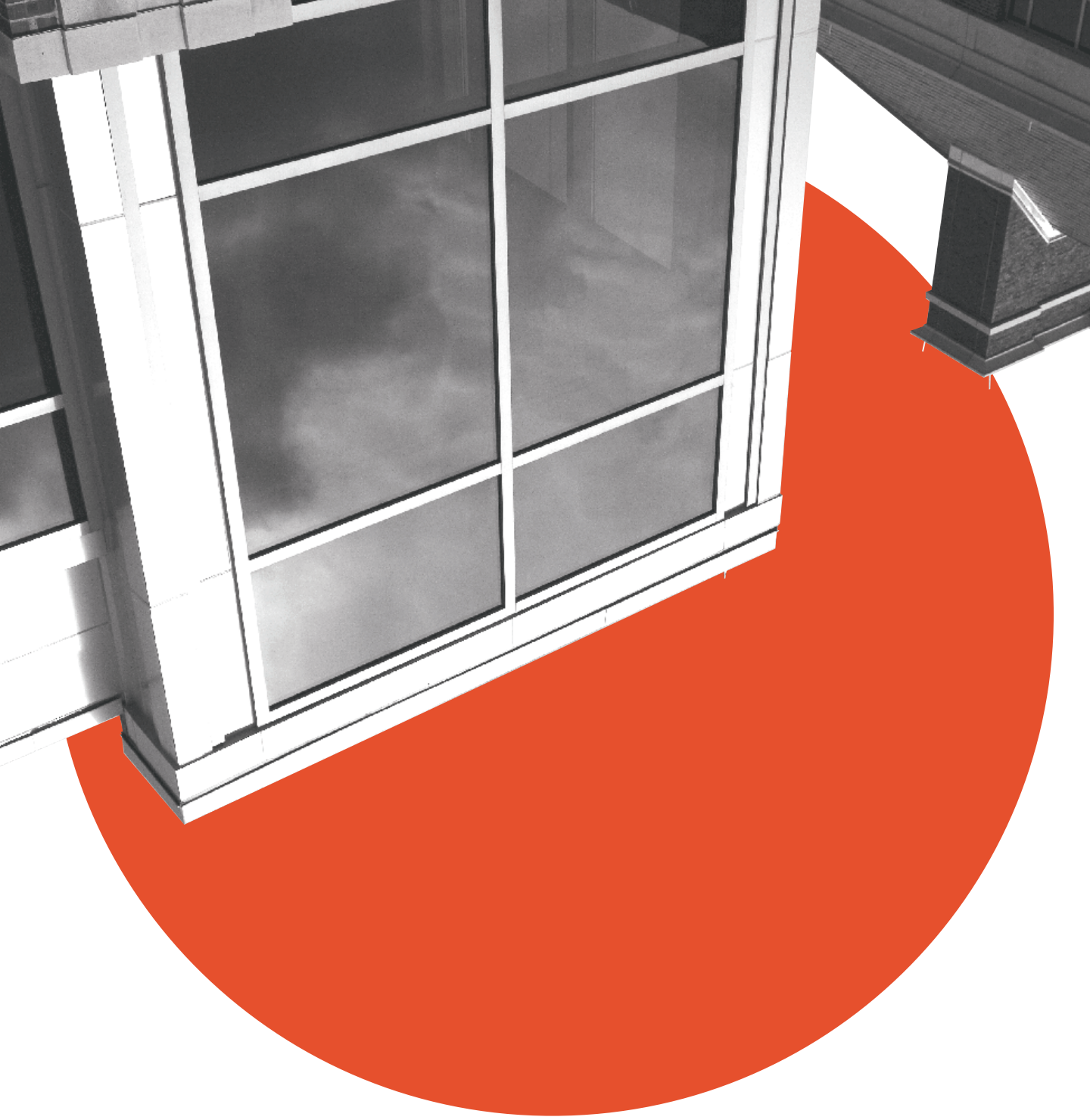




Science is here.

2025 Annual Report

Carl R. Woese

Institute for Genomic Biology

Message from the Director

01

About the IGB

04

IGB Stories from 2025

06

Evolving
Ecosystems

08

Growing
Efficiency

24

Tracing Pathways to
Treatment

38

Delivering on
Better Health

54

Designing Stronger
Systems

70

FY25 IGB Numbers

86

Credits

97

Acronyms

Beckman: Beckman Institute
for Advanced Science and
Technology

DOD: Department of Defense

DOE: Department of Energy

NCSA: National Center for
Supercomputing Applications

NIH: National Institutes of Health

NSF: National Science Foundation

USDA: U.S. Department of
Agriculture



Modern scientific institutions communicate on the timescale of research.

Each new grant announcement represents the inception of a project; each new publication represents the culmination of a project. These are important milestones to recognize, and talking about them invites collaborators, stakeholders, and the public into the research process.



But when we tell these discrete stories of research, we can sometimes lose sight of the longer chronicle of science. The Carl R. Woese Institute for Genomic Biology was built around overarching research goals; themes are brought together by the scale and importance of their aims. Securing the food supply of a growing world population, curing intractable cancers, or reinventing the way biological laboratories work are not efforts that can be supported by a single five-year grant or described in a single publication. Because of this, their progress may sometimes feel slow or uncertain. **These quiet times represent months and years of steady and careful work before the next breakthrough.**

In this year's annual report, we are shining a light on these longer arcs of science. Each section introduces one of our research areas, then follows the trajectory of one particular strand of work within that area. Considering the stories

that come after, of research milestones reached this year, it is inspiring to remember that each is one step in its own timeline of scientific progress.

Viewing our work in this way also allows us to appreciate the resilience of the scientific process. A research project that spans decades will inevitably meet setbacks in addition to successes. To achieve the progress we share here – the opening of a first-of-its-kind biological foundry, the establishment of a robust and versatile method for disease detection, insight into the mitigation of an environmental toxin's impacts – our members moved forward in the face of funding challenges and complex findings. Looking even further back in time, each of these projects shows itself to be grounded in earlier efforts that were similarly driven by pursuit of truth and commitment to advancing the communities we all share.

We cannot always live within the long-term view. Each new

year brings changes, both challenges and opportunities, that we face in the moment. This is particularly true for me this year; after 15 years leading the IGB, I have made the decision to step down as director in order to serve as CEO of the Discovery Partners Institute. DPI is a campus institute whose mission is on a similar grand scale to the IGB's. It aims to increase the impact of our university in Chicago through innovative programs in research, workforce development, economic development, and public engagement that focus on the application of artificial intelligence to science, technology, and society.

While I am excited for the challenges and opportunities this new position will bring, it has been the high point of my career to serve as director of the IGB. Our membership – faculty, staff, and students – has always worked hard to help IGB achieve great success and impact.

**As we move
forward under new
leadership, together
with the community
with which we are
inextricably connected,
we are also continuing
to write the chronicles
of genomic biology and
all that it can do
for society.**



A handwritten signature in black ink, reading "Gene E. Robinson". The signature is fluid and cursive, written across the bottom of the orange semi-circle.

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

About the IGB



Research Themes

Anticancer Discovery from Pets to People (ACPP) provides successful anticancer therapies in dogs and cats that translate to clinical trials in human subjects.

Biosystems Design (BSD) engineers microorganisms and plants to help overcome hurdles in health and sustainability.

Center for Artificial Intelligence and Modeling (CAIM) aims to unravel complicated scientific processes using modeling and machine learning.

Center for Genomic Diagnostics (CGD) employs new technologies to diagnose and treat diseases at a lower cost.

Center for Indigenous Science (CIS) uses Indigenous Science frameworks to provide alternative scientific models, promoting research that is ethical, sustainable, and community-focused.

Crops And Microbes for BioEconomy Resilience and Sustainability (CAMBERS) re-designs crops, microbes and ecosystems to produce next-generation biofuels and bioproducts.

Environmental Impact on Reproductive Health (EIRH) explores the effects of environment, diet, and stress on reproductive health and fertility.

Gene Networks in Neural and Developmental Plasticity (GNDP) uses gene expression to explain why animals are highly diverse, even though the

fundamentals are conserved across species.

Genomic Security and Privacy (GSP) studies advancing technologies with the aim of protecting the privacy and security of genomic information.

Infection Genomics for One Health (IGOH) works to describe microbial communities and their genes across different natural and man-made environments.

Microbiome Metabolic Engineering (MME) seeks to understand the positive effects of the microbiome on human health and how harmful environmental factors reduce those effects.

Mining for anti-infectious Molecules from Genomes (MMG) identifies undiscovered microbial sources with medical potential for new antibiotics and other beneficial drugs.

Multi-Cellular Engineered Living Systems (M-CELS) creates machines made of living cells that could serve as a solution to challenging real-world problems.

Photosynthesis and Food Security (PFS) develops new crops and management methods to maintain agricultural ecosystems in the face of a changing climate.

Regenerative Biology and Tissue Engineering (RBTE) studies organ regeneration techniques in animals and aims to translate these to humans.

the power of genomics for the improvement and sustainable use of biodiversity across Africa.

Biohub employs AI-powered biology to study how cells operate and organize to understand why disease happens, and how to correct it.

High Performance Biological Computing (HPCBio) supplies infrastructure, user support, training, and R&D capability in computational genomics to the Illinois research community.

Microbial Systems Initiative (MSI) addresses critical problems in health, agriculture, and energy while building collaboration across disciplines.

NSF Illinois Biofoundry (iBioFoundry) develops research infrastructure integrating AI/ML, robotic automation, and synthetic biology to democratize access to high-throughput autonomous experimentation.

Personalized Nutrition Initiative (PNI) facilitates transdisciplinary collaborative efforts across campus to answer fundamental questions regarding how nutrition modulates health and disease, translating to clinical care.

Strategic Partners

African Biogenome Project (AfricaBP) is a coordinated pan-African effort to harness

IGB Stories from

20

Leading edge (*noun*): The unprotected edge of a roof, floor, or other walking-working surface that is under construction. The leading edge changes location as work on the surface progresses.

At the IGB, we work on leading edges of genomic research. Each new project adds to our basic knowledge and pushes innovation toward new heights. We often focus on reporting our work from this forward perspective. We look to future opportunities that are exciting and too novel to be certain. Here, we are expanding our view to take in the stable foundation that many years of steady work have built.







Evolving Ecosystems

Human societies around the globe have elaborated and expanded so much that we often think of them as displacing the environment. In reality, we remain an inseparable part of the ecosystem even as we reshape it through our activities. From towering trees and wild and domestic animals to microbes more numerous than stars in our galaxy, we are interconnected with a vast array of coinhabitants on Earth.

The study of biology began with the desire to appreciate the diversity of life and the complexity of its systems. It continues with the increasingly pressing aim to remake our societies to be sustainable for every type of organism, including humans. How have our previous activities impacted the environment, including in ways that were neither intended nor suspected? Each new decade of research has uncovered new ecological considerations with origins in the past. Our growing knowledge grants the capability to set a better course for the future.



Can collective action reverse a chemical crisis?

'17

The countless varieties of organisms found in any ecosystem are tied together by their need for water. Water is at once a vital nutrient and a vehicle that carries away waste, a dual role that amplifies the environmental impacts of modern human activities.

Almost three decades ago, a landmark court ruling helped to bring a particular class of industrial waste to public and scientific attention. Per- and polyfluoroalkyl substances, a category of compounds referred to as PFAS, are noteworthy for their stability and longevity. These chemical properties led to their use in nonstick coatings, fabric, insulation, and fire suppressants. Their ubiquity in manufacturing led to the discovery of their toxicity; a finding that is elevated by their persistent and pervasive presence into a quiet health and environmental crisis.

Early epidemiological studies by multiple groups around the country demonstrated the cancer-causing effects of PFAS exposure through their presence in the water supply, particularly near industrial sites. However, the biological mechanisms by which PFAS promote cancers remain unclear. When Joseph Irudayaraj arrived at Illinois, he brought with him a determination to work via multiple collaborations and approaches to discover how PFAS spread through the water system and harm people who consume them.



