IGB NEWS

Upcoming Events
Monthly Profiles
Happenings at IGB

Image Of The Month
Research News
Department Announcements

Volume 12 Number 4

UPCOMING EVENTS

Campus-Wide Computational Biology Brown Bag Seminar Series

What Single-Cell Transcriptomics Can Teach Us About the Honey Bee Brain and Behavior

May 31, 2019, 12:00 p.m.
1040 NCSA

Ian Traniello
Neuroscience, University of Illinois

Postdoctoral Association Presents: Faculty Job Search Session One

Learn how to assemble an academic job application package with relevant comparisons to industry

June 13, 2019, 12:00 p.m.
612 Carl R. Woese Institute for Genomic Biology

Erik R. Nelson, PhD
Assistant Professor of
Molecular and Integrative Physiology
University of Illinois

Postdoctoral Association Presents: Faculty Job Search Session Two

Do's and don'ts of the academic interview and the art of a successful job talk with the opportunity to receive feedback on an application package

July 11, 2019, 12:00 p.m.
607 Carl R. Woese Institute for Genomic Biology

Erik R. Nelson, PhD
Assistant Professor of
Molecular and Integrative Physiology
University of Illinois

IGB Seminar - ONC-PM

August 27, 2019, 12:00 p.m.
612 Carl R. Woese Institute for Genomic Biology

Catherine Klapperich, PhD
Boston University; Associate Dean
for Research and Technology
Development Professor

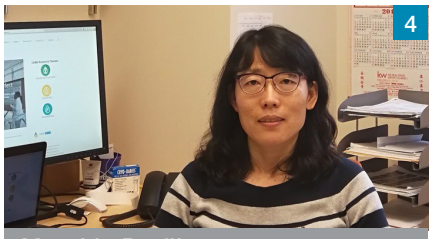
FEATURED NEWS


2

Drugs reprogram genes in breast tumors


3

Breakthrough to measure plant improvements boosts production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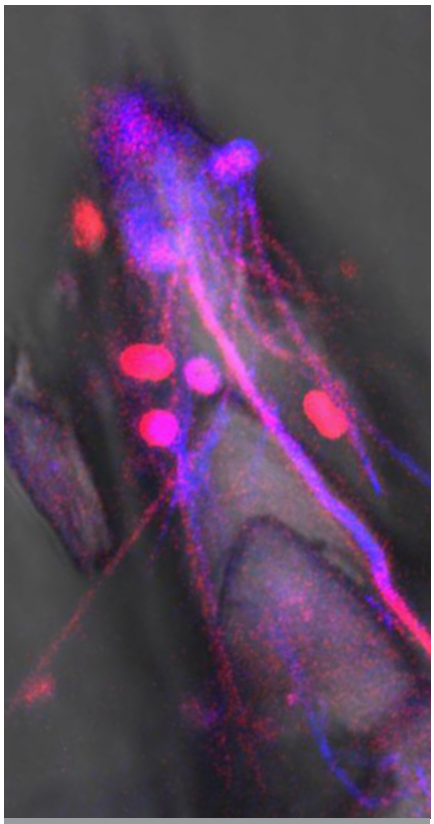
Monthly Profile: Li-Qing Chen


