

Upcoming Events

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Image Of The Month

IP @ IGB

Department Announcements

Volume 10 Number 6

UPCOMING EVENTS

IGB Seminar (MME)

Complex Carbohydrate Metabolism by Human Gut Bacteria During Health and Disease October 17, 2017, 12:00 p.m. 612 Carl R. Woese Institute for Genomic Biology

Eric Martens, PhD University of Michigan, Microbiology and Immunology

Enduring Legacy of Sol Spiegelman

October 20, 2017 to October 22, 2017 Alice Campbell Alumni Center 601 S. Lincoln Avenue

A national panel of speakers will be presenting on current and future work in their respective fields. Full info at spiegelman2017.igb.illinois.edu

IGB Pioneers Seminar (GEGC)

The Role of Hybridization in the Evolution of Crops, Weeds, and New Species October 24, 2017, 12:00 p.m. 612 Carl R. Woese Institute for Genomic Biology

Loren Rieseberg, PhD University of British Columbia Department of Botany

Fox Family Innovation and Entrepreneurship Lecture

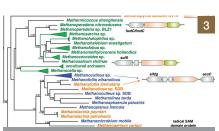
A Novel Series of Efflux Pump Inhibitors to Combat Multidrug Resistant Enterobacteriaceae December 5, 2017, 12:00 p.m. 612 Carl R. Woese Institute for Genomic Biology

Tim Opperman, PhD Senior Proposal Scientist, Microbiotix, Inc.

FEATURED NEWS



DOE Grant to Fund Sorghum
Research at Illinois



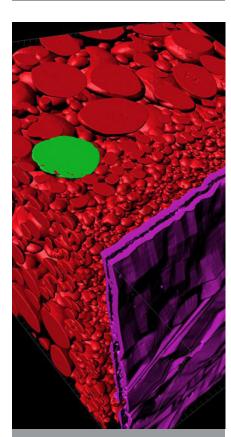
Unique Property of Critical Methane-producing Enzyme



Monthly Profile: Christopher Brooke



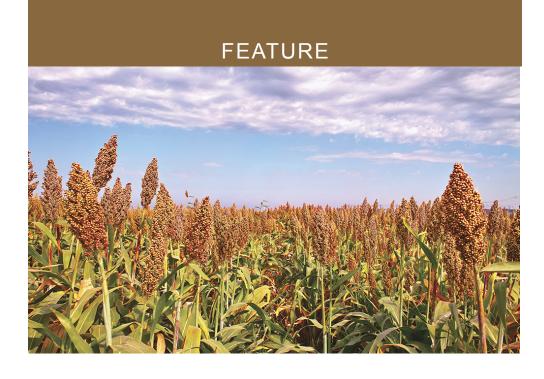
IMAGE OF THE MONTH



This month's image features segmented cross sections of a clawed frog egg. The image was taken with a Zeiss Sigma VP 3View Serial Block-Face SEM (SBF-SEM), segmented in Microscopy Image Browser and imported into Imaris to create a surface. Image provided by Kingsley Boateng of Core Facilities and Aurora Turgeon of the Jing Yang Laboratory. Research was funded by NIH.

IGB News

Share your news with the IGB. Send deas on stories, articles, and features to avasi@illinnis.edu.



U.S. Department of Energy Grant to Fund Sorghum Research at Illinois

An Illinois professor is part of a multi-institutional research project that has received a 5-year, \$16 million grant from the U.S. Department of Energy (DOE) to work with sorghum in an effort to optimize photosynthesis and water use efficiency.

Andrew Leakey, professor in the Department of Plant Biology and IGB faculty in the Genomic Ecology of Global Change research theme, is part of the project, based at the Donald Danforth Plant Science Center, that will expand upon earlier research on green foxtail grass (Setaria viridis) to identify new genes and pathways that contribute to photosynthesis and enhanced water use efficiency. Sorghum, a grass grown worldwide, is a particularly ideal crop to research for solar energy conversion and use of water.

The research team—which also includes researchers from Washington State University, Carnegie Institution for Science, University of Rhode Island, University of Minnesota, and the United States Department of Agriculture—will then deploy these genes using tools of the emerging field of synthetic biology to accelerate development of elite energy sorghum varieties for production under marginal environments.

