

070809  
101112  
131415  
162017

REDEFINING LIFE'S LIMITATIONS: 10 YEARS AND COUNTING  
2017 ANNUAL REPORT  
CARL R. WOESE INSTITUTE FOR GENOMIC BIOLOGY



## ABBREVIATIONS AND ACRONYMS

### RESEARCH THEMES AND CENTERS

ACPP  
Anticancer Discovery from Pets to People

BCXT  
Biocomplexity

BSD  
Biosystems Design

CABBI  
Center for Advanced Bioenergy and Bioproducts Innovation

CGRH  
Computing Genomes for Reproductive Health

EBI  
Energy Biosciences Institute

GEGC  
Genomic Ecology of Global Change

GNDP  
Gene Networks in Neural and Developmental Plasticity

IGOH  
Infection Genomics for One Health

MME  
Microbiome Metabolic Engineering

MMG  
Mining Microbial Genomes

ONC-PM  
Omics Nanotechnology for Cancer Precision Medicine

RBTE  
Regenerative Biology and Tissue Engineering

---

## OTHER ABBREVIATIONS AND ACRONYMS

DOE  
Department of Energy

IGB  
Carl R. Woese  
Institute for Genomic Biology

IUB  
NASA Astrobiology Institute  
for Universal Biology

NIH  
National Institutes of Health

NSF  
National Science Foundation

USDA  
United States Department of Agriculture

# 1

---

Director's Message  
GENE ROBINSON

p.2-5

# 2

---

About the IGB

IGB Themes, Partnerships  
and Facilities

p.6-9

# 3

---

2007-2017:  
Highlights from our first ten years

p.10-33

2017:  
This year in detail

p.34-83

# 4

---

IGB numbers, publications,  
and awards

p.84-90

Giving and Donor Roll

p.91

World of Genomics (Image to the right)

For three days last May, visitors to the Chicago Field Museum of Natural History were introduced to IGB research as they explored six special exhibits interspersed with the Field Museum's iconic offerings. Read more on page 45.



# 1

---

Director's Message  
GENE ROBINSON

Science endeavors to use the past to predict and prepare for the future. Success requires the systematic collection and evaluation of evidence. What are we observing? Do we know all the factors involved and their relative importance? When we synthesize the information we have gathered, can we produce a trend line that points toward a clear prediction? In addition to careful, precise work, some of the most revolutionary science has involved what can seem like a sixth sense for which details will matter.

CONTINUED ON P.4



ILLINOIS  
GENE ROBINSON

WORLD OF GOMICS  
WORLD OF GEN

150  
100

---

## Director's Message

GENE ROBINSON



Genomic Biology finds a new home on campus: the IGB under construction in 2005.

In 2007, the Carl R. Woese Institute for Genomic Biology became the functioning embodiment of a prediction that the apparent rise of genomics would continue to accelerate. That rise had begun years before with the first handful of published genome sequences and the inception of the Human Genome Project; growing excitement in the field helped to spark the idea that led to the IGB's formation. Illinois administrators and faculty came together in the late 1990s to discuss the need to centralize genomic biology research on campus, and in a few years gained state government support for a new institute, housed in a custom-designed building and led by Harris Lewin, the IGB's founding director.

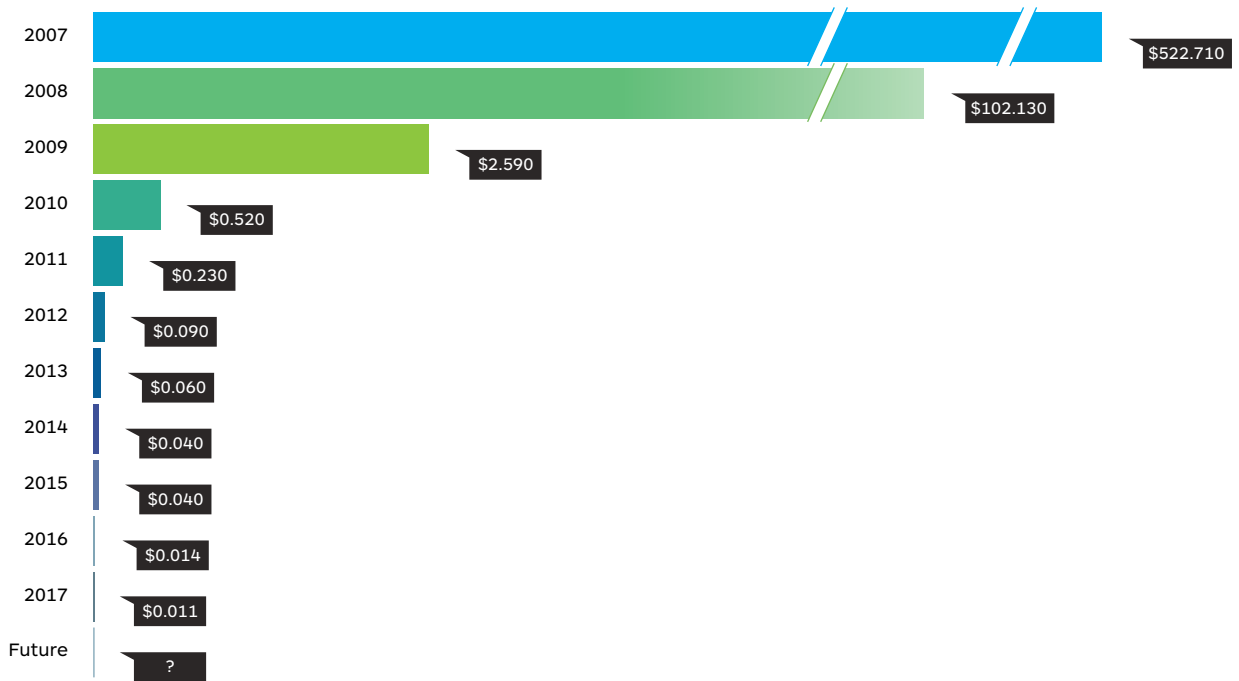
The trend that campus researchers, the university administration, and the state government united to take advantage of is one that has continued to soar. Since 2007, the number of organisms with sequenced genomes swelled from about 3,000 to over 130,000 and the average cost of sequencing a megabase of DNA dropped from just over \$500 to its recent low of just over a cent. Sequencing projects that would once have been moonshots are now as routine as a day trip to a local park.

The establishment of the IGB created a space that allowed researchers to thrive in this technological and scientific boom, and thrive they did. IGB projects in the last ten years have moved us closer to sustainable food and fuel security, to using personal genomic data to empower at-risk populations, to probing the origins and most basic principles of life itself. The larger scientific community celebrated technological developments that were once barely imaginable, including the storage of readable data in synthesized DNA, the characterization of the gut microbiome, and the explosion of CRISPR-based genome editing approaches and applications.

Our researchers have responded to these and other developments by forging paths in the scientific territory they have revealed. Some of our thematic research groups have incorporated new initiatives and directions: Mining Microbial Genomes has leveraged new sequencing and computation capabilities to further its investigative aims. Others have assembled or reimagined themselves in response to fresh challenges and opportunities: Gene Networks in Neural and Developmental Plasticity has embraced systems approaches to exploring complex phenotypes, and Biosystems Design and Metabolic Microbiome Engineering were instigated, in part, in response to novel genome editing technologies and their synergy with the biochemical power of microbial communities.

The same flexibility has helped shape our community engagement efforts. In the last decade, the IGB has had the privilege of creating a science-inspired art exhibit that has been displayed around the nation and beyond, and implementing a multi-day outreach event on the main floor of the Chicago Field Museum. We continue to look for new ways to share with the public the same types of stories you will find in this Annual Report, of the discovery of

## Cost of sequencing per megabase 2007-2017



*Thanks to next-generation sequencing technologies, the cost of DNA sequencing has dropped dramatically in the last ten years, at a rate exceeding Moore's Law. Future technological improvements may reduce this cost still further, but the next major challenge is addressing the computational demands of genomic data analysis and storage.*

more effective strategies to produce potentially therapeutic stem cells; the identification of interactions between molecular pathways and diet that could lead to new breast cancer treatments; and the development of tools that allow researchers to produce custom strains of yeast for bioproduct manufacturing.

These and other research stories from within and beyond the walls of the IGB have additional value as data points for future trends. Genomics has come a long way, but for all the thousands of genomes sequenced so far, we have still only explored a tiny fraction of the genomic frontier represented in the diversity of life on earth. In addition to affording us one more opportunity for reflection, this report represents our enthusiasm for future efforts. How can we position ourselves to make the next ten

years and beyond as productive as the last ten? We anticipate that the coming decade will bring an increasing need for better computational resources, more efficient ways to translate discovery into practical solutions for health conditions or food and fuel needs, and studies that serve the needs of broader, more diverse populations. Whether these needs or more unexpected ones turn out to be our greatest challenges, we are determined to continue to build on the IGB's trajectory of excellence.

Gene E. Robinson  
Director, Carl R. Woese Institute for Genomic Biology

# 2

---

## About the IGB

### Our origins

The Carl R. Woese Institute for Genomic Biology (IGB) was founded in 2007 with the intention of facilitating cohesion of genomic research and resources across the campus.

### Our present

The tenth anniversary of IGB's establishment was an occasion to celebrate the diversity and productivity of our membership.

### Our future

We are determined to continue strengthening our connections with communities in academia, industry, and society to ensure the relevance and positive impact of our work.

---

At the IGB, as throughout the scientific world, change is a constant. The questions we ask, the approaches we embrace, and the goals we pursue will continue to adapt as genomics progresses, but our commitment to collaboration and diversity is unwavering.

Image: Scientists and community members come together at the annual Art of Science opening reception to appreciate the beauty of biology.





Our thematic research groups and partnerships have grown and coevolved over the last ten years, converging into a comprehensive portfolio of fundamental and applied genomic research.

## Strategic Partnerships


### **Energy Biosciences Institute**

BP, Shell, UC Berkeley, Lawrence Berkeley National Laboratory




### **Center for Advanced Bioenergy and Bioproducts Innovation**

Boston University, Brookhaven National Laboratory, Colorado State University, HudsonAlpha Institute for Biotechnology, Institute for Systems Biology, Iowa State University, Lawrence Berkeley National Laboratory, Mississippi State University, Princeton University, USDA-Agricultural Research Service, UC Berkeley, University of Florida, University of Idaho, University of Nebraska-Lincoln, University of Wisconsin-Madison, West Virginia University



### **Center for Nutrition, Learning and Memory**

Abbott Nutrition, Beckman Institute



### **Omics Nanotechnology for Cancer Precision Medicine**

Macro and Nanotechnology Laboratory




### **ZEISS Labs@Location Partnership**

ZEISS Microscopy




### **CompGen Initiative**

Coordinated Science Laboratory, Abbott Molecular, Dow Agro Sciences, Eli Lilly and Co., IBM Systems, Strand Life Sciences, Intel Corporation, Xilinx Inc., OSF Healthcare



### **High Performance Biological Computing**

Carver Biotechnology Center



HEALTH


TECHNOLOGY

ENVIRONMENT

## Research Themes


### **Anticancer Discovery from Pets to People (ACPP)**

Develops cancer treatments in pet animals that translate to human disease




### **Biocomplexity (BCXT)**

Explores the origin of life and the behavior of biological systems




### **Biosystems Design (BSD)**

Applies engineering principles to real and artificial biological systems




### **Computing Genomes for Reproductive Health (CGRH)**

Examines the interplay among genetic and environmental factors that influence disorders of reproduction



### **Gene Networks in Neural & Developmental Plasticity (GNDP)**

Examines the effects of coordinated gene activity on biological diversity




### **Genomic Ecology of Global Change (GEGC)**

Studies the intersection of plant genomics and global climate change




### **Infection Genomics for One Health (IGOH)**

Examines how microbes in human-inhabited environments influence health and disease




### **Microbiome Metabolic Engineering (MME)**

Explores the relationships between human microbiota, environment, and health




### **Mining Microbial Genomes (MMG)**

Discovers small molecules that might provide new medical solutions




### **Omics Nanotechnology for Cancer Precision Medicine (ONC-PM)**

Develops new technology to identify and manage cancerous tumors



### **Regenerative Biology & Tissue Engineering (RBTE)**

Studies the replacement or regeneration of tissues and organs



HEALTH

TECHNOLOGY

ENVIRONMENT

# 3

---

A look back at the last  
10 years and a review of  
what happened in 2017

For 10 years our institute has sought answers both practical and fundamental: our search horizons extend from the smallest of particles to the broadest patterns of life itself. Join us as we highlight the markers from the previous

decade that guided us and revisit the most recent developments defining our future direction. Ten years means many things to us: a notable milestone, a worthwhile struggle, and perhaps most meaningfully, a promising beginning.

## 2007 IN GENOMICS



NUMBER OF SPECIES SEQUENCED

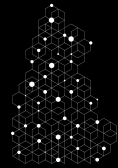
2,952

---

ARCHAEA	111
BACTERIA	1,986
EUKARYA	855

---

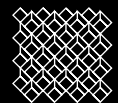
↑ 872 TOTAL SPECIES SINCE 2006



COST OF SEQUENCING PER  
MEGABASE

\$522.71

↓ \$176.49 SINCE 2006



NUMBER OF "GENOMICS"  
PUBLICATIONS

17,580

↑ 2,683 SINCE 2006

## GENOMICS MADE THE HEADLINES:

For the first time, scientists store data in engineered, biocompatible DNA

Skin cells successfully converted into stem cells, offering the promise of future cures

Image: Complex systems are found in biological processes at all levels, from microscopic to global.

20  
07

In 2007, IGB receives its third major research award, \$5 million from the NSF Frontiers in Biology Research program to investigate the emergence of life.

The scientific shift from genetics to genomics contained a conceptual shift from the singular to the collective. Where researchers had once been focused on the structure and function of individual genes, they could now take advantage of techniques that allowed them to ask how the actions of genes influenced one another, and how biological processes emerged holistically from activity across the entire genome.

Given this crucial expansion of focus, it is no surprise that the Biocomplexity (BCXT) theme was one of the first proposed and formed during the construction of the IGB. The shared challenge that united its members was to address a deep and fundamental question that can be asked at every level of biological organization: how do the parts of a complex system come together to create a coherent whole?

Driven by the work of theme member and IGB co-founder Carl Woese, the theme's purview naturally expanded into the speciation of microbial communities, the identification of key molecular biosignatures within diverse environments, and later the development of the Institute for Universal Biology, a NASA Astrobiology Institute housed within the IGB to address perhaps some of the most fundamental questions facing society: what is the origin of life and how does it evolve? Their research into the fundamentals of living systems has resulted in broad and unexpected applications, from a partnership with Mayo Clinic to study the similarities between kidney stones and travertine, a form of limestone found in hot springs, and the impact that extreme microbial populations can have on global concerns such as climate change.

## IGB THEME METRICS

### BIOCOMPLEXITY (BCXT)

Explores the origin of life and the behavior of biological systems

---

#### Current Members

**13** **9**  
Faculty Affiliates

---

#### Represented Departments

**13**

Animal Sciences; Anthropology; Bioengineering; Cell and Developmental Biology; Chemistry; Civil and Environmental Engineering; Computer Science; Geology; Mathematics; Microbiology; Physics; Plant Biology

---

#### Publications since 2007

**677**

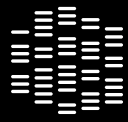
---

#### Member Awards Since Inception

**23**

---

## 2008 IN GENOMICS



NUMBER OF SPECIES SEQUENCED

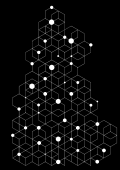
3,829

---

ARCHAEA	143
BACTERIA	2,690
EUKARYA	996

---

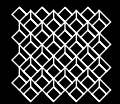
↑ 877 TOTAL SPECIES SINCE 2007



COST OF SEQUENCING PER  
MEGABASE

\$102.13

↓ \$420.58 SINCE 2007



NUMBER OF "GENOMICS"  
PUBLICATIONS

20,673

↑ 3,093 SINCE 2007

### GENOMICS MADE THE HEADLINES:

Chemists synthesize the first DNA molecule made from lab-produced components

20  
08

---

Image: Close-up view of a leaf of Miscanthus, also known as elephant grass, a high-performing biofuel crop.

---

In 2008, IGB researchers begin planting the 320-acre Energy Farm, a "living laboratory" in which to develop and test biofuel crops.



In a year where many saw gas prices reach—and then surpass—the \$4.00 per gallon mark, a large, cross-institutional collaboration focused on alternative fuel and energy sources set the example for multidisciplinary public-private partnerships and set the tone for the development of the IGB as an emerging research leader at Illinois. Backed by a \$500 million investment from energy company BP and combining the established agricultural strengths of Illinois with the biotechnology and chemical synthesis facilities at The University of California, Berkeley and the Lawrence Berkeley National Lab, the Energy Biosciences Institute (EBI) began operations in earnest.

What followed was a comprehensive effort to address issues in the energy sector, in the areas of biofuels production, bioconversion, feedstock engineering, biomass degradation, societal and economic impact, and later algal biofuels production and microbial recovery of hydrocarbons, including the most difficult problem of an efficient and cost-effective process to harness sugars stored in woody material of energy crops. A shifting economy and reprioritization of BP's research investments resulted in a scaled-down and reimagined EBI, but their core mission to produce sustainable next-generation energy sources remained the same. With major breakthroughs in fermentation abilities of yeast, identification of deep subsurface microbes that enhance the ability to explore for and recover oil and gas, mapping the genome of promising energy crops, and developing bio-based aviation fuels, members of the EBI continue their efforts to solve the energy needs of future generations.

## IGB THEME METRICS

### ENERGY BIOSCIENCES INSTITUTE (EBI)

Utilizes innovative approaches to produce sustainable next-generation energy sources

---

#### Current Members

**7**  
Faculty

---

#### Represented Departments

**4**

Animal Sciences; Chemical and Biomolecular Engineering; Civil and Environmental Engineering; Plant Biology

---

#### Publications since 2007

**1,341**

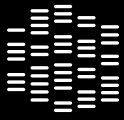
---

#### Member Awards Since Inception

**23**

---

## 2009 IN GENOMICS



NUMBER OF SPECIES SEQUENCED

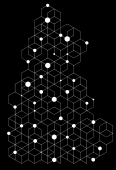
5,843

---

ARCHAEA	174
BACTERIA	4,446
EUKARYA	1,223

---

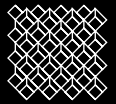
↑ 2,014 TOTAL SPECIES SINCE 2008



COST OF SEQUENCING PER  
MEGABASE

\$2.59

↓ \$99.54 SINCE 2008



NUMBER OF "GENOMICS"  
PUBLICATIONS

24,018

↑ 3,345 SINCE 2008

### GENOMICS MADE THE HEADLINES:

Medical scientists create the first comprehensive catalog of cancer-causing mutations

Image: Genomic research has the potential to improve the prognosis for individuals suffering from many types of cancer, including the small cell lung cancer visible in this sample.

# 20 09

In 2009, the first research articles documenting the cancer-fighting properties of PAC-1 are published.

Some of the most promising breakthroughs in cancer therapy have involved the development of innovative cancer drugs that hit new targets. One of the IGB's earliest themes, Cellular Decision Making in Cancer (CDMC), was built upon this idea. When the theme was reimagined as Anticancer Discovery From Pets to People (ACPP), it added a unique approach: using companion animals such as cats and dogs as model organisms. Drugs are commonly tested on mice and rats, but researchers believe that the disease progression, and therefore treatment, is more likely to be similar in humans and pets, making them a better model to use to discover breakthroughs in treating human cancers.

Research in ACPP uses genomic methods to identify novel cancer targets. After finding molecules that can hit these targets, researchers can test their efficiency as probes or therapeutics. When compounds can hit new targets, they are often more successful in human trials and can be developed at a lower cost.

One of the most significant endeavors, begun in CDMC and carried forward by ACPP, has been the development of PAC-1, an experimental drug used to treat anaplastic astrocytoma, a rare malignant tumor, and glioblastoma multiforme, an aggressive brain cancer.

PAC-1 has already been safely tested in dogs and is now being tested in human clinical trials. It will take years to fully determine its safety and effectiveness, but researchers have hope that it can provide a way to treat one of the world's deadliest cancers.

## IGB THEME METRICS

### ANTICANCER DISCOVERY FROM PETS TO PEOPLE (ACPP)

Develops cancer treatments in pet animals that translate to human disease

---

#### Current Members

6

Faculty

1

Affiliate

---

#### Represented Departments

6

Biochemistry; Bioengineering;  
Comparative Biosciences; Chemistry;  
Physics; Veterinary Clinical Medicine

---

#### Publications since 2007

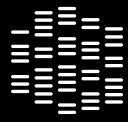
357

---

#### Member Awards Since Inception

5

## 2010 IN GENOMICS



NUMBER OF SPECIES SEQUENCED

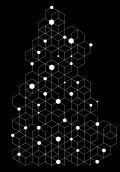
8,378

---

ARCHAEA	308
BACTERIA	6,395
EUKARYA	1,675

---

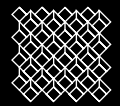
↑ 2,535 TOTAL SPECIES SINCE 2009



COST OF SEQUENCING PER  
MEGABASE

\$0.52

↓ \$2.07 SINCE 2009



NUMBER OF "GENOMICS"  
PUBLICATIONS

27,774

↑ 3,756 SINCE 2009

### GENOMICS MADE THE HEADLINES:

Scientists announce the creation of a living cell with a synthetic genome

# 20 10

---

Image: Large, complex proteins called enzymes, like the one seen here, are vital to almost every cellular function.

---

In 2010, IGB receives a \$33.9 million award from the NIH to establish the Enzyme Function Initiative.