5

On the Grid: Happenings at IGB

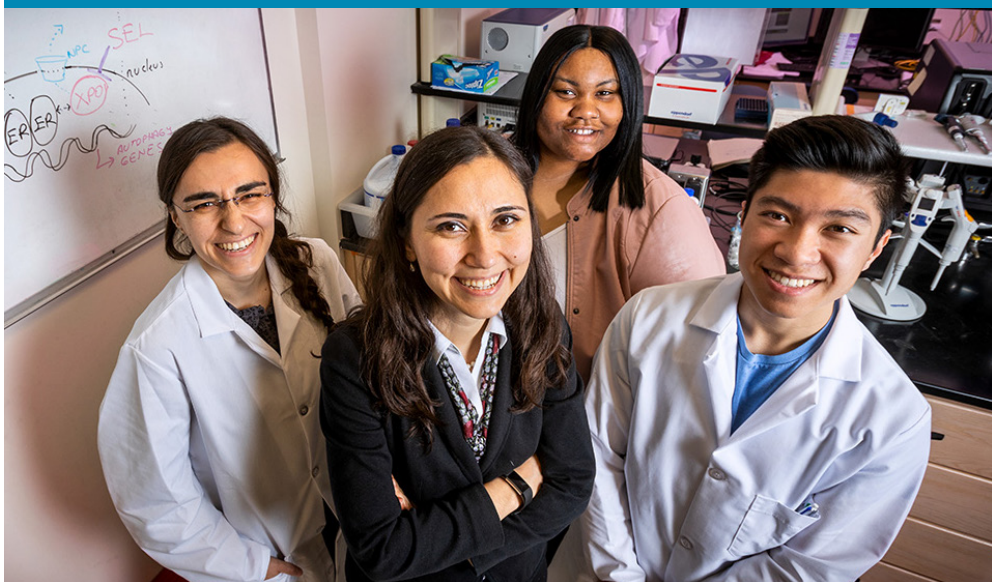
IMAGE OF THE MONTH



This month features an image which merges transmitted plane-light (brightfield) with Airyscan Superresolution autofluo-rescence, showing a rapidly extending travertine crystal intimately associated with thermophilic sulfide oxidizing bacterial filaments (Sulfurihydrogenibium yellow-stonense) and unknown rod-to-coccoid shaped bacteria. Provided by Mayandi Sivaguru and Bruce W. Fouke.

IGB News

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



Drugs reprogram genes in breast tumors
to prevent endocrine resistance

Treating breast tumors with two cancer drugs simultaneously may prevent endocrine resistance by attacking the disease along two separate gene pathways, scientists at the University of Illinois found in a new study.

The two drugs used in the study, selinexor and 4-OHT, caused the cancer cells to die and tumors to regress for prolonged periods, said food science and human nutrition professor Zeynep Madak-Erdogan (ONC-PM), the principal investigator on the study.

The study, published recently in the journal *Cancers*, involved human breast cancer cells that were implanted in mice and analyses of the genes expressed by endocrine-resistant breast tumors.

While endocrine therapy currently is the most effective form of treatment for hormone-responsive breast cancer, some patients will either not respond or will develop resistance to the drugs over time. This condition, called endocrine resistance, causes metastases and is responsible for a majority of women's deaths from hormone-responsive breast cancer.

Based upon the team's prior research, the researchers hypothesized that two elements might work together to cause endocrine resistance – the hormone receptor ERa, which is responsive to estrogen and is expressed in 70 percent of all breast cancers, and the nuclear transport gene XPO1, which removes foreign materials from cells' nuclei.

Combining the drugs selinexor, which prevents XPO1 anti-cancer proteins from functioning, and 4-OHT, which inhibits estrogen receptors from responding to the hormone, might be more effective than either drug alone, the researchers hypothesized.

In a 2016 study published in *Molecular Endocrinology*, Madak-Erdogan's team found that women who expressed higher levels of XPO1 and a "signature" of other nuclear transport genes were more likely to be endocrine resistant.

That paper was co-written by epidemiology professor Rebecca Smith, then-graduate student Karen Chen, research assistant Kinga Wrobel and graduate student Eylem Kulkoyluoglu-Cotul, who was the first author of the current study.

(above) From left, graduate student Eylem Kulkoyluoglu-Cotul, food science and human nutrition professor Zeynep Madak-Erdogen, graduate student Brandi Patrice Smith and undergraduate student Kevin Duong.

In the current study, the team treated endocrine-resistant tumor cells with 4-OHT or selinexor alone, or with a combination of both drugs to determine how each of these treatment protocols affected the tumors' survival and functioning. The drug combination was more effective at reducing the tumor cells' viability than either drug was by itself, they found.

When they tested the three treatments on human breast tumor cells implanted in mice, they found that the combination of 4-OHT and selinexor caused the tumors to regress faster and more completely than either drug alone – effects that continued for several weeks after treatment ended, according to the study.