'20

In a cluster of publications, Irudayaraj's research team focused in on a potential explanation for the carcinogenic activity of PFAS: studies in multiple types of tissues suggested that PFAS exposure resulted in epigenetic changes rather than sequence changes to genomic DNA. When the researchers examined the distribution of methyl groups,

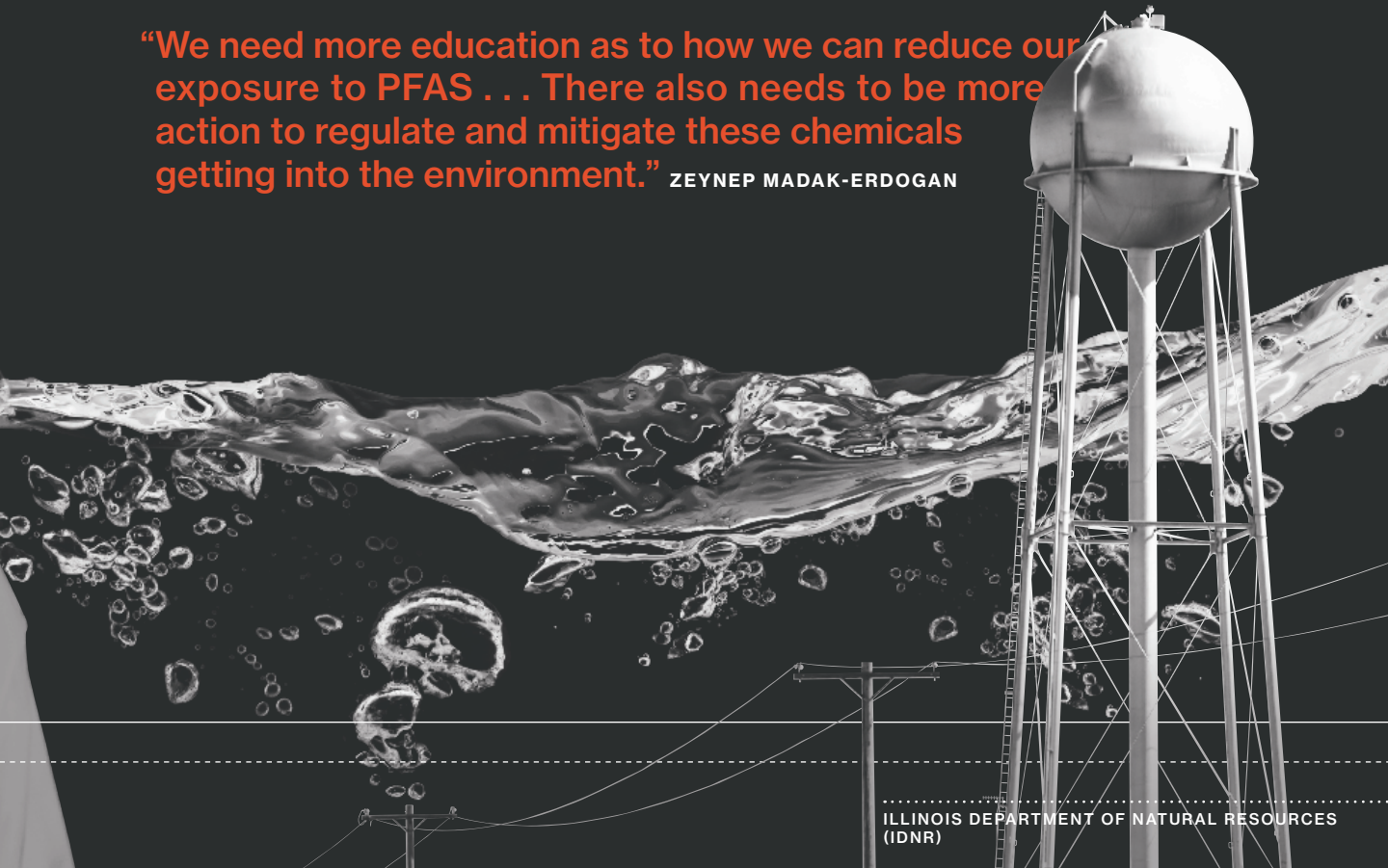
small chemical tags on the DNA strand that change how available a sequence is to be transcribed into RNA, they found that exposed cells had a different methylation pattern than unexposed cells.

These findings fit with similar results from other institutions, pointing to a hypothesis for the role of PFAS in cancer risk – PFAS exposure might reduce overall DNA methylation in tissues throughout the body, leading to atypical patterns of gene activity resembling those found in some cancers.

'21

A team led by Zeynep Madak-Erdogan, Michael Spinella, and Irudayaraj continued to work the problem of PFAS' toxicity from the clinical side. The carcinogenic activity of these compounds is difficult to determine via epidemiological studies in part because so many different factors influence cancer risk. Previous studies had nonetheless provided strong evidence for an association between exposure and the occurrence of prostate cancer. The researchers found that in a mouse model study of prostate cancer, PFAS altered cell energy usage, enabling treated cells to proliferate at three times the rate of nonexposed cells. When exposure was combined with a high-calorie diet, the effect of PFAS exposure on tumor growth was heightened still further.

"We need more education as to how we can reduce our exposure to PFAS . . . There also needs to be more action to regulate and mitigate these chemicals getting into the environment." ZEYNEP MADAK-ERDOGAN



'23

PFAS' deleterious effects are made all the more concerning by their persistence in the environment. The molecular stability that made them valuable accentuates their threat to health. A separate arm of research at Illinois is addressing this ecological challenge with chemistry. Xiao Su, Diwakar Shukla, and their colleagues combined laboratory testing and computer simulations to help design an electrode able to attract and capture a range of PFAS from environmental waters. Research continues to develop this technology's capability to mitigate PFAS.

'24

Meanwhile, Madak-Erdogan, Spinella, and Irudayaraj were still working to trace a path from PFAS exposure to tumor formation and growth. Just as in their mouse models of prostate cancer, they documented testicular cancer cell and tumor growth in response to dosing with PFAS – the first study to demonstrate this causal link.

The hypothesized connection between PFAS and aberrant DNA

methylation tied this work to a decades-long focus on testicular cancer in Spinella's laboratory. This form of cancer is closely associated with both environmental PFAS exposure and distinct patterns of DNA methylation. The 2024 publication added yet more evidence for PFAS' carcinogenic activity via epigenetic changes; in the testicular tumor cells, PFAS altered gene activity related to DNA methylation.

“By showing that PFAS can induce specific epigenetic changes, we provide evidence that long-term exposure from drinking water, food and consumer products could have lasting health consequences.” JOSEPH IRUDAYARAJ

'25

With evidence accumulating that PFAS acts through epigenetic changes to promote cancer, Irudayaraj and his team asked whether those changes could be more specifically catalogued and – in a step toward future medical interventions – whether they could be reversed. They discovered an array

of specific genes whose activity was disrupted by PFAS-related methylation changes in lab-grown kidney cells. Using a version of the gene editing tool CRISPR that is able to add or remove methyl groups from DNA, they successfully reversed those changes and restored normal functions in treated cells.

Elucidating the deleterious effects of PFAS is moving us closer to the capability to mitigate their impact in the body and their presence in waterways around the world. It can be overwhelming to consider that this is just one front of the war we are waging on behalf of the global ecosystem we have altered so significantly, yet cannot live without. This is a fight for which centuries of scientific inquiry have equipped us. If we keep moving forward together, we can accomplish a great deal.



People Mentioned

Joseph Irudayaraj (CGD/EIRH), bioengineering; **Zeynep Madak-Erdogan** (CGD/EIRH/GSP), food science and human nutrition; **Michael Spinella** (ACPP/EIRH), veterinary clinical medicine

People Involved

Younan Adam, Saeed Ahmad, Ahmed Balboula (University of Missouri), Raya Boyd, Johannes Elbert, Muhammed Fayyaz, Zeeshan Fazal, Jianan Feng, Sarah Freemantle, Wen-Yang Hu (University of Illinois Chicago), Ozan Berk Imir, Joseph Irudayaraj, Musarrat Jabeen, Tor Jensen, Samantha Johnson, Alanna Zoe Kaminsky, Michael La Frano, Jiho Lee, Mindy Lin, Wenjie Liu, Yu-Jeh Liu, Zeynep Madak-Erdogan, Christine Powell, Aashna Prakash, Gail Prins (University of Illinois Chicago), Huanyu Qiao, Faizan Rashid, Brayden Rennels, Anaira Román Santiago, Arshveer Sachdeva, Mia Sands, Doha Shokry, Diwakar Shukla, Ratnakar Singh, Edgar Soto-Moreno (University of Missouri), Michael Spinella, Xiao Su, Yi Wen, Song Yin, Xing Zhang, Qian-Ying Zuo

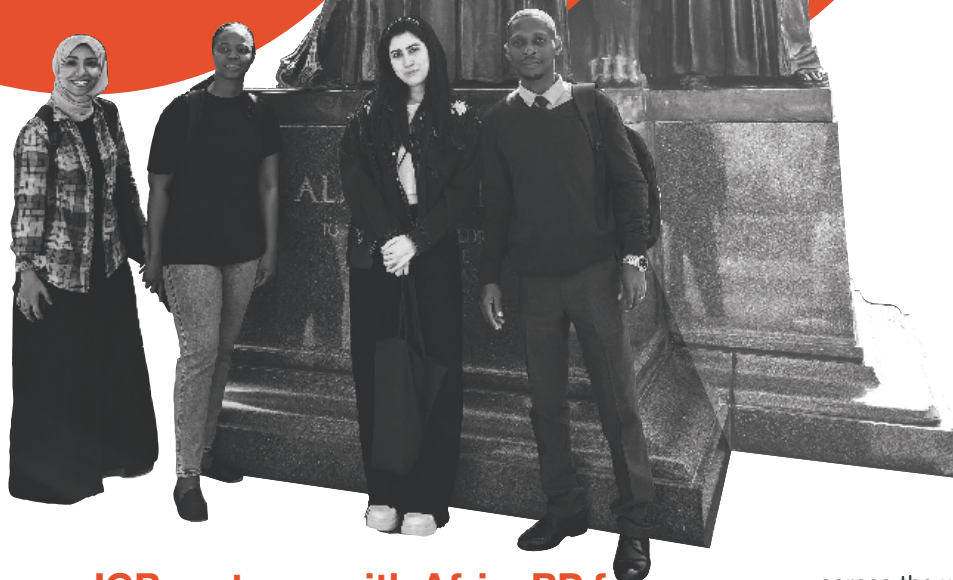
Publications

Liu, et al., *Food Chem. Toxicol.* **141**, 2020; Rashid, et al., *Toxics* **8** (3), 2020; Jabeen, et al., *Toxics* **8** (112), 2020; Imir, et al., *Nutrients* **13** (11), 2021; Feng, et al., *Cell Prolif.* **56**, 2022; Boyd, et al., *Toxics* **12** (4), 2024; Román Santiago, et al., *J. Am. Chem. Soc.* **145** (17), 2023; Boyd, et al., *Environ. Toxicol. Pharmacol.* **120**, 2025; Sands, et al., *Environ. Health* **3** (11), 2025



Briefs

Evolving Ecosystems



IGB partners with AfricaBP for inaugural cohort of leadership program

People Mentioned

Sarah Schwartz, external relations coordinator

Tracy Parish, director of external relations and strategic partnerships

Victor Ezebuiro, University of Port Harcourt, Nigeria

Ichrak Hayah, Mohammed V University

Tshepo Mafokwane, University of South Africa

Shaimaa Reda, Nile University

Huimin Zhao (BSD leader/CAMBERS/CGD/MMG), chemical and biomolecular engineering

Xing Wang (CGD), bioengineering

Laurie Leonelli (PFS), agricultural and biological engineering

The IGB hosted its first scholar cohort as part of the African Biodiversity Fellowship for Emerging Genomics Leaders program. The comprehensive leadership program, aimed to train Africa's next generation of leaders in genomics and bioinformatics, was organized in partnership with the African BioGenome Project. AfricaBP was launched in 2021 as a coordinated effort to harness the power of genomics for the improvement and sustainable use of biodiversity across the African continent.

For the program's first year, four scientists traveled

across the world to Illinois to take part in a four-month international exchange at the IGB, after completing a month-long internship or residency at an African institution. In addition to attending professional development workshops, each scholar worked within one of IGB's research themes and was matched with a group that fit their interests.

"Our partnership with AfricaBP is designed to give early career scientists from across the African continent an opportunity to learn new skills, including team science best practices, and build their professional networks," said Sarah Schwartz, who led the program with Tracy Parish.

Scientists and faith leaders discuss evolution at Genomics for Faith

People mentioned

Becky Fuller (GNBP), evolution, ecology, and behavior
John MacLean, english
Todd Daly, Urbana Theological Society
Susan Barreto, Lutheran Alliance for Faith, Science and Technology
Amy Felty, Bahá'í Faith
Tim Bossenbroek, Hessel Park Church
Dan Urban, regional outreach program manager
Claudia Lutz, assistant director of outreach

Supported by

Wayfarer Foundation

For the sixth installment of the IGB's Genomics for Faith workshop series, scientists and faith leaders explored the theory of evolution, how faith traditions have interacted with this concept from its proposal to the present day, and sources of misunderstanding that have inhibited trust among religious and scientific groups.

This was followed by group discussion facilitated by scientists and local faith leaders, including Dan Urban, Becky Fuller, John MacLean, Todd Daly, Susan Barreto, Amy Felty, and Tim Bossenbroek.