Mirroring the structure of the IGB to emphasize collaboration across disparate disciplines, the National Institute of General Medical Sciences supported a “Glue Grant” program, so named for its intent to “glue” together multidisciplinary research teams to address complex biomedical problems too large for any one research group. A proposal by the Mining Microbial Genomes (MMG) theme secured one of these awards, a \$33.9M five-year grant to form the Enzyme Function Initiative (EFI). The EFI was tasked with developing a strategy to discover the functions of unknown enzymes by using bioinformatic and computational prediction to determine enzymatic reactions.

An estimated 163 million proteins have been sequenced, yet only half that number have known functions. By developing specialized tools and methods, selected enzymes and their biochemical pathways can be identified and that knowledge applied broadly—in effect the identification of a single protein enables identification of hundreds more. Focusing on enzymes found in bacterial genomes to better understand their role in the microbiome, the EFI seeks to discover new chemical and medical applications and broaden our fundamental understanding of organismal biology. To date, the freely available web-based EFI Enzyme Similarity Tool (EFI-EST) remains one of the most valuable resources for researchers to visualize protein sequence relationships and identify functions for unknown enzymes, contributing to several functional discoveries outside of those initially targeted by the grant.

## IGB THEME METRICS

### MINING MICROBIAL GENOMES (MMG)

Discovers small molecules that might provide new medical solutions

---

#### Current Members

8

Faculty

6

Affiliates

---

#### Represented Departments

6

Biochemistry; Bioengineering;  
Chemical and Biomolecular Engineering;  
Chemistry; Electrical and Computer  
Engineering; Microbiology

---

#### Publications since 2007

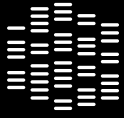
1,247

---

#### Member Awards Since Inception

35

## 2011 IN GENOMICS



NUMBER OF SPECIES SEQUENCED

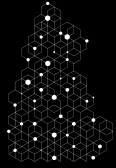
11,412

---

ARCHAEA	377
BACTERIA	8,992
EUKARYA	2,043

---

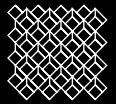
↑ 3,034 TOTAL SPECIES SINCE 2010



COST OF SEQUENCING PER  
MEGABASE

\$0.23

↓ \$0.29 SINCE 2010



NUMBER OF "GENOMICS"  
PUBLICATIONS

31,640

↑ 3,866 SINCE 2010

### GENOMICS MADE THE HEADLINES:

Researchers characterize the  
diversity of human gut microbiota

# 20 11

---

Image: By studying the social interactions of honey bees and other organisms, researchers can learn about healthy and disordered social behavior in humans.

---

In 2011, researchers begin development of an automated system to monitor honey bee social networks, a step toward high-throughput quantitation of social behavior.

Many of the earliest genome sequencing projects focused on organisms whose biological study had clear biomedical applications: nematode worms, fruit flies, mosquitos, mice, and humans. Yet for non-traditional model organisms—such as bees and stickleback fish—largely left on the sidelines of genetic research, genomics became an equalizing entry point into molecular-level science.

The Gene Networks in Neural & Developmental Plasticity (GNDP) theme was formed around some of the most fundamental biological questions made accessible by this approach. How do nature and nurture work together to produce the complex of traits that define an individual or a species? A key idea underlying the work of the theme has been the recognition that genomes are not static blueprints, but living documents that change to reflect and respond to experiences within an individual's lifetime.

One project that grew to involve multiple IGB themes was the design of a tiny barcode tag that fit on the back of a honey bee, allowing for computer-aided tracking of behavior inside the hive. Behavior-tracking technology is now being applied to multiple theme projects, enabling IGB researchers to ask new questions about how the control of gene activity within the body and brain relates to behaviors and other complex traits. With these developments, the area of greatest need may now be shifting from the creation of high-throughput data generation tools to the computational strategies required to make sense of those data. Through partnerships with KnowEnG and CompGen, the theme and the IGB as a whole are hopeful to meet this latest challenge head-on.

## IGB THEME METRICS

### GENE NETWORKS IN NEURAL AND DEVELOPMENTAL PLASTICITY (GNDP)

Examines the effects of coordinated gene activity on biological diversity

---

#### Current Members

**6**  
Faculty

**34**  
Affiliates

---

#### Represented Departments

**16**

Animal Biology; Animal Sciences; Applied Research Institute; Biochemistry; Bioengineering; Cell and Developmental Biology; Computer Science; Crop Sciences; Electrical and Computer Engineering; Entomology; Medical Information Science; Molecular and Integrative Physiology; Physics; Psychology; Sociology; Statistics

---

#### Publications since 2007

**1,710**

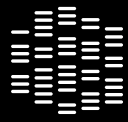
---

#### Member Awards Since Inception

**31**

---

## 2012 IN GENOMICS



NUMBER OF SPECIES SEQUENCED

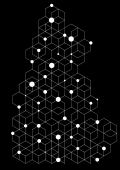
22,828

---

ARCHAEA	507
BACTERIA	18,215
EUKARYA	4,106

---

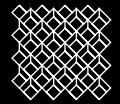
↑ 11,416 TOTAL SPECIES SINCE 2011



COST OF SEQUENCING PER  
MEGABASE

\$0.09

↓ \$0.14 SINCE 2011



NUMBER OF "GENOMICS"  
PUBLICATIONS

35,734

↑ 4,094 SINCE 2011

### GENOMICS MADE THE HEADLINES:

Molecules from the adaptive bacterial immune system, CRISPR, yield revolutionary genome-editing method

---

Image: An aerial view of an experimental field of sorghum, an important food and biofuel crop.

20  
12

---

In 2012, IGB receives \$25 million from the Bill & Melinda Gates Foundation to help achieve food security by developing more productive variants of key food crops.



Across the globe, approximately 815 million people are chronically undernourished. Scientists understand that the growing population of our planet will require an increase in food production, but climate change is making this prospect more challenging. In the Genomic Ecology of Global Change (GEGC) theme, scientists have worked to understand how plants and ecosystems will be affected by our changing climate. Their goal is to understand how well plants adapt when they are challenged by aspects of climate change—such as an increase in carbon dioxide, drought, and more frequent interactions with plant pathogens. They hope to translate this knowledge into models that can be used to predict how climate change may affect future ecosystems.

One of the major projects in GEGC is Realizing Increased Photosynthetic Efficiency (RIPE), which was funded in 2012 by a \$25 million grant from the Bill & Melinda Gates Foundation. The project received a \$45 million reinvestment in 2017 to continue its transformative work on increasing the efficiency of photosynthesis to increase crop yields. RIPE is dedicated to engineering new crops and getting them into the hands of farmers in sub-Saharan Africa and Asia, areas where food security has recently worsened. So far, their work has shown promising results. Scientists demonstrated they can alter the photosynthesis of a tobacco plant to increase productivity by up to 20 percent. They hope that technologies like these can be transferred to food crops and eventually contribute to reducing hunger and poverty worldwide.

## IGB THEME METRICS

### GENOMIC ECOLOGY OF GLOBAL CHANGE (GEGC)

Studies the intersection of plant genomics and global climate change

---

#### Current Members

7

Faculty

12

Affiliates

---

#### Represented Departments

5

Agricultural and Biological Engineering;  
Cell and Developmental Biology;  
Crop Sciences; Entomology; Plant Biology

---

#### Publications since 2007

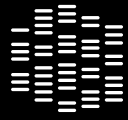
829

---

#### Member Awards Since Inception

27

## 2013 IN GENOMICS

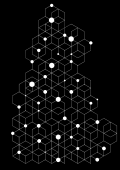


NUMBER OF SPECIES SEQUENCED

40,458

ARCHAEA 783  
BACTERIA 31,413  
EUKARYA 8,262

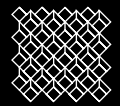
↑ 17,630 TOTAL SPECIES SINCE 2012



COST OF SEQUENCING PER  
MEGABASE

\$0.06

↓ \$0.03 SINCE 2012



NUMBER OF "GENOMICS"  
PUBLICATIONS

39,920

↑ 4,186 SINCE 2012

### GENOMICS MADE THE HEADLINES:

U.S. Supreme Court rules that naturally occurring DNA sequences cannot be patented

Image: The iBioFAB robotic system automates multiple molecular and microbiological laboratory tasks, streamlining genomic engineering work.

# 20 13

In 2013, the iBioFAB robotic system, which automates key laboratory processes of synthetic biology research, is installed at the IGB.

Synthetic biology is changing. As research becomes more rich with data, the creation of complex artificial biological systems requires more precision, efficiency and versatility. Like many other fields, automation has helped to usher in these changes. In the Biosystems Design (BSD) theme, researchers embraced the benefits of automation through the development of a one-of-a-kind robotic system, the Illinois Biological Foundry for Advanced Biomanufacturing or iBioFAB, which can automatically produce and analyze synthetic biological systems.

iBioFAB is driven by algorithms that make its work more reliable and repeatable. The system is programmable, modular and able to work with complex systems—such as genomes containing thousands of genes. iBioFAB was built to elevate synthetic biology research and the capabilities of researchers. The system embodies the changes occurring in the field of synthetic biology—changes that require automation and standardization so tasks like DNA synthesis and genome engineering can be done efficiently and affordably.

Technologies like these raise the bar for researchers who want to approach problems in a unique and innovative way, and the BSD theme hopes this innovation can help address important issues in health and sustainability. Researchers in the theme are interested in applying novel technologies to improving the efficiency of photosynthesis in food and biofuel crops, altering the protein content of food crops, enabling fundamental biological research, and more. iBioFAB is just one example of how groundbreaking technologies can help us get closer to achieving these goals.

## IGB THEME METRICS

### BIOSYSTEMS DESIGN (BSD)

Applies engineering principles to real and artificial biological systems

---

#### Current Members

**7**  
Faculty

**12**  
Affiliates

---

#### Represented Departments

**11**

Bioengineering; Cell and Developmental Biology; Chemical and Biomolecular Engineering; Chemistry; Computer Science; Crop Sciences; Electrical and Computer Engineering; Food Science and Human Nutrition; Industrial and Enterprise Systems Engineering; Mechanical Science and Engineering; Plant Biology

---

#### Publications since 2007

**2,029**

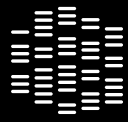
---

#### Member Awards Since Inception

**26**

---

## 2014 IN GENOMICS



NUMBER OF SPECIES SEQUENCED

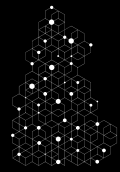
51,606

---

ARCHAEA 963  
BACTERIA 39,794  
EUKARYA 10,849

---

↑ 11,148 TOTAL SPECIES SINCE 2013

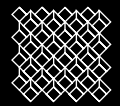


COST OF SEQUENCING PER  
MEGABASE

\$0.04

---

↓ \$0.02 SINCE 2013



NUMBER OF "GENOMICS"  
PUBLICATIONS

44,416

---

↑ 4,496 SINCE 2013

### GENOMICS MADE THE HEADLINES:

Scientists report successful use of artificial DNA bases by a living bacterial cell

---

Image: Exploring the developmental biology of model organisms such as pigs (a porcine skull is shown here) reveals potential therapeutic pathways to treat animal and human injury and disease.

# 20 14

---

In 2014, a custom 3D-printed tracheal splint, developed at the IGB, is used to save the life of an infant born with an anatomical defect.

From the beginning, scientists at the IGB have tackled large scale, real world problems. In the Regenerative Biology and Tissue Engineering (RBTE) theme, researchers are taking on organ malformation, damage and failure. These issues affect over a million people each year. Organ and tissue growth and regeneration involve complex cellular and developmental processes that scientists in the theme have been working to understand.

Research in RBTE involves using stem cell and development approaches to learn how organs form and regenerate, and then using this knowledge to regenerate tissues and organs in model and non-model organisms. Eventually, their research can be translated from models to humans. The theme's goal is to increase our knowledge of tissue and organ growth and develop technologies to replace or regenerate human tissues and organs. By doing this, their work could contribute to solving major health issues and improving human welfare.

In one case, RBTE researchers developed a 3D-printed splint that saved the life of an infant with a severe, life-threatening birth defect that causes the airway to collapse. They first tested the splint in animal models and later successfully implanted a splint into a six-week-old infant with the defect. The project exemplified how RBTE research can be translated from the lab to change lives around the world.

## IGB THEME METRICS

### REGENERATIVE BIOLOGY AND TISSUE ENGINEERING (RBTE)

Studies the replacement or regeneration of tissues and organs

#### Current Members

**10** **23**  
Faculty Affiliates

#### Represented Departments

**11**

Animal Sciences; Anthropology; Bioengineering; Cell and Developmental Biology; Chemical and Biomolecular Engineering; Electrical and Computer Engineering; Kinesiology and Community Health; Materials Science and Engineering; Mechanical Science and Engineering; Molecular and Cellular Biology; Veterinary Clinical Medicine

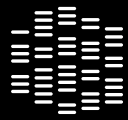
#### Publications since 2007

**1,634**

#### Member Awards Since Inception

**54**

## 2015 IN GENOMICS

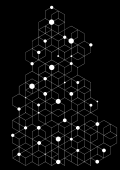


NUMBER OF SPECIES SEQUENCED

61,078

ARCHAEA 1,117  
BACTERIA 45,939  
EUKARYA 14,022

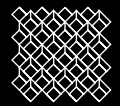
↑ 9,472 TOTAL SPECIES SINCE 2014



COST OF SEQUENCING PER  
MEGABASE

\$0.04

↓ \$0.00 SINCE 2014



NUMBER OF "GENOMICS"  
PUBLICATIONS

49,330

↑ 4,914 SINCE 2014

### GENOMICS MADE THE HEADLINES:

Scientists release the first complete map of the human epigenome

Image: Sociogenomic research seeks to help us understand how the environment acts through the genome to impact social behavior.

In 2015, IGB researchers initiate and progress efforts to relate genomic and epigenomic profiles to traits such as resilience to environmental stress.

# 2015

The study of sociogenomics involves not only the effects of gene expression on behavior, but also how the environment can influence and alter the physical properties of organisms such as health and wellness. What conclusions can we draw when we look to the residents of urban neighborhoods with high levels of crime and violence, where stress, PTSD, and preterm birth are prevalent?

These questions and other research goals coalesced in the form of the Computational Genomics for Reproductive Health (CGRH) theme, combining aspects of precision medicine with analytical practices in Big Data to establish predictive preventative methods. Looking at the intersection of environment, genome, and health, the theme explores new directions such as the Developing Responses to poverty through Education And Meaning (DREAM) initiative to track changes in gene expression and improve well-being in black mothers and daughters on the South Side of Chicago, and developing protocols for the rapid processing of biological samples to determine the prevalence of PTSD and other mental illnesses through sampling community residents in Detroit, a city that experiences twice the national number of PTSD cases per capita.

Placing significant focus on obstetrical syndromes, major contributors to infant and maternal mortality that also increase the risk of adult metabolic, cognitive, and psychiatric disorders, the theme leverages both clinical research and theoretical data to help develop new treatments to improve pregnancy outcomes.

## IGB THEME METRICS

### COMPUTING GENOMES FOR REPRODUCTIVE HEALTH (CGRH)

Examines the interplay among genetic and environmental factors that influence disorders of reproduction

---

#### Current Members

**11** **23**  
Faculty Affiliates

---

#### Represented Departments

**20**

Animal Biology; Animal Sciences; Anthropology; Applied Research Institute; Bioengineering; Civil and Environmental Engineering; Comparative Biosciences; Computer Sciences; Crop Sciences; Electrical and Computer Engineering; Entomology; Food Science and Human Nutrition; Mechanical Science and Engineering; Medical Information Science; Microbiology; Molecular & Integrative Physiology; Physics; Psychology; Sociology; Statistics

---

#### Publications since 2007

**986**

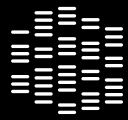
---

#### Member Awards Since Inception

**14**

---

## 2016 IN GENOMICS

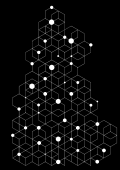


NUMBER OF SPECIES SEQUENCED

99,571

ARCHAEA 1,326  
BACTERIA 78,692  
EUKARYA 19,553

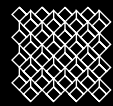
↑ 38,493 TOTAL SPECIES SINCE 2015



COST OF SEQUENCING PER  
MEGABASE

\$0.014

↓ 0.026 SINCE 2015



NUMBER OF "GENOMICS"  
PUBLICATIONS

54,625

↑ 5,295 SINCE 2015

## GENOMICS MADE THE HEADLINES:

Human patient treated with CRISPR  
gene editing for the first time

# 20 16

Image: Cross section of the  
second most common form  
of skin cancer, squamous  
cell carcinoma.

In 2016, IGB researchers  
bring a unique blend of  
engineering and genomic  
approaches to bear on  
public health via the  
development of a hand-  
held clinical screening  
device and an effort to  
reverse engineer health  
human microbiota.



The IGB is unique in that new research themes can be proposed by any academic community member on campus, and that existing themes evolve and reform over time. From this philosophy, two new themes emerged: one using modern technology to address one of healthcare's most difficult challenges, cancer, and the other to hone in on unexplored aspects in a field rapidly gaining momentum—the microbiome.

Born from the meeting of several members at an imaging conference discussing the topic of cancer diagnostics, a partnership quickly developed between members at the IGB, the Illinois Micro & Nanotechnology Laboratory, the University of Wisconsin, and Mayo Clinic to address the need for affordable, genomics-based diagnostics for cancer biomarkers. Looking to mitigate cost and equipment requirements, Omics Nanotechnology for Cancer Precision Medicine (ONC-PM) focuses on “liquid biopsies,” beginning with development of a handheld spectral analyzer that would enable a smartphone to perform clinical tests on blood or saliva. This cheap and mobile ability to collect and track samples could help identify cancers and suggest individualized treatment strategies for patients world-wide.

The second theme, Microbiome Metabolic Engineering (MME), was formed to explore how the millions of genomes that form each individual's microbiome affect their health. Their proposal to create an external microbiota allowing direct interaction to track changes in the microbial community and measure the effect of pathogens could lead to a more fundamental understanding of microbiome development. In addition to adult gut microbiota, the theme investigates infant microbiomes, collaborating with two Illinois studies linking health with factors such as obesity, environmental toxins, and activity level: the Illinois Kids Development Study (IKIDS) and the Synergistic Theory and Research on Obesity and Nutrition Group (STRONG).

## IGB THEME METRICS

### OMICS NANOTECHNOLOGY FOR CANCER PRECISION MEDICINE (ONC-PM)

Develops new technology to identify and manage cancerous tumors

### MICROBIOME METABOLIC ENGINEERING (MME)

Explores the relationships between human microbiota, environment, and health

#### Current Members

<b>6</b>	<b>5</b>	<b>9</b>	<b>10</b>
Faculty ONC-PM	Affiliates ONC-PM	Faculty MME	Affiliates MME

#### Represented Departments

**7**

ONC-PM: Biochemistry; Bioengineering; Chemistry; Electrical and Computer Engineering; Food Science & Human Nutrition; Molecular and Cellular Biology; Veterinary Clinical Medicine

**9**

MME: Animal Sciences; Anthropology; Biochemistry; Bioengineering; Chemical and Biomolecular Engineering; Civil and Environmental Engineering; Comparative Biosciences; Food Science and Human Nutrition; Microbiology

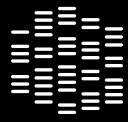
#### Publications since 2007

<b>866</b>	<b>665</b>
ONC-PM	MME

#### Member Awards Since Inception

<b>4</b>	<b>3</b>
ONC-PM	MME

## 2017 IN GENOMICS

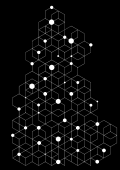


NUMBER OF SPECIES SEQUENCED

133,911

ARCHAEA 1,584  
BACTERIA 94,555  
EUKARYA 37,772

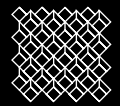
↑ 34,340 TOTAL SPECIES SINCE 2016



COST OF SEQUENCING PER  
MEGABASE

\$0.011

↓ 0.003 SINCE 2016



NUMBER OF "GENOMICS"  
PUBLICATIONS

59,939

↑ 5,314 SINCE 2016

## GENOMICS MADE THE HEADLINES:

FDA approves three gene therapies  
for general use on human patients

20  
17

Image: Newly identified  
H1N1 influenza virus,  
taken in the CDC Influenza  
Laboratory.

In 2017, IGB establishes its  
newest theme, which seeks  
to combat the continued  
threat of infectious disease.

Human health depends on the health of agricultural, industrial and natural ecosystems. What links these ecosystems together are microbes, and if scientists can predict how microbes move between these ecosystems, they can effectively address threats to human health. In 2017, IGB's newest theme, Infection Genomics for One Health (IGOH), was created to develop a broad predictive framework to address these threats, which range from antimicrobial resistance to the emergence of infectious diseases.

One example of the theme's exploration in this area includes research that revolves around an inventive idea: what if antiviral drugs could evolve alongside viruses, such as influenza virus, and stop antiviral drug resistance? The research aims to combat antiviral drug resistance—which has long been a problem in modern society—by creating a therapeutic inspired by the biology of viruses themselves. Not only will this research help scientists understand influenza infection and how viruses evolve, but it could also have an impact on driving influenza virus to extinction.

IGOH breaks with tradition by encouraging collaboration across fields, connecting with researchers from areas such as ecology, evolution, and agricultural and food sciences. This cross-disciplinary teamwork, paired with the application of novel methods and the integration of big data, aims to create novel high-throughput methods to analyze important microbes. The theme takes into account interactions at all levels—from the gene and genome up to the population and community—in order to deeply understand the dynamics between them that influence environmental and human health.

## IGB THEME METRICS

### INFECTION GENOMICS FOR ONE HEALTH (IGOH)

Examines how microbes in human-inhabited environments influence health and disease

---

#### Current Members

9

Faculty

8

Affiliates

---

#### Represented Departments

14

Anthropology; Bioengineering; Civil and Environmental Engineering; Computer Science; Entomology; Food Science and Human Nutrition; Integrative Biology; Mathematics; Microbiology; Molecular and Cellular Biology; Molecular and Integrative Physiology; Pathobiology; Plant Biology; Veterinary Medicine

---

#### Publications since 2007

415

---

#### Member Awards Since Inception

3

---

# 20 17

MONTH 01 02 03 04 05 06  
07 08 09 10 11 12



#### HEALTH

Research that seeks to understand the origins and mechanisms of disease and discovers new ways to promote wellness.