In analyzing genetic activity in human endocrine-resistant breast tumors, they found that the drug combination increased the expression of more than 100 genes and decreased the expression of 132 other genes that were not affected by either drug alone.

The drug combination appeared to promote sustained tumor regression by decreasing the activity of genes that were associated with endocrine resistance and metastasis. Among these were sets of genes regulated by the protein Akt that control cells' survival, proliferation and migration.

However, in endocrine-resistant tumors, XPO1 helped the cells mutate by modulating Akt's activity, "rewiring breast cancer cells' metabolism to provide them with new survival or escape routes," she said. "By decreasing the expression of certain genes, the 4-OHT and selinexor combination prevented tumor cells from activating these survival pathways, which were prominent when the tumors were treated with either drug alone."

Pathologist Dr. Sunati Sahoo and medical oncologist Dr. Barbara Haley, both of the University of Texas Southwestern Medical Center, co-wrote the paper along with Hua Chang and Yosef Landesman, both of Karyopharm Therapeutics.

Other U. of I. co-authors included Wrobel, graduate student Brandi Patrice Smith and undergraduate students Kevin Duong and Ozan Berk Imir. Caitlin O'Callaghan and Aditi Mehta, both participants in the Cancer Center at Illinois' ResearcHStart program, also contributed to the project.

The research was supported by the U.S. Department of Agriculture's National Institute of Food and Agriculture, a Karyopharm Investigator grant, the U. of I. Office of the Vice Chancellor for Research, an Arnold O. Beckman Award and private donors.

Written by Sharita Forrest. Photo by red Zwicky.

Breakthrough to measure plant improvements helps boost production

An international team is using advanced tools to develop crops that give farmers more options for sustainably producing more food on less land. To do this, thousands of plant prototypes must be carefully analyzed to figure out which genetic tweaks work best. In a special issue of the journal *Remote Sensing of Environment*, scientists have shown a new technology can more quickly scan an entire field of plants to capture improvements in their natural capacity to harvest energy from the sun.

"The method we developed allows us to measure improvements we have engineered in a plant's photosynthesis machinery in about ten seconds, compared to the traditional method that takes up 30 minutes," Katherine Meacham-Hensold, a postdoctoral researcher at the University of Illinois, who led this work for a research project called Realizing Increased Photosynthetic Efficiency (RIPE). "That's a major advance because it allows our team to analyze an enormous amount of genetic material to efficiently pinpoint traits that could greatly improve crop performance."

RIPE, which is led by Illinois, is engineering crops to be more productive by improving photosynthesis, the natural process all plants use to convert sunlight into energy and yield. RIPE is supported by the Bill & Melinda Gates Foundation, the Foundation for Food and Agriculture Research (FFAR), and the U.K. Government's Department for International Development (DFID).

The traditional method for assessing photosynthesis analyzes the exchange of gases through the leaf; it provides a huge amount of information, but it takes 30 minutes to measure each leaf. A faster, or "higher-throughput" method, called spectral analysis, analyzes the light that is reflected back from leaves to predict photosynthetic capacity in as little as 10 seconds.

"The question we set out to answer is: can we apply spectral techniques to predict photosynthetic capacity when we have genetically altered the photosynthetic machinery," said RIPE research leader Carl Bernacchi (CABBI/GEGC), a scientist with the U.S. Department of Agriculture, Agricultural Research Service, who is based at Illinois' Carl R. Woese Institute for Genomic Biology. "Before this study, we didn't know if changing the plant's photosynthetic pathways would change the signal that is detected by spectral measurements."

Although they can prove this method can be used to screen crops that have been engineered to improve photosynthesis, researchers have not uncovered what spectral analysis measures exactly. "Spectral analysis requires custom-built models to translate spectral data into measurements of photosynthetic capacity that must be recreated each year," Meacham said. "Our next challenge is to figure out what we are measuring so that we can build predictive models that can be used year after year to compare results over time."