"Understanding the network of genes involved in photosynthesis and drought tolerance will provide targets for plant breeders and genetic engineers to re-design sorghum specifically as a high value bioenergy feedstock to be grown on marginal soils and thus not compete with food crops," said lead principal investigator, Thomas Brutnell, director of the Enterprise Rent-A-Car Institute for Renewable Fuels at the Danforth Center.

According to Leakey, Illinois will receive approximately \$2.1 million of the DOE grant to contribute to the project.

"New infrastructure for experimentally manipulating water supply to large field-grown crops at the University of Illinois will be leveraged, along with advances in phenotyping crop carbon and water relations, in order to develop and field-test high water use efficiency sorghum," he said.

"New infrastructure for experimentally manipulating water supply to large field-grown crops at the University of Illinois will be leveraged, along with advances in phenotyping crop carbon and water relations."

This project aims to deliver stress-tolerant sorghum lines, addressing DOE's mission in the generation of renewable energy resources. The development of a low input, environmentally safe and highly productive sorghum germplasm will help establish a lignocellulosic energy economy that can provide jobs to rural communities, ensure energy security and benefit the

Sorghum is a member of the grass family and is grown worldwide. Sorghum is very resilient to drought and heat stress. Natural genetic diversity in sorghum makes it a promising system for identifying stress-resistance mechanisms in grasses that may have been lost during the domestication of related cereal crops. It is among the most efficient crops in conversion of solar energy and use of water, making it an ideal crop to target for improvement.

Founded in 1998, the Donald Danforth Plant Science Center is a not-for-profit research institute with a mission to improve the human condition through plant science. Research, education and outreach aim to have impact at the nexus of food security and the environment, and position the St. Louis region as a world center for plant science. The Center's work is funded through competitive grants from many sources, including the National Institutes of Health, U.S. Department of Energy, National Science Foundation, and the Bill & Melinda Gates Foundation.

The Department of Plant Biology at Illinois is part of the School of Integrative Biology.

Written by Donald Danforth Plant Science Center and Dave Evensen. Photo by L. Brian Stauffer.



Andrew Leakey is part of multi-

Methanomassiliicoccus luminyensis Methanomassiliicoccales archaeon RumEn M2 Methanoplasma termitum Methanomethylophilus alvus Thermoplasmatales archaeon BRNA1 methanogenic archaeon mixed culture ISO4-G1 methanogenic archaeon ISO4-H5 Methermicoccus shenaliensis Methanoperedens nitroreducens Methanoperedens sp. BLZ1 Methanosarcina sp. Methanohalophilus sp. Methanohalobium evestigatum Methanolobus sp. Methanomethylovorans hollandica Methanococcoides sp. uncultured archaeon Methanoculleus sp. Methanofollis ethanolicus Methanoculleus sp. SDB Methanolinea tarda

Researchers Discover Unique Property of Critical Methane-producing Enzyme

An unexpected discovery has given scientists a greater understanding of an important methane-producing enzyme.

A team of researchers at the IGB published a paper in eLife that outlined their findings on an enzyme

called methyl-coenzyme M reductase, or MCR.

Their findings overturn what was previously believed to be true in the field: that a set of unique modifications present in MCR were essential to how the enzyme functions.

They discovered that these modifications were in fact not essential, a finding that will bring scientists a step closer to fully understanding this enzyme, which plays an important role in methane production and the carbon cycle.

Methane is an important greenhouse gas that contributes to approximately 20 percent of the greenhouse effect, which contributes to the warming of earth.

Methane comes from both geological sources and biological sources, including from a group of microorganisms called methanogens. These microscopic organisms, which are a member of the domain Archaea, produce methane as the byproduct of their metabolism. Gigatons of methane are produced by methanogens every year.

Methanogens have the enzyme MCR, which is the only enzyme that makes methane. It's critical for both the production and consumption of methane.