Kicking off the workshop, Urban, whose scientific background is in evolutionary developmental biology, explained the history of the study of evolution. In the conversation that followed, workshop participants examined how a lack of common definitions have helped or hindered communication among science and faith practitioners. This discussion of language by Darwin and his scientific successors emphasized the importance of open dialogues both historically and today.

"One valuable insight I gained in listening to participants discuss this topic is the way scientific language choices have sometimes aided acceptance of evolution, and at other times inhibited it," Claudia Lutz said. "While these historical misunderstandings feel daunting, it is helpful to recognize that faith and science communities are not separate, but overlapping, with individuals who exemplify different ways of bridging the two."

Exploring the gut's potential to treat disease

Our microbiome is critical to our overall health, yet scientists have only recently begun to understand how we are affected by the microorganisms in our gut, influencing our digestion, immune system, and even mental health. What if we recruit these microbes for even more specific roles in our health? A team of researchers is looking more closely at the microbiome's potential to produce medical treatments from inside the body.

People Mentioned

Shannon Sirk (MME/MMG), bioengineering

Supported by

NIH

Their work, which was published in *Nature Communications*, looked at the drug-production capabilities of *Bacteroides*, some of the most abundant bacteria in our gut. However, we still lack genetic tools to easily develop new strains.

Shannon Sirk's lab has developed a system to enable *Bacteroides* to make proteins they don't normally produce and efficiently guide those proteins into the gut. These bacteria naturally produce peptide signals to communicate with nearby cells; the research team designed a gene that fuses one of these peptide sequences with that of a therapeutic protein.

In order to control production of this hybrid protein, the

researchers also added a genetic sequence that acts as a switch: the protein will be produced when the bacteria are fed a particular "inducer" compound. If the system proves to be safe and effective within the human gut, it holds immense promise to improve the lives of individuals with chronic gastrointestinal diseases such as inflammatory bowel disease.



Genomic survey uncovers evolutionary origins of secretoglobins

Twenty-five years after their classification, a super family of proteins called secretoglobins remain a biological mystery. Secretoglobins were grouped together by the similarity of their gene sequence, and with the hope that studying them together might eventually reveal their unknown functions within the body. Researchers recently dived into the evolutionary origins of these genes to learn more.

People Mentioned

Christina Laukaitis (EIRH/RBTE), Carle Illinois College of Medicine

Bob Karn (GNBP), Carle Illinois College of Medicine

This bioinformatic survey reported that secretoglobins, or SCGBs – originally thought to be exclusive to mammals – are also found in turtles, crocodilians, lizards, and birds. These findings, published in *Genome Biology and Evolution*, suggest that these proteins evolved earlier than dinosaurs and share a basic function that still eludes discovery.

“We have a series of *Scgb* genes within the human genome, but no one knows what their function is,” said Christina Laukaitis, who coauthored the study with Robert Karn. “If we want to understand ourselves,

we have to understand what we share and don’t share with other organisms.”

Previously, SCGBs had mainly been studied in the context of human health; establishing their evolutionary origins has yielded insights that this limited vantage point could not. One hypothesis suggested by these results is that some SCGBs play a role in animal communication. Moving forward, Karn and Laukaitis plan to explore this hypothesis further and hope that overall, their findings bring a renewed excitement for this field of research.

Researchers trace genetic code’s origins to early protein structures

The genetic code enables DNA to contain instructions for the complex processes that make organisms function. But how and why did it come to be the way it is? A recent study in *the Journal of Molecular Biology* sheds new light on the origin and evolution of the genetic code, providing valuable insights for genetic engineering and bioinformatics.

“Why does life rely on two languages – one for genes and one for proteins?” said corresponding author Gustavo Caetano-Anollés. “We still don’t know why this dual system exists or what drives the connection between the two. The drivers couldn’t be in RNA, which is functionally clumsy. Proteins, on the other hand, are experts in operating the sophisticated molecular machinery of the cell.”

When considering the emergence of life on Earth, some scientists believe RNA-based enzymatic activity came first, while others suggest proteins first started working together. Work by Caetano-Anollés and his colleagues supports the latter view. For this most recent study, the research team analyzed a dataset of 4.3 billion dipeptide sequences, combinations of two amino acids, from organisms throughout the tree of life.

People Mentioned

Gustavo Caetano-Anollés (PFS), crop sciences

Supported by

NSF; University of Illinois; USDA



The study suggests that dipeptides represent a primordial protein code emerging in response to the structural demands of early proteins, alongside an early RNA-based operational code. Uncovering these evolutionary roots deepens our understanding of life's origin and informs modern fields of innovation.

Team finds regional, age-related trends in exposure to drug-resistant pathogen

Campylobacter infections are the most common foodborne illnesses in the U.S., sickening an estimated 1.5 million people each year. A study that examined records of *Campylobacter jejuni* infections from 10 states identified patterns of risk based on both region and patient age, as well as trends in antibiotic resistance. The findings were reported in the *International Journal of Antimicrobial Agents*.

The main source of human *Campylobacter* infections is the consumption of contaminated, improperly prepared meat, especially poultry. Many infections are mild, but some individuals, including children and the elderly, may experience serious illness. To see how risk is evolving over time, the study examined publicly available data collected by the National

Antimicrobial Resistance Monitoring System, which tracks reports on infectious bacteria in 10 representative states.

"These sites are monitoring foodborne pathogens in the local population," said Csaba Varga, who led the research. "We analyze this surveillance data because we are interested in emerging and long-term trends."

The study found that young adults were infected with drug-resistant *C. jejuni* at higher rates than all other age groups, and that drug resistance was unevenly distributed across regions. The findings are particularly interesting because most human cases of *C. jejuni* are not treated with antibiotics, Varga said. These data emphasize the need for further study aimed at limiting the spread of antibiotic resistance in food-borne and other pathogens.

People Mentioned

Csaba Varga (IGOH), pathobiology

**Could
nanoplastics in
the environment
turn *E. coli* into a
bigger villain?**

People Mentioned

Pratik Banerjee (MME), food science
and human nutrition

Supported by

USDA

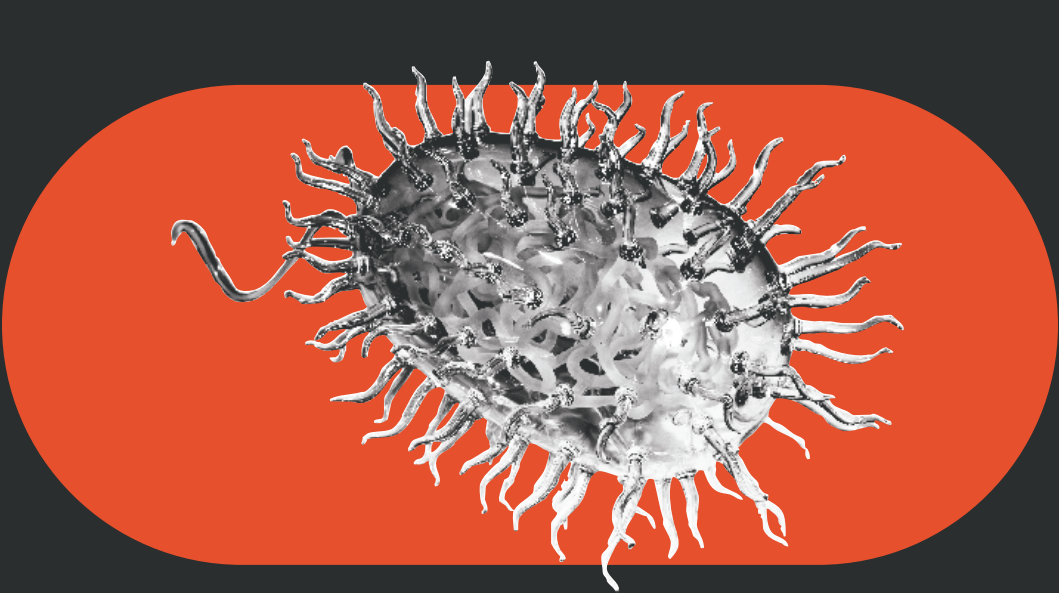
Nanoplastics are everywhere. These fragments are so tiny they can accumulate on bacteria and be taken up by plant roots; they're in our food, our water, and our bodies. Scientists don't know the full extent of their impacts on our health, but a recent food science study published in the *Journal of Nanobiotechnology* suggests certain nanoplastics may make foodborne pathogens more virulent.

"We focused on one of the key pathogens implicated in outbreaks of foodborne illness – *E. coli* O157:H7," said senior study author Pratik Banerjee. "One of our goals was to see what happens when this human pathogen, which is commonly transmitted via food, encounters these nanoplastics from the vantage point of a biofilm," a group of bacteria growing together within a communally-

generated protective gel of sugar and protein.

Banerjee's team found that nanoplastics with positively charged surfaces were more likely to cause physiological stress in biofilms of a disease-causing strain of *E. coli* called O157:H7. Just as a stressed dog is more likely to bite, the stressed bacteria became more virulent, pumping out illness-causing toxin.

Interactions with plastic particles may be doing more than increasing *E. coli*'s toxicity; based on the results obtained by other research efforts, Banerjee's group has studies underway to look at the transfer of resistance genes, as well as changes in virulence and transmission patterns of major foodborne pathogens in food products and other environments.



A call to decarbonize agriculture by expanding policies aimed at low-carbon biofuels

A team of agricultural economists, environmental scientists and policy experts envisions a path toward a carbon-neutral agricultural future by expanding the reach of policies that promote low-carbon biofuels. In a publication in *Science*, the researchers proposed policies that would reward farmers for adopting “climate-smart” practices when growing biofuel crops, while removing the hurdles that currently thwart such efforts.

People Mentioned

Madhu Khanna (CAMBERS), agricultural and consumer economics

Supported by

Council on Food, Agricultural and Resource Economics; DOE; NSF; USDA

Climate-smart practices include techniques that build soil carbon, like cover-cropping, and those that reduce the carbon footprint of crop production, like electrifying farm vehicles. The researchers used data from past studies to project that, if adopted globally, such practices could reduce carbon emissions by 4-8 billion metric tons – between 10-20% of total emissions – per year.

“Currently, our biofuel policies don’t reward farmers for adopting climate-smart practices,” said Madhu Khanna, lead author of the report. “By accounting for differences in practices implemented at the farm level . . . biofuel policies can incentivize adoption of these practices.”

At present, the channels for crediting farmers for climate-friendly practices are segregated from the markets that provide credits for low-carbon biofuels, Khanna said. Farmers must navigate a series of extra hurdles to be compensated. She and her colleagues proposed an approach for merging the biofuel feedstock market and climate-offset market into a single channel, reducing barriers to compensation and leading to more widespread adoption of climate-smart practices.



Two-step method to prevent biofilm regrowth is a SLAM dunk

Most people have encountered the slimy stains of bacterial biofilms built up on the bathroom tiles or kitchen sink. Even after vigorous scrubbing and strong cleaning chemicals, this grime stubbornly grows back. A study published in *Chemical Engineering Journal* reports a novel, two-step method to effectively dismantle bacterial biofilms and prevent regrowth.

“Biofilms are everywhere, from bathrooms to food factories,” said Hyunjoon Kong, lead researcher on the study. “Biofilms are also responsible for cross-contamination between patients at hospitals, and they can be found on medical instruments like tooth or bone implants.”

Many types of bacteria form complex communities, producing an external molecular scaffolding for protection. The researchers explored this by treating *Pseudomonas aeruginosa* biofilms with chemical disinfectants and then imaging the biofilm remnants. Although chemical treatment removed more than 50% of the entire biofilm, a large portion of the matrix was left behind; this allowed surviving cells to repopulate.

To disrupt this resistant matrix, the researchers took advantage of self-locomotive antibacterial microbubblers, or SLAM, previously developed by the Kong group. When activated with hydrogen peroxide, the SLAM particles generate oxygen bubbles that expand and rupture in the biofilm, leading to mechanical disruption. When SLAM treatment was followed by a traditional disinfectant, biofilm resurgence was further prevented for over two months. Moving forward, Kong looks to translate this technology into real-world applications.

People Mentioned

Hyunjoon Kong (M-CELS leader/EIRH/RBTE), chemical and biomolecular engineering

Supported by

Korean Ministry of Trade, Industry and Energy; NIH; NSF; SerVaas Laboratories, TechnipFMC

New model can accurately predict a forest’s future

Ecosystems comprise a complex web of interactions among species and aspects of their shared environment, and their dynamics over time are correspondingly difficult to anticipate. In a recent report in *Science*, researchers detailed their development of a new model that can predict future fluctuations in the relative abundance of those species, using a tree census and genomic data collected from multiple species in a forest.