"While there are still hurdles ahead, spectral analysis is a game-changing technique that can be used to assess a variety of photosynthetic improvements to single out the changes that are most likely to substantially, and sustainably, increase crop yields," said RIPE executive committee member Christine Raines, a professor of plant molecular physiology at the University of Essex, whose engineered crops were analyzed with the technique. "These tools can help us speed up our efforts to develop high-yielding crops for farmers working to help feed the world."

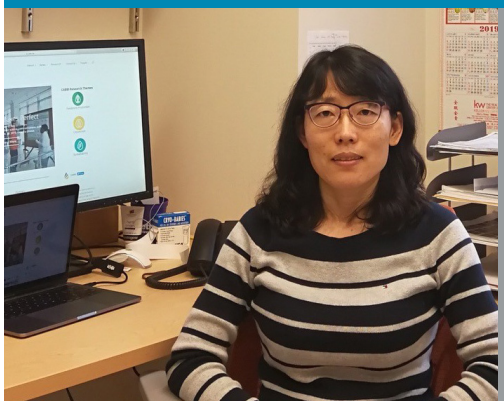
Realizing Increased Photosynthetic Efficiency (RIPE) is engineering staple food crops to more efficiently turn the sun's energy into food to sustainably increase worldwide food productivity, with support from the Bill & Melinda Gates Foundation, the Foundation for Food and Agriculture Research, and the U.K. Government's Department for International Development.

RIPE is led by the University of Illinois in partnership with The Australian National University, Chinese Academy of Sciences, Commonwealth Scientific and Industrial Research Organisation, Lancaster University, Louisiana State University, University of California, Berkeley, University of Essex, and U.S. Department of Agriculture, Agricultural Research Service. ■

Written by Claire Benjamin. Photos by RIPE project.

Scientist Katherine Meacham and an international team have found a method that allows them to measure improvements they have engineered in a plant's photosynthesis machinery much faster.

MONTHLY PROFILE



Li-Qing Chen is an assistant professor in the Department of Plant Biology, whose research focuses on unraveling regulatory networks in plants as a basis for engineering and optimizing assimilates allocation, using a combination of in vivo biochemistry, cell biology, molecular genetics, systems and synthetic biology.

Li-Qing Chen

Understanding plant processes at a deeper level

Growing up in the countryside of China, Li-Qing Chen understood the challenges of farming from a young age. Her family owned a small farm, so she became aware of the many conditions and stresses that plants face.

When Chen began her college education, she decided that she wanted to learn more about plants at a deeper level.

"As farmers, we don't care much about what is going on within plants at the molecular and the genetic level," she said. As a scientist, Chen could finally work toward understanding the fundamental mechanisms of plants.

Now an assistant professor in the Department of Plant Biology and an affiliate of IGB's GEGC theme, Chen is researching how plants control the flow of sugar from their source tissues, such as leaves, to their sink tissues, such as roots, flowers and seeds.

Sugar is an important part of plant nutrition. Plants' source tissues can make enough sugar for themselves and other parts of the plant, but their sink tissues need to import sugar to support their own growth.

Chen wants to understand how this flow of sugar is regulated at the molecular level—a process that is not well understood.

"We only know a little about sugar flux regulation," Chen said. "That's why I feel that my research is so urgent."

This fundamental research can have a real-world application. Sugar-rich tissues are a favorable trait for some crops because sugar can be converted into biodiesel and ethanol fuel, two major alternative renewable fuels. Sugar also contributes greatly to crop yields.

If scientists can better understand how sugar is allocated through plants, they may be able to one day manipulate these processes to increase the amount of sugar in the plant and maximize crop yields.

"Can we allocate more sugar to the desirable tissues to increase crop yields and/or biofuel production?" Chen said. "That's our goal."

Chen is also a faculty member of the Center for Advanced Bioenergy and Bioproducts Innovation (CABBI), a collaboration between the IGB and the Institute for Sustainability, Energy and Environment.

> *"Can we allocate more sugar to the desirable tissues to increase crop yields and/or biofuel production? That's our goal."*

CABBI's aim is to research and develop sustainable biofuels and bioproducts.