"This is a hugely important enzyme," said Professor of Molecular and Cellular Biology William Metcalf, co-author of the paper and leader of IGB's Mining Microbial Genomes (MMG) theme. "I would argue it's one of the most important enzymes on earth for the carbon cycle."

MCR also has some unusual properties. Unlike most enzymes, MCR has a series of modifications

From left to right: G. William Arends Professor in Molecular and Cellular Biology William Metcalf, Associate Professor of Chemistry Douglas Mitchell, IGB Fellow Dipti Nayak, and postdoctoral researcher Nilkamal Mahanta.

that change the enzyme's amino acids. These modifications were previously believed to have been essential to the enzyme's functions.

Before now, it's been impossible to do a genetic analysis of these enzymes -- which would include taking away these modifications and looking at how the enzyme works without them.

"It was believed that if you did that, the enzyme wouldn't work," Metcalf said. "Because that enzyme is required for viability of the organism, it was thought to be an essential gene."

But Douglas Mitchell, a professor of chemistry and faculty member of IGB's MMG theme, thought otherwise. He and his research laboratory had been studying a class of molecules that had one of the modifications that is also present in MCR. They figured out how this modification was done and predicted that the same enzymatic machinery used

to modify MCR in methanogens was the same machinery used to make antibiotics and bacteria.

However, their lab had a limitation, according to Nilkamal Mahanta, a postdoctoral researcher in Mitchell's lab who was involved with the research.

> Their lab was limited in its ability to perform the kind of experiment needed to see if this was true. The organisms they wanted to study exist only in anaerobic environments, which do not contain oxvgen.

> IGB Fellow Nayak had recently developed a novel genetic tool that could manipulate this type of organism. She used this tool to study the physical properties of MCR and understand how it works and found that the modification was not essential to the enzyme's function.

This came as a surprise to many in this field of research, and to Metcalf and Nayak as well.

"When I started this project, I didn't quite know as much about the importance of these modifications," Nayak said. "As the project moved along . . . I realized the impact of the discovery we made, that this modification we thought was important and involved in making methane or breaking down methane, suddenly was not playing as important a role as people in the literature had been talking about for the last 10 or 15 years - maybe even longer, actually."

Their findings suggest there is more to be uncovered about this enzyme and the role it plays in producing and consuming methane.

Written by Emily Scott. Photos by L. Brian Stauffer.

Assistant Professor of Microbiology Christopher Brooke and his lab study how RNA viruses (especially influenza viruses) replicate, transmit, and evolve, particularly in how diversity and collective interactions within viral populations influence their transmission and evolution—critical for expanding fundamental understanding of virology and evolutionary biology.

Christopher Brooke

Combating antiviral drug resistance with dynamic therapeutics

Antiviral drug resistance has long been a problem in modern society. As viruses evolve, they develop resistance to antiviral drugs, which become less effective at treating diseases such as influenza.

Now, a group of researchers is approaching this problem with a new idea: what if antiviral drugs could evolve along with viruses to stop this resistance?

Christopher Brooke, assistant professor of microbiology and member of IGB's Infection Genomics for One Health (IGOH) theme, is part of a DARPA-funded program called INTERfering and Co-Evolving Prevention (INTERCEPT) that hopes to achieve this.

The program's goal is to develop a new class of biological therapeutics that can coevolve with viruses. That way, as the virus develops resistance to the therapeutic, the therapeutic would evolve and develop anti-resistance.

"It would be as dynamic as the pathogen, and so that would, ideally, eliminate or at least blunt the problem of evolved resistance," Brooke said.

Nine teams in the program are targeting other viruses such as HIV and Zika virus, but Brooke's team of five researchers will work on developing a therapeutic specifically for influenza.

They hope to do this by creating therapeutics with a design based on viruses themselves. This idea is based on a natural phenomenon known as defective interference.

Under certain conditions, many viruses spontaneously produce virus mutants that are missing parts of their genome. These mutants, called defective interfering particles, compete with the virus and inhibit its ability to replicate.

Influenza produces these defective interfering particles regularly, and it has generally been believed that they're detrimental to the virus.

"We're not totally convinced that's the case," Brooke said.

He and his colleagues will instead use the particles as a starting point. They plan to make changes to the particles and see if they have a detrimental effect on the viral population.