#### TECHNOLOGY

Research that imagines, develops, and refines new tools that enable discovery and create solutions.



#### ENVIRONMENT

Research that explores and protects ecosystems, especially those we rely on for food and fuel.



#### FUNDAMENTAL RESEARCH

“Blue Sky” research that creates the knowledge base needed for future progress.



#### COMMUNITY ENGAGEMENT

Programs that promote open dialogue between genomic research and society.

## JANUARY

Study: Climate change will affect carbon storage levels, richness in Midwest soil



[go.igb.illinois.edu/CarbonStorage](http://go.igb.illinois.edu/CarbonStorage)

**Midwest soil may lose as much as 15 percent of its stored carbon—and thus its agricultural fertility—over the next 100 years due to the effects of global climate change.** This prediction

arose from research led by Plant Biology Professor Evan DeLucia (GEGC), Plant Biology Professor Carl Bernacchi (GEGC), graduate student Christopher K. Black and Ohio University Assistant Professor of Environmental Studies Sarah C. Davis and University of Idaho Professor of Natural Resources Tara Hudiburg.

During a three-year field trial at Illinois, researchers exposed pockets of a traditional corn-soy rotation agriculture site to the kinds of increased temperatures and atmospheric carbon dioxide levels the region is expected to experience in 50 years' time.

As ambient carbon dioxide levels increase in the air surrounding plants, they actually “breathe” in more carbon dioxide and store it (via photosynthesis) in their root systems—a net gain of carbon in the soil. However, as temperatures simultaneously increase, the soil microbes become increasingly active, eating up more soil matter and releasing more carbon.

“The story here is that the kind of warming we are expecting to see is accelerating the decomposition of carbon in the soil, which accelerates the rate of global warming, which takes more carbon out of the soil, which accelerates global warming, etc.,” DeLucia said of the study, which was published in *Global Change Biology*. Portions of the research were funded by the DOE.



Researchers found that compared to top leaves, lower leaves of C4 crops such as corn underperform, costing farmers about 10 percent of potential yield.

## Crop Achilles' heel costs farmers 10 percent of potential yield



[go.igb.illinois.edu/CropHeel](https://go.igb.illinois.edu/CropHeel)

Scientists have assumed leaves at the top of a plant would be the best at turning higher levels of light into carbohydrates through the process of photosynthesis, while the lower, shaded leaves would be better at processing the low light levels that penetrate the plant's canopy of leaves. A closer look has revealed that in two of our most productive crops, these shaded leaves are less efficient than the top leaves, thus limiting yield. These findings, published in the *Journal of Experimental Botany*, could help scientists further boost the yields of corn and Miscanthus, as well as other C4 crops that have evolved to photosynthesize more efficiently than C3 plants such as wheat and rice.

"Today we grow these crops in ever-denser stands, and provide them with nitrogen and water so that they can produce many more layers of leaves. But as a result, the proportion of leaves that are shaded has increased, and the production of grain will depend more and more on the contribution of this increasing proportion of shaded leaves," said principal investigator Stephen Long (BSD/GEGC), Gutsell Endowed Professor of Plant Biology and Crop Sciences. **This loss of efficiency in the lower leaves may cost farmers roughly 10 percent of potential yield—an Achilles' heel that likely applies to other C4 relatives, such as sugarcane and sorghum.**

This work was supported by the EBI.

Patients like the individual with leukemia who gave this blood sample could someday be treated with lab-grown stem cells.

## Changing the environment within bone marrow alters blood cell development



[go.igb.illinois.edu/BoneMarrow](http://go.igb.illinois.edu/BoneMarrow)

Researchers reported in *Science Advances* they were able to alter blood cell development by using biomaterials designed to mimic characteristics of bone marrow, a first step toward developing more effective bone marrow treatments for diseases like leukemia and lymphoma.

Blood cells flow throughout the body delivering life-supporting oxygen and nutrients. As these cells are used and recycled, they are regenerated by bone marrow, the soft tissue inside the body's long and hollow bones.

"The tissue environment that surrounds these cells in the bone marrow provides a wealth of signals that can alter how

these precursor cells behave. This paper looked at the signals provided by the tissue matrix itself," said Chemical and Biomolecular Engineering Professor Brendan Harley (RBTE leader).

This project is only the first step in controlling the signals from the matrix that influence hematopoietic stem cells, which give rise to blood cells. **Research continues to identify other features of the matrix that can be manipulated to increase the number of stem cells and make them more effective in transplantation.**

The NSF, NIH and the American Cancer Society of Illinois supported this research.



The life history of gray short-tailed opossum allows researchers to easily study ear and jaw development.

## In the developing ears of opossums, echoes of evolutionary history

  | [go.igb.illinois.edu/OpossumEar](http://go.igb.illinois.edu/OpossumEar)

Hidden in the development of opossums is one possible version of the evolutionary path that led from the simple ears of reptiles to the more elaborate and sensitive structures of mammals, including humans. This discovery, published in *Proceedings of the Royal Society B*, emerged from work by animal scientists at Illinois, King's College London, and the University of Chicago, led by Associate Professor of Animal Biology Karen Sears (RBTE, now at University of California, Los Angeles).

To get a better idea of how the mammalian ear might have evolved, Sears and colleagues chose to study the gray short-tailed opossum, a small and charismatic South American marsupial whose key stages of jaw and ear development take place gradually and after birth. The team also identified a set of genes whose increased activity correlates with the self-destruction of the cells that connect the future jaw to the future ear.

**“The improved auditory sensitivity of these newly freed middle ear ossicles would have been a remarkable boon for early mammals. Most of these would have been very small, nocturnal insectivores,”** said IGB Fellow Daniel Urban (also now at University of California, Los Angeles). “Confinement to activity during the night hours would have helped them avoid becoming prey, while at the same time, improved hearing would have aided in their own predatory abilities.”

---

### MARCH

## New tool RODEO captures breadth of microbial biosynthetic potential

  | [go.igb.illinois.edu/RODEO](http://go.igb.illinois.edu/RODEO)

A team of researchers led by Associate Professor of Chemistry Douglas Mitchell (MMG) has created a tool that searches through microbial genomes, identifying clusters of genes that indicate an organism's ability to synthesize therapeutically promising molecules, as reported in *Nature Chemical Biology*.

“With genome sequencing going at the pace it has . . . there's a dearth of functional information about what these genes are doing,” Mitchell said. “It becomes increasingly important to make sense of and interpret metabolic

pathways, especially biosynthetic gene clusters encoded by microbes.”

The informatics tool that Mitchell's laboratory designed, named Rapid Open reading frame Description and Evaluation Online, or RODEO, **identified 1,300 novel peptides (called lasso peptides for their looping structure) including several with particularly unusual structures that make them promising as potential therapeutics.** The researchers confirmed that the empirically determined structures matched those predicted by the software.

This work was supported by the NIH, the American Chemical Society, the David and Lucile Packard Foundation, and Robert C. and Carolyn J. Springborn Endowment for Student Support Program.

## Study links sulfide-producing bacteria and colon cancer in African Americans


 | [go.igb.illinois.edu/ColonCancer](http://go.igb.illinois.edu/ColonCancer)

A new study reported in the journal *Gut* reveals that African Americans have measurable differences in the number and type of bacteria that live in the colon, and those differences are related to higher-than-average colon cancer risk.

Review of colonic tissue biopsies from 197 African Americans and 132 non-Hispanic whites collected over a two-year period found that African Americans have more sulfide-producing bacteria in their colon than do non-Hispanic whites in the U.S. Although these microbes are a normal part of the gut ecosystem, an overabundance of sulfide in the colon can lead to inflammation and can damage DNA, said Animal Sciences Professor Rex Gaskins (RBTE) who led the research with



## IGB announces new partnership with ZEISS labs@location program

 | [go.igb.illinois.edu/ZEISSlabs](http://go.igb.illinois.edu/ZEISSlabs)

A new agreement between the IGB and Carl Zeiss Microscopy LLC has named the Core Facilities at IGB as an official ZEISS labs@location Partner. The model facility will allow researchers from around the U.S. to test-drive new instruments in the IGB's Core Facilities Microscopy Suite, the first North American location of the ZEISS labs@location partner program.

“With this special partnership with IGB Core Facilities, we transfer a successful labs@location program from Europe to the U.S.,” said Jim Sharp, President of Carl

Zeiss Microscopy LLC. “labs@location is a community of our ZEISS customers and partners providing in-depth knowledge and dedicated services. We are very excited that the IGB becomes our first American ZEISS labs@location.”

The agreement will allow IGB and Illinois researchers access to select cutting edge technologies immediately following—or in some cases before—their broad release, as well as training, demos, and classes taught by ZEISS personnel at the IGB.





Left: Professor in the Departments of Animal Sciences and Pathobiology Rex Gaskins, right, with graduate student Patricia Wolf.



Right: Mary-Claire King, Professor of Genome Sciences and of Medicine at the University of Washington School of Medicine.

colleague Nathan Ellis, scientific director of the Cancer Biology Research Program at the University of Arizona Cancer Center in Tucson.

Native Africans have dramatically lower colon cancer rates than African Americans, suggesting that environmental factors, including dietary habits, are a key to the problem, along with genetics. A previous study involving Gaskins found that switching rural South African Zulus who normally ate a low-fat, high-fiber diet to a diet with a lot of meat and animal fat led to increases in sulfide-producing bacteria in their colon in less than two weeks.

**“We are now beginning to connect the dots between these dietary factors and one’s risk of developing colon cancer,” Gaskins said. “Our research adds to the evidence that the microbes that inhabit the colon are part of the equation and should not be overlooked.”**

The NIH and the American Cancer Society supported this research.

## Geneticist Mary-Claire King delivers IGB Distinguished Public Lecture

 | [go.igb.illinois.edu/MCKing](http://go.igb.illinois.edu/MCKing)

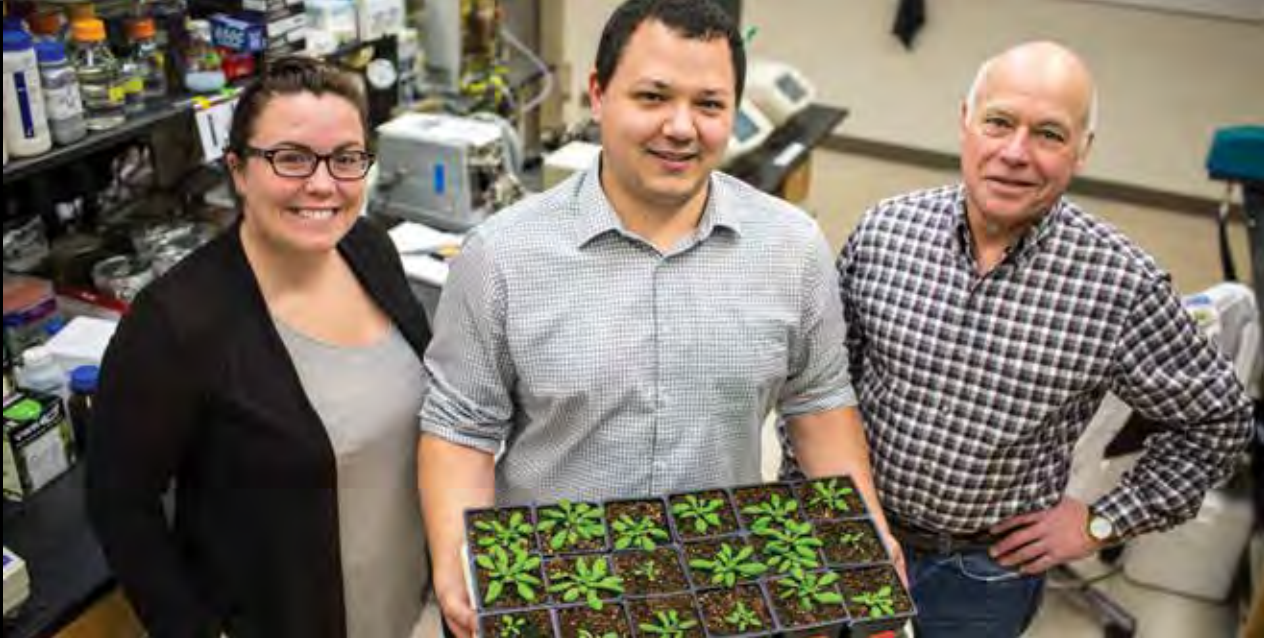
Mary-Claire King, Professor of Genome Sciences and of Medicine at the University of Washington School of Medicine, spoke as part of the IGB Distinguished Public Lecture series to a full auditorium at the Alice Campbell

Alumni Center on the Illinois campus during the spring semester of 2017. King’s work includes the genetics and interaction of genetics and environmental influences on human conditions such as HIV, lupus and inherited deafness. **She is well-known for her discovery that a single gene on chromosome 17, later known as *BRCA1*, is responsible for many breast and ovarian cancers.** Her research revolutionized the study of numerous other common diseases, and King had successfully identified the gene before the Human Genome Project had been fully developed. The technique King developed to identify *BRCA1* has since proven valuable in the study of many other illnesses, and King has built on that research by identifying *BRCA2* and extending her technique to other diseases and conditions.

## Newly characterized protein has potential to save U.S. farmers millions annually

  | [go.igb.illinois.edu/BASS6](http://go.igb.illinois.edu/BASS6)

During photosynthesis, many plants accidentally convert carbon into a plant-toxic compound that is recycled through a process called photorespiration. Project lead Don Ort (BSD/GEGC), USDA/ARS scientist and Robert Emerson Professor of Plant Biology, and colleagues report in *Plant Cell* the discovery of a key protein in this process, which they hope to manipulate to increase plant productivity.



During photosynthesis in C3 crops, such as wheat and rice, the enzyme Rubisco sometimes reacts with oxygen (instead of carbon dioxide), creating a plant-toxic compound that must be recycled, wasting energy. Researchers—including USDA/ARS scientist Paul South (center), Robert Emerson Professor of Plant Biology and USDA/ARS scientist Don Ort (right), and Amanda Cavanagh (left)—reported the discovery of a key protein in this process.

The team identified photorespiration—a process that requires significant amounts of fixed carbon and energy—as a primary target to improve photosynthetic efficiency as a strategy to improve crop yield.

**“We could feed around 200 million people with the calories lost to photorespiration each year just in the Midwestern United States,”** said co-author Berkley Walker, an Alexander von Humboldt Postdoctoral Fellow at the University of Düsseldorf, citing his recently published simulations. “While we can’t get all that yield back, even saving 5 percent of the energy lost in photorespiration would be worth millions of dollars annually.”

This work is supported by Realizing Increased Photosynthetic Efficiency (RIPE), an international collaboration funded by the Bill & Melinda Gates Foundation.

## Governor recognizes IGB for 10 years of scientific contribution to Illinois

[go.igb.illinois.edu/IGB10](http://go.igb.illinois.edu/IGB10)

Illinois Gov. Bruce Rauner recognized the IGB for celebrating 10 years of genomic research addressing major societal issues in the areas of agriculture, environmental conservation, health, and technology. A proclamation issued by Rauner officially records March 29, 2017 as the 10th anniversary of the Institute and recognizes its societal, scientific, and scholarly contributions made to research within the state of Illinois.

“By uniting the genomic resources and expertise on campus with the newest technologies and approaches, we are able to address grand challenges in science,” said IGB Director and Swanlund Professor of Entomology Gene Robinson. **“We are honored to have led in the application of genomics to life science research in the state of Illinois for the past 10 years and are strongly committed to continuing to do so for the next 10 years, and beyond.”**

---

## APRIL

### Giving with purpose



Dr. Mark Tracy, founder and president of Tracy BioConsulting, LLC and University of Illinois alumnus, gifted a financial contribution dedicated to introducing Illinois students in the sciences to the biotechnology industry and biopharmaceutical product development. The Illinois International Genetically Engineered Machine (iGEM) team, sponsored in part by the IGB, inspired him to make this donation.

Dr. Tracy is an avid proponent of introducing undergraduate science students to biotechnology industry research, **motivated by his passion for harnessing science to develop new medicines quickly and affordably.** He hopes that exposing students with different backgrounds to biopharma industry research, the drug development process, and the business of developing new medical products during their undergraduate years will promote interest in solving important medical problems and foster greater awareness of rewarding opportunities in the industry. He hopes this gift will be a catalyst that ultimately will help us to address important medical challenges facing future generations.

---

## MAY

### Scientists engineer sugarcane to produce biodiesel, more sugar for ethanol



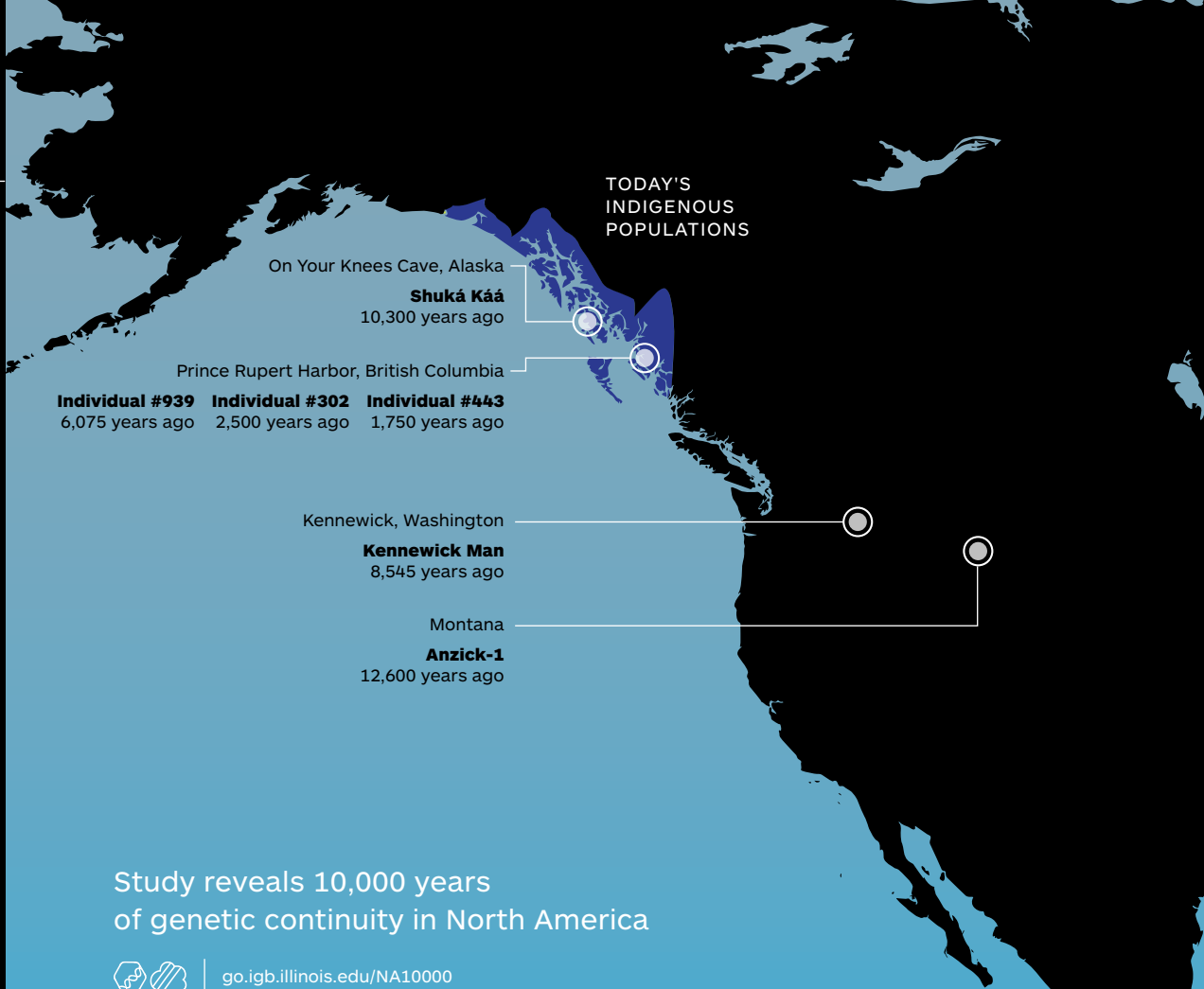
A multi-institutional team led by Illinois has proven sugarcane can be genetically engineered to produce oil in its leaves and stems for biodiesel production, and to produce more sugar that could be used for ethanol production. The dual-purpose bioenergy crops are predicted to be over five times more profitable per acre than soybeans, two times more profitable than corn, and can be grown on marginal land. Stephen Long, Gutgsell Endowed Professor of Plant Biology and Crop Sciences (BSD/GEGC) and lead on the Plants Engineered to Replace Oil in Sugarcane and Sorghum (PETROSS) project, co-authored a paper published in *Biocatalysis and Agricultural Biotechnology* that analyzes the project's first genetically modified sugarcane varieties. Using a juicer, the researchers extracted about 90 percent of the sugar and 60 percent of the oil from the plant; the juice was then fermented to produce ethanol and later treated with organic solvents to recover the oil. The team



Researchers extract juice from sugarcane that has been engineered to produce oil for biodiesel in addition to the plant's sugar that is used for ethanol production.

has patented the method used to separate the oil and sugar.

“While fuel prices may be considered low today, we can remember paying more than \$4 per gallon not long ago,” Long said. **“As it can take 10-15 years for this technology to reach farmers’ fields, we need to develop these solutions to ensure our fuel security today and as long as we need liquid fuels into the future.”** The PETROSS project and this work are supported by the Advanced Research Projects Agency-Energy (ARPA-E).