James O’Dwyer, who co-led the research with external collaborators Andy Jones and James Lutz, has spent most of his career studying the factors that drive ecological change. He uses this knowledge to build models that reliably predict how individual species and forest communities will change over time.

The study used data from the Wind River Forest Dynamics Plot, part of the Smithsonian Forest Global Earth Observatory. Jones led an effort to collect genomic data from the most abundant species of trees within the plot. By integrating these data with tree census data in their model, the team was able to accurately predict species fluctuations over a five-year period, outperforming other models.

“This work is crucial because changes in abundance or loss of a species from a forest can have cascading effects on other species,” O’Dwyer said. “We identified certain combinations of life histories across plant communities that act to maintain diversity over longer timescales, while other combinations would lead to lower diversity.”

People Mentioned

James O’Dwyer (CAIM), plant biology
Andy Jones, Oregon State University
James Lutz, Utah State University

Supported by

NSF; Simons Foundation



**Nobel laureate
Thomas R. Cech
gives IGB
distinguished
public lecture**

This April, Nobel Laureate Thomas R. Cech gave the IGB Distinguished Public Lecture in Genomics on “The Magic of RNA: New Medicines, Immortality, and the Power to Control Evolution.” His talk, which drew over 400 people from the Champaign-Urbana community, was followed by a signing of his recent book, *The Catalyst: RNA and the Quest to Unlock Life’s Deepest Secrets*.

In 1982 Cech and his research group announced that an RNA molecule from *Tetrahymena*, a single-celled pond organism, cut and rejoined chemical bonds in the complete absence of proteins. This discovery of self-splicing RNA provided the first exception to the long-held belief that biological reactions are always catalyzed by proteins.

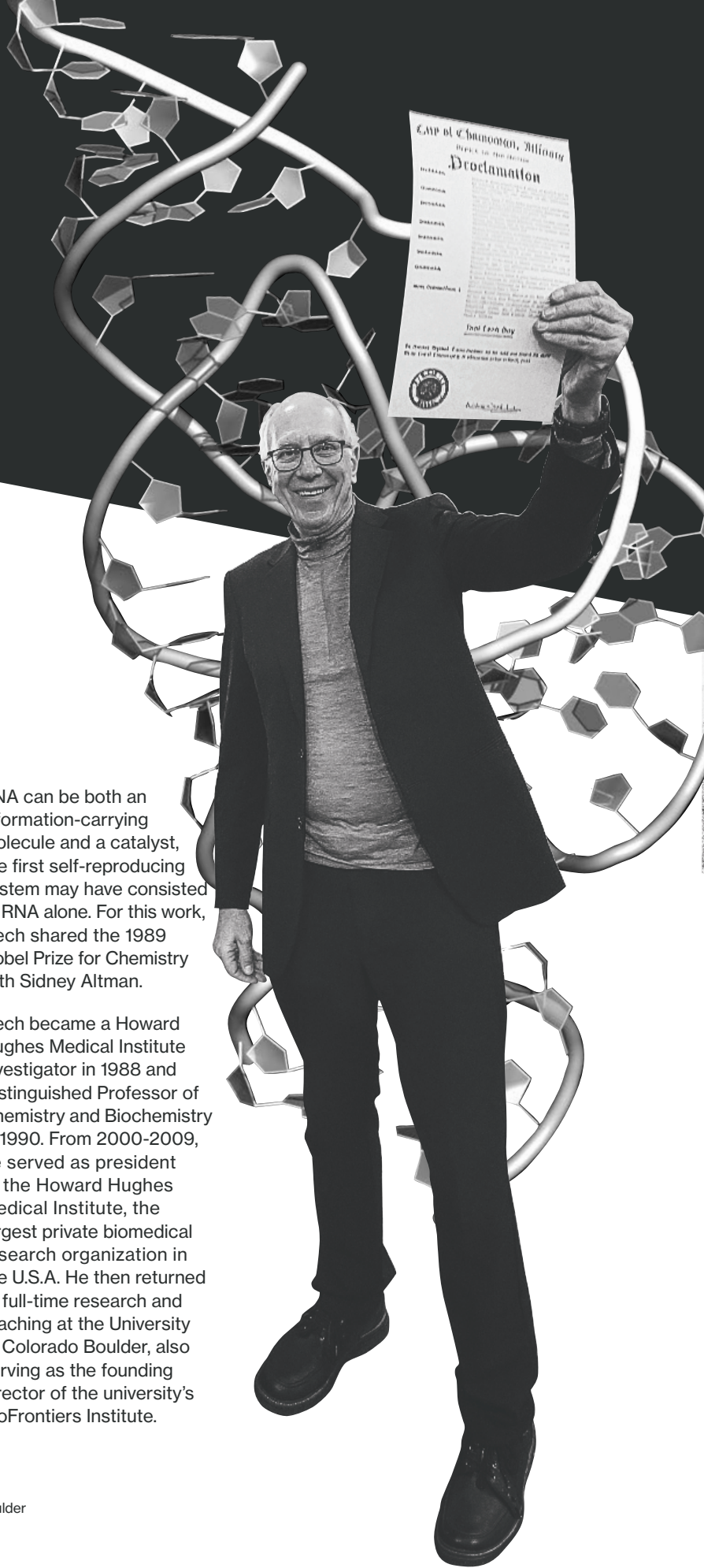
In addition, Cech’s groundbreaking finding provided important evidence for a new, plausible scenario for the origin of life; because

RNA can be both an information-carrying molecule and a catalyst, the first self-reproducing system may have consisted of RNA alone. For this work, Cech shared the 1989 Nobel Prize for Chemistry with Sidney Altman.

Cech became a Howard Hughes Medical Institute investigator in 1988 and Distinguished Professor of Chemistry and Biochemistry in 1990. From 2000-2009, he served as president of the Howard Hughes Medical Institute, the largest private biomedical research organization in the U.S.A. He then returned to full-time research and teaching at the University of Colorado Boulder, also serving as the founding director of the university’s BioFrontiers Institute.

People Mentioned

Thomas R. Cech, University of Colorado Boulder





Awards recognize excellence in public engagement

Individuals and teams from Illinois who have made a visible impact on society were recognized with the 2025 Campus Awards for Excellence in Public Engagement. Faculty, staff members, students and community members who engage the public to address critical civic and community issues at the local, state, national and global levels were honored for their efforts.

The IGB Communications and Outreach team was the recipient of the Team Award

for Excellence in Public Engagement. Ever since the founding of the institute in 2007, the team has worked to translate complex ideas to the public in eloquent and playful ways, channeling the IGB's motto: "Where Science Meets Society."

One of the sustained successes from the team is hosting the annual Pollen Power summer camp, which has impacted more than 300 area students since its inception in 2012. On a regional scale, the IGB team

also led the 2024 return of World of Genomics, a multi-day event hosted at Chicago's Griffin Museum of Science and Industry that attracted thousands of attendees. A recent priority for the communications and outreach team has also involved deepening the quality of the institute's community relationships, partnering with an array of groups to offer relevant and timely information about genomics.





Growing Efficiency

The energy that plants capture from sunlight through photosynthesis provides the source of nearly all of humanity's food and a growing portion of its fuel. As our scientific knowledge of this process has grown, our dependence upon it has made us acutely aware of its inefficiencies. Evolution does not yield the ideal food crops, but rather plants that survived the changing environments of the past.

Fundamental discoveries in photosynthesis have pointed to many ways to boost its power to produce. From the match between a plant and its ecosystem, to the way it takes in and transforms sunlight, to the downstream use of its biomass, there are many points of potential optimization. Each one carries its own technical challenges and potential rewards.

Researchers have spent decades building a systems view of plant biology that provides a foundation to pursue all these pathways to food and security simultaneously. The steady development of resilient, reliable food and fuel crops is coming to fruition.

How long does it take for a better crop to reach harvest?

'12

As far back as the 1960s, researchers at Illinois were studying photosynthesis with the aim of extending the successes of the Green Revolution. Bill Ogren earned recognition throughout the plant science world for his efforts on a quixotic enzyme called Rubisco. Rubisco drives a key reaction of photosynthesis. It also enables one of its most pernicious inefficiencies.

Rubisco – the world's most abundant protein – is responsible for capturing carbon dioxide and starting it on its chemical pathway to become a part of a sugar molecule. About a third of the time, Rubisco errs and captures oxygen instead. Correcting this chemical misstep through an alternate process called photorespiration costs the plant energy and time.

In 2012, a team of researchers led by Stephen Long and Donald Ort received a five-year, \$25-million grant from the Gates Foundation for a project entitled Realizing Increased Photosynthetic Efficiency. From the start, the RIPE project spanned institutions, continents, and scientific approaches to enhancing food crop resilience and yield. One of its key goals was to find ways to prevent or shortcut photorespiration.

'15

As work on the RIPE project moved forward, Long and two colleagues, Amy Marshall-Colon and Xin-Guang Zhu, issued a call to action to the scientific world in a review paper in *Cell*. Their case for a concerted effort to improve photosynthetic efficiency was twofold. First, emerging scientific technologies, including computational modeling, high-throughput sequencing, and gene editing had put once unattainable crop improvement strategies within reach. Second, the time frame between the development of a new plant variety in the lab and the widespread availability of that plant to farmers and consumers is on the order of decades. To feed future world populations, the time to act was immediately.

“If we have a success today, it won't appear in farmers' fields for 15 years at the very earliest. We have to be doing today what we may need in 30 years.”

STEPHEN LONG

NATIONAL SCIENCE FOUNDATION

GATES FOUNDATION

ARPA-E

'19

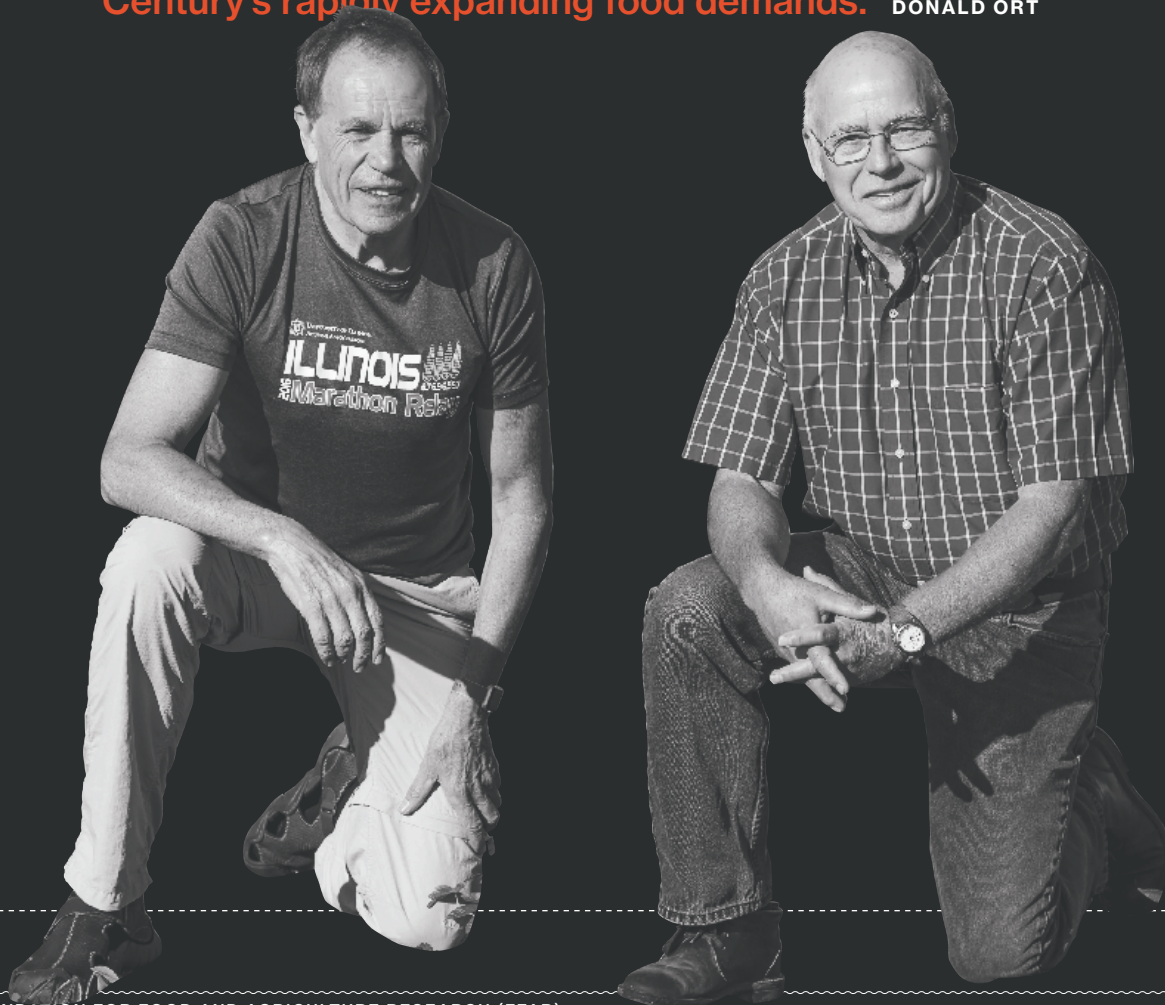
After several years of studies identifying theoretical workarounds for photorespiration and testing genetic constructs in the laboratory, Ort, Paul South, and colleagues transformed an experimental crop with genes borrowed from microbes, predicted by *in silico* models to offer a new pathway to divert the products of photorespiration.