"This program is basically trying to see if we can take that idea... and engineer versions of these that can act as therapeutics," Brooke said.

A major part of this research will involve the creation of mathematical models that will help them better understand influenza infection.

Mathematical modeling, which involves using mathematical concepts to describe real world situations, can help the researchers make useful predictions. Two mathematicians on Brooke's team will work with experimenters to try and predict what a defective interfering particle that could serve as an efficacious therapeutic might look like.

Mathematical modeling is common in biology research, but there is typically a communication gap between those doing the modeling and those doing experimental work.

"There's not a huge amount of crosstalk," Brooke said. "But this program is bridging that to some extent."

Each side brings a level of expertise that can help the other — for example, experimental researchers don't always have precise control over what they're testing.

"Say we add a virus to a well of cells. We can't dic-

tate exactly how many virus particles go into every cell... We just can't do that," Brooke said. "But in a mathematical model, you can do whatever you want."

Using the advantages of mathematical modeling, they can decide which particles they want to test in the lab.

"What I really like about the mathematical modeling is that it allows us to test hypotheses that we may have . . . in a much more quantitatively rigorous way than we can through experimentation," Brooke said. "It also allows us to test things that we can't really test experimentally."

Brooke explained that having input from the theoretical side of biology will give the project greater insight.

"The more times you bring more perspectives to one problem, the greater your chances are of finding some sort of insight...it's one of the things I'm most excited about."

With mathematicians and experimenters working side by side and having access to higher quality data, Brooke predicts the resulting models will be more accurate.

For now, Brooke and his team are working on identifying and characterizing every possible defective interfering particle that can be generated by influenza virus.

"We're going to try and capture different ones that we think will behave differently," he said. "We have no idea what to expect and we can't necessarily predict or judge who would be more likely to be efficacious, so we're just going to test everything."

They will analyze how the particles affect viral rep-

MONTHLY PROFILE

lication and transmission, how they affect the host cell, and more.

Their end goal is to identify a particle known as a therapeutic interfering particle that could be introduced to an individual infected with influenza.

"It will dramatically decrease disease severity and forward transmission of the virus," Brooke said. "It would do so without the virus being able to evolve resistance to it."

Regardless of whether this research will have impact on driving influenza virus to extinction, the researchers expect to gain valuable information on how virus populations evolve, which is an area Brooke and his lab have already been exploring.

In the 20th century, vaccines were introduced against diseases such as poliovirus, measles virus, and influenza virus, which all have similar mutation rates. Poliovirus and measles were controlled by vaccines, but influenza was not. It has remained a public health issue despite the fact that most people are immune to some influenza virus strains.

This leaves many large-scale questions that Brooke and his lab hope to answer: Why is influenza so good at outrunning host immunity? Why are other viruses not? How does influenza's genome affect how it evolves?

Through this research, parts of these questions could be answered.

"We're going to learn a huge amount about how influenza virus populations behave and evolve," Brooke said. "That's going to be useful for the development of this class of therapeutics, but also just more generally in terms of improving vaccines."

For Brooke, this research is a chance for him to continue studying viruses, which consistently fascinate

"They're super weird and they're really interesting," he said. "They're always surprising us in terms of what we find them doing and how they work."

Written by Emily Scott. Photo courtesy of Microbiology.

ON THE GRID HAPPENINGS AT THE IGB

NEW ARRIVALS



THOMAS KEHL-FIE

Professor Thomas Kehl-Fie has joined the IGB as an affiliate member in the Mining Microbial Genomes (MMG) Research Theme. He received his Ph.D. from Washington University, and subsequently was a postdoctoral research associate at Vanderbilt University. Professor Kehl-Fie is currently an Assistant Professor in the Department of Microbiology. His research interests are in the areas of host-pathogen interactions, microbial physiology, protein structure, regulation of gene expression and signal transduction.