## Study reveals 10,000 years of genetic continuity in North America



[go.igb.illinois.edu/NA10000](http://go.igb.illinois.edu/NA10000)

A study of the DNA in ancient skeletal remains adds to the evidence that indigenous groups living today in southern Alaska and the western coast of British Columbia are descendants of the first humans to make their home in northwest North America more than 10,000 years ago, as reported in the *Proceedings of the National Academy of Sciences*.

The study, led by anthropology professor Ripan Malhi (CGRH/RBTE), looked at genomic data from Shuká Káa (Tlingit for “Man Before Us”), an ancient individual whose remains—found in a cave in southeastern Alaska—date to about 10,300 years ago. Researchers also analyzed the genomes of three more individuals from the nearby coast of British Columbia whose remains date to between 6,075 and 1,750 years ago.

The descendants of some of these lineages are still living in the same region today, and a few are co-authors on the

new study. Their participation is the result of a long-term collaboration between the scientists and several native groups who are embracing genomic studies as a way to learn from their ancestors. Collaborators include co-author Rosita Worl, director of the Sealaska Heritage Institute in Juneau, Alaska, who is Tlingit, Ch’áak’ (Eagle) moiety of the Shangukeidí (Thunderbird) Clan from the Kawdliyaayi Hít (House Lowered From the Sun) in Klukwan, Alaska.

“We supported DNA testing of Shuká Káa because we believed science ultimately would agree with what our oral traditions have always said—that we have lived in southeast Alaska since time immemorial.

**The initial analysis showed the young man was native, and now further studies are showing that our ancestral lineage stems from the first initial peopling of the region,”** said Worl, who also is an anthropologist. **“Science is corroborating our oral histories.”**

## Modified soybeans yield more in future climate conditions



[go.igb.illinois.edu/SoybeanYield](http://go.igb.illinois.edu/SoybeanYield)

In a three-year field study published in the *Journal of Experimental Botany*, researchers demonstrated that engineered soybeans yield more than conventional soybeans in future predicted climatic conditions.

“Our climate system and atmosphere are not changing in isolation from other factors—there are actually multiple facets,” said USDA/ARS scientist Carl Bernacchi (GEGC), an associate professor of plant biology. “The effect of carbon dioxide in and of itself seems to be very

generalized, but neglects the complexity of adding temperature into the mix. This research is one step in the right direction towards trying to figure out a way of mitigating those temperature-related yield losses that will likely occur even with rising carbon dioxide concentrations.”

**The study found the modified crop yielded more when subjected to both increased temperature and increased carbon dioxide levels, suggesting we can harness genetic changes to help offset the detrimental effects of rising temperature.**

*Soybeans grown in fields that simulate 2050 temperatures show signs of stress. Researchers have discovered modified soybeans that yield more than current varieties in 2050 field conditions.*



## New capabilities for genome-wide engineering of yeast



[go.igb.illinois.edu/EngYeast](http://go.igb.illinois.edu/EngYeast)

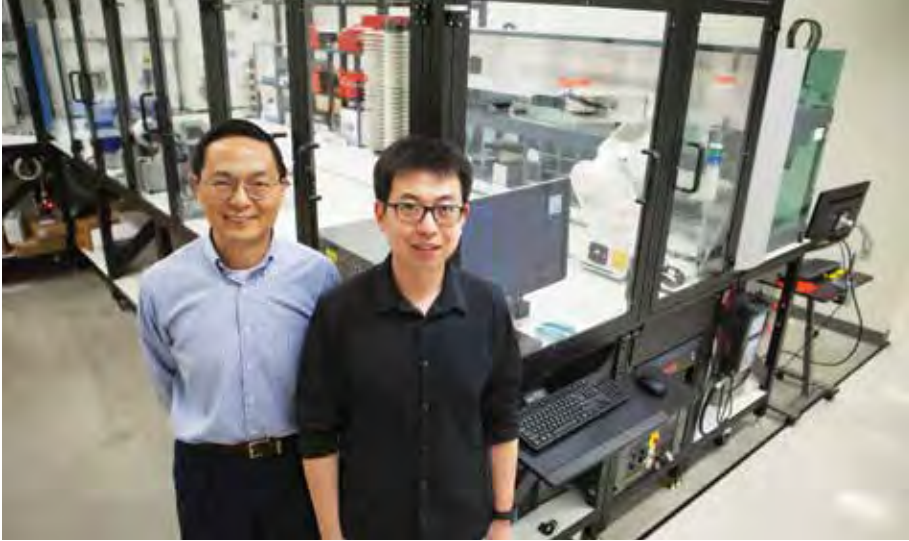
In a *Nature Communications* paper, Illinois researchers described how their successful integration of several cutting-edge technologies—creation of standardized genetic components, implementation of customizable genome editing tools, and large-scale automation of molecular biology laboratory tasks—enhances our ability to work with yeast and the potential to produce valuable novel strains of yeast for industrial use.

“The goal of the work was really to develop a genome-scale engineering tool for yeast . . . traditional metabolic engineering focused on just

a few genes and the few existing genome-scale engineering tools are only applicable to bacteria, not eukaryotic organisms like yeast,” said Steven L. Miller Chair of Chemical and Biomolecular Engineering Huimin Zhao (BSD leader/MMG), who led the study. “A second innovation is the use of synthetic biology concepts, the modularization of the parts, and integration with a robotic system, so we can do it in high-throughput.”

Because yeast and other fungi, like humans, are eukaryotes—organisms with a compartmentalized cellular structure and complex mechanisms that control their gene activity—study of yeast genome function is also a key component of biomedical research.

**Zhao and his colleagues examined the ability of the CRISPR-Cas system to make precise cuts in the yeast genome, into which**



**the standardized genetic parts from their library could insert themselves.**

Analyzing the modified genomes of the most promising yeast strains, they identified combinations of genes whose altered activities contributed to desirable traits. The functions of some of these genes were previously unknown, demonstrating the technique's ability to generate new biological knowledge and paving the way for similar approaches to broad-scale, automated genome engineering of other eukaryotic species.

Steven L. Miller Chair of Chemical and Biomolecular Engineering Huimin Zhao, left, with IGB Research Fellow Tong Si in front of the Illinois Biological Foundry for Advanced Biomanufacturing (iBioFAB) robotic system.

This work was funded by the Roy J. Carver Charitable Trust, IGB, Defense Advanced Research Program Agency, and National Academies Keck Futures Initiative on Synthetic Biology.

Three IGB members  
elected to National  
Academy of Sciences



[go.igb.illinois.edu/NAS17](http://go.igb.illinois.edu/NAS17)

The National Academy of Sciences, the most prestigious scientific society in the U.S., announced the election of their 2017 members. Three members of IGB were among those elected: John Cronan (MMG), Professor and Head of Microbiology and Professor of Biochemistry; Donald Ort (GEGC leader/BSD), Robert Emerson Professor of Plant Biology, USDA/ARS Photosynthesis Research Unit and Adjunct Professor of Crop Sciences; and

Left to right: Elected to the NAS, John Cronan, Jeffrey Moore, and Donald Ort.

Jeffrey Moore (BSD), Murchison-Mallory Professor of Chemistry and Professor of Materials Science and Engineering.

**Members are chosen by their peers for their distinguished and continuing achievements in original research** and are formally inducted into the NAS during its annual meeting.



## World of Genomics brings IGB research to Chicago



[go.igb.illinois.edu/ChicagoGenomics](http://go.igb.illinois.edu/ChicagoGenomics)

From May 18th to 20th in Chicago, over 15,000 visitors experienced the World of Genomics at the Field Museum of Natural History, a three-day event presented by the Carl R. Woese Institute for Genomic Biology. A large, blue-lit funnel representing the tree of life dominated the space; beneath it, the world's smallest sequencer read out the genomes of never-before-sequenced organisms currently studied at the IGB.

With six learning stations distributed across Stanley Field Hall, the main floor of the museum where famous *T. rex* Sue is displayed, World of Genomics represented the full scope of IGB research in health, technology, and the environment, with hands-on activities and exhibits for all ages.

"In all of the outreach events I've been a part of, I've never experienced such an engaged audience that asked so many excellent, relevant questions about our research," said

Beryl Jones, one of the over 60 volunteers from the IGB who staffed the event. "World of Genomics was truly one of the most rewarding experiences of my PhD, and I feel honored to have been a part of an event that reached so many people."

Jones was one of the volunteers tasked with running the Brains and Behavior learning station, which focused on the shared genomic underpinnings of behavior between humans and honey bees. To bring their work to life, researchers presented explorable brain models in virtual reality as well as an observation hive with live bees.

"It was an amazing experience," said Michelle Goettge. She was a volunteer with the DNA to Drugs learning station, which presented information and activities based on antibiotic resistance, the development of new therapeutics, and high-throughput screening. "I've done outreach before, but it usually focuses



on just one group—kids or adults. World of Genomics really engaged with everyone, and people were so excited to learn about the science, it was unbelievable.”

Other learning stations included Food and Fuel, where visitors could remotely control a miniature agricultural robot and view examples of engineered crop plants; and Personalized Health, which presented a suite of activities demonstrating biological differences between individuals as well as their commensal microbial communities to explain concepts in human health and development.

A fifth station, the sprawling Emergence of Life, partnered with Zeiss to bring high-end microscopy to the Field. There, visitors viewed the intricacies of coral and travertine at the nanoscale; remote microscopy from the Core Facilities SEM was also on hand to image human kidney stones from the IGB at an even higher resolution.

In all, the event represented IGB's largest outreach effort to date, and perhaps most successful: not only in the number of people reached, but in the quality of the interactions between scientists and guests.

**Members' Nights attendees responded with high praise, with comments such as “The World of Genomics was absolutely amazing,” “Loved the virtual reality experience by the bees,” and**





**“More research information booths like U of I. Those were amazing.” The volunteers especially made a lasting impression, with responses including “The U of I people explaining the exhibits were all very enthusiastic, patient, and knowledgeable,” and “I enjoyed the exhibits by the university students. First of all, they were interesting. Even more importantly, they gave us a vision of the future—the next generation of scientists.” When asked for favorites, attendees responded “Crop robot and talk on GMO vs other, viewing the 3D printer, virtual reality” and, simply, “Bees.”**

“We reached everyone from young children to their grandparents, from those who had never heard of us to Chicago alumni, friends of the university, even the University of Illinois President,” said IGB Director and Swanlund Professor of Entomology Gene Robinson. “The entire floor was abuzz with rapt and engaged visitors, who immersed themselves into each exhibit, learning about our research, talking to our people, and gaining a new understanding of how fundamental genomics is to their lives.”

JUNE

## Social experience tweaks genome function, behavior

 | [go.igb.illinois.edu/SocialStress](http://go.igb.illinois.edu/SocialStress)

What changes in the brain of an animal when its behavior is altered by experience? Research led by Professor of Cell and Developmental Biology Lisa Stubbs (GNBP leader) focuses on the collective actions of genes to answer this, identifying gene network activity involved in the response to social stress in a *Genome Research* publication.

“The goal of this study was to understand the downstream events in mice, and how they are conveyed across interacting brain regions . . . how they might set the stage for emotional learning in response to social threat,” Stubbs said. Answers to these questions could help scientists understand how the brains of other animals, including humans, generate social behavior, as well as what goes wrong in disorders of social behavior.

The researchers looked for associations between the responses of specific genes to social experience and their epigenetic state. How different regions of DNA are packaged into the cell can influence



Professor of Cell and Developmental Biology Lisa Stubbs leads the IGB’s Gene Networks in Neural & Developmental Plasticity research theme.

the activity of genes, and so-called epigenetic modifications, changes to this structure, help to modify that activity in different situations. **Their hope is that by identifying genomic mechanisms of social behavior basic enough to be shared even between distantly related animal species, they can discover which biological mechanisms are most central.**

Co-authors on the study, which was funded by the Simons Foundation, included IGB Fellow Michael Saul and graduate student Christopher Seward.

## Foundation for food and agriculture research supports Crops *in silico*

 | [go.igb.illinois.edu/FFARCIS](http://go.igb.illinois.edu/FFARCIS)

Amy Marshall-Colón (GEGC), Assistant Professor of Plant Biology, is developing a suite of virtual plant models that may help resolve a growing gap between food supply and demand in the face of global climate change. Under new funding for the Crops *in silico* (Cis) project, her team will examine the effects of environmental challenges on a molecular, cellular, and



Assistant Research Professor of Astronomy Matthew Turk, left, and Assistant Professor of Plant Biology Amy Marshall-Colón and other researchers collaborated to bring virtual plant modeling to the Crops *in silico* project.

organ level within a plant to determine the best targets for genetic engineering. The ability to computationally mimic the growth, development, and response of crops to the environment will allow researchers to conduct many more experiments than can realistically be achieved in the field.

**The team will work to integrate above- and below-ground models of plants to create never-before-seen “whole views” of them. They will then subject these newly built virtual plants to computer-simulated extreme growing conditions—from flood to severe drought to increased ambient carbon dioxide—and compare the model’s predicted plant reaction to observed responses from field studies.** This will help “dial in” the model’s accuracy.

Beyond a technological breakthrough, the *Cis* team also aims to achieve a research community shift, uniting largely isolated efforts into a connected and collaborative community that will take full advantage of advances in computation science and mechanistic understanding of plant processes and their responses to the environment.

The Crops *in silico* project was seed-funded in 2015 by a \$350,000 grant from the Institute for Sustainability, Energy, and Environment to Stephen Long, Gutgsell Endowed Professor of Crop Sciences and Plant Biology (BSD/GEGC). The National Center for Supercomputing Applications awarded additional seed funding, and both provide matching funds to support the *Cis* team and its work. Funding for Marshall-Colón’s research is provided by the Foundation for Food and Agriculture Research.



Members of the Infection Genomics for One Health theme include (left to right) Joanna Shisler, Rebecca Smith, Patrick Degnan, Rachel Whitaker, and Rebecca Stumpf.

## Rachel Whitaker receives Allen Distinguished Investigator award



[go.igb.illinois.edu/WhitakerADI](http://go.igb.illinois.edu/WhitakerADI)

Rachel Whitaker, Associate Professor of Microbiology (IGOH leader/BCXT), received an Allen Distinguished Investigator award from the Paul G. Allen Frontiers Group. The award is given to researchers conducting pioneering research in epigenetics, aging, and evolution.

Whitaker’s award, in the area of microbial evolution, focuses on recent research that has unearthed regions of the genome that are capable of moving rapidly between cells, creating a sea of dramatic and unpredictable genetic changes. These mobile genetic elements (MGEs) are particularly

exploited by infectious bacteria, which evade antibiotics through rapid evolution. **While the scientific response to infectious disease has focused on identifying new ways to target and kill bacteria, antimicrobial resistance, virulence, and many other properties of pathogens are evolutionary problems driven by mobile elements.** An evidence-based predictive understanding of the evolutionary forces that drive the emergence and spread of these traits is needed to stop them. This project will create models of MGEs and their evolutionary roles within a human system and compare and refine those models against longitudinal data in order to capture and better understand this crucial evolutionary process.

The award will advance the research goals of IGOH as a whole and involve collaboration with colleagues at Illinois, University of Chicago and Geisel School of Medicine at Dartmouth. Their joint expertise will allow progress toward the shared objective of developing a promising new evolutionary paradigm.

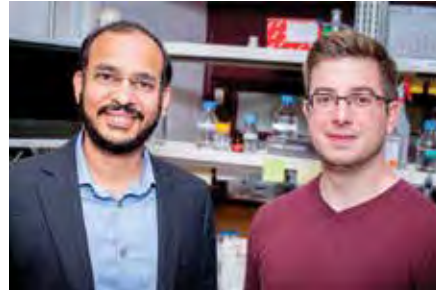
## Study identifies key player in heart enlargement



[go.igb.illinois.edu/LargeHeart](http://go.igb.illinois.edu/LargeHeart)

A study of mouse hearts led by Assistant Professor of Biochemistry Auinash Kalsotra (GNBP/ONC-PM) revealed a previously unknown mechanism by which heart cells control their size by ramping up or ceasing production of a key factor called PABPC1. **The findings, published in *eLife*, could assist in the development of therapeutics that promote healthy heart growth and prevent disease.**

During exercise, heart cells adapt over time to increased stress by boosting production of specific proteins, allowing the cells to increase in size. After a prolonged period without exercise, the heart cells return to their original size. In this study, researchers focused on PABPC1, a protein that binds to RNA and aids in the process of translating the RNA



Biochemistry professor Auinash Kalsotra, left, graduate student Joseph Seimetz and their colleagues identified a mechanism that allows heart cells to grow larger.

into protein. Scientists had long assumed all cells needed PABPC1 to survive and make new proteins. This study challenges this assumption—even though PABPC1 RNA is present in all human and mouse cells, the protein itself is absent in the adult heart, explaining why heart cells produce much lower levels of new proteins than other tissues in the body.

The NIH supported this research.

## JULY

### The Walk of Life: A celebration of the past and a path to future discovery



[go.igb.illinois.edu/WalkOfLife](http://go.igb.illinois.edu/WalkOfLife)

Just west of the IGB building is a stretch of sidewalk paved with multicolored stones that form a double helix. This area, called the Walk of Life, contains commemorative paver stones engraved in honor of gracious donors to the IGB.

Past contributors to the Walk of Life have used their pavers to address future generations in a variety of ways, while some were dedicated to a specific objective or field of interest. **Dr. Howard Grundy, MD, alumnus and native of DeKalb, Illinois, developed a deep appreciation for the skills and insights of the American farmer and chose to dedicate his paver to American agriculture and science.** David and Frances Hubbard, both alumni of the University of Illinois, hold strong ties to the region and to the university, raising four children who all attended the University of Illinois. Their daughter Dr. Carol Hubbard Seery devoted a paver to her parents in order to celebrate the significant role that Illinois played in the lives of the Hubbard family. Drs. Tobias and Annette Erb, both microbiologists, accepted postdoctoral fellowships at the IGB in 2009 and saw their gifted pavers as a way to celebrate the significant impact that the IGB had on their personal lives.

The IGB is proud to honor our donors with this unique showcase, which simultaneously reflects our mission of transformative research and technology in life sciences and allows our supporters to become a permanent part of IGB history.

## New grant to study fish genomics, behavior



[go.igb.illinois.edu/FishEDGE](http://go.igb.illinois.edu/FishEDGE)

The three-spined stickleback is a funny sort of fish. They are somewhat non-distinct: drabish silver, small, and minnow-like, native to salt- and freshwater bodies throughout most of the Northern hemisphere. However, different

stickleback populations have evolved very distinct morphological traits, demonstrating a natural diversity that makes them an ideal candidate with which to examine the mechanics of adaptive evolution and ecology. **More strikingly, they display a wide number of behaviors related to breeding, territorial disputes, and foraging that make them fascinating models for the study of animal behavior, particularly as to how genomics can both influence and be influenced by social dynamics.**

A new grant through the NSF's Enabling Discovery through Genomic Tools (EDGE) program promises to expand our knowledge of the three-spined stickleback, a foundational fish species. The award is supported by several co-PIs including Associate Professor of Animal Biology Alison Bell (GNBP), who collaborates with the team to develop new strategies for genetic manipulation that will make decoding the already-sequenced fish genome easier to decipher. They also aim to develop stock lines that will enable researchers to better standardize and replicate experiments, and create training tools to benefit the 100+ labs working on stickleback research worldwide.

Bell's lab focuses on behavior; other investigators are examining host-parasite and host-microbe interactions, evolution, ecological genetics, and more. They believe that in the process of developing needed tools to address their own specific research aims, they can simultaneously improve the tools and techniques used to study sticklebacks in the broader research community, benefiting labs worldwide.

The EDGE program is administered by the NSF's Biological Sciences Directorate.



Male three-spined sticklebacks interacting.

## Brief interactions spur lasting waves of gene activity in the brain



[go.igb.illinois.edu/BrainWaves](http://go.igb.illinois.edu/BrainWaves)

A five-minute encounter with an outsider spurs a cascade of changes in gene activity in the brain that can last for hours, researchers report in a study of three-spined stickleback fish published in *PLoS Genetics*.

Associate Professor of Animal Biology Alison Bell (GNBP) and colleagues tracked changes in gene expression 30, 60 and 120 minutes after an encounter. They focused on two parts of the brain—the telencephalon, which is important to learning and memory, and the diencephalon, which integrates social

information and hormonal influences. They compared the results between fish that had the encounter and fish that remained alone in their tanks.

Hundreds of genes were expressed differently in the experimental and control fish. They also varied in the expression of numerous transcription factors, which regulate the activity of other genes. The team then analyzed the functions of groups of genes whose expression patterns paralleled one another at specific intervals, revealing that genes changing in tandem over time had similar functions. In the experimental fish, hormone gene expression was highest at 30 minutes, metabolism genes peaked at 60 minutes and genes linked to immune function and

## DOE funds major bioenergy research center at Illinois through IGB and iSEE



[go.igb.illinois.edu/AnnounceCABBI](http://go.igb.illinois.edu/AnnounceCABBI)

The DOE announced funding of the \$115 million Center for Advanced Bioenergy and Bioproducts Innovation (CABBI), a collaboration between the Institute for Sustainability, Energy, and Environment (iSEE) and the IGB. CABBI includes 16 partner institutions, with Evan DeLucia, G. William Arends Professor of Plant Biology and Baum Family Director of iSEE (GEGC) serving as CABBI Director.

**“As the United States seeks energy independence, we need to look at the most efficient ways to grow, transform, and market biofuels,”** DeLucia said. “This grant is a game-changer, and CABBI will be at the forefront as we press toward a new bio-based economy. Our Center’s holistic approach will generate new products directly from biomass,

reducing our nation’s dependence on fossil fuels and making us more secure.”