Chen is a member of CABBI's Feedstock Production theme, which focuses on using plants as "factories" to create biofuels, bioproducts, and important molecules.

With CABBI, Chen is working on understanding why sweet sorghum can accumulate more sugar in its stem than grain sorghum can.

Sorghum, a versatile crop, is one of the world's highest producers of biomass, a renewable source of energy. Sweet sorghum has mainly been grown for its sugary syrup, but it has recently become a promising crop for biofuel and chemical production.

"We know sweet sorghum can accumulate a lot of sugar. Can we maximize this potential?" Chen said. "That's a fundamental question—we have to get a better understanding of the mechanism behind it."

Chen has been affiliated with the IGB since she came to the University in 2015. She can see how her expertise in sugar allocation fits into the GEGC theme's research on photosynthesis and other plant processes.

"I can see lots of collaborative opportunities with other members in the IGB," she said.

She also believes that her research and expertise can contribute to solving several crucial problems our world faces today—including urgent needs for renewable fuels due to fossil fuel depletion, and food insecurity due to growing populations and the loss of arable land.

"I think I may be able to contribute to resolving these issues, a little bit," Chen said. "That's my career goal too. That drives me to continue the research in this field." ■

Written by Emily Scott. Photo by Li-Qing Chen.

CABBI
CENTER FOR ADVANCED BIOENERGY AND BIOPRODUCTS INNOVATION

The Center for Advanced Bioenergy and Bioproducts Innovation (CABBI) integrates recent advances in agronomics, genomics, and synthetic and computational biology to increase the value of energy crops—using a holistic approach that will help reduce our nation's dependence on fossil fuels, thus increasing national security.

ON THE GRID
HAPPENINGS AT THE IGB

AWARD

STEPHEN LONG

Stephen P. Long, a professor of crop sciences and plant biology at the University of Illinois, has been elected to the National Academy of Sciences, one of the highest professional honors a scientist can receive. He is one of 100 new members and 25 foreign associates recognized for "distinguished and continuing achievements in original research."

EVENT

WORLD OF GENOMICS AT THE NATIONAL ACADEMY OF SCIENCES

In April the IGB co-hosted with the National Academies a massive outreach event in Washington, D.C. called DecisionTown in the World of Genomics, merging the NAS concept of DecisionTown with our own outreach activities. The event drew several thousand attendees to the NAS building, where IGB volunteers were on hand to lead activities at 6 different interactive booths. IGB faculty members were in attendance to interact with the public at our stations and to give talks in the NAS auditorium. The effort was made possible with support from the Kleinmuntz Center, and we were happy that Catherine Kleinmuntz herself was able to attend.

Our thanks to the faculty, volunteers, staff, and IGB leadership for putting together one of the most complicated World of Genomics events to date!

PROJECT

EBP DIRECTORS VISIT D.C.

IGB Director Gene Robinson, left, and founding IGB Director Harris Lewin, right, met with Congressman Ami Bera to speak about the Earth Biogenome Project, a joint grand challenge to sequence, catalog and characterize the genomes of all of Earth's eukaryotic biodiversity over a period of ten years.

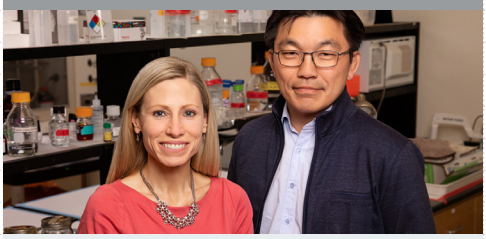
EXHIBIT

ART OF SCIENCE AT THE SPRINGER CULTURAL CENTER

The IGB celebrated the opening of the 9th annual Art of Science exhibit, in new location the Springer Cultural Center in Champaign. Several hundred attendees came to see the newest version of the show, with special guest speakers including IGB Director Gene Robinson, co-sponsor and President of BodyWork Associates Doug Nelson, graduate student from the Harley Lab Emily Chen, and Assistant Professor of Anthropology Jessica Brinkworth. Both Emily and Jessica had work in the show, and spoke about the connections between their research and the artwork presented.