DAVID KRANZ

Professor David Kranz has jointed the IGB as a faculty member in the Anticancer Discovery from Pets to People (ADPP) Research Theme. He is a professor in the Department of Biochemistry and is the Phillip A Sharp Professor. Research in his laboratory is directed toward understanding a fundamental issue in immunology: how mammals can eliminate millions of different antigens that are "foreign" (e.g. viruses, bacteria) without destroying antigens that are "self" (e.g. one's own tissues).



IDOIA OCHOA

Professor Idoia Ochoa has joined the IGB as an affiliate in the Computing Genomes for Reproductive Health (CGRH) Research Theme. Before joining the Department of Electrical and Computer Engineering as an Assistant Professor, she was a postdoctoral research associate at Stanford University. Her research interests are in the areas of bioinformatics, computational biology, data compression, machine learning, statistical learning and information theory and coding.

ON THE GRID HAPPENINGS AT THE IGB

AWARDS



KRISTOPHER KILIAN

Kristopher Kilian, Associate Professor of Materials Science and Engineering (RBTE) was named a 2017 Young Innovator of Cellular and Molecular Bioengineering (CMBE).



GIRISH CHOWDHARY

Girish Chowdhary, Assistant Professor of Agricultural and Biological Engineering (GEGC) was elected to the grade of Associate Fellow, Class of 2018 in the American Institute of Aeronautics and Astronautics (AIAA).



THOMAS KEHL-FIE

Thomas Kehl-Fie, Assistant Professor of Microbiology (MMG) was named a 2017 Vallee Scholar by the Vallee Foundation, which supports original, innovative, and pioneering work by early career scientists.



ANDREW ALLEYNE

Andrew Alleyne, Professor of Mechanical Science & Engineering (BSD) was awarded the Society of Women Engineers (SWE) Advocating Women in Engineering Award.

SYMPOSIUM



THE ENDURING LEGACY OF SOL SPIEGELMAN

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

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

GENOME DAY



GENOME DAY IS COMING NOVEMBER 4

Genome Day is an opportunity to educate the community about genomes, genes, DNA, and evolution, held each year at the Orpheum Children's Science Museum in Champaign.

Our next Genome Day will take place on November 4, 2017! Admission to the event and museum is free, and activities will run continuously in an open house format.

We need volunteers! Sign up online here.

PROFILE



NIGEL GOLDENFELD INTERVIEWED BY QUANTA MAGAZINE

Quanta magazine recently interviewed Swanlund Professor of Physics and leader of IGB's Biocomplexity research theme, Nigel Golden-

Professor Goldenfeld speaks of his diverse work in physics, the origin of life, NASA, and much more. Read the full article at http://bit.ly/2iOeplE.

ANNUAL REPORT



IGB ANNUAL REPORT

The 2016 IGB Annual Report is now available. This Annual Report has plenty of stories of achievement, but also glimpses of the most fundamental origins of science and of scientists, and the individual philosophies that keep researchers going when achievement feels like a distant goal.

Download a copy at http://bit.ly/2yHX1Cb or if you'd prefer a hardcopy please contact nvasi@illinois.edu.

ON THE GRID HAPPENINGS AT THE IGB

EVENTS



IGB OCTOBER EVENTS

Don't miss the following events coming up at the end of October at the IGB:

IGB Blood Drive

October 30, 9:00am - 1:00pm 612 Conference Room

Halloween party

October 30, 4:00pm - 5:30pm Array Cafe

Join us for a Halloween party for IGB members and their families, and participate in our costume contest for kids and adults. Winners will be announced at 5:30pm!

POSTDOC ASSOCIATION



IGB POSTDOCTORAL ASSOCIATION EVENTS

The IGB Postdoctoral Association will be hosting two events, free of charge and open to all.

Question and Answer Session with Richard Harris

Friday, October 20th, 3:00pm 612 Conference Room

Award-winning NPR journalist Richard Harris has reported on a wide range of topics in science, medicine and the environment since joining NPR in 1986. Bring your questions and join us for coffee with Richard.



Postdoctoral Career Development with Pamela J. Hines

Thursday, October 26th, 3:00pm 612 Conference Room

Pamela J. Hines is a Senior Editor at Science covering research and review papers in developmental neurobiology and plant science. Bring your questions and join us for a conversation with Dr. Hines concerning career development and postdoctoral career options.