CABBI researchers will develop fuels and products by integrating three highly interconnected DOE priority areas. Feedstock Development, led by Professor of Crop Sciences Stephen Moose (BSD/GEGC/MME), will integrate recent advances in genomics, synthetic biology, and computational biology to increase the value of biomass crops. Conversion, led by Steven L. Miller Chair in Chemical Engineering Huimin Zhao (BSD leader/MMG), will develop a versatile, automated “biofoundry” for rapidly engineering microbial strains that can efficiently produce diverse, high-value molecules such as biodiesel, organic acids, jet fuels, lubricants, and alcohols. Sustainability, led by ACES Distinguished Professor in Environmental Economics Madhu Khanna, will provide an overarching framework for viewing outcomes from the Feedstocks and Conversion themes through an environmental and economic lens.

homeostasis were most upregulated two hours after the encounter.

**“We’re seeing changes in gene expression even two hours after the fish interacts with an intruder. Clearly, those changes are not about the animal’s initial behavior,”** Bell said. **“We haven’t studied learning and memory, but we think that these chromatin modifications and changes in gene expression are all about setting up their brains to respond to threats in the future.”**

This research was funded by the Simons Foundation.

Animal Biology Professor Alison Bell (right), graduate student Syed Abbas Bukhari and their colleagues tracked changes in gene expression in the stickleback brain after the fish encountered an intruder.



## Two undergrads improve plant carbon-cycle models



[go.igb.illinois.edu/UndergradStomata](http://go.igb.illinois.edu/UndergradStomata)

In the summer of 2012, two Illinois undergraduate students tackled a problem that plant ecology experts had overlooked for 30 years. Mark Abordo, a mathematics major, and Kevin Wolz, a biology and civil and environmental engineering major, demonstrated that different plant species vary in how they take in carbon dioxide and emit water through stomata, the pores in their leaves. The data, reported in *Nature Ecology and Evolution*, boosted the accuracy of mathematical models of carbon and water fluxes through plant leaves by 30 to 60 percent.

This oversight of previous research stems in part from the fact that few plant biologists know how—or are naturally inclined—to convert their biological insights into the mathematical equations that modelers need to improve the accuracy of their work, said Andrew Leakey, Associate Professor of Plant Biology (GEGC) who mentored both students and is a co-author of the study.

The two students collected leaves during the summer from 15 tree species and used gas exchange equipment to measure how the leaves responded to different light and atmospheric conditions. Each leaf underwent a range of tests lasting



Left: Mark Abordo was a mathematics major at the time of the study. “It was a nice change from working on chalkboards all the time to doing lab experiments and working out in the fields,” he said. Right: Kevin Wolz majored in civil engineering and biology as an undergraduate at Illinois. This allowed him to appreciate both the complexity of the natural world and the simplicity and power of mathematical models.

roughly six hours. **The team found a significant amount of variation in the way that different tree species responded to factors such as light, heat, carbon dioxide concentration and humidity. Altering standard models with the new data dramatically improved the models’ accuracy, the researchers found.**

The NSF and EBI supported this research.

## Study finds parallels in variation in social responsiveness in bees and humans



[go.igb.illinois.edu/BeeSocial](http://go.igb.illinois.edu/BeeSocial)

A recent *Proceedings of the National Academy of Sciences* study has uncovered parallels between bees and humans who are less responsive to certain social stimuli. Research led by IGB Director and Swanlund Professor of Entomology Gene Robinson found that some genes associated with autism spectrum disorders in humans are regulated differently in less responsive honey bees than in their more responsive nest mates.

Postdoctoral researcher Hagai Shpigler observed that some bees were unmoved by the presence of a queen larva—a stimulus that typically spurs diligent action in bees involved in caring for young in the hive. Some bees responded with aggression toward intruders, while others seemed indifferent. Surprisingly, a few bees responded to neither type of stimulus.

To explore the biological mechanisms that might drive this behavioral variation, the team analyzed 246 groups of bees from seven genetically distinct honey bee colonies, carefully tested each bee in various social contexts, and then analyzed levels of gene expression in their brains. They found that more than 1,000 genes were regulated differently between less responsive bees, nurse bees, and guards.





**The researchers found a significant overlap between the less responsive honey bees' gene expression profile and genes associated with autism in humans. Further analyses found no significant overlap with human genes associated with depression, schizophrenia or several other mental disorders.**

"It's important to point out some caveats," Robinson said. "Humans are not big bees and bees are not little humans. The social responsiveness depends on context, and is different in the two cases. Autism spectrum disorder is very complex, and unresponsiveness is not the only behavior associated with it."

While social behavior likely evolved independently in honey bees and humans, Robinson said, "our data reveal that they make use of common toolkits, common building blocks."

The Simons Foundation and the NSF supported this research.

## How iBioFAB is building on changes in synthetic biology

  | [go.igb.illinois.edu/iBioFAB17](https://go.igb.illinois.edu/iBioFAB17)

In the IGB's Biosystems Design theme, an innovative robotic system is allowing researchers to pursue synthetic biology in a new way.

iBioFAB, which stands for Illinois Biological Foundry for Advanced Biomanufacturing, is a platform for the automatic production and analysis of synthetic biological systems. It performs tasks with its robotic arm in a fully-automated fashion, making it more reliable and opening up countless possibilities in synthetic biology research. iBioFAB allows researchers to perform DNA synthesis, pathway optimization, and genome engineering efficiently and at a low cost.

The algorithms used by iBioFAB allow tasks to be easily repeated and make it easier to find where things went wrong in an experiment. The robot can also handle more complex systems, which is important as synthetic biology becomes more rich with data.

One of the first projects iBioFAB was a part of involved a yeast genome, which has approximately 6,000 genes. Researchers showed that the system could be used to automate the genome-scale engineering workflow of this genome.

Professor Huimin Zhao (BSD leader/MMG), Steven L. Miller Chair of Chemical and Biomolecular Engineering, said he is excited to see how iBioFAB could fuel advances in drug discovery and metabolic engineering, which involves engineering a microorganism to produce a particular chemical. **This can sometimes take years to accomplish, but with a technology like iBioFAB, Zhao said the time can be reduced to one year.**

### Research to investigate oil field biosouring with new technology

 [go.igb.illinois.edu/Biosour](http://go.igb.illinois.edu/Biosour)

A research project is seeking to solve a \$90 billion global problem in the oil industry while working to make oil drilling less harmful to the environment.

Bruce Fouke (BCXT), Professor of Geology and Microbiology and the director of the Roy J. Carver Biotechnology Center, was awarded a three-year grant from the Dow Chemical Company to study a process known as oil field biosouring.

Biosouring results from a common procedure in oil drilling: seawater is pumped deep underground in order to maximize the amount of extracted oil. This action significantly affects the microbes that live in the Earth's deep subsurface.

Biosouring also creates a byproduct called sulfide that is highly corrosive and harmful to human health. Sulfide causes the largest maintenance expense for oil companies: replacement of underground oil field pipes and plumbing systems. Globally, almost \$90 billion is spent each year on replacing damaged pipes.

**Dow Chemical Company is interested in applying IGB research to understand how biosouring happens and developing ways to reduce or stop it, Fouke said. He and his colleagues will use a technology they developed called the GeoBioCell, a microfluidics test bed, that can recreate biosouring so they can study the process.** They will test different temperatures, chemicals, food sources and water chemistries to try and reduce or stop biosouring.

Fouke said results from the experimentation will enhance our understanding of how oil and gas are produced while better protecting the environment.

Professor of Geology and Microbiology Bruce Fouke, shown here with his research team at Yellowstone National Park, will study oil field biosouring as part of a new three-year grant.



---

AUGUST

Disease-causing bacteria like *Yersinia enterocolitica*, pictured, communicate with chemical signals that allow them to respond collectively to environmental changes. Researchers hope to harness these signals to fight bacterial infections.

## Slowing dangerous bacteria may be more effective than killing them



[go.igb.illinois.edu/SlowBacteria](https://go.igb.illinois.edu/SlowBacteria)

Researchers have discovered a mechanism that allows bacteria of the same species to communicate when their survival is threatened. The study suggests that it may be possible to slow dangerous infections by manipulating the messages these microbes send to each other, allowing the body to defeat an infection without causing the bacteria to develop resistance to the treatment.

The study, published in the *Proceedings of the National Academy of Sciences*, was co-authored by Professor of Biochemistry Satish Nair (MME/MMG), postdoctoral researcher Shi-Hui Dong, and colleagues. The study was supported by funds from the NIH.

When bacteria compete with other microbes for scarce resources, they produce antibiotics to kill off the other species. Once population growth of one group of bacteria outpaces availability of the nutrients it needs to survive, the group produces another unique molecule that tells it to go into a dormant, but more virulent, state and slow growth until more food is available.

Over time, bacteria have adapted to resist antibiotics. Nair said bacteria share adaptations easily, and with so many out there, each with different adaptations to share, they develop resistance quickly.

Nair and Dong's new study targets the language that bacteria use to slow down growth rather than the antibiotic signal to kill. Slowing them down lessens the chance of resistance developing. The researchers say understanding how bacteria produce the dormancy-signal molecule paves the way for developing molecules that can disrupt the communication of specific bacteria, with little chance for drug resistance to develop.



## Woese Undergraduate Research Scholar selected

 [go.igb.illinois.edu/WURS17](http://go.igb.illinois.edu/WURS17)

Yuhao Min, double major in chemistry and molecular and cellular biology, studied anticancer compounds as the Woese Undergraduate Research Scholar, a position that funds undergraduate students to pursue interdisciplinary research at IGB over the summer.

As the scholarship recipient, Min pursued research with Steven L. Miller Chair Huimin Zhao, Professor of Chemical and Biomolecular Engineering (BSD leader/MMG) and Wilfred van der Donk, Richard E. Heckert Chair in Chemistry (MMG). Their collaborative research project is focused on engineering a peptidic anticancer compound.

Min's research is focused on nisin, a peptide that has been used as a food preservative but also has a broad antimicrobial spectrum. It has been shown to be a potential therapeutic for treating cancers such as head and neck squamous cell carcinoma. **Min's project focused on engineering nisin as an effective anticancer agent by creating variant DNA libraries, introducing mutations into nisin's precursor gene. He worked with the lab to isolate nisin mutants with improved anticancer activities through high-throughput screening, a common drug discovery method.**

## Girls learn about plants inside and out at Pollen Power camp

 [go.igb.illinois.edu/PollenPower17](http://go.igb.illinois.edu/PollenPower17)

**Over the summer, a group of middle school girls attended Pollen Power camp at the IGB to learn about plants and insects, explore fiber optics and lenses, use microscopes and create green screen recordings.**

The camp, offered for the fifth consecutive year, was funded in part by the NSF and the IGB. The camp is co-organized by plant biologists Lisa Ainsworth (GEGC) and Andrew Leakey (GEGC), the IGB Core Facilities microscopy suite, and IGB Outreach staff. Female graduate students acted as counselors for the plant science-themed camp, providing examples for attendees of what a future career in science could look like.

In addition to basics of plants and pollination, campers learned about the relationship of plant biology to animal pollinators, evolution, and global climate change through a series of projects and activities. The girls used high-powered microscopes and fabrication equipment to explore pollen grains and other plant structures up close. They wrote and

---

Above: Pollen Power camp participants get hands-on experience with Illinois flora and fauna.

produced their own short videos about Earth's present and future climate.

Talks by female scientists and visits to laboratories and research field sites around the Illinois campus helped provide a broad view of the many forms that scientific work can take and a more concrete picture of its day-to-day realities. The ultimate goal of the camp is not just to educate, but also to make a career in STEM, particularly plant science or engineering, more appealing and achievable to those who attend.

## Auinash Kalsotra awarded MDA grant for studying myotonic dystrophy



[go.igb.illinois.edu/MDAMD](http://go.igb.illinois.edu/MDAMD)

Assistant Professor of Biochemistry Auinash Kalsotra (GNBP/ONC-PM) was awarded a nationally competitive research award from the Muscular Dystrophy Association (MDA). The grant provides Kalsotra with \$300,000 over a three-year period to study the molecular basis for cardiac arrhythmias in myotonic dystrophy, a multi-systemic disease that affects about 1 in 8,000 people and has no cure.

"Myotonic dystrophy type 1 (DM1) is caused by an unusual mutation in which a small DNA segment of the mutated gene is repeated hundreds of times," Kalsotra said. "The mutated gene, when copied into RNA, becomes toxic and particularly harmful because instead of its normal exit to the cytoplasm, the RNA with repeats gets trapped within the nucleus, which alters the normal function of many genes, not just the gene with the mutation."

**Cardiac defects, particularly arrhythmias, are the second leading cause of death among DM1 individuals, but the underlying mechanisms responsible remain poorly understood. Kalsotra's laboratory is investigating the disrupted function of a previously unknown RNA binding protein in DM1 cardiac pathogenesis.** The team will be using novel CRISPR-based mouse models, *in vitro* cell culture systems, and next-generation

sequencing approaches to decipher the exact role of this RNA binding protein in promoting cardiac arrhythmias in DM1.

"The value of MDA research funding cannot be underestimated in making this line of investigation possible in my laboratory," Kalsotra said. "The support of MDA allows us to generate exciting new tools for research and study previously unrecognized pathogenic mechanisms for this debilitating disease."

## New microscope technique reveals internal structure of live embryos



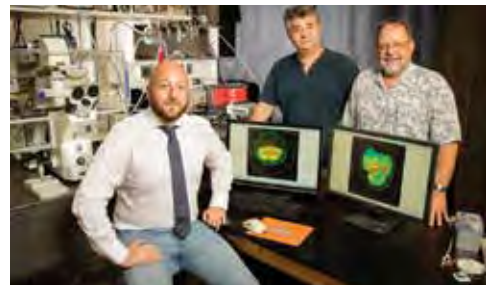
[go.igb.illinois.edu/3Dembryo](http://go.igb.illinois.edu/3Dembryo)

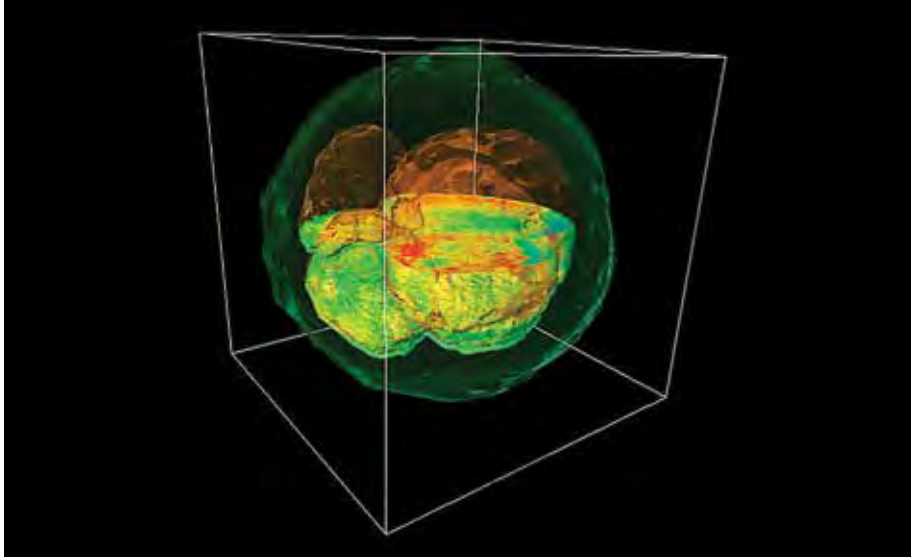
A group of researchers have developed a way to produce 3D images of live cattle embryos that could help determine embryo viability before *in vitro* fertilization in humans.

The new method, published in *Nature Communications*, was developed by Gabriel Popescu, Professor of Electrical and Computer Engineering and Matthew Wheeler (RBTE), Professor of Animal Science.

Infertility can be devastating for those who want children. Many seek treatment, but the cost of a single *in vitro* fertilization cycle can be \$20,000, making it desirable to succeed in as few attempts as possible. Additional knowledge regarding the health of embryos could help physicians select those that

Left to right: Marcello Rubessa, Gabriel Popescu and Matthew Wheeler teamed up to produce 3D images of live cattle embryos that could help determine embryo viability before *in vitro* fertilization in humans.





A GLIM image of a cow embryo, displayed to reveal internal structures.

are most likely to lead to successful pregnancies.

The researchers' method, called gradient light interference microscopy, or GLIM, solves a challenge that other methods have struggled with—imaging thick, multicellular samples.

In many forms of traditional biomedical microscopy, light is shined through thin slices of tissue to produce an image. Operators sometimes use chemical or physical markers so they can find a specific object in a thick sample, but those markers can be toxic to living tissue.

**GLIM can probe deep into thick samples by controlling the path length over which light travels through the specimen. The technique allows researchers to produce images from multiple depths, which are then composited into a single 3D image.**

The team hopes to apply GLIM technology to human fertility research and treatment, as well as a range of different types of tissue research.

## New handheld spectral analyzer uses smartphone to detect disease



[go.igb.illinois.edu/TRIphone](http://go.igb.illinois.edu/TRIphone)

Researchers have developed technology that enables a smartphone to perform lab-grade medical diagnostic tests that typically require large, expensive instruments. Costing only \$550, **the spectral Transmission-Reflectance-Intensity (TRI) Analyzer attaches to a smartphone and analyzes patient blood, urine or saliva samples as reliably as clinic-based instruments that cost thousands of dollars.**

The technology was developed in the lab of Bioengineering and Electrical and Computer Engineering Professor Brian Cunningham (ONC-PM leader/MMG). His team used the TRI Analyzer to perform two commercially available assays. Their test results were comparable to those done with clinic-grade spectrometer instrumentation.

The TRI Analyzer operates by converting the smartphone camera into a high-performance spectrometer. The analyzer illuminates a sample fluid with the phone's internal white LED flash or with an inexpensive external green laser diode.



The spectral transmission-reflectance-intensity (TRI) Analyzer attaches to a smartphone and analyzes patient blood, urine, or saliva samples as reliably as clinic-based instruments that cost thousands of dollars.

The light from the sample is collected in an optical fiber and guided into the phone's rear-facing internal camera. These optical components are all arranged within a 3D-printed plastic cradle.

Additionally, the technology can analyze multiple samples quickly and reliably, making the Analyzer suitable for patients who lack convenient access to a clinic or hospital with diagnostic test facilities, or for patients with urgent health situations requiring rapid results.

Cunningham said the TRI Analyzer can also be applied to point-of-use applications that include animal health, environmental monitoring, drug testing, manufacturing quality control, and food safety. The patented technology is available for license.

## Combating antiviral drug resistance with dynamic therapeutics



[go.igb.illinois.edu/ViralCombat](http://go.igb.illinois.edu/ViralCombat)

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. 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?



Assistant Professor of Microbiology Christopher Brooke seeks to develop biological therapeutics that evolve to combat viral resistance.

Assistant Professor of Microbiology Christopher Brooke (GOH) is part of a DARPA-funded program that hopes to achieve this. The program's goal is to develop a 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. Brooke's team is developing a therapeutic specifically for influenza.

The team's approach is based on a natural phenomenon known as defective interference. Under certain conditions, many viruses spontaneously produce virus mutants known as defective interfering particles. These were believed to be detrimental to the virus, but Brooke is not totally convinced this is the case.

**He and his colleagues will instead make changes to these particles and see what effect they have on the viral population. Their goal is to identify a particle that could be introduced to an infected individual and decrease disease severity and forward transmission of influenza without the virus developing resistance.**

Regardless of whether this research will facilitate eradication of the influenza virus, the researchers expect to gain valuable information on how viral populations evolve.

## Workshop “bridges” empirical, theoretical understandings of climate and crop yield

  | [go.igb.illinois.edu/BridgeWorkshop](http://go.igb.illinois.edu/BridgeWorkshop)

Researchers from Illinois, University of Birmingham, and other institutions around the world gathered at the IGB for a set of intense discussions on how to improve predictions of the impact of climate on future crop yield. The workshop was supported by a seed grant from the Birmingham-Illinois Partnership for Discovery, Engagement and Education (BRIDGE).

**“Our objective is to improve the ability of computer models to simulate the way crops are going to respond to rising carbon dioxide concentrations. That’s an important exercise because the models are used to make projections about how future climate will impact food and fuel availability,”** said co-organizer and Associate Professor of Plant Biology Andrew Leakey (GEGC).

Leakey and colleagues identified a specific strategy for the improvement of crop models: bring together the model developers, those who work to assemble the puzzle pieces of the changing climate’s impact, with experimentalists, those whose work to understand the biological mechanisms of response. Modeling experts at the workshop focused on representing and ultimately predicting the impact of rising carbon dioxide levels on crop yield. The assumption is that more carbon dioxide, the gas that is incorporated by photosynthesis into the sugars produced by plants, helps crops grow faster or yield more. However, interactions between plants and their environment are incredibly complex, representing a synthesis of factors including atmospheric and soil composition, plant respiration, water availability, and weather.

A further experimental challenge, to gather real data on how crop plants respond to variations in carbon dioxide levels and other aspects of climate, is addressed through SoyFACE, the Soybean Free Air Concentration Enrichment facility at Illinois.





## NSF awards Illinois \$3 million for interdisciplinary graduate student training

[go.igb.illinois.edu/NSFRT](http://go.igb.illinois.edu/NSFRT)

The NSF recently granted \$3 million to the University of Illinois for an interdisciplinary graduate student training program to help form new insight on the brain and expand participation in the field of neuroscience.

Sixty graduate students from across campus will participate in the five-year NSF Research Traineeship, led by Martha Gillette (GNDP), Professor of Cell and Developmental Biology and director of the Neuroscience Program at Illinois. Hyunjoon Kong (RBTE), Professor of



Left to right: Martha Gillette and Hyunjoon Kong.

Chemical and Biomolecular Engineering, is a co-principal investigator.

The program's primary goal is to provide students with an immersive research experience that blends techniques from multiple disciplines to better understand the many aspects of the human body's most complex organ. The program is also designed to increase the participation of women, underrepresented minorities, and students with disabilities in the field of brain science. A third goal is to improve scientists' communication skills with the public.