Their field trials were the first time that a biochemical solution to the problem of photorespiration had been tested in real-world agronomic conditions.

The team developed an experimental variety of tobacco, an ideal model plant for crop research because it is easier to modify and test than food crops, develops a leafy

canopy, and can be tested in the field. Over two years of replicated field studies, they found that their transformed plants developed faster, grew taller, and produced about 40 percent more biomass. In a subsequent study, they found that the plants were more resilient to heat stress, which often increases photorespiration rates.

“We could feed up to 200 million additional people with the calories lost to photorespiration in the Midwestern U.S. each year...Reclaiming even a portion of these calories across the world would go a long way to meeting the 21st Century’s rapidly expanding food demands.” DONALD ORT



'24

After over a decade of work and striking successes in tobacco test crops, the RIPE team was ready to see what their alternative photorespiratory pathway could do for a true food crop. They introduced their genetic construct into potatoes, a staple food crop around the world. As in their previous field trials, the experimental crop outperformed expectations, showing 30% increases in tuber mass under heatwave conditions.

Combined with promising results from field testing

of other improvements in photosynthetic efficiency, including in soybeans, these findings validated the approach put forward by Long, Ort, and their colleagues years before. Katherine Meacham-Hensold, who led the study on alternative respiratory pathways in potatoes, aims to carry this approach forward into other staple crops. Cassava, another tuber that is a vital food source in sub-Saharan Africa, is a key target.

'25

As the RIPE project continues to move forward, its impacts extend far beyond the pressing problem of photorespiration. Other targets for improved efficiency of photosynthesis relate to improving the penetration of sunlight through crops' leaf canopy, as well as helping plants more quickly shift from protective mechanisms used in high-intensity light to optimal light-gathering in cloudy conditions. Researchers are also identifying the genomic origins of heat-, drought- and flood-tolerance of different varieties of specific crop plants in hopes of replicating and amplifying these valuable attributes.



Even as the race against population growth, hunger, and a changing climate becomes more urgent, new scientific tools – including artificial intelligence and lab automation – promise to boost our capacity to push forward another Green Revolution. Thanks to seeds of scientific endeavor planted years ago, there is hope to feed and fuel the future world.



People Mentioned

Stephen Long (BSD/CAMBERS/PFS), plant biology (deceased); **Amy Marshall-Colón** (CAMBERS/PFS), plant biology (deceased); **Katherine Meacham-Hensold**, RIPE program project manager; **William Ogren**, USDA-ARS (deceased); **Donald Ort** (PFS leader/BSD/CAMBERS), plant biology, crop sciences; **Paul South**, Louisiana State University; **Xin-Guang Zhu**, Chinese Academy of Sciences

People Involved

Elizabeth Ainsworth, **Carl Bernacchi**, **Ryan Boyd**, **Steven Burgess**, **Elizabete Carmo-Silva** (Lancaster University), **Amanda Cavanagh**, **Ryan Dilger**, **Nicholas Ferrari**, **Jessica Fowler**, **Jooyeon Jeong**, **Martin Jonikas** (Princeton University), **Johannes Kromdijk** (University of Cambridge), **Justin Larkin**, **Moonsub Lee**, **Helen Liu**, **Stephen Long** (deceased), **Benedict Long** (University of Newcastle), **Amy Marshall-Colón** (deceased), **Katherine Meacham-Hensold**, **Donald Ort**, **Diwakar Shukla**, **Peyton Sorensen**, **Paul South**, **Samantha Stutz**, **Yu Wang**, **Robert Wilson** (Massachusetts Institute of Technology)

Publications

Zhu, et al., *Cell* **161**, 2015; **South, et al.**, *Science* **363** (6422), 2019; **Meacham-Hensold, et al.**, *Glob. Change Biol.* **30** (12), 2024; **Cavanagh, et al.**, *Plant Biotechnol. J.* **20** (4), 2025; **Long, et al.**, *Cell* **188** (24), 2025

Briefs

Growing Efficiency



Traditional breeding falls short in boosting soybean photosynthesis

A study of the biology behind crop development has determined that improving a key component of soybean photosynthesis is unlikely to come from traditional breeding methods. Instead, gene editing is likely the key to unlocking soybean potential.

Photosynthesis, the natural process all plants use to convert sunlight into energy and yields, is not optimized for current agricultural systems. This is because wild species don't evolve to maximize yield, but rather to survive unpredictable stressors.

Photosynthesis is also poorly adapted to the managed conditions of a modern field; when a crop plant has extended sun exposure, that excess energy can actually hurt its growth potential.

Steven Burgess and his team planted, collected, and analyzed field trials for three years, gathering data about how plants protect themselves from excess sunlight, along with environmental data such as precipitation and temperature. Seeing how different soybean genotypes compared in a variety of times and conditions gave the scientists the best overall picture of how these genetics would perform in other fields and environments. Their work was published in *The Plant Journal*.

"There's not a huge amount of room to improve the light-harvesting efficiency of soybean photosynthesis at a cellular level using what's available naturally from traditional breeding," said Burgess. "If people are going to pursue this strategy, it really needs to be either gene editing or transgenic approaches."

People mentioned

Steven Burgess (CAMBERS/PFS), plant biology

Supported by

RIPE/Gates Ag One

New approach makes AI adaptable for computer vision in crop breeding

Crop scientists have gained a powerful tool to help track plant traits in the field. A research effort combined machine learning software development with ongoing plant breeding data to produce an AI tool that can teach itself, with minimal external guidance, to analyze aerial images of growing crops.

The computational model, described in the journal *Plant Physiology*, learns to differentiate between aerial images of flowering and nonflowering *Miscanthus* grasses. *Miscanthus* is an important potential biomass crop with thousands of varieties, each of which has its own flowering traits and timing.

“Flowering time is a key trait influencing productivity and the adaptation of many crops, including *Miscanthus*, to different growing regions,” said Andrew Leakey, a coauthor of the project. “But repetitive visual inspections of thousands of individual plants grown in extensive field trials is very labor intensive.”

People mentioned

Andrew Leakey (CAMBERS leader/PFS), plant biology, crop sciences

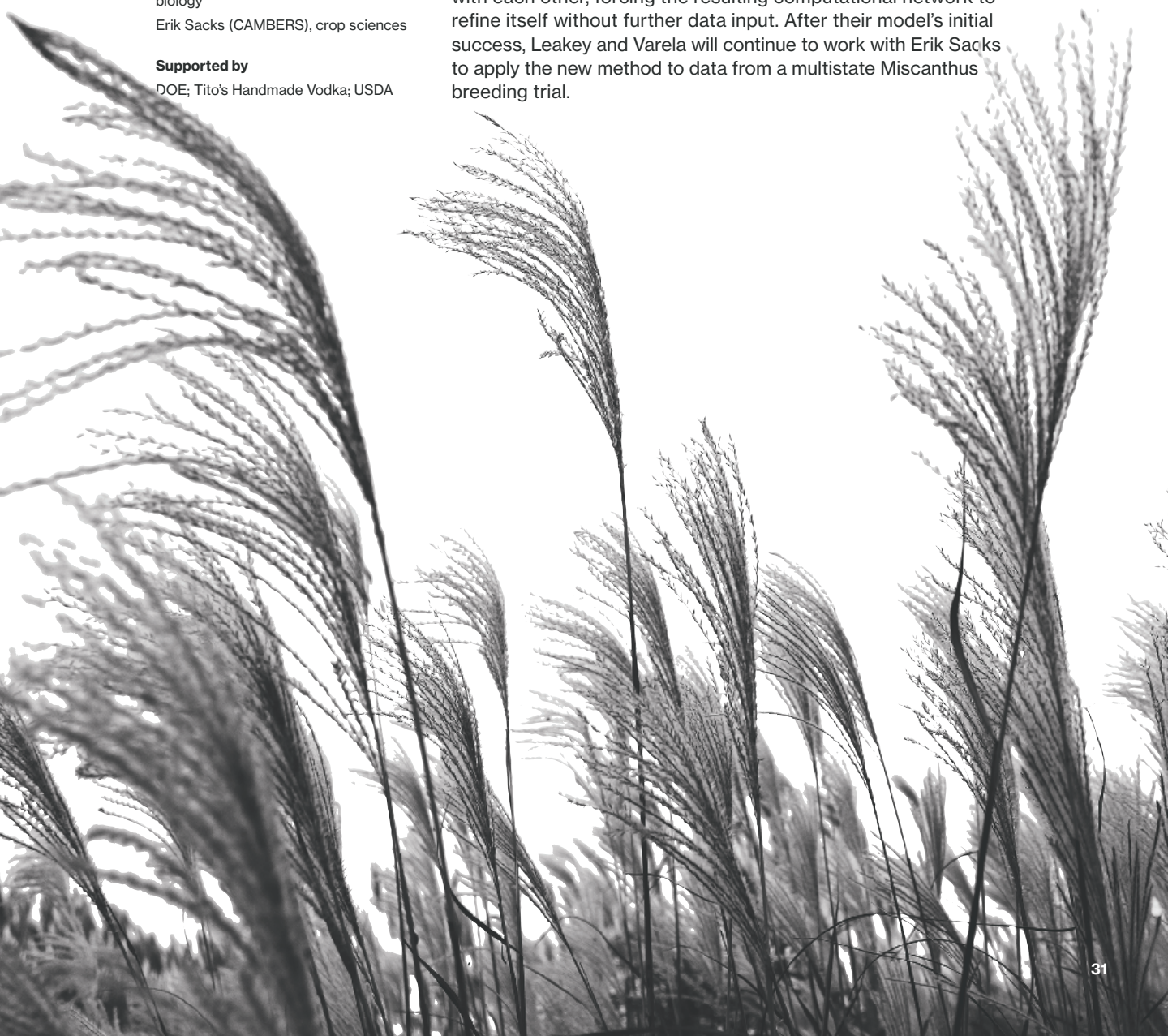
Sebastian Varela (CAMBERS), plant biology

Erik Sacks (CAMBERS), crop sciences

Supported by

DOE; Tito's Handmade Vodka; USDA

Machine learning models, a promising alternative, are almost always reliant on very large and well-annotated data sets. To bypass this limitation, Leakey and colleague Sebastian Varela used an existing method that prompts two AI models to compete with each other, forcing the resulting computational network to refine itself without further data input. After their model's initial success, Leakey and Varela will continue to work with Erik Sacks to apply the new method to data from a multistate *Miscanthus* breeding trial.



Microalgae and bacteria team up to convert CO₂ into useful products

Scientists have spent decades genetically modifying the bacterium *Escherichia coli* and other microbes to convert carbon dioxide into useful

People mentioned

Yong-Su Jin (BSD/CAMBERS/MME/PFS), food science and human nutrition

Supported by

Department for International Development in the U.K.; DOE; Foundation for Food and Agricultural Research; Korea Institute for Advancement of Technology; Ministry of Trade, Energy and Industry in Korea; RIPE/Gates Ag One; USDA

biological products. Most methods require additional carbon sources, adding to the cost. Microbiologists have found a way to overcome this limitation by combining the photosynthetic finesse of a single-celled algae with the production capabilities of the bacteria *E. coli*.

Previous studies have used photosynthetic bacteria to convert CO₂ into sugars that are then taken up by other microbes as a carbon source, said study lead Yong-Su Jin. The new method, published in *Metabolic Engineering*, differs from those because the microalga used takes in CO₂ and excretes an organic acid, glycolate. Unlike most organisms, *E. coli* readily consumes glycolate.

“Sometimes sugars are better for the production of certain products,” Jin said. “But if we use glycolate instead of sugar, we have less chance of contamination with outside organisms.”

The microalga, a mutant form of *Chlamydomonas reinhardtii*, will eventually produce so much glycolate that it poisons itself. But when co-cultured with *E. coli*, the bacteria will consume the glycolate, keeping the microalgae alive and relatively healthy. The researchers tested the potential uses of this setup by successfully generating two valuable compounds: lycopene, a carotenoid antioxidant, and green fluorescent protein, which is widely used in biochemical research.