DEPARTMENT ANNOUNCEMENTS

BUSINESS OFFICE

ANNUAL CHARITABLE FUND DRIVE

The 2016 Campus Charitable Fund drive is underway September 19th - November 11th. Please consider contributing! Take a moment to read the brochure by visiting the website at www.ccfd.illinois.edu.

A few things you might want to remember:

We encourage everyone to give by on-line payroll deduction.

If you are giving by payroll deduction, please remember to type in the annual amount you wish to donate. There is no limit to the number of agencies that you may select, but the minimum ANNUAL donation is \$24.00 (\$2 per month).

When making a one-time donation, make your check(s) payable to the umbrella organization(s) listed on the Pledge Form, not to designations within the umbrella. If you have any questions throughout the campaign, please contact Jacinda King at 244-2276 or jkking@igb.illinois.edu. The deadline is November 10, 2017. ■

COMMUNICATIONS

ILLINOIS TRANSITIONS TO ONE LOGO

Beginning October 13th, 2017 the Illinois system will now use one logo for all branding, rather than using the "column I" and the "block I" as in the past. The column I will be retired and per the university guidelines "Using the block "I" as the only logo consolidates and strengthens the university brand's impact. This return to a single graphic (logo) ensures that the entire campus can leverage the full benefit of our legacy and take advantage of the instant global recognition the block "I" enjoys."

Existing physical materials with the column I can be used until the supply is depleted, any new items created must have the block I as the primary identity. If you have any questions about proper usage of the logo, refer to http://creativeservices.illinois.edu/brand/ or feel free to contact Nicholas Vasi at <u>nvasi@illinois.edu</u>. ■

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.

Zamroziewicz, M. K., Talukdar, M. T., Zwilling, C. E., & Barbey, A. K. (2017). Nutritional status, brain network organization, and general intelligence. *NeuroImage*, 161, 241-250. DOI: 10.1016/j.neuroimage.2017.08.043

Moran, R. L., Zhou, M., Catchen, J. M., & Fuller, R. C. (2017). Male and female contributions to behavioral isolation in darters as a function of genetic distance and color distance. *Evolution*. DOI: 10.1111/evo.13321

Proskuryakova, A. A., Kulemzina, A. I., Perelman, P. L., Makunin, A. I., Larkin, D. M., Farré, M., ... Graphodatsky, A. S. (2017). X chromosome evolution in cetartiodactyla. *Genes*, 8(9), [2016]. DOI: 10.3390/genes8090216

Yao, L., Li, H., Martin, R. D., Moreau, C. S., & Malhi, R. S. (2017). Tracing the phylogeographic history of Southeast Asian long-tailed macaques through mitogenomes of museum specimens. *Molecular Phylogenetics and Evolution*, 116, 227-238. DOI: 10.1016/j.ympev.2017.08.006

Schwarcz, H. P., Abueidda, D., & Jasiuk, I. (2017). The ultrastructure of bone and its relevance to mechanical properties. *Frontiers in Physics*, 5(SEP), [39]. DOI: 10.3389/fphy.2017.00039

Moon, H., Comi, T. J., Dunham, S. J. B., Kwon, B., Sweedler, J. V., & King, W. P. (2017). Microscale transport physics during atomic force microscopy mass spectrometry and improved sampling efficiency. In TRANSDUCERS 2017 - 19th International Conference on Solid-State Sensors, Actuators and Microsystems (pp. 24-27). [7993978] *Institute of Electrical and Electronics Engineers Inc.*. DOI: 10.1109/TRANSDUCERS.2017.7993978

Saba, C. F., Vickery, K. R., Clifford, C. A., Burgess, K. E., Phillips, B., Vail, D. M., ... Thamm, D. H. (2017). Rabacfosadine for relapsed canine B-cell lymphoma: Efficacy and adverse event profiles of 2 different doses. *Veterinary and Comparative Oncology*. DOI: 10.1111/vco.12337