If you missed the show, an online gallery can be viewed on the IGB website.

RESEARCH



INJECTIONS AND EXERCISE PROMOTE MUSCLE REGROWTH AFTER ATROPHY

By injecting cells that support blood vessel growth into muscles depleted by inactivity, researchers say they are able to help restore muscle mass lost as a result of immobility.

The research, conducted in adult mice, involved injections of cells called pericytes, which are known to promote blood vessel growth and dilation in tissues throughout the body. The injections occurred at the end of a two-week period during which the mice were prevented from contracting the muscles in one of their hind legs.

"Just as the mice were becoming mobile again, we transplanted the pericytes and we found that there was full recovery of both muscle mass and the vasculature, too," said University of Illinois kinesiology and community health professor Marni Boppart, who led the research with chemical and biomolecular engineering professor HyunJoon Kong (RBTE) and their colleagues. The mice that received the injections had significantly better improvement than those that regained mobility without the injections. Boppart is a member of the IGB's Regenerative Biology & Tissue Engineering research theme, as well as a researcher in the Beckman Institute for Advanced Science and Technology and in the Carle Illinois College of Medicine at Illinois.

The team reports the new findings in *The FASEB Journal.*

The National Institute of Arthritis and Musculoskeletal and Skin Diseases and the National Heart, Lung, and Blood Institute of the U.S. National Institutes of Health supported this research.

DEPARTMENT ANNOUNCEMENTS

BUSINESS

FY20 BENEFIT CHOICE ENROLLMENT FOR UNIVERSITY OF ILLINOIS EMPLOYEES

The FY20 Benefit Choice period will begin on Wednesday, May 1, 2019 and end on Friday May 31, 2019 with an effective date of July 1, 2019.

If you are eligible for State of Illinois insurance and benefits, you will no longer use NESSIE to make Benefit Choice changes. Instead, you will use the state's new CMS MyBenefits Marketplace website: https://mybenefits.illinois.gov/account/login/choseclient.

There are two helpful resources for using the new MyBenefits site:

- MyBenefits Tips blog post found at https://blogs.illinois.edu/view/1418/472472 is a quick-start guide for registering, logging in, and using the site.
- MyBenefits Marketplace FAQs found at https://www.hr.uillinois.edu/benefits/segip/mybenefitsFAQ will help to address some common questions.

Questions
For assistance with your state benefit plans (health, dental, and life insurance, and flexible spending accounts) contact the MyBenefits Marketplace Service Center. Bilingual customer service representatives are available.

- Phone: 844-251-1777 or TTY 844-251-1778
- Hours: 8:00 a.m. – 6:00 p.m. CT Monday through Friday

For questions about university plans or benefit counseling, please contact University Payroll and Benefits by sending an e-mail to benefits@uillinois.edu or via phone at (217) 265-6363. ■

CNRG

CNRG has replaced the default nodes in Biocluster with five 72 core, 1.2 TB systems. The costs of these systems remain the same as the previous nodes while offering improved networking, processing capability, and a larger memory pool. If you have any questions about these new resources, please contact CNRG at help@igb.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.

Jeong, H., Arif, B., Caetano-Anolles, G., Kim, K. M., & Nasir, A. (2019). Horizontal gene transfer in human-associated microorganisms inferred by phylogenetic reconstruction and reconciliation. *Scientific Reports*, 9(1), [5953]. https://doi.org/10.1038/s41598-019-42227-5

Xing, M., Wei, Y., Zhou, Y., Zhang, J., Lin, L., Hu, Y., ... Zhang, Y. (2019). Radical-mediated C-S bond cleavage in C2 sulfonate degradation by anaerobic bacteria. *Nature communications*, 10(1), [1609]. https://doi.org/10.1038/s41467-019-09618-8

Thirawatananond, P., McPherson, R. L., Malhi, J., Nathan, S., Lambrecht, M. J., Brichacek, M., ... Gabelli, S. B. (2019). Structural analyses of NudT16–ADP-ribose complexes direct rational design of mutants with improved processing of poly(ADP-ribosyl)ated proteins. *Scientific Reports*, 9(1), [5940]. https://doi.org/10.1038/s41598-019-39491-w