Study identifies gene clusters in rhizobia linked to robust legume growth

How do plant roots and soil microbes work together? To dig into this question, scientists used nearly every tool in their toolkit – genomics, transcriptomics, greenhouse experiments, and advanced statistical methods – and emerged with new insights into the complex chemical interactions that take place within root nodules.

The study, which examined how soil microbes called rhizobia exchange vital nutrients with the roots of legumes, was reported in the *Proceedings of the National Academy of Sciences*. Its results identified clusters of rhizobial genes that appear to move rapidly through bacterial populations and drive greater plant biomass in the host plants.

where a lot of evolutionary history has shaped a very intimate interaction,” said Katy Heath, who led the study with Amy Marshall-Colón. “Legumes like soybeans, peas or peanuts develop these special relationships with rhizobia.”

To explain those relationships, Heath and her colleagues studied a specific legume-rhizobial pair, inoculating plants with one of 20 different bacterial strains. They determined which plant and bacterial genes were associated with the most vigorous plant growth and paired this with genome sequence information. Combining these many types of data revealed that key genes were clustered together. Future studies will examine whether other plant-microbe pairs maintain the same pattern.

People Mentioned

Katy Heath (IGOH), plant biology

Amy Marshall-Colón (CAMBERS/PFS), plant biology (deceased)

Supported by

Consejo Nacional de Ciencia y Tecnología, Mexico; IGB; NSF

“Just like us, plants are full of microbes, and some form these tightly co-evolved symbioses



Easy CowPEAsy: RIPE team develops new gene expression tool for cowpea

A team from the Realizing Increased Photosynthetic Efficiency project has developed a tool that will enable scientists to better explore cowpea gene expression with the click of a button. CowPEAsy is an open-access interactive web tool that allows researchers to look at specific genes within three levels of the plant canopy, which are associated with different light levels, during two points of the growing season. A description of the tool was published in *Plant, Cell & Environment*.

Previously, most datasets with measures of gene activity have not included associated canopy position or plant development data. Members of Laurie Leonelli's research group collected and consolidated these data types in a single place, giving users a way to explore research questions

without requiring expertise in coding or computational biology. Scientists who have a specific gene in mind can use the tool to see how it is responding under a particular set of conditions. For a more exploratory project, the tool can instead help determine genes of interest.

"Cowpea is a vitally important source of sustenance for certain areas of the world. The more we can learn about how it interacts with its light environment through its gene expression, the better positioned we will be to design strategies to improve its photosynthetic productivity, and in turn, increase its yield," Leonelli said. **"We are really excited to see where this leads."**

People mentioned

Laurie Leonelli (PFS), agricultural and biological engineering

Supported by

RIPE/Gates Ag One



How drought and ozone pollution team up to reduce soybean yield

In a decisive study published in *Plant Physiology*, crop scientists at the University of Illinois Urbana-Champaign and the USDA's Agricultural Research Service showed that soybeans are doubly damaged by drought and ozone pollution, both of which are increasing across the globe.

The study settles the question of whether drought stress could actually protect soybean plants from the damaging effects of ozone. When plants sense drought, they close their stomata – microscopic pores in their leaves – to conserve water. Some early studies suggested that by causing stomata to close, drought may also prevent ozone from entering leaves and damaging sensitive tissues.

To test the strength of this hypothesis, Lisa Ainsworth's team grew soybeans in the field for three years under high ozone concentrations, while excluding about 40% of each season's rainfall. They measured health characteristics in the growing plants, as well as yield at harvest. What they found contradicted earlier indications: even in drought conditions, elevated ozone consistently reduced photosynthetic efficiency and reduced yield, with fewer and smaller seeds in each pod.

People Mentioned

Lisa Ainsworth (CAMBERS/PFS), crop sciences, plant biology

Supported by

USDA

"Drought and ozone pollution are just part of our growing environment today. Understanding how these factors interact will help us design practices that could mitigate their effects," Ainsworth said. "As we're thinking about targets for crop improvement, regardless of whether there's drought or not, improving ozone tolerance will be key."

Heat-resilient crops are within reach – given enough time and money

Laboratory and field experiments have repeatedly shown that modifying the process of photosynthesis or the physical characteristics of plants can make crops more resilient to hotter temperatures. Scientists can now alter the abundance or orientation of leaves, change leaf chemistry to improve heat tolerance, and adjust key steps in the process of photosynthesis to overcome

bottlenecks, researchers reported in a review in *Science*.

Timing is critical to overcoming the heat-related challenges of climate change. Projected temperature increases between 2010 and 2050 are expected “to depress yields of the major grains by 6%-16%, against a backdrop of a potential >50% increase in demand over this period,” the authors reported.

Through alteration of plant traits, including increasing the reflectivity of plant leaves or regulating water loss through leaf pores, crop development can produce plants that survive hotter and dryer growing

conditions. Traditional breeding methods, however, are not always able to produce the desired characteristic, and require years of work. Gene editing technologies work quickly and safely, but still require a careful progression of laboratory and field tests to validate.

“There are real opportunities to address temperature increases, to future-proof the crop against rising temperatures,” Stephen Long said. “It isn’t an impossibility. But it’s going to mean significant, very significant effort.”

People mentioned

Stephen Long (BSD/CAMBERS/PFS), plant biology, crop sciences (deceased)

Supported by

RIPE/Gates Ag One

Illinois research shows benefits of prairie grass for sustainable aviation fuel

Switchgrass has gripped Midwestern soils for millions of years, but soon, the earthbound prairie grass could fly. Detailed economic and environmental evaluations have highlighted switchgrass as a candidate source for sustainable aviation fuel.

Scientists have been studying switchgrass for its bioenergy potential for decades. But previous studies used less productive switchgrass cultivars or were grown in suboptimal conditions. In two recent

studies, researchers grew modern “energy” cultivars at the field scale across the Midwest to determine which cultivars are most profitable where, and how they compare to corn in terms of ecosystem services.

“With these energy-type cultivars, farmers can put marginal lands to use and see returns after two years,” said Muhammed Umer Arshad, who worked on the project with DoKyoung Lee. “Our results can help guide decision-makers to optimize input strategies for biomass production and meet renewable energy demands.”

Beyond producing great quantities of biomass, switchgrass can also be harvested annually for a decade or more, requires minimal nitrogen fertilizer,

thrives on marginal land, and performs important ecosystem services. The research team said that as the market prepares for bioenergy aviation fuel, switchgrass cultivars will be getting ready as well.

People Mentioned

DoKyoung Lee (CAMBERS), crop sciences

Muhammed Umer Arshad, crop sciences

Supported by

DOE



The coming of age of Miscanthus

Can an ornamental grass change the world? Giant, versatile, and genetically complex, Miscanthus poses unique opportunities for the farm economy, domestic manufacturing, next-generation biofuels, and the environment. An emerging biomass crop, its harvested leaves are used commercially for a multitude of high-value products, including fuel for heat and electricity, compostable packaging, and erosion control.

Work around the country shows that this grass needs infrequent replanting and little fertilization, tolerates both drought and cool temperatures, and can efficiently sequester carbon. But bringing all of its desirable traits together into a perennial that can grow in varied U.S. climates is a breeding challenge. That's been a focus of researchers at the Center for Advanced Bioenergy and Bioproducts Innovation.

In a recently published study, a research team led by Erik Sacks examined the effect of day length on flowering and growth in Miscanthus from a range of environments around the world. All tended to flower earlier with shorter days, but the plant's sense of a "short day" varied based on where it originated. For varieties from northern regions, even a small drop in daylight would cause the plant to flower quickly; for those from the subtropics, a much shorter day was needed. A current study of another Miscanthus species is showing the same trends.

"We're creating a foundation for miscanthus research and development," Sacks said. "It's a liftoff of this giant endeavor, involving people with a wide array of specialties collaborating. That's what CABBI allows us to do: pull that all together. That's the really critical piece."

People Mentioned

Erik Sacks (CAMBERS), crop sciences

Supported by
DOE

Pollen Power camp: science on the summer horizon

The IGB's week-long day camp, Pollen Power, returned this summer for its 12th year. The camp, offered in partnership with Champaign's Unit 4 School District since 2022, helps the middle school-aged children who attend to envision a future career in science by blending authentic lab experiences with classic summer fun.

"This camp is in its third year of collaboration with IGB. This year we have students from eight Champaign Unit 4 schools," said Zanne Newman. "Students are provided Unit 4 transportation, free lunches and fabulous learning opportunities. Families love this camp and often attend for multiple years. It is an exciting experience for our students to be on the University of Illinois campus meeting scientists, going on field trips and engaging in nature-centered activities."

This year, campers visited several campus highlights, including the recently opened CABBI greenhouse facilities, the Rare Book and Manuscript Library, and the IGB Core

Facilities, where they learned to use research instrumentation to image and digitally reconstruct pollen grains.

Working as a group, campers also designed and conducted a week-long plant growth experiment in which they tested how different conditions affect germination and health. Other activities included modeling the mechanical properties of carnivorous plants, touching and holding newly emerged honey bees, isolating chlorophyll from leaves, and viewing plant stomata under the microscope.

People mentioned

Zanne Newman, Franklin STEAM Academy

Supported by
DOE; IGB







Tracing Pathways to Treatment

At its origin, a new medical threat is almost always based on a tiny and nearly invisible change. A difference in a DNA sequence; a few cells growing out of place; a little less of a particular cellular signal, or a little more. Escalation follows. The sooner these sometimes insidious changes are detected, the more likely it is that full-blown disease can be prevented.

Many technological innovations follow this process in-reverse. Engineers combine the

knowledge and tools at hand to build something new – a system that is elaborate enough to pull a single bacterial gene from an ecosystem of microbes or a key molecule from a few microliters of blood. After this initial breakthrough come many rounds of careful refinement, paring down a technology from something that can be understood by a few to something that can be used by many. If everything goes right, what remains in the end is an elegant means to find and foil a disease process before it can really start.

What does it take to find a disease almost before it starts?

EARLY
'00s

Since the early 2000s, Brian Cunningham's Nanosensors research group has followed many paths toward a basic aim – to build diagnostic devices that can uncover trace levels of biomarkers: proteins, nucleic acids, or other molecules that can indicate if healthy or disease processes are occurring in the body. They do so using materials that are engineered on the same scale as the molecules they want to capture. This focus is strategic; nanomaterials rival biological materials in the potential sensitivity of their molecular interactions.

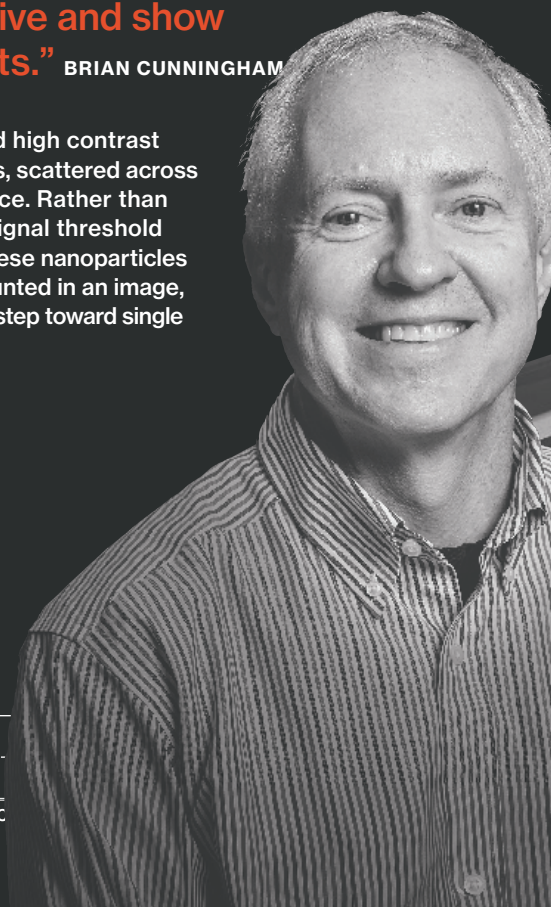
To achieve enhanced biomarker detection, the Nanosensors group integrated photonic crystal technologies into prototype devices. Photonic crystals manipulate how light is absorbed and reflected on the nanoscale, due to tiny grooves patterned on their surface. These technologies showed promise for development into technologies for point-of-care diagnostic testing, but were often too expensive, unwieldy, or challenging to operate in their initial form.

'14

Most biosensors share a basic design; a component within the device recognizes and captures the target molecule, which prompts a signal that can be detected and measured. Often, fluorescent tags are used as reporters, emitting light that must accumulate and exceed a certain threshold to provide a measurable result. Cunningham's group investigated an alternative: they tried using metallic gold nanoparticles, also called AuNPs, to tag biomarkers. They found that when light is reflected off the photonic crystal, AuNPs on its surface can quench the light's intensity.