Wai, C. M., VanBuren, R., Zhang, J., Huang, L., Miao, W., Edger, P. P., ... Ming, R. (2017). Temporal and spatial transcriptomic and microRNA dynamics of CAM photosynthesis in pineapple. *Plant Journal*, 92(1), 19-30. DOI: 10.1111/tpj.13630

Mendenhall, R., Linear, T. I. A., McKee, M. W., Lamers, N. A., & Mouawad, M. B. (2017). Chicago African American mothers' power of resistance: Designing Spaces of Hope in global contexts. *Advances in Education in Diverse Communities: Research, Policy and Praxis*, 12, 409-428. DOI: 10.1108/S1479-358X20140000012019

Gabrys, R., Kiah, H. M., & Milenkovic, O. (2017). Asymmetric Lee Distance Codes for DNA-Based Storage. *IEEE Transactions on Information Theory*, 63(8), 4982-4995. [7918539]. DOI: 10.1109/TIT.2017.2700847

Chen, C., Somavat, P., Singh, V., & Gonzalez de Mejia, E. (2017). Chemical characterization of proanthocyanidins in purple, blue, and red maize coproducts from different milling processes and their anti-inflammatory properties. *Industrial Crops and Products*, 109, 464-475. DOI: 10.1016/j. indcrop.2017.08.046

Bell, A. M., & Stein, L. R. (2017). Transgenerational and developmental plasticity at the molecular level: Lessons from Daphnia. *Molecular Ecology*. DOI: 10.1111/mec.14327

Badea, A., McCracken, J. M., Tillmaand, E. G., Kandel, M. E., Oraham, A. W., Mevis, M. B., ... Nuzzo, R. G. (2017). 3D-Printed pHEMA Materials for Topographical and Biochemical Modulation of Dorsal Root Ganglion Cell Response. ACS Applied Materials and Interfaces, 9(36), 30318-30328. DOI: 10.1021/acsami.7b06742

Berenbaum, M. R. (2017). Communicating about Science Communication: A Brief Entomological History. *Annals of the Entomological Society of America*, 110(5), 435-438. DOI: 10.1093/aesa/sax060

Tasan, I., & Zhao, H. (2017). Targeting Specificity of the CRISPR/Cas9 System. *ACS Synthetic Biology*, 6(9), 1609-1613. DOI: 10.1021/acssynbio.7b00270

Chen, S., McCutchen, M., Cao, P., Qadeer, S., & Iyer, R. K. (2017). SV-Auth – A single-sign-on integration solution with runtime verification. In *Runtime Verification - 17th International Conference*, RV 2017, Proceedings (Vol. 10548 LNCS, pp. 349-358). (Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics); Vol. 10548 LNCS). Springer Verlag. DOI: 10.1007/978-3-319-67531-2 21

Abeysirigunawardena, S. C., Kim, H., Lai, J., Ragunathan, K., Rappé, M. C., Luthey-Schulten, Z., ... Woodson, S. A. (2017). Evolution of protein-coupled RNA dynamics during hierarchical assembly of ribosomal complexes. *Nature Communications*, 8(1), [492]. DOI: 10.1038/s41467-017-00536-1

Venugopal, S., & Viswanathan, M. (2017). The subsistence marketplaces approach to poverty: Implications for marketing theory. *Marketing Theory*, 17(3), 341-356. DOI: 10.1177/1470593117704282

Dau, H., & Milenkovic, O. (2017). Latent Network Features and Overlapping Community Discovery via Boolean Intersection Representations. *IEEE/ACM Transactions on Networking*. DOI: 10.1109/ TNET.2017.2728638

Yang, B., Cui, L., Perez-Enciso, M., Traspov, A., Crooijmans, R. P. M. A., Zinovieva, N., ... Megens, H. J. (2017). Genome-wide SNP data unveils the globalization of domesticated pigs. *Genetics Selection Evolution*, 49(1), [71]. DOI: 10.1186/s12711-017-0345-y

Zhai, C. (2017). Probabilistic topic models for text data retrieval and analysis. In SIGIR 2017 - Proceedings of the 40th International ACM SIGIR Conference on Research and Development in Information Retrieval (pp. 1399-1401). Association for Computing Machinery, Inc. DOI: 10.1145/3077136.3082067

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