The training program will bridge two research paradigms: cognitive and behavioral studies and cell and tissue studies. **To meet these goals, the program will guide graduate students through specialized courses to broaden their knowledge beyond their own specific fields. Students will also have opportunities to visit and work with laboratories of international partners.**

Co-directors of the project include Rashid Bashir (RBTE), Professor of Bioengineering, Electrical and Computer Engineering, and Jonathan Sweedler (BSD/MMG), James R. Eiszner Family Endowed Chair in Chemistry.

---

## SEPTEMBER

### New genetic engineering method is indispensable biotechnological tool

 [go.igb.illinois.edu/GETool](http://go.igb.illinois.edu/GETool)

Research by Professor Huimin Zhao (BSD leader/MMG), Steven L. Miller Chair of Chemical and Biomolecular Engineering, and graduate student Behnam Enghiad is advancing a new method of genetic engineering for basic and applied biological research and medicine. Their work, reported in *ACS Synthetic Biology*, could open new doors in genomics research by improving the precision and adherence of sliced DNA.

Restriction enzymes are an important tool in genomic research: by cutting DNA at a specific site, they create a space where foreign DNA can be introduced for gene-editing purposes. This process can also be achieved by artificial restriction enzymes, or AREs.

Though useful in genetic engineering, AREs don't generate "sticky ends"—an uneven break in the DNA ladder structure that leaves complementary overhangs, improving adhesion when introducing new DNA.

However, restriction enzymes also have a drawback: the recognition sequence that prompts them to cut is very short.

Researchers rely on finding a restriction enzyme whose cut site appears only once in the genome—a difficult proposition when the DNA could be thousands of base pairs long.

Enghiad and Zhao developed a new technique that creates AREs by using a protein called *PfAgo*. **Led by two DNA guides, *PfAgo* can recognize much longer sequences when finding its cut**

**site, making it more specific. It can also create longer sticky ends than restriction enzymes.**

They believe their technology will have broad applications in biological research, ranging from discovery of small molecule drugs to engineering microbial cell factories for creating fuels and chemicals. The study was supported by the University of Illinois and 3M Corporation.

## A new tool for genetically engineering the oldest branch of life

 [go.igb.illinois.edu/ArchaeaEdit](http://go.igb.illinois.edu/ArchaeaEdit)

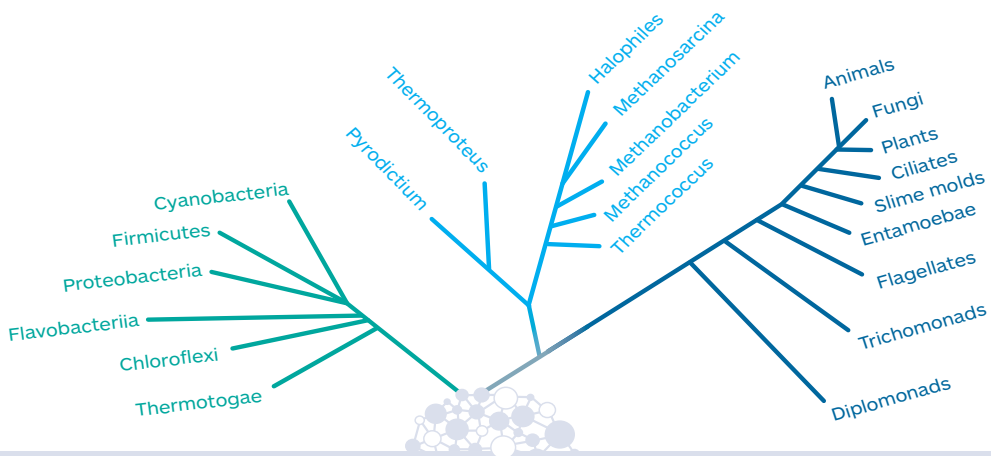
A new study by G. Williams Arends Professor of Microbiology William Metcalf (MMG leader) and IGB fellow Dipti Nayak has documented the use of CRISPR-Cas9 mediated genome editing in the third domain of life, Archaea, for the first time.

Their groundbreaking work, reported in *Proceedings of the National Academy of Sciences*, has the potential to vastly accelerate future studies of these organisms, with implications for research including global climate change.

Previous methods for doing research with *Methanosarcina acetivorans*, the specific archaeon they worked with, could take

months. With CRISPR-Cas9, they were able to speed up the process.

By using the introduced Non-Homologous End Joining repair system to perform what are known as “knock-out” studies, where a single gene is removed or silenced to see what changes are produced and what processes that gene might affect, Nayak says that **future research will be able to assemble a genetic atlas of *M. acetivorans* and other archaeal species. Such an atlas would be incredibly useful for a variety of fields of research involving Archaea and climate change, an area of particular interest to the Metcalf lab.**



### BACTERIA

Most abundant and diverse single-celled organisms

### ARCHAEA

The only class of organisms that can produce methane

### EUKARYA

Plants, animals, fungi, and protists



G. William Arends Professor of Microbiology and theme leader of the IGB's Mining Microbial Genomes theme William Metcalf, left, with IGB Fellow Dipti Nayak.

This research represents an exciting new direction in studying and manipulating Archaea.

This work was supported by the DOE.



## Scientists discover spring-loaded mechanism in unusual species of trap-jaw ant

 [go.igb.illinois.edu/AntJaw](http://go.igb.illinois.edu/AntJaw)

Researchers revealed how a group of trap-jaw ants can snap their jaws shut at speeds of up to 50 miles an hour—just fast enough to capture their elusive prey.

Animal Biology Professor Andrew Suarez (GNBP) and former graduate student Frederick Larabee, now a postdoctoral researcher at the Smithsonian Institution's National Museum of History, reported their findings in the *Journal of Experimental Biology*.

The ants they studied belong to the genus *Myrmoteras*, and are one of four groups of ants that have independently evolved the ability to quickly snap their powerful jaws shut to capture speedy prey. Until they encounter their prey, *Myrmoteras* ants hold their jaws open at a 280-degree angle. Latched in this

position, their jaws store elastic energy that, when released, snaps the jaws shut in a fraction of a second.

To visualize the ants' jaws, Larabee used a microscope and microcomputed tomography, which exposes tiny specimens to X-rays to discern their internal structures. **His observations allowed him to determine how the jaws likely work: a feature of the ant's mandible allows it to lock its jaws open. Just before a strike, a lobe on the back of the ant's head compresses. A trigger muscle releases the jaws, executing a strike.**

Suarez said studying these ants "gives us insight into solutions for real-world issues related to energy storage and high-speed systems."

The NSF, Peter Buck Fellowship and the National Geographic Society supported this research.

## Seeing emergent physics behind evolution

 [go.igb.illinois.edu/GoldenfeldQuanta](http://go.igb.illinois.edu/GoldenfeldQuanta)

The physicist Nigel Goldenfeld (BCXT leader/CGRH/GNDP) hates biology—"at least the way it was presented to me" when he was in school, he said. "It seemed to be a disconnected collection of facts. There was very little quantitation."

That sentiment may come as a surprise to anyone who glances over a list of the myriad projects Goldenfeld's lab is working on. He and his colleagues monitor the individual and swarm behaviors of honey bees, analyze biofilms, watch genes jump, assess diversity in ecosystems, and probe the ecology of microbiomes. Goldenfeld himself is director of the NASA Astrobiology Institute for Universal Biology, and he spends most of his time not in the physics department at Illinois but in his biology lab.

Goldenfeld is one in a long list of physicists who have sought to make headway on questions in biology: In the 1930s, Max Delbrück transformed the understanding of viruses; later, Erwin Schrödinger published



Nigel Goldenfeld, leader of the IGB Biocomplexity research theme and director of the NASA Astrobiology Institute for Universal Biology, applies biology studies to the informative principles of condensed matter physics and emergent states.

*What is Life? The Physical Aspect of the Living Cell*; Francis Crick, a pioneer of X-ray crystallography, helped discover the structure of DNA.

Goldenfeld wants to make use of his expertise in condensed matter theory, in which he models how patterns in dynamic physical systems evolve over time, to better understand diverse phenomena including turbulence, phase transitions, geological formations and financial markets. **His interest in emergent states of matter has compelled him to explore one of biology's greatest mysteries: the origins of life itself. And he's only branched out from there.**

"Physicists can ask questions in a different way," Goldenfeld said. "My motivation has always been to look for areas in biology where that kind of approach would be valued. But to be successful, you have to work with biologists and essentially become one yourself. You need both physics and biology."

This article is adapted from and available in full on [www.quantamagazine.org](http://www.quantamagazine.org).

## Airlines could fly thousands of miles on biofuel from new promising feedstock

 [go.igb.illinois.edu/AirBiofuel](http://go.igb.illinois.edu/AirBiofuel)

A Boeing 747 burns one gallon of jet fuel each second, but a recent analysis from researchers at Illinois estimate that this aircraft could fly for 10 hours on bio-jet fuel produced on 54 acres of specially engineered sugarcane.

Plants Engineered to Replace Oil in Sugarcane and Sorghum, or PETROSS, is funded by the DOE Advanced Research Projects Agency - Energy (ARPA-E). They have developed sugarcane that produces oil, called lipidcane, that can be converted into biodiesel or jet fuel in place of sugar that is currently used for ethanol production.

"Oil-to-Jet is one of the direct and efficient routes to convert bio-based feedstocks to jet fuel," said Vijay Singh (GEGC), Professor of Agricultural and Biological Engineering. "Reducing the feedstock cost is critical to improving process economics of producing bio-jet fuel. Lipidcane allows us to reduce feedstock cost."

**PETROSS sugarcane could be grown on an estimated 23 million acres of marginal land in the southeastern U.S. If this acreage was used to produce renewable jet fuel from lipidcane, it could replace about 65 percent of national jet fuel consumption.**



Deepak Kumar, postdoctoral researcher and lead analyst on the study, said they estimate that this biofuel would cost the airline industry \$5.31 per gallon, which is less than renewable jet fuels from other sources.

## The time is RIPE to transform agriculture and feed the world



[go.igb.illinois.edu/RIPEreinvest](http://go.igb.illinois.edu/RIPEreinvest)

Political and agricultural leaders gathered at the University of Illinois to see transformative work by scientists in the Realizing Increased Photosynthetic Efficiency (RIPE) research project.

A \$45 million, five-year reinvestment from the Bill & Melinda Gates Foundation, the Foundation for Food and Agriculture Research, and the U.K. Department for International Development will enable the researchers to continue their work to address the global food challenge.

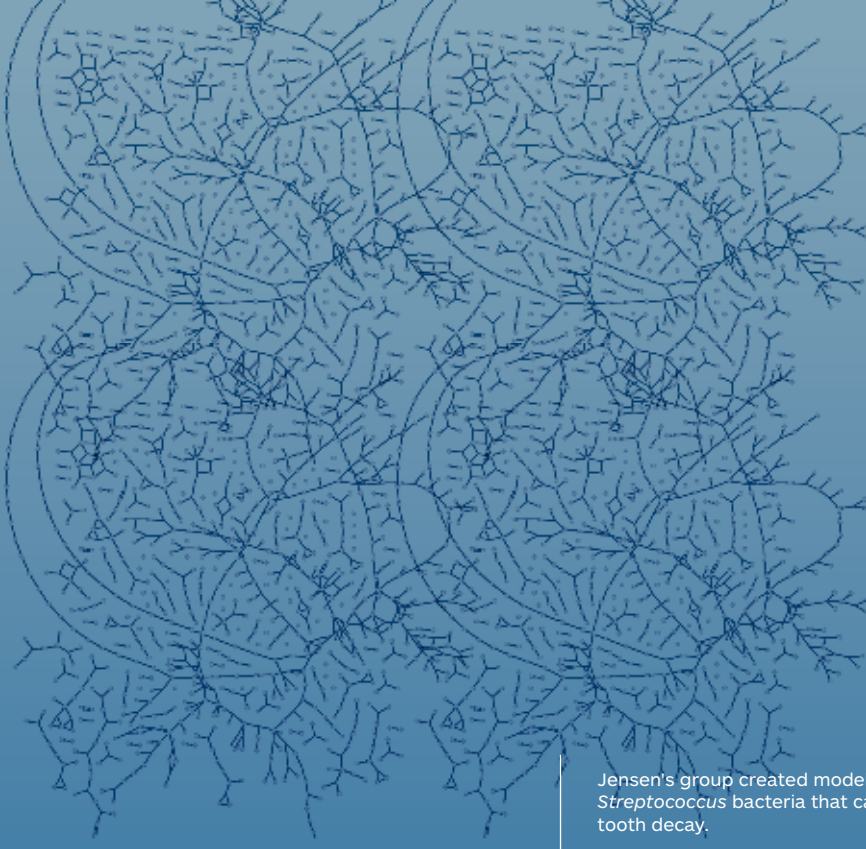
Building on half a century of photosynthesis research at Illinois, including several landmark discoveries enabled by state and federal

Researchers prepare field trials to discover the resilience of specially engineered plants to temperatures that simulate the predicted climate of 2050.

partnerships, RIPE researchers simulated the 170-step process of photosynthesis and identified seven potential pipelines to improve photosynthesis. With the support of an initial \$25 million, five-year grant from the Gates Foundation, RIPE began work in 2012 to turn their ideas into sustainable yield increases.

In a study published in the journal *Science*, the team demonstrated that one of their approaches could **increase crop productivity by as much as 20 percent—a dramatic increase over typical annual yield gains of one percent or less. Two other RIPE pipelines have now led to even greater yield improvements in greenhouse and preliminary field trials.**

RIPE and its funders will ensure that their high-yielding food crops are globally available and affordable for smallholder farmers to help feed the world's hungriest and reduce poverty, particularly in sub-Saharan Africa and southeast Asia.



Jensen's group created models of *Streptococcus* bacteria that cause tooth decay.

## Researchers use computation and genomics to battle tooth decay



[go.igb.illinois.edu/ToothDecay](http://go.igb.illinois.edu/ToothDecay)

An expert in using computational and experimental techniques to combat infectious diseases, Bioengineering Professor Paul Jensen (MMG) is taking aim at one of the most prevalent chronic diseases in the U.S.—tooth decay.

Jensen received funding from the National Institute of Craniofacial Research to apply a data-driven approach to understanding the role that certain bacteria play in cavity formation.

Cavities occur when the good and bad bacteria in our mouth become imbalanced. The bad bacteria, *Streptococcus mutans*, forms a biofilm, then takes the sugars we eat and ferments them into acid, which decalcifies our teeth and causes decay.

Another harmful bacteria, *S. sobrinus*, accelerates tooth decay in some people, but very little is known about this microbe and its function—it's also much more difficult to work with in the lab than *S. mutans*.

Jensen and his students were the first researchers to ever complete the entire genome of *S. sobrinus*. They also built a genome-scale model of *S. mutans*, which enables them to study a full network of its metabolism. They are now applying their increased knowledge to develop a similar model for *S. sobrinus*.

**They hope to create simulations to develop therapeutic measures that can alter the levels of *S. sobrinus* and *S. mutans* in the mouth. Their research could identify places where genes could be targeted in order to change the microbes' destructive function. The team will create a short list of promising drug targets for further experiments.**

## Researchers awarded NSF grant to fund 3D bioprinter



[go.igb.illinois.edu/3Dbioprint](http://go.igb.illinois.edu/3Dbioprint)

A team of researchers from IGB's RBTE theme was awarded an NSF grant that will provide funding for a new 3D-bioprinting instrument.

The Major Research Instrumentation grant will fund the purchase of an EnvisionTEC 3D-Bioplotter, a bioprinting system that is essentially a 3D printer for tissues.

Bioprinting uses 3D printing technology to create cell patterns and fabricate biomaterials. Much of the research in the RBTE theme involves developing approaches to regenerate tissues in order to address problems in human health.

**The bioplotter will be housed within the IGB as a shared-use facility that will be accessible to researchers across campus. Several research efforts at the IGB and Illinois are dedicated to developing tissue engineering solutions that could impact a range of important healthcare issues such as cancer, stem cell behavior and more.**

Brendan Harley (RBTE leader), Associate Professor of Chemical and Biomolecular Engineering, said he hopes researchers will look to the IGB and RBTE theme as a hub for tissue engineering on campus.

"We're going to be able to do some really exciting new work," Harley said. "Everything's in place to really attack big, challenging problems."

## Researchers discover unique property of critical methane-producing enzyme



[go.igb.illinois.edu/MethaneEnzyme](http://go.igb.illinois.edu/MethaneEnzyme)

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

A team of IGB researchers 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 brings scientists a step closer to fully understanding this enzyme that plays an important role in methane production and the carbon cycle.

William Metcalf (MMG leader), G. Williams Arends Professor of Microbiology and co-author of the paper, argues that MCR is one of the most important enzymes on Earth for the carbon cycle.

The study employed a novel genetic tool, developed by IGB fellow Dipti Nayak, which helped them realize that the modifications were not essential to the enzyme's function. This came as a surprise to many in this field of research.

"We have this important enzyme, but we really don't understand why it's made the way it is," Metcalf said. "If we want to understand that enzyme, and how that enzyme fits in the organism, and how that organism fits into the global environment—we really have to be able to tease this puzzle apart piece by piece."

Metcalf and Nayak hope to use the genetic tool Nayak created to investigate other modifications of MCR that have yet to be studied.



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

## Group develops gene circuit design strategy to advance synthetic biology



[go.igb.illinois.edu/GeneCircuit](http://go.igb.illinois.edu/GeneCircuit)

Over the last 17 years, scientists and engineers have developed synthetic gene circuits that can program the functionality, performance and behavior of living cells. Engineered gene circuits hold great promise in medical and biotechnological applications. They could combat superbugs, produce advanced biofuels, and manufacture functional materials.

Most circuits are made through trial and error, and this process can often be inefficient. To address this design challenge, researchers have turned to quantitative modeling. But the current modeling program is often incapable of effectively describing circuit behaviors.

Bioengineering Associate Professor Ting Lu (BCXT/BSD/MME) and his graduate students, Chen Liao and Andrew Blanchard, created an integrated modeling framework for quantitatively describing and predicting gene circuit behaviors. Using *E. coli* as a model host, the framework consists of a mechanistic description of host physiology.

**Their framework, published in *Nature Microbiology*, was able to capture and predict a large set of experimental data concerning the host and simple gene overexpression. The framework also has potential to be generalized for describing multiple host organisms. According to Lu, this work advances the quantitative understanding of gene circuit behaviors and facilitates the transformation of gene network design from trial and error to rational forward engineering.**

This research was supported by the NSF, the Office of Naval Research, and the American Heart Association.

---

### OCTOBER



## DOE grant to fund sorghum research at Illinois



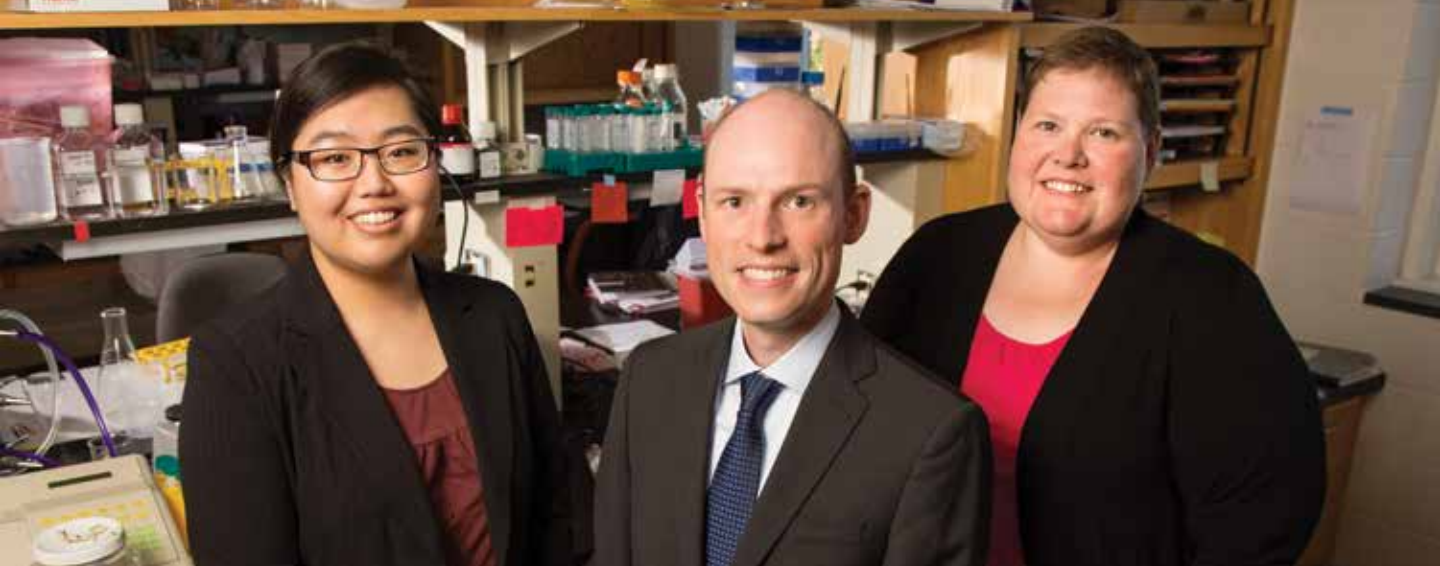
[go.igb.illinois.edu/SorghumEfficiency](http://go.igb.illinois.edu/SorghumEfficiency)

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

Andrew Leakey (GEGC), a professor in the Department of Plant Biology, is involved in the project which, will expand upon earlier research on green foxtail grass to identify new genes and pathways that contribute to photosynthesis and enhanced water use efficiency.

The research team, which includes researchers from several universities





and the USDA, will then deploy these genes using synthetic biology tools to accelerate development of elite energy sorghum varieties for production on marginal lands.

Sorghum is a member of the grass family and is grown worldwide. **It 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. Sorghum is among the most efficient crops in conversion of solar energy and use of water, making it an ideal crop to target for improvement.**

The 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 environment.