“The photonic crystals act like a mirror, but only for the color red. The gold nanoparticles are non-reflective and show up as dark spots.” BRIAN CUNNINGHAM

This method yielded high contrast images of the AuNPs, scattered across the biosensor surface. Rather than hitting a minimum signal threshold like fluorescence, these nanoparticles could be visually counted in an image, which is a promising step toward single molecule resolution.



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BECKMAN INSTITUTE

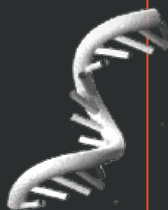
U.S. DEPARTMENT OF AGRICULTURE

MAYO CLINIC



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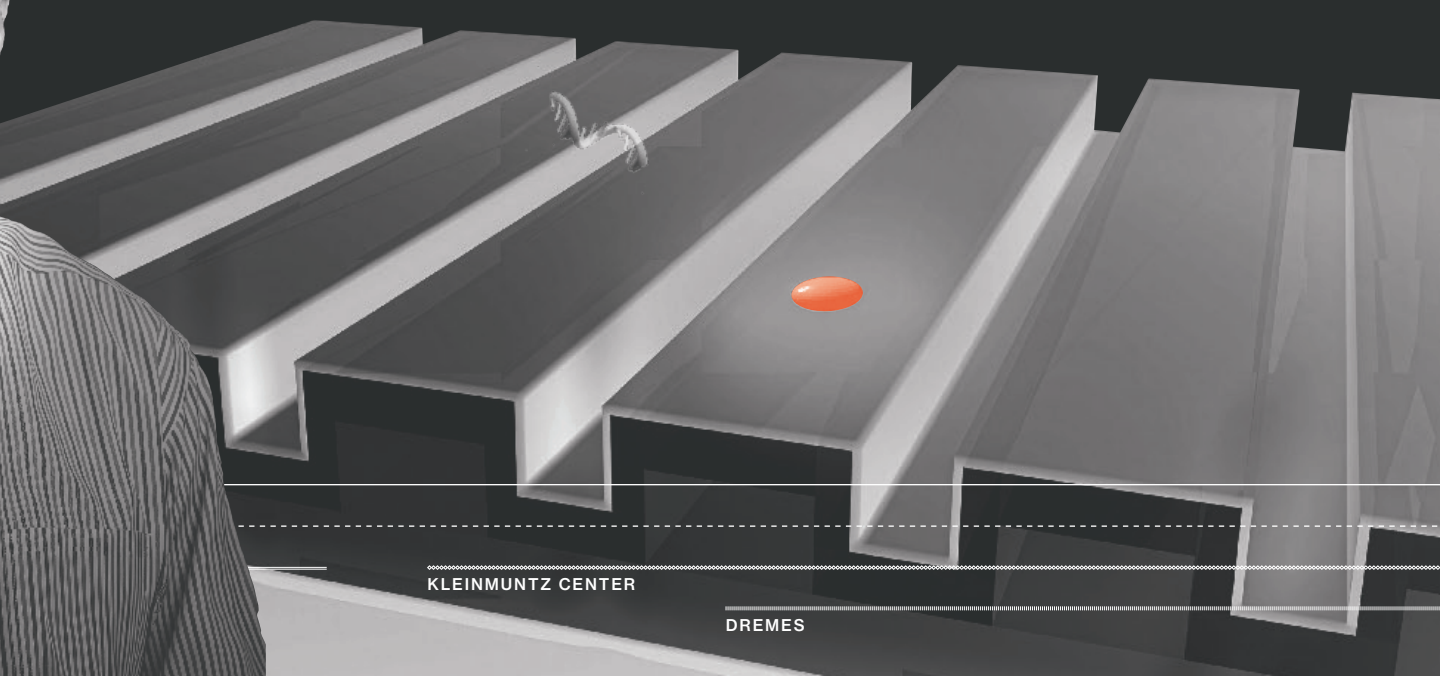
The team reported their development of a biosensing method called Photonic Resonator Absorption Microscopy, or PRAM, to capture and count cancer-associated biomarkers. The method employed AuNPs, functionalized with nucleic acid probes that can bind to the target microRNA sequences. With the biomarker in tow, the microRNA then attaches to the photonic crystal surface for detection. Using a commercial microscope, the PRAM images are acquired, and the dark spots – each representing a single, AuNP-tagged microRNA – are counted. With collaborators in Florida, the researchers successfully sensed ultralow levels of two microRNAs that are known, blood-based biomarkers for prostate cancer.



'21

While PRAM was successfully applied for biomarker detection, the system used was expensive and the size of a ping pong table, making it unsuitable for clinical, point-of-care applications. Traditional medical diagnostic tests are often performed offsite, in a process that can be long and expensive and require laboratory expertise. Point-of-care diagnostics, like home pregnancy tests and blood glucose meters for diabetes, are instead rapid, low cost, and easy to use.

Researchers in the Nanosensors group moved closer to this goal by developing ap-PRAM, a compact and cheaper version of the system that uses a red LED light and simplified image acquisition technology. Rather than moving the biosensor on a stage and collecting measurements pixel-by-pixel, it instead captures a single, wide frame image using a webcam-quality sensor.



‘22 ‘23

Cunningham’s group continued finding new ways improve their biosensors, including methods to further amplify biomarker signal and speed up detection.

‘24

Because the cost and size of ap-PRAM would still be prohibitive for certain users, Cunningham’s group pushed the engineering further to make the PRAM Mini. The prototype, which links to smartphones via Bluetooth, is more portable and user-friendly than past iterations. While the researchers report that some image quality is sacrificed as they try to reduce the size and cost – estimated around \$500 to manufacture – PRAM Mini still achieves similar detection limits to prior models.

“If you have a simple, fast and sensitive test like that, it can be used for detecting cancer, monitoring cancer treatment effectiveness, and following up with treatment. We envision this method being used in a health clinic so you wouldn’t have to take a sample, send it to a lab, and wait several days.”

BRIAN CUNNINGHAM



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KLEINMUNTZ CENTER

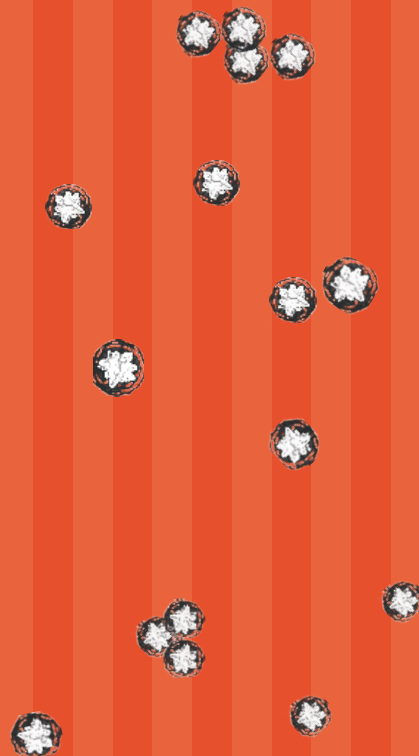
DREMES

'25

In order to make PRAM better suited for point-of-care environments, researchers integrated a deep learning method, called Localization with Context Awareness, to automate image analysis. But while it removes the need for expert analysis, the AI's performance is tied to the quality of its training data. Even to the trained eye, a speck of dust can be difficult to differentiate from a true spot.

To ensure accurate counting, Cunningham's team spent hours cross-referencing black spots against ground truth electron microscope images of the AuNPs on the photonic crystal surface. As a result, LOCA-PRAM surpassed conventional techniques in accuracy, detecting lower levels of the biomarkers and minimizing rates of false-positive and negatives.

The many rounds of refinement involved in developing PRAM, or any other disease detection technique, have dual goals. One is to make it work. The other is to make it usable. Success is realized when a technique is out in the world, promoting well-being by preventing disease.



People Mentioned

Brian Cunningham (CGD leader), electrical and computer engineering

People Involved

Takhmina Ayupova, Taylor Canady, Congnyu Che, Weili Chen, Edmond Chow, Brian Cunningham, Utkan Demirci (Stanford University), Diego Diel (Cornell University), Minh Do, Erika Falkiewicz, Ying Fang, Shreya Ghosh, Prashant Gupta (Washington University), Huan Hu, Young-Gu Ju (Kyungpook National University), Kodchakorn Khemtonglang, Chansong Kim, William King, Manish Kohli (Huntsman Cancer Institute), Hankeun Lee, Nantao Li, Siyan Li, Weinan Liu, Leyang Liu, Kenneth Long, Meng Lu, Yi Lu (UT Austin), Shuming Nie, Ege Onal, Isabella Rose Palm, Michael Rathslag, Skye Shepherd, Srikanth Singamaneni (Washington University), Lucas Smith, Andrew Smith, Tingjie Song, Limei Tian (Washington University), Joseph Tibbs, Weijing Wang, Xiaojing Wang, Yanyu Xiong, Ruiyang Xue, Yihong Yang (Zhejiang University), Hojeong Yu, Zhao Yuan, Bin Zhao, Yue Zhuo

Publications

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Briefs

Tracing Pathways to Treatment



Study identifies hotspots of disease-carrying ticks in Illinois

Scientists analyzed the distribution of three potentially harmful tick species in Illinois, identifying regions of the state with higher numbers of these ticks and, therefore, at greater risk of infection with multiple tick-borne diseases.

“We knew that tick-borne diseases from the most common, medically important tick species are here in Illinois, so we wanted to see if the

hotspots for ticks match with the incidence of diseases transmitted by those ticks,” said Abrar Hussain.

The researchers gathered tick-occurrence and tick-borne-disease data from several sources and reported their findings in the journal *Ticks and Tick-borne Diseases*. Data included 1,414 ticks collected through active surveillance in 80 Illinois counties from 2018-2022. The team built spatial statistical models to identify county-level clusters with higher-than-expected tick distributions.

Their analyses found that of the three species tracked, the lone star tick, *Amblyomma*

americanum, is most prevalent in southern Illinois; the black-legged tick or deer tick, *Ixodes scapularis*, is more common in northern and central Illinois; and the dog tick, *Dermacentor variabilis*, dominates the central and southern parts of the state.

“Just because there isn’t a county-level hotspot near you doesn’t mean that there’s no ticks,” said Rebecca Smith, who urges people to protect themselves from ticks whenever they venture out into wild areas, road edges, parks, woodlands or prairies. The analysis offers insights that will allow health and safety officials to concentrate their resources accordingly.

People Mentioned

Rebecca Smith (IGOH co-leader/CGD),
veterinary clinical medicine
Abrar Hussain, pathobiology

Researchers develop enhanced method for wastewater surveillance of antibiotic resistance

When exposed to antibiotics, surviving bacteria can adapt to this chemical threat. Resulting antibiotic resistance decreases treatment effectiveness in subsequent infections. Resistance is also passed among different bacteria through the transfer of small pieces of bacterial DNA called antibiotic resistance genes, or ARGs.

“Wastewater detection of ARGs with clinical significance allows public health authorities and physicians to anticipate what is circulating in communities,” Helen Nguyen said.

Wastewater contains DNA from many different organisms; along with other bacterial genome fragments, wastewater samples contain traces of many different ARGs. These traces are at such a low concentration that they are difficult to detect with standard metagenomic methods.

Metagenomics involves breaking all the sample DNA into millions of smaller fragments, simultaneously sequencing these fragments, and then using computational algorithms to piece together and identify the full DNA sequences. In collaboration with Joanna Shisler, Nguyen’s team leveraged the CRISPR-Cas9 system – a highly effective tool for gene editing – to enrich the amount of ARG-associated fragments in wastewater samples for metagenomic analysis. The new method identified over 1000 low abundance ARGs in wastewater samples.

People Mentioned

Helen Nguyen (IGOH), civil and environmental engineering
Yuqing Mao, civil and environmental engineering
Joanna Shisler, microbiology

Supported by

Environmental Protection Agency;
NTU/U of I Joint Research and Innovation Seed Grants Program;
Water Research Foundation

“Our new CRISPR method increases the abundance of ARG fragments in the sample, which increases their chances to be read and detected,” Yuqing Mao said.

AI-human task-sharing could cut mammography screening costs by up to 30%

Breast cancer screening is a critical public health tool, with nearly 40 million mammograms performed annually in the U.S. alone. Yet the process is time-intensive and costly, in both labor and follow-up procedures triggered by false positives. Artificial intelligence could help healthcare providers streamline this process.

A study published in the journal *Nature Communications* finds that a “delegation” strategy – where AI helps triage low-risk mammograms and flags higher-risk cases for closer inspection by human radiologists – could reduce screening costs by as much as 30% without compromising patient safety.

“AI is excellent at identifying low-risk mammograms that are relatively straightforward and easy to interpret,” Mehmet Ahsen said. “But for high-risk or ambiguous cases, radiologists still outperform AI. The delegation strategy leverages this strength: AI streamlines the workload, and humans focus on the toughest cases.”