Sonam, S., Srnak, J. A., Perry, K. J., & Henry, J. J. (2019). Molecular markers for corneal epithelial cells in larval vs. adult Xenopus frogs. *Experimental Eye Research*, 184, 107-125. https://doi.org/10.1016/j.exer.2019.04.010

Dewey, M. J., Johnson, E. M., Weisgerber, D. W., Wheeler, M. B., & Harley, B. A. (2019). Shape-fitting collagen-PLA composite promotes osteogenic differentiation of porcine adipose stem cells. *Journal of the Mechanical Behavior of Biomedical Materials*, 95, 21-33. https://doi.org/10.1016/j.jmbbm.2019.03.017

Dodd, L. D., Nowak, E., Lange, D., Parker, C. G., DeAngelis, R., Gonzalez, J. A., & Rhodes, J. S. (2019). Active feminization of the preoptic area occurs independently of the gonads in *Amphiprion ocellaris*. *Hormones and Behavior*, 112, 65-76. https://doi.org/10.1016/j.yhbeh.2019.04.002

Jiang, S., Yildiz, G., Ding, J., Andrade, J., Rababahb, T. M., Almajwalc, A., ... Feng, H. (2019). Pea Protein Nanoemulsion and Nanocomplex as Carriers for Protection of Cholecalciferol (Vitamin D3). *Food and Bioprocess Technology*, 12(6), 1031-1040. https://doi.org/10.1007/s11947-019-02276-0

Li, Q., Singh, V., Demejia, E., & Somavat, P. (2019). Effect of sulfur dioxide and lactic acid in steeping water on the extraction of anthocyanins and bioactives from purple corn pericarp. *Cereal Chemistry*, 96(3), 575-589. https://doi.org/10.1002/cche.10157

RECENT PUBLICATIONS

Schilling, B., Basisty, N., Christensen, D. G., Sorensen, D., Orr, J. S., Wolfe, A. J., & Rao, C. V. (2019). Global lysine acetylation in *Escherichia coli* results from growth conditions that favor acetate fermentation. *Journal of bacteriology*, 201(9), [e00768-18]. https://doi.org/10.1128/JB.00768-18

Qin, E. C., Kandel, M. E., Liamas, E., Shah, T. B., Kim, C., Kaufman, C. D., ... Kong, H. J. (2019). Graphene oxide substrates with N-cadherin stimulates neuronal growth and intracellular transport. *Acta Biomaterialia*, 90, 412-423. https://doi.org/10.1016/j.actbio.2019.04.005

Son, K., You, J. S., Yoon, M. S., Dai, C., Kim, J. H., Khanna, N., ... Chen, J. (2019). Nontranslational function of leucyl-tRNA synthetase regulates myogenic differentiation and skeletal muscle regeneration. *Journal of Clinical Investigation*, 129(5), 2088-2093. https://doi.org/10.1172/JCI122560

Moskát, C., & Hauber, M. E. (2019). Sex-specific responses to simulated territorial intrusions in the common cuckoo: a dual function of female acoustic signaling. *Behavioral Ecology and Sociobiology*, 73(5), [60]. https://doi.org/10.1007/s00265-019-2665-0

Iyer, R. R., Liu, Y. Z., & Boppart, S. A. (2019). Automated sensorless single-shot closed-loop adaptive optics microscopy with feedback from computational adaptive optics. *Optics Express*, 27(9), 12998-13014. https://doi.org/10.1364/OE.27.012998

Berenbaum, M. R. (2019). Speaking of gender bias. *Proceedings of the National Academy of Sciences of the United States of America*, 116(17), 8086-8088. https://doi.org/10.1073/pnas.1904750116

Mei, R., Kim, J., Wilson, F. P., Bocher, B. T. W., & Liu, W-T. (2019). Coupling growth kinetics modeling with machine learning reveals microbial immigration impacts and identifies key environmental parameters in a biological wastewater treatment process. *Microbiome*, 7(1), [65]. https://doi.org/10.1186/s40168-019-0682-x