## Cholesterol byproduct hijacks immune cells, lets breast cancer spread



[go.igb.illinois.edu/BreastCholesterol](https://go.igb.illinois.edu/BreastCholesterol)

High cholesterol levels have been associated with breast cancer spreading to other sites in the body, but doctors and researchers don't know what causes this. A study in *Nature Communications* found that the culprit is a byproduct of cholesterol metabolism that acts

A cholesterol byproduct facilitates breast cancer's spread by hijacking immune cells, a new University of Illinois study found. Pictured, from left: Postdoctoral researcher Amy Baek, professor Erik Nelson and breast cancer survivor Sarah Adams.

on specific immune cells so that they facilitate the cancer's spread instead of stopping it.

The study, supported by the NIH and Susan G. Komen, identifies new potential drug targets that could inhibit the creation or actions of the dangerous cholesterol byproduct, a molecule called 27HC. The work was led by Erik Nelson (CGRH), a professor of molecular and integrative physiology, and postdoctoral researcher Amy Baek.

**Their research on mice involved inhibiting the enzyme that makes 27HC during cholesterol metabolism. By doing this, they found a suppressor effect on breast cancer metastasis, the development of additional malignant growths. This suggests that a drug treatment targeting this enzyme could be an effective therapeutic.**

Because 27HC acts through the immune system, and not on breast cancer itself, the researchers believe their findings have broad applicability for solid tumors. They performed experiments looking at colon cancer, lung cancer, melanoma and pancreatic cancer, and found that 27HC increased metastasis for all the tumor types, suggesting that a treatment targeting 27HC could be effective across multiple cancer types.

The team is working with Carle Foundation Hospital to establish whether the 27HC pathway is similar in mice and humans. They hope to develop small-molecule drugs to inhibit 27HC.



## Nutrition scientist Sharon Donovan elected to National Academy of Medicine

 [go.igb.illinois.edu/DonovanNAM](http://go.igb.illinois.edu/DonovanNAM)

Sharon M. Donovan (CGRH/MME), a professor of nutrition and the Melissa M. Noel Endowed Chair in Nutrition and Health, was elected to the National Academy of Medicine (NAM).

Induction into NAM recognizes individuals who have demonstrated outstanding professional achievements and commitments to service. It is considered one of the highest honors in the fields of health and medicine.

**Donovan and her research group conduct research in pediatric nutrition, focusing on three areas: optimal intestinal development of neonates, prevention of childhood obesity, and determinants of picky eating in 2- to 5-year-old children.**

Her work has garnered numerous honors, including awards from the International Life Sciences Institute North America and the American Society for Nutrition (ASN). She is an active ASN member, serving as that organization's president from 2011 to 2012, and she is currently the president-elect of the

Food Science and Human Nutrition Professor Sharon Donovan, center, is among 70 new members elected to the National Academy of Medicine.

International Society for Research on Human Milk and Lactation.

"Being inducted into NAM is an incredible honor that very few people achieve," said Kim Kidwell, the dean of the College of Agricultural, Consumer and Environmental Sciences. "Sharon Donovan embodies the spirit of this honor through the incredible contributions she has made to advancing our understanding of digestive tract and brain development, childhood obesity and autism. Sharon's work helps people throughout the world to live better lives. I am thrilled that she has been acknowledged for her contribution in this way and am very proud that she is a member of the ACES family."

## Expanding Brazilian sugarcane could dent global carbon dioxide emissions

 [go.igb.illinois.edu/BrazilCane](http://go.igb.illinois.edu/BrazilCane)

Vastly expanding sugarcane production in Brazil for conversion to ethanol could reduce current global carbon dioxide emissions by as much as 5.6 percent,

according to a report published in *Nature Climate Change*.

The study, led by Stephen Long (BSD/GEGC), Gutzsell Endowed Professor in Crop Sciences and Plant Biology, states this would require the conversion of hundreds of thousands of square miles—more than the combined land area of Texas and California—to sugarcane fields.

But this can be accomplished without impinging on environmentally sensitive areas in Brazil, while allowing for the expansion of other agricultural crops and human needs.

The research, which was supported by the DOE and EBI, relied on a new approach to modeling the precise behavior of sugarcane crops growing in regions that vary in soil composition, temperature, rainfall and numerous other parameters.

Amanda De Souza, a postdoctoral researcher and co-author of the study, said Brazil has already accomplished a lot with its sugarcane-to-ethanol industry. The study concluded that

expanding the industry further could “make a significant contribution to decarbonizing fuel,” according to Long.

**“This expansion does not have to stop at Brazil,” Long said. “Many acres that once grew sugarcane—from the Caribbean to Hawaii—lie idle today. Sugarcane-to-ethanol production would provide a use for this land again.”**

Crop Sciences and Plant Biology Professor Stephen P. Long and his colleagues calculated the environmental consequences of expanding Brazil’s use of sugarcane for biofuel production.



---

## NOVEMBER

### Cell phone software creates new possibilities for precision medicine



[go.igb.illinois.edu/COPDapp](http://go.igb.illinois.edu/COPDapp)

Professor of Medical Information Science Bruce Schatz (CGRH) and colleagues have been developing software for Android phones that uses the phone’s native motion sensor to predict a lung patient’s disease state. In a study published in *Telemedicine and e-Health*, they demonstrated that the software is now able to monitor a patient’s status while they perform everyday tasks outside of the hospital.

Traditionally, patients with respiratory conditions, including chronic obstructive pulmonary disease (COPD), can be assessed via several measures, with a simple breath test or a measure known as the six minute walk test. Schatz’s team had already developed and

tested software that can predict the result of either of these tests with high accuracy. **To quickly identify when a patient’s condition may be deteriorating or collect the volume of health data that a precision medicine effort would require, medical practitioners need an easier, more scalable way to monitor patients.**

Schatz’s team adapted the software to effectively monitor relevant data about gait during everyday life. In a clinical setting, a change in a healthy person’s gait might be related to lung function; in other settings, it might instead indicate common activities. Researchers improved their software’s ability to focus only on movements that occurred during intervals when walking was the only activity.

Schatz plans to continue expanding the functionality of this software to make it possible to collect much more robust data sets to further efforts in predictive or precision medicine.

From left, IGB Director Gene Robinson, postdoctoral researcher Arian Avalos, and Professor of Crop Sciences Matthew Hudson and their colleagues found genomic signatures associated with the evolution of gentle behavior in Puerto Rico's Africanized honey bees.



## Genomic study explores evolution of gentle 'killer bees' in Puerto Rico



[go.igb.illinois.edu/GentleBees](http://go.igb.illinois.edu/GentleBees)

A genomic study of Puerto Rico's Africanized honey bees—which are more docile than other so-called “killer bees”—revealed that they retain most of the genetic traits of their African honey bee ancestors, but that a few regions of their DNA have become more like those of European honey bees. According to findings published in *Nature Communications*, these changes likely contributed to the bees' rapid evolution toward gentleness in Puerto Rico, a change that occurred within 30 years.

Africanized honey bees arrived in Puerto Rico—most likely on a ship, by accident—in the 1990s, and within three decades had evolved into the gentle, yet hardy, Africanized bees that dominate the island today. To gain insight into how the bees became gentle, the researchers sequenced the genomes of 30 gentle Puerto Rican bees, 30 Africanized bees from Mexico and 30 European honey bees from central Illinois.

Illinois postdoctoral researcher Arian Avalos conducted the research with IGB Director and Swanlund Professor of Entomology Gene Robinson; crop sciences professor Matthew Hudson (CGRH/ GNDP); and Guojie Zhang and Hailin Pan of the Chinese Academy of Sciences. **The team discovered that, for the most part, the genomes of the gentle bees resembled those of their Africanized forebears. Specific regions of the DNA, however, had shifted in the gentle bees, reflecting more of their European heritage.** These regions appeared to be under “positive selection.” The scientists hypothesize that the bees evolved to be more docile because they lived on a densely populated island from which they could not easily escape. Humans likely eradicated the most aggressive bees, aiding their more docile counterparts.

The NSF, BGI and the University of Illinois supported this research.

## In microbe populations, bioengineers find balance of opposing genomic forces



[go.igb.illinois.edu/MicrobeForces](http://go.igb.illinois.edu/MicrobeForces)

Sergei Maslov (BCXT), a professor of bioengineering and physics, sees a “universe in a grain of sand.” His research seeks to explore that universe by focusing on the genomic diversity of its constituents: the millions of microbes that thrive and reproduce within it. His recent study published in *Genetics* examined the dynamics that govern this diversity by modeling the effects of several different factors on evolution of the genome sequence.

In an effort to understand how bacterial species form and what forces keep them coherent, Maslov questioned: within a universe of microbes, how does mutation—chance errors in genome sequence that expand the variation found within a strain—compare to the binding “gravitational force” of recombination? He and his coauthors set out to answer this question with the aid of the ever-growing

public database of bacterial genomic data. They developed a computational model that captured the basic elements of bacterial evolution: the existing level of genomic diversity between pairs of individuals within a population, the rate of chance mutations, and the capacity for recombination. The model quantified the relationships between all these factors as they influence genome sequence within a population of bacteria. The researchers found that the balance between these factors creates a fairly sharp division between two distinct states—metastability and divergence. Frequent recombination events can keep a population of bacteria in a metastable state, one in which speciation is unlikely to occur even over the course of many generations. A larger population in which the mutation rate can outweigh homogenizing effects of recombination will diverge quickly.

**By elucidating basic features of bacterial speciation, this work addresses fundamental questions about evolution and could eventually contribute to efforts to track and prevent the development of drug resistance or virulence in disease-causing pathogens.**



## Hacking evolution, screen technique may improve most widespread enzyme



[go.igb.illinois.edu/EnzymeScreen](http://go.igb.illinois.edu/EnzymeScreen)

Plants evolved over millions of years into an environment that has dramatically changed in the 150 years since the Industrial Revolution began. Carbon dioxide levels have increased by 50 percent and the average global temperature has increased by nearly 2 degrees Fahrenheit. While natural adaptation has been unable to keep up, scientists have developed tools to simulate millions of years of evolution in days to help plants adapt.

Researchers reported a novel screening strategy in the *Journal of Biological Chemistry* that has enabled them to identify, for the first time, a much more efficient form of Rubisco, the enzyme that catalyzes the first step of

fixing carbon dioxide en route to creating plant biomass in photosynthesis.

The research shows that Rubisco's efficiency and ability to differentiate carbon dioxide from oxygen can be improved. "Although the most abundant and arguably the most important enzyme on our planet, Rubisco may not have been evolution's finest moment. Rubisco evolved when oxygen was absent from the atmosphere, and as a result, it was not forced to learn to differentiate between life-sustaining carbon dioxide molecules and oxygen molecules that create a toxic compound that costs the planet energy to recycle," said Don Ort, Deputy Director of Realizing Increased Photosynthetic Efficiency (RIPE), which supported this work. Ort is a physiologist with the USDA/ARS Photosynthesis Research Unit and the Robert Emerson Professor of Plant Biology and Crop Sciences

The team tested 250,000 mutant Rubiscos from cyanobacteria in *E. coli* bacteria that was engineered so that their survival depends on the efficiency of the enzyme. **Eighteen Rubisco mutants survived the screen, and eleven were found to be much more efficient at fixing carbon dioxide. They found these mutations are localized to a specific, previously unexplored region of cyanobacterial Rubisco. Now they hope to make similar tweaks to improve Rubisco in crops and increase their growth and yield.**

## Study reveals how bacteria steal nutrients from human hosts



[go.igb.illinois.edu/NutrientTheft](http://go.igb.illinois.edu/NutrientTheft)

A study published in *mBio* exposes a zinc-import system in bacteria that could contribute to their ability to cause infection. The study looked at how the bacterium *Staphylococcus aureus*, which can infect virtually all of the tissues in the human body, competes with the immune system for the essential nutrient zinc.

To combat infection, the immune system hoards zinc and other critical nutrients in an effort to weaken the bacteria, which is also trying to obtain the metal away from the host.

Professor of Microbiology Thomas Kehl-Fie (MMG) and his colleagues discovered a new system that enables *S. aureus* to acquire zinc from the body. The discovery explains how *S. aureus* is able to grow well even in zinc-limited environments.

The system imports zinc into the bacteria even when the amount of zinc in the environment is extremely low. Even with the immune system acting in full-force against these bacteria, they can still obtain this essential nutrient in the human body.

**"This discovery not only means we know more about how these bacteria infect the human body, but could open up new ways to help fight infection of this type,"** Kehl-Fie said. "The continued emergence and spread of antibiotic resistance highlights the need for new therapeutics to treat bacterial infections."



Graduate student, Kyle Grim, left, and Thomas Kehl-Fie studied how bacteria compete for zinc in the human body.

## Four IGB researchers rank among world's most influential

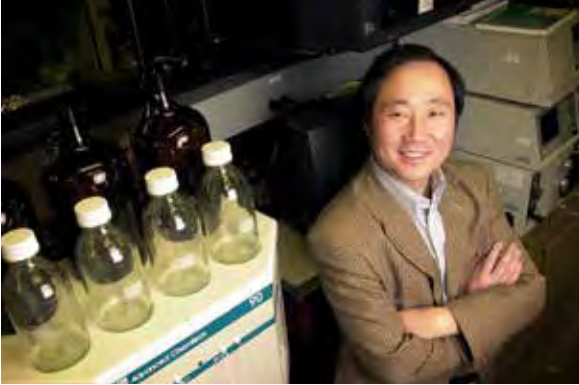
[go.igb.illinois.edu/HighlyCited17](http://go.igb.illinois.edu/HighlyCited17)

Four faculty members from the IGB were named to the 2017 Clarivate Analytics Highly Cited Researchers list.

**The list recognizes "leading researchers in the sciences and social sciences from around the world." It**



Clockwise: Crop Sciences and Plant Biology Professor Lisa Ainsworth, Crop Sciences and Plant Biology Professor Stephen P. Long, Psychology Professor Brent Roberts, and Chemistry Professor Yi Lu.



**is based on an analysis of journal article publication and citation data, an objective measure of a researcher’s influence, from 2005 to 2015.**

The highly cited IGB researchers include Crop Sciences and Plant Biology Professor Lisa Ainsworth (GEGC), Crop Sciences and Plant Biology Professor Stephen P. Long (BSD/GEGC), Chemistry Professor Yi Lu (BSD/ONC-PM), and Psychology Professor Brent Roberts (GNDP).

Ainsworth’s research focuses on plant mechanism, photosynthesis and molecular variation within species and how those factors contribute to plant responses to global change. A key goal of her work is to maximize crop production in the future.

Long is the Gutsell Endowed Professor in the departments of crop sciences and plant biology. He uses computational and experimental approaches to improve photosynthesis efficiency, and works to address the effects of climate change on crop yield.

Lu, the Jay and Ann Schenck Professor of Chemistry at Illinois, focuses on the design and engineering of metalloenzymes and their applications as biocatalysts in alternative energy applications and as sensors and imaging agents.

Roberts is a professor of psychology in the field of personality psychology. He studies continuity

and change in personality throughout adulthood, with an emphasis on understanding the factors that influence change.

### Theory suggests flexibility is at the heart of human intelligence

 | [go.igb.illinois.edu/IQflex](http://go.igb.illinois.edu/IQflex)

A theory published in *Trends in Cognitive Sciences* makes the case that the brain’s dynamic properties are the best predictors of intelligence in the human brain.

“When we say that someone is smart, we understand intuitively what that means,” said psychology professor Aron Barbey (GNDP), the author of the theory. “Usually, we’re referring to how good they are at making decisions and solving particular types of problems. But recently in neuroscience, there’s been a focus on understanding in biological terms how general intelligence arises.”

Research on general intelligence has studied two primary facets of intelligence—crystallized intelligence, the pathways that encode prior knowledge and experience, and fluid intelligence, flexible adaptive reasoning and problem-solving skills.

Although researchers have known that flexibility is an important characteristic of human brain function, only recently has the



idea emerged that flexibility provides the basis for human intelligence.

“General intelligence requires both the ability to flexibly reach nearby, easy-to-access states—to support crystallized intelligence—but also the ability to adapt and reach difficult-to-access states—to support fluid intelligence,” Barbey said.

**“What my colleagues and I have come to realize is that general intelligence does not originate from a single brain region or network. Emerging neuroscience evidence instead suggests that intelligence reflects the ability to flexibly transition between network states.”**

## Light green plants save nitrogen without sacrificing photosynthetic efficiency

 | [go.igb.illinois.edu/LightGreen](http://go.igb.illinois.edu/LightGreen)

A modeling study found that leaves with reduced chlorophyll content do not improve canopy-level photosynthesis, but instead conserve a significant amount of nitrogen that the plant might be able to reinvest to improve light use efficiency and increase yield.

Berkley Walker, an Alexander von Humboldt postdoctoral fellow at the University of Dusseldorf, led this work, which is supported by RIPE. Walker explained how leaves at the top of the canopy absorb a lot

of light, but they aren't efficient with that light energy, while leaves at the bottom of the canopy are very efficient.

Scientists have designed plants with light green leaves to allow more light to penetrate the crop canopy to increase photosynthesis and yield; however, models show these plants likely require less nitrogen and photosynthesis is hardly affected.

of light, but they aren't efficient with that light energy, while leaves at the bottom of the canopy are very efficient.

**“So, if you could just take some of that light that's being hogged up at the top, and move it down deeper in the canopy, theoretically, you'd have a more efficient canopy,” Walker said.**

As described in *Plant Physiology*, researchers tested this idea using a computer simulation incorporating data from nearly 70 varieties of soybeans with varying levels of chlorophyll from the USDA germplasm bank. They found that plants with 20 percent less chlorophyll theoretically require 9 percent less nitrogen with no penalty to carbon gain (biomass) and yield.

When the plants' chlorophyll was decreased, more light was lost to reflection, and the plant didn't get the full benefits of getting light deeper into the canopy where it could be absorbed, according to RIPE Deputy Director Don Ort (GEGC leader/BSD).

**Next, they are exploring if these nitrogen savings could be used to fix photosynthetic bottlenecks or increase light penetration into the canopy.**



## Cancer drug starts clinical trials in human brain cancer patients



[go.igb.illinois.edu/PAC1b](http://go.igb.illinois.edu/PAC1b)

**A drug that spurs cancer cells to self-destruct was cleared for use in a clinical trial of patients with anaplastic astrocytoma, a rare malignant brain tumor, and glioblastoma multiforme, an aggressive late-stage cancer of the brain.**

This clinical trial will determine if the experimental drug PAC-1 can be used safely in combination with temozolomide, a standard brain cancer chemotherapy drug.

Professor of Chemistry Paul Hergenrother (ACPP leader/MMG) discovered PAC-1's anticancer effects more than a decade ago. After tests in human cell lines and rodents proved promising, Hergenrother and Professor of Veterinary Clinical Medicine Timothy Fan (ACPP/ONC-PM) tested PAC-1 in pet dogs with a variety of naturally occurring cancers.

PAC-1 has been evaluated in pet dogs with naturally occurring osteosarcoma, lymphoma and, most recently, glioma—a brain cancer similar to glioblastoma in humans. The trials in dogs continue and have found PAC-1 to be safe, with few observable side effects apart from the occasional gastrointestinal distress.

So far, the clinical trials of PAC-1 alone have seen no significant side effects in humans. The team cannot report on clinical outcomes in a phase 1 clinical trial, as such trials are designed to measure safety, not efficacy. As with any investigational agent, determining the true safety and efficacy profile of PAC-1 will take several years of human clinical trials, which are currently taking place at three locations.



Veterinary oncologist Dr. Timothy Fan, top, Chemistry Professor Paul Hergenrother and their colleagues are testing the safety of a new cancer drug in a clinical trial for humans with late-stage brain cancer. The compound has worked well in canine patients with brain cancer, lymphoma and osteosarcoma.

Pretzel, above, had a brain tumor which shrank more than 40 percent after treatment in a clinical trial for dogs with glioma.



## Research expands potential and efficiency of metabolic engineering



[go.igb.illinois.edu/NewMeta](http://go.igb.illinois.edu/NewMeta)

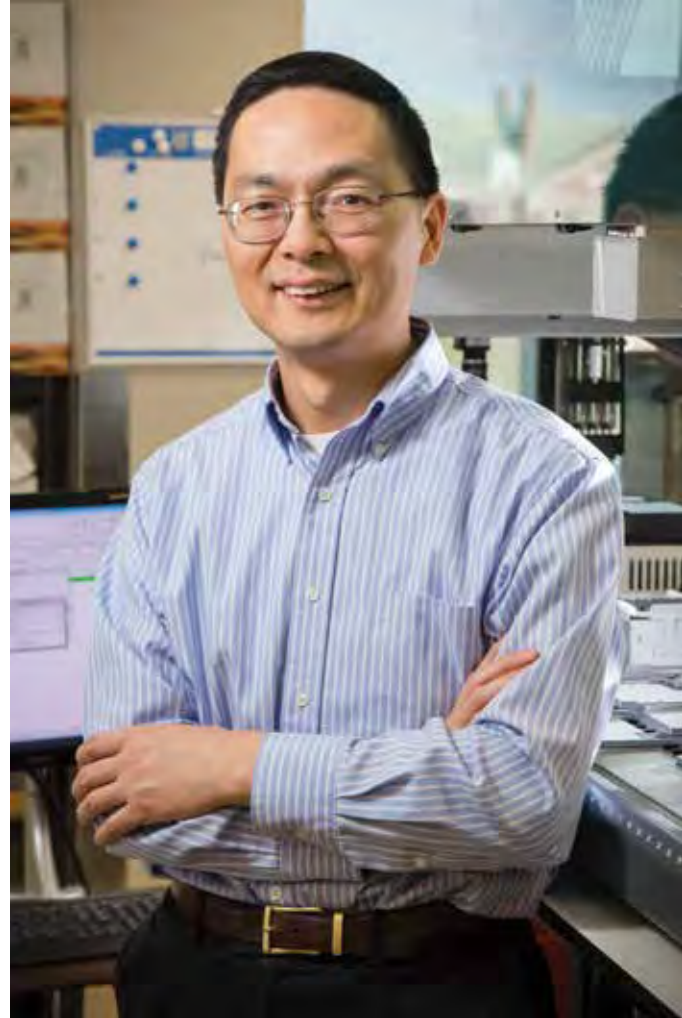
Researchers in the Biosystems Design theme have pursued new projects that could change the field of metabolic engineering.