The findings could help shape how hospitals and clinics integrate AI into their diagnostic workflows amid a growing demand for early breast cancer detection and a shortage of radiologists. The delegation strategy could also be applicable to other areas of medicine such as pathology and dermatology.

People Mentioned

Mehmet Eren Ahsen (CGD), business administration

Study links urinary tract bacteria to prostate cancer

People Mentioned

Jason Ridlon (MME), animal sciences
Joseph Irudayaraj (CGD/EIRH),
bioengineering
Saeed Ahmad, bioengineering
Karen Sfanos, Johns Hopkins University

Supported by

CCIL; DOD; National Cancer Institute;
Prostate Cancer Foundation

A study published in *Nature Microbiology* has revealed that bacteria in the urinary tract can turn corticosteroids into androgens – hormones that help prostate cancer grow.

“Bacteria in our bodies are an overlooked part of our hormone system,” said Jason Ridlon. In 2015, Ridlon’s Sterolbiome group began hypothesizing that gut and urinary tract bacteria contribute to hormone-driven cancer. Some bacteria convert drugs used in androgen-deprivation therapy, like prednisone, into androgens, stimulating cancer cell growth.

In the recent study, the team identified two bacterial genes, *desF* and *desG*, that make hormone-like compounds. One big surprise was that a hormone called epitestosterone, thought to block cancer, actually caused prostate cancer cells to grow even more. These findings by Ridlon’s lab were enabled by experiments using microbial bead technology developed by Joseph Irudayaraj’s research group.

“When we developed the microbial bead technology, we did not realize the broad impact of its applications,” Irudayaraj said. “Saeed Ahmad was instrumental in extending the methods to encapsulate anaerobic bacteria in the beads.”

The team also collaborated with Karen Sfanos, a pioneer in studying the link between the microbiome and prostate cancer. Moving forward, they are now focused on mapping additional bacterial pathways that metabolize steroids.

Mutation increases enzyme in mouse brains linked to schizophrenia behaviors

People mentioned

Uwe Rudolph (GNBP), comparative biosciences

Supported by

Broad Institute; Harvard Brain Science Initiative Bipolar Disorder Seed Grant; McLean Hospital; NIH; Shervert Frazier Research Institute; Stanley Center for Psychiatric Research

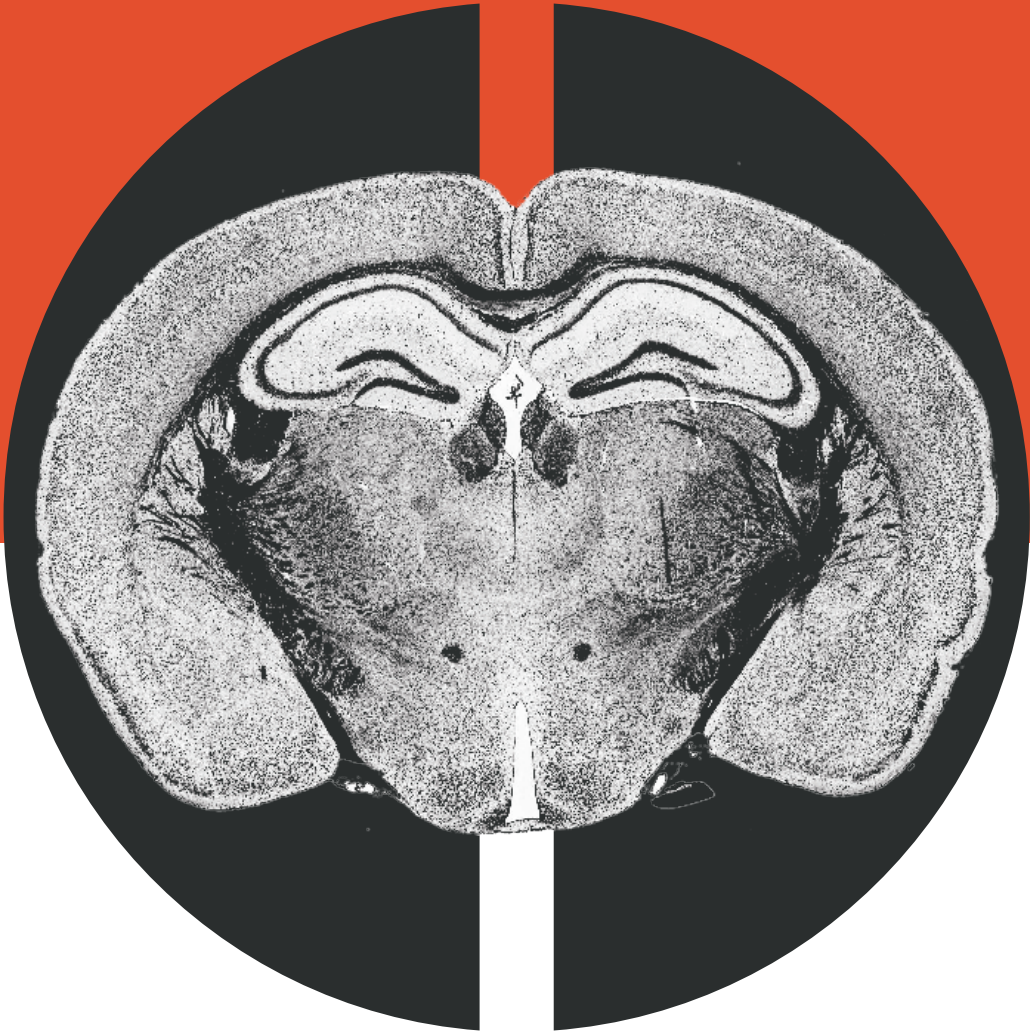
In a collaborative study published in the journal *Molecular Psychiatry*, researchers reported a rare finding of a direct genetic link to psychosis.

“The genetics of schizophrenia is very complex, and it is rare that mutations found in patients can be linked directly to the disease,” said study leader Uwe Rudolph.

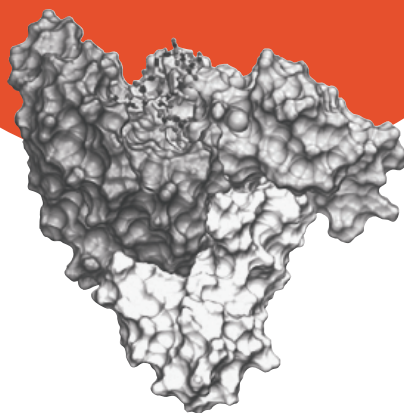
Researchers at McLean Hospital reached out to Rudolph when they found a genetic mutation in two human patients with schizophrenia. The patients’ DNA had multiple copies of the gene for a protein called glycine decarboxylase, or GLDC. This enzyme is responsible for regulating levels of glycine, a chemical signal that is essential for many brain functions, including learning and memory.

Rudolph’s research group created a line of mice with the same mutation and observed that these mice also showed schizophrenia-associated behaviors. With the help of collaborators, the team then investigated why multiple copies of the *glc* gene had such a strong effect on behavior. They found that mice with the mutation had lower amounts of glycine available in a specific subregion of the brain called the dentate gyrus. Subsequent functional studies and biochemical analysis of the dentate gyrus revealed some pathways previously implicated in schizophrenia had reduced activity.

WT



4c9R



Kidney fibrosis linked to molecule made by gut bacteria

Diabetic kidney fibrosis is a major cause of kidney failure worldwide, yet the key drivers of it have remained a mystery. Research from the University of Illinois and Mie University in Japan investigated how corisin – a small peptide produced by *Staphylococcus* bacteria in the gut – could lead to kidney damage.

“Many people with longstanding diabetes eventually develop kidney fibrosis, and once it progresses, there are limited options beyond dialysis or kidney transplantation,” Dr. Taro Yasuma said.

After finding high levels of corisin in the blood of patients with diabetic kidney fibrosis, the researchers used computer simulations and tissue and mouse experiments to track how corisin affects the kidneys, how it gets there from the gut, and a possible method of countering it with antibody treatment.

People Mentioned

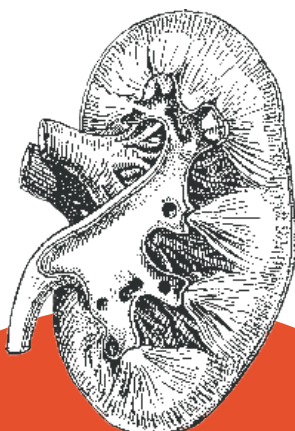
Isaac Cann (MME), animal sciences
Taro Yasuma, Mie University

Supported by

Charles and Margaret Levin Family Foundation; Daiwa Security Foundation; Eli Lilly Japan Innovation Research Grant; Japan Association for Diabetes Education and Care; Japan Society for the Promotion of Science; Japan Science and Technology Agency; Takeda Science Foundation

“Our earlier studies showed corisin can damage cells and worsen tissue scarring and fibrosis in other organs, so we suspected it might be a hidden driver of kidney fibrosis,” Isaac Cann said. “Our new findings suggest corisin is indeed a hidden culprit behind progressive kidney damage in diabetes, and that blocking it could offer a new way to protect kidney health in patients.”

Next, the researchers plan to test anticorisin treatments in more advanced animal models, such as pigs, to explore how they could be adapted for safe use in humans. The researchers published their findings in the journal *Nature Communications*.



Researchers capture new antibiotic resistance mechanisms with trace amounts of DNA

Scientists have developed a method to isolate genes from tiny amounts of microbial DNA. How tiny? It would take 20,000 of these DNA samples to weigh as much as a single grain of sugar. The new method, called METa assembly, was used to discover previously unknown antibiotic resistance genes in

bacterial DNA isolated from human stool and from fish tanks at Chicago's Shedd Aquarium.

“With antibiotic resistance on the rise, it's more important than ever to understand the full diversity of mechanisms bacteria may be using to inactivate or avoid antibiotics,” said Terence Crofts.

Crofts developed METa assembly to improve upon previously existing microbiology approaches that enable researchers to study bacterial genes in the environment. METa assembly

requires 100 times less DNA than standard approaches.

“Because aquatic samples are usually less dense with microbes, you usually can't get as much DNA out of them, but we showed that we could still make good libraries from the aquarium sample,” Crofts said.

Crofts plans to deploy his METa assembly method to agricultural systems – sampling soil and from “nose to tail” in livestock – since antibiotic resistance not only occurs on the farm, it often originates there.

People Mentioned

Terence Crofts (IGOH), animal sciences

Supported by

Florida State University Council for Research and Creativity; USDA's National Institute of Food and Agriculture

In challenging times, a legacy of mentorship and kindness lives on

Eric Jakobsson, an integral member of the University of Illinois and Champaign-Urbana communities for 50 years, is remembered for his legacy of kind and thoughtful leadership. Until his death in 2021, he was an intelligent, calm, and seemingly tireless source of ideas and mentorship in every realm of his life: his family, his laboratory group, his city, and the scientific circles he helped to bridge.

A gift made by his wife Naomi Jakobsson is continuing his legacy through timely and impactful support to research trainees at the IGB. The gift, made in Eric's name, will enable undergraduate and graduate researchers to engage in full-time research experiences.

“Eric was so supportive of his graduate students,” Naomi said, explaining her thought process in planning the gift. “He would just spend hours working with a student, helping them, whether they were

writing something or working out something.”

Remembrances of Eric's academic career invariably highlight both his high level of scientific achievement and his warmth and generosity toward everyone with whom he worked.

Sagar Pandit, who worked with Eric as a postdoctoral fellow, said, “He had a quiet but powerful presence, and his impact on my work, and on me personally, has been lasting.”

Zeeshan Fazal, who completed his graduate degree in Eric's laboratory group, also spoke about the impact of his mentorship.

“He saw me not just as a researcher, but as a person with dreams, struggles, and a family – and he embraced all of it with a heart full of generosity,” Fazal said.

People Mentioned

Eric Jakobsson, molecular and integrative physiology (deceased)

Naomi Jakobsson, former member, Illinois House of Representatives

Sagar Pandit, University of South Florida

Zeeshan Fazal, NIH



Summer EIP pitch contest winners chosen

At the IGB, innovation doesn't take a break for summer! The 10-week IGB Early Innovator Program, offered to IGB graduate students and postdoctoral researchers, is designed to teach participants the skills necessary to become innovative leaders in their fields, and to support IGB scientists in considering creative ways to bring science to society. Trainees learn from subject matter experts about the process of innovation,

People Mentioned

Han Keun Lee, (CGD) electrical and computer engineering

Lauana Pereira de Oliveira (CAMBERS/PFS), plant physiology

Quanhui Ye (CAMBERS), environmental engineering

Seemesh Bhaskar (CGD), photonics and plasmonics

Joshua Ye