Mirts, E. N., Bhagi-Damodaran, A., & Lu, Y. (2019). Understanding and Modulating Metalloenzymes with Unnatural Amino Acids, Non-Native Metal Ions, and Non-Native Metallocofactors. *Accounts of chemical research*, 52(4), 935-944. https://doi.org/10.1021/acs.accounts.9b00011

Wallberg, A., Bunikis, I., Pettersson, O. V., Mosbech, M. B., Childers, A. K., Evans, J. D., ... Webster, M. T. (2019). A hybrid de novo genome assembly of the honeybee, *Apis mellifera*, with chromosome-length scaffolds. *BMC genomics*, 20(1), [275]. https://doi.org/10.1186/s12864-019-5642-0

Banerjee, S. S., Kalbarczyk, Z. T., & Iyer, R. K. (2019). AcMC 2: Accelerated Markov Chain Monte Carlo for Probabilistic Models. In ASPLOS 2019 - 24th International Conference on Architectural Support for Programming Languages and Operating Systems (pp. 515-528). (International Conference on Architectural Support for Programming Languages and Operating Systems - ASPLOS). *Association for Computing Machinery*. https://doi.org/10.1145/3297858.3304019

Lin, C. Y., Alexander, C., Steelman, A. J., Warzecha, C. M., Cattai de Godoy, M. R., & Swanson, K. S. (2019). Effects of a *Saccharomyces cerevisiae* fermentation product on fecal characteristics, nutrient digestibility, fecal fermentative end-products, fecal microbial populations, immune function, and diet palatability in adult dogs. *Journal of animal science*, 97(4), 1586-1599. https://doi.org/10.1093/jas/skz064

Hauber, M. E., Bond, A. L., Kouwenberg, A. L., Robertson, G. J., Hansen, E. S., Holford, M., ... Dale, J. (2019). The chemical basis of a signal of individual identity: Shell pigment concentrations track the unique appearance of Common Murre eggs. *Journal of the Royal Society Interface*, 16(153), [20190115]. https://doi.org/10.1098/rsif.2019.0115

Lombardi, L., Zoppo, M., Rizzato, C., Bottai, D., Hernandez, A. G., Hoyer, L. L., & Tavanti, A. (2019). Characterization of the *Candida orthopsilosis* agglutinin-like sequence (ALS) genes. *PloS one*, 14(4), [e0215912]. https://doi.org/10.1371/journal.pone.0215912

Argueso, C. T., Assmann, S. M., Birnbaum, K. D., Chen, S., Dinneny, J. R., Doherty, C. J., ... Williams, C. M. (2019). Directions for research and training in plant omics: Big Questions and Big Data. *Plant Direct*, 3(4), [e00133]. https://doi.org/10.1002/pld3.133

Kim, D. H., Park, H. J., Park, H. S., Lee, J. U., Ko, C., Gye, M. C., & Choi, J. M. (2019). Estrogen receptor α in T cells suppresses follicular helper T cell responses and prevents autoimmunity. *Experimental and Molecular Medicine*, 51(4), [41]. https://doi.org/10.1038/s12276-019-0237-z

Farré, M., Kim, J., Proskuryakova, A. A., Zhang, Y., Kulemzina, A. I., Li, Q., ... Larkin, D. M. (2019). Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. *Genome Research*, 29(4), 576-589. https://doi.org/10.1101/gr.239863.118

Henry, J. J., Perry, K. J., & Hamilton, P. W. (2019). *Ex Vivo* Eye Tissue Culture Methods for Xenopus. *Cold Spring Harbor protocols*, 2019(4). https://doi.org/10.1101/pdb.prot101535

Henry, J. J., Perry, K. J., & Hamilton, P. W. (2019). Methods for Examining Lens Regeneration in Xenopus. *Cold Spring Harbor protocols*, 2019(4). https://doi.org/10.1101/pdb.prot101527

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