDA will implement their public access plans.

For background information, these plans are in response to the White House's Office of Science and Technology Policy (OSTP) memo "Increasing Access to the Results of Federally Funded Scientific Research" (**http://go.illinois.edu/OSTP_Memo**).

If you have questions about or would like guidance on these requirements, please contact Sarah Williams, the Life Sciences Data Services Librarian (*scwillms@illinois.edu*), or the Research Data Service, headquartered in the University Library (**http://researchdataservice.illinois.edu/**). ■

BUSINESS

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 Manager, at *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.

Gomez A, Rothman JM, Petrzelkova K, et al. Temporal variation selects for diet-microbe co-metabolic traits in the gut of gorilla spp. *ISME J*. 2015.

Yendrek CR, Koester RP, Ainsworth EA. A comparative analysis of transcriptomic, biochemical, and physiological responses to elevated ozone identifies species-specific mechanisms of resilience in legume crops. *J Exp Bot*. 2015.

Eerkens JW, Carlson T, Malhi RS, et al. Isotopic and genetic analyses of a mass grave in central california: Implications for precontact hunter-gatherer warfare. *Am J Phys Anthropol*. 2015.

Choi JS, Mahadik BP, Harley BAC. Engineering the hematopoietic stem cell niche: Frontiers in biomaterial science. *Biotechnol J*. 2015.

Wang X, Vukovic L, Koh HR, Schulten K, Myong S. Dynamic profiling of double-stranded RNA binding proteins. *Nucleic Acids Res*. 2015;43(15):7566-7576.

Freestone TS, Zhao H. Combinatorial pathway engineering for optimized production of the anti-malarial FR900098. *Biotechnol Bioeng*. 2015.

Wang M, Yu C, Zhao H. Directed evolution of xylose specific transporters to facilitate glucose-xylose co-utilization. *Biotechnol Bioeng*. 2015.

Hollister SJ, Flanagan CL, Zopf DA, et al. Design and quality control for translating 3D-printed scaffolds. *Essentials of 3D Biofabrication and Transl*. 2015:43-59.

Sears KE, Maier JA, Rivas-Astroza M, et al. The relationship between gene network structure and expression variation among individuals and species. *PLoS Genet*. 2015;11(8).

Smith CE, Ernenwein D, Shkumatov A, et al. Hydrophilic packaging of iron oxide nanoclusters for highly sensitive imaging. *Biomaterials*. 2015;69:184-190.

Si T, HamediRad M, Zhao H. Regulatory RNA-assisted genome engineering in microorganisms. *Curr Opin Biotechnol*. 2015;36:85-90.

Raghavan M, Steinrücken M, Harris K, et al. Genomic evidence for the pleistocene and recent population history of native americans. *Science*. 2015;349(6250).

Caetano-Anollés D, Caetano-Anollés G. Ribosomal accretion, apriorism and the phylogenetic method: A response to petrov and williams. *Front Genet*. 2015;6(JUN).

Chen W, Long KD, Kurniawan J, et al. Planar photonic crystal biosensor for quantitative label-free cell attachment microscopy. *Adv Opt Mater*. 2015.

Baumann K, Venail J, Berbel A, et al. Changing the spatial pattern of TFL1 expression reveals its key role in the shoot meristem in controlling arabidopsis flowering architecture. *J Exp Bot*. 2015;66(15):4769-4780.

Rittschof CC, Grozinger CM, Robinson GE. The energetic basis of behavior: Bridging behavioral ecology and neuroscience. *Curr Opin Behav Sci*. 2015;6:19-27.

Logue MW, Amstadter AB, Baker DG, et al. The psychiatric genomics consortium posttraumatic stress disorder workgroup: Posttraumatic stress disorder enters the age of large-scale genomic collaboration. *Neuropsychopharmacology*. 2015;40(10):2287-2297.

Nguyen N-D, Mirarab S, Kumar K, Warnow T. Ultra-large alignments using phylogeny-aware profiles. *Genome Biol*. 2015;16(1).

Rich MH, Lee MK, Marshall N, et al. Water-hydrogel binding affinity modulates freeze-drying-induced micropore architecture and skeletal myotube formation. *Biomacromolecules*. 2015;16(8):2255-2264.

Van Hoeck N, Watson PD, Barbey AK. Cognitive neuroscience of human counterfactual reasoning. *Front Human Neurosci*. 2015;9:1-18.

Bishop KA, Betzelberger AM, Long SP, Ainsworth EA. Is there potential to adapt soybean (glycine max merr.) to future [CO2]? an analysis of the yield response of 18 genotypes in free-air CO2 enrichment. *Plant Cell Environ*. 2015;38(9):1765-1774.

Urban DJ, Sorensen DW, Maier JA, et al. Conjoined twins in a wild bat: A case report. *Acta Chiropterologica*. 2015;17(1):189-192.

Stephens ZD, Lee SY, Faghri F, et al. Big data: Astronomical or genomical? *PloS Biol*. 2015;13(7).

Feng Y, Kumar R, Ravcheev DA, Zhang H. Paracoccus denitrificans possesses two BioR homologs having a role in regulation of biotin metabolism. *MicrobiologyOpen*. 2015;4(4):644-659.

Miao R, Hennessy DA. Optimal protein segregation strategies for wheat growers. *Can J Agric Econ*. 2015;63(3):309-331.

Way DA, Long SP. Climate-smart agriculture and forestry: Maintaining plant productivity in a changing world while minimizing production system effects on climate. *Plant Cell Environ*. 2015;38(9):1683-1685.

Pan JJ, Solbiati JO, Ramamoorthy G, et al. Biosynthesis of squalene from farnesyl diphosphate in bacteria: Three steps catalyzed by three enzymes. *ACS Cent Sci*. 2015;1(2):77-82.

Mahadik BP, Pedron Haba S, Skertich LJ, Harley BA. The use of covalently immobilized stem cell factor to selectively affect hematopoietic stem cell activity within a gelatin hydrogel. *Biomaterials*. 2015;67:297-307. ■

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www.igb.illinois.edu 15.118