Metabolic engineering involves modifying the gene networks within cells in order to increase an organism's ability to produce a specific substance. For example, cells can be made to create useful products such as chemicals and biofuels.

During the metabolic engineering process, gene expression is changed or deleted to modify the organism's genome. This involves modifying several targets in the genome, and these targets are usually tested individually in a series of time-consuming steps. Huimin Zhao (BSD leader/MMG), Steven L. Miller Chair of Chemical and Biomolecular Engineering, and his colleagues **created a method that combines all of these steps and executes them simultaneously, making the process faster and easier.**

Zhao is also leading a new research endeavor that aims to gain a better understanding of two unique non-model organisms that could be engineered to create specific products. **Understanding these non-model organisms means that there will be more choices for production hosts, and thus a greater variety of products that can be made in the future.**

Zhao and a group of co-investigators are doing this through a five-year, \$8.3 million grant from the DOE. In addition to learning more about the non-model organisms, they hope to develop tools that would reveal which genetic manipulations are useful for the production of chemicals and fuels in a more efficient manner.



Professor Huimin Zhao, Steven L. Miller Chair of Chemical and Biomolecular Engineering, leads the IGB's Biosystems Design research theme.



## Alumnus funds graduate students researching brain tissue cultures



[go.igb.illinois.edu/FisherFund](https://go.igb.illinois.edu/FisherFund)

Scott Fisher believes learning how to solve a problem can be as valuable as solving one. This belief is what drove him to create a fund that will support IGB research in the area of regenerative biology and tissue engineering, primarily in the RBTE theme.

The fund will aid the research needs of graduate students working in this area of study—specifically those who are developing technologies to culture brain tissue to learn about brain cancer, traumatic brain injuries and neurological disorders.

Fisher, an alumnus of the University of Illinois and a retired program manager at Ecolab, created the fund to give back to the university and to honor his late wife, Bonita J. Fisher, who

Illinois alumnus and former manager of Ecolab Scott Fisher (center) with graduate student Samantha Zambuto (left) and Research Scientist Sara Pedron Haba (right).

was diagnosed with multiple sclerosis. No cure for this disease exists, but Fisher believes that multidisciplinary research, like the research being done in IGB's RBTE theme, can eventually solve this and other difficult diseases.

Studying brain tissue is particularly difficult because it is unlike any other tissue in the body. Because of this, the tissue engineering community has struggled to build models of brain tissue. **The RBTE theme's goal is to build a model that will enable researchers to study tissue outside of the brain. Researchers in the theme are currently using a primary culture of brain tissue to study brain tumors.** The IGB research team receives the cancer cells directly from Mayo Clinic, a partner on this project.



## Viruses share genes with organisms across the tree of life



[go.igb.illinois.edu/ViralTree](http://go.igb.illinois.edu/ViralTree)

A study reported in *Frontiers in Microbiology* found that viruses share some genes exclusively with cells that are not their hosts. The research adds to the evidence that viruses swap genes with a variety of cellular organisms and are agents of diversity.

COMSATS Institute of Information Technology researcher Arshan Nasir led the new research with Gustavo Caetano-Anolles, a professor of crop sciences (GEGC), and Kyung Mo Kim, a senior scientist at the Korea Polar Research Institute.

The team used a bioinformatics approach to analyze the genomes of organisms and the viruses that infect them. They examined the functional components of proteins, which are called folds, and found hundreds of folds that are present across all superkingdoms of life and in all types of viruses. This suggests they came from an ancient ancestor of all life forms.

**Their data point to other mechanisms that allow viruses to exchange**

Professor of Crop Sciences Gustavo Caetano-Anolles and colleagues found evidence of gene sharing between viruses and organisms that are not their hosts.

**genetic material with cells. They also discovered a large subset of virus-specific protein folds that were not present in any cellular genomes, suggesting that viruses can create new genes and potentially transfer those genes to cellular organisms.**

The research was supported by the Higher Education Commission in Pakistan, the NSF, and the NIH.

## Team receives funding to study bacterial community dynamics



[go.igb.illinois.edu/MicrobialDynamics](http://go.igb.illinois.edu/MicrobialDynamics)

Bioengineering Assistant Professor Roy Dar (GNBP) is part of a multi-institutional research team that will study long-term microbial community dynamics with the help of a \$169,000 grant through Scialog: Molecules Come to Life, an initiative cosponsored by the Research Corporation for Science Advancement and the Gordon and Betty Moore Foundation.

The research team will work on establishing a spatially and temporally “tunable” microfluidic platform for studying the dynamics between two interacting bacteria populations in a biofilm. Their goal is to harness “quorum sensing,” or cell-to-cell signaling, abilities of the bacterium *Vibrio cholerae*.

Quorum sensing allows bacterial cells in a community to cooperate by synchronously expressing sets of genes in response to self-produced chemical signals. The *Vibrio*



Bioengineering  
Assistant Professor  
Roy Dar.

microbe can cause fatal disease by thriving in the human gut, and has recently been shown to kill adjacent competitor bacteria by piercing them with a toxin-tipped nanoweapon called a Type 6 Secretion System.

The researchers will create a microfluidic device and re-engineered *Vibrios* that activate genes for the nanoweapon only in response to quorum sensing signals that are made by competitors, rather than self-produced. They will also develop mathematical models to characterize the interactions occurring between the bacterial community members. **Because their work involves biofilms produced by a disease-causing microbe, this study could have important implications for industrial, environmental and human health issues.**

## Unsuspected flexibility offers new pathway to cancer drug development



[go.igb.illinois.edu/VesselGrowth](http://go.igb.illinois.edu/VesselGrowth)

A study led by Assistant Professor of Bioengineering Princess Imoukhuede (RBTE) has added a layer of nuance to our understanding of the signals that direct blood vessel growth.

Blood vessels are the supply lines of the human body, bringing nutrients and oxygen to cells and carrying away waste. Controlling the

growth of these supply lines can be an effective tactic to combat several different types of disorders, including cancer, stroke, and injury.

Imoukhuede's research team examined two distinct signaling systems that influence blood vessel growth and discovered that molecules from one system were able to interact with molecules from the other. The work was published in *Science Reports*.

Growth factors are molecules produced by the body that direct tissue growth and encourage cells to divide. They play a unique role in specific tissues and phases of development. Imoukhuede and her coauthors examined the strength of every combination of paired interactions between two specific growth factors and their families of receptors. They found that one growth factor could form a bond with one of the other growth factor's receptors, and they were surprised by the strength of that chemical attraction.

The group hopes that exploring these types of complexities in growth factor signaling will eventually contribute to the development of more effective therapies—either to promote signaling to aid recovery from conditions such as injury or stroke, or to inhibit it to block tumor growth.

Assistant Professor of Bioengineering Princess Imoukhuede is a member of the IGB's Regenerative Biology & Tissue Engineering theme.



# 4

---

IGB numbers,  
publications, and awards

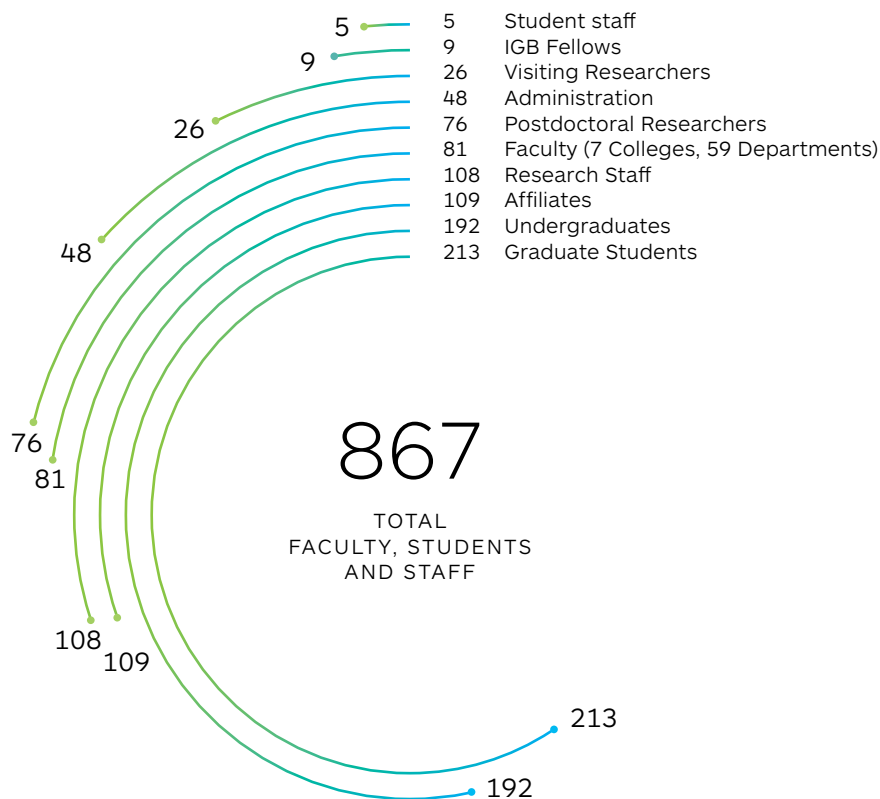
With each passing year, we remain grateful for the opportunities we have to delve deeper into the scientific questions that excite us, and to apply what we're learning to real-world problems. This section is another way of looking at what we have been up to and where we are going next.

Image: Awards from funding agencies, like the NSF grant that supports the Pollen Power summer camp for middle school girls, enable the IGB to broaden the reach of its community engagement.



IGB numbers,  
publications, and awards

People



FY17 Economic Development

10

Disclosures

12

Patent Applications

3

Licenses Optioned

3

Patents Issued

“Production of Xylitol from a Mixture of Hemicellulosic Sugars”  
Ryan Woodyer, Nikhil Unni Nair, **Huimin Zhao**, Michael Racine

“Separation Process of Oil and Sugars from Biomass”  
Haibo Huang, **Stephen Long, Vijay Singh**

“Procaspace Activating Compounds”  
Karson S. Putt, Jennifer M. Pearson, Grace Chen,  
**Paul Hergenrother**, Quinn P. Peterson, Diana C. West



## 2017 Publications

# 934

934 papers published  
4 *Science* and 3 *Nature*  
IGB faculty in bold

Born, D. A., Ulrich, E. C., Ju, K. S., Peck, S. C., **Van Der Donk, W. A.**, & Drennan, C. L. (2017). Structural basis for methylphosphonate biosynthesis. *Science*, 358(6368), 1336-1339. DOI: 10.1126/science.aao3435

Campbell-Staton, S. C., Cheviron, Z. A., Rochette, N., **Catchen, J.**, Losos, J. B., & Edwards, S. V. (2017). Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. *Science*, 357(6350), 495-498. DOI: 10.1126/science.aam5512

Grillo, A. S., SantaMaria, A. M., Kafina, M. D., Cioffi, A. G., Huston, N. C., Han, M., Seo, Y. A., Yien, Y. Y., Nardone, C., Menon, A. V., Fan, J., Svoboda, D. C., Anderson, J. B., Hong,

J. D., Nicolau, B. G., Subedi, K., Gewirth, A. A., Wessling-Resnick, M., Kim, J., Paw, B. H., **Burke, M. D.** (2017). Restored iron transport by a small molecule promotes absorption and hemoglobinization in animals. *Science*, 356(6338), 608-616. DOI: 10.1126/science.aah3862

**Robinson, G. E.**, & Barron, A. B. (2017). Epigenetics and the evolution of instincts: Instincts may evolve from learning and share the same cellular and molecular mechanisms. *Science*, 356(6333), 26-27. DOI: 10.1126/science.aam6142

4D Nucleome Network (2017). The 4D nucleome project. *Nature*, 549(7671), 219-226. DOI: 10.1038/nature23884

**O'Dwyer, J. P.** (2017). Ecology: Contests between species aid biodiversity. *Nature*, 548(7666), 166-167. DOI: 10.1038/nature23103

Erclik, T., **Li, X.**, Courgeon, M., Bertet, C., Chen, Z., Baumert, R., Ng, J., Koo, C., Arain, U., Behnia, R., Del Valle Rodriguez, A., Senderowicz, L., Negre, N., White, K. P., Desplan, C. (2017). Integration of temporal and spatial patterning generates neural diversity. *Nature*, 541(7637), 365-370. DOI: 10.1038/nature20794

## IGB Core Facilities Usage

# 121

Research Groups

# 291

Active Users

IGB numbers,  
publications, and awards  
continued

## Grant Funding

\$20,773,359 FY17

<b>NIH</b>	\$9,237,707
<b>NSF</b>	\$2,637,357
<b>USDA</b>	\$28,000
<b>UCB/BP</b>	\$554,134
<b>Other</b>	\$8,316,161

\$45,759,904 FY18 projected

<b>DOE</b>	\$19,427,601
<b>NIH</b>	\$8,479,967
<b>NSF</b>	\$1,036,981
<b>UCB/BP</b>	\$326,999
<b>UCB/Shell Oil</b>	\$1,709,720
<b>Other</b>	\$14,778,636

## Outreach

50+ events

12,000+ people

### World of Genomics

A 3-day long event at the Chicago Field Museum with hands-on activities for the public featuring research in health, technology and the environment.

### Genome Day

Community event with learning activities for all ages that present concepts in environment, ecology, energy use, DNA and evolution.

### Art of Science

New art installations in Urbana, MATTER Chicago, Springfield, Bloomington and Harold Washington Library.

### After School Visits and Field Trips

Hands-on activities with schools in Champaign, Urbana, Chicago and Rantoul.

### Genomics for™ Workshops

Educational programs that target specific groups exploring basic science and genomics concepts.

### Public Lectures

Science talks around Champaign and Urbana featuring a lecture from world-renowned human geneticist Mary-Claire King.

### Summer internship for Indigenous peoples in Genomics (SING)

A workshop to discuss the ethical uses of genomics as a tool for indigenous peoples' communities.

### Pollen Power

A summer camp for middle school girls to learn about pollen, plant biology and climate change.

### IGB Training

Training for IGB students and postdoctoral researchers including lectures on entrepreneurship and participation in the iGEM international competition.

## Awards

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

**Rashid Bashir**, Bioengineering Professor (RBTE) received the 2018 Robert A. Pritzker Distinguished Lecture Award from the Biomedical Engineering Society, and received a Campus Award for Excellence in Faculty Leadership.

**Carla Cáceres**, Professor of Animal Biology (IGOH) elected a 2017 Fellow of the American Association for the Advancement of Science.

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

**John Cronan**, Professor and Head of Microbiology and Professor of Biochemistry (MMG) elected to the National Academy of Sciences.

**Brian Cunningham**, Professor of Electrical and Computer Engineering (ONC-PM Theme leader/MMG) appointed a Center for Advanced Study

(CAS) Associate, Class of 2018-2019.

**Sharon Donovan**, Professor of Nutrition and Melissa M. Noel Endowed Chair in Nutrition and Health (CGRH/ MMG) elected to the National Academy of Medicine.

**John Gerlt**, Gutsell Professor of Biochemistry (MMG) awarded the 2017 Gordon Hammes Lectureship, sponsored jointly by Biochemistry and the ACS Division of Biological Chemistry.

**Paul Hergenrother**, Professor of Chemistry (ACPP leader) received the Arthur C. Cope Scholar Award by the American Chemistry Society.

**Hannah Holscher**, Assistant Professor of Nutrition (MME) received the New Innovator in Food and Agriculture Research award from the Foundation for Food and Agriculture Research.

**Princess Imoukhuede**, Assistant Professor of Bioengineering (RBTE) received a National Science Foundation Faculty Early Career Development Program CAREER Award.

**Thomas Kehl-Fie**, Assistant Professor of Microbiology (MMG) named a 2017 Vallee Scholar by the Vallee Foundation.

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

**Hyunjoon Kong**, Professor and Centennial Scholar in Chemical and Biomolecular Engineering (RBTE) named an American Institute for Medical and Biological Engineering Fellow.

**Stephen Long**, Gutsell Endowed Professor in the Departments of Crop Sciences and Plant Biology (BSD/GEGC) appointed the Newton Abraham Visiting Professorship in the Department of Plant Sciences at the University of Oxford, United Kingdom.

**Zeynep Madak-Erdogan**, Assistant Professor of Nutrition (ONC-PM) awarded a 2017-18 NCSA Faculty Fellowship.

**Ruby Mendenhall**, Associate Professor in Sociology, African American Studies, Urban and Regional Planning, and Social Work

---

IGB numbers,  
publications, and awards  
continued

(CGRH/GNDP) awarded a 2017-18 NCSA Faculty Fellowship, and received the Black Metropolis Research Consortium Fellowship, sponsored by the Melon Foundation.

**Jeffrey Moore**, Murchison-Mallory Professor of Chemistry and Professor of Materials Science and Engineering (BSD) elected to the National Academy of Sciences.

**Donald Ort**, Robert Emerson Professor of Plant Biology, USDA/ARS Photosynthesis Research Unit and Adjunct Professor of Crop Sciences (GEGC leader/BSD) elected to the National Academy of Sciences.

**Gene Robinson** (Director) appointed member of the Convergence Advisory Group of the National Academies of Sciences, Engineering, and Medicine.

**Rachel Smith-Bolton**, Assistant Professor of Cell and Developmental Biology (GNDP/RBTE) named an I. C. Gunsalus Scholar in the College of Liberal Arts and Sciences.

**Rebecca Stumpf**, Associate Professor of Anthropology (BCXT/CGRH/IGOH) appointed a Center for Advanced Study

(CAS) Associate, Class of 2018-2019, and received a Campus Award for Excellence in Undergraduate Teaching.

**Jonathan Sweedler**, James R. Eiszner Family Endowed Chair in Chemistry (BSD/MMG) named to the 2017 "Magnificent Tens" Power List by The Analytical Scientist magazine.

**Andrew Suarez**, Professor of Animal Biology (GNDP) received a Campus Award for Excellence in Undergraduate Teaching.

**Monica Uddin**, Associate Professor of Psychology (CGRH) named a Richard and Margaret Romano Professional.

**Tandy Warnow**, Founder Professor of Bioengineering and Computer Science (BCXT/CGRH) elected a 2017 Fellow of the International Society for Computational Biology.

**Rachel Whitaker**, Associate Professor of Microbiology (IGOH leader/BCXT) received an Allen Distinguished Investigator award.

**Dave Zhao**, Assistant Professor of Statistics (CGRH/GNDP) named a recipient of the Lincoln Excellence for Assistant Professors award by the College of Liberal Arts & Sciences.

**Huimin Zhao**, Steven L. Miller Chair in Chemical and Biomolecular Engineering (BSD leader/MMG) selected as the 2018 Awardee for the Marvin Johnson Award by the Biochemical Technology Division of the American Chemical Society, and received the 2017 Biotechnology Progress Award for Excellence in Biological Engineering Publication by the Society for Biological Engineering.

---

## Giving and Donor Roll

July 1 2016 – June 30, 2017, including corporate gifts related to World of Genomics.

Abbott	Illinois State Beekeepers Association	California, Inc.
Abbvie Inc.	John Wiley & Sons Ltd	Renaissance Charitable Foundation, Inc.
American Society of Plant Biologists	Marsha and Dale Johnston	Julia and Gene Robinson
Annual Reviews	Jay and Rosalyn Kesan	Schwab Charitable Fund
Bill & Melinda Gates Foundation	Barbara and Charles* Kucera	Thomas and Carol Seery David and Jan Sholem
Isaac Cann and Tae Hosotani	Andrew Leakey and Elizabeth Ainsworth	Simons Foundation
Sarah and Steve Case	Life Sciences Research Foundation	Mark Taylor
Cystic Fibrosis Foundation	George and Harriette* Lewin	Regina Taylor
Walter Donovan and Marilyn Lang	Martha and Joaquin* Loustaunau	Tracy BioConsulting LLC
Francis and Carol Egan	Kenneth Luehrsen	Mark Tracy and Wendy Putnam
Elanco	Melissa McKillip	Nicholas Vasi and Heidi Imker
Eli Lilly & Company	Diane and Paul* Mortensen	Ursula Melissa Vera
Scott and Bonita* Fisher	National Aeronautics and Space Administration	Daniel Wolf
Kathy Fosnaugh and John Commeree	Opentrons	Jerrold and Carol Zar
Friedrich-Alexander-University Erlangen-Nuremberg	Don and Sara Ort	ZEISS
Illinois Soybean Association	Pacific Biosciences of	* Deceased

---

## Credits

**Managing Editor**  
Nicholas Vasi

**Design**  
Mirhee Lee

**Writing**  
Claudia Lutz and Emily Scott

**Printing**  
Curtis 1000

*Writing Contributors: Steph Adams, Sarah Banducci, Claire Benjamin, Jordana Cepelewicz, Department of Bioengineering, Dave Evensen, Sharita Forrest, Olivia Harris, Tony Mancuso, Kathryne Metcalf, Laura Schmitt, Serina Tajula, Samantha Jones Toal, Gregory Toreev, Liz Ahlberg Touchstone, Nicholas Vasi, Diana Yates, Lois Yoksoolian*

*Images contributors: Mark Abordo, Steph Adams, Claire Benjamin, AJ Christensen, College of Engineering, Department of Bioengineering, Noah Dibert, Kathryn Faith, Don Hamerman, Seth Lowe, NASA, Jennifer Oosthuizen, Gabriel Popescu, Steven O. Shattuck, L. Brian Stauffer*



UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN  
CARL R. WOESE INSTITUTE FOR GENOMIC BIOLOGY

Where science meets society  
[igb.illinois.edu](http://igb.illinois.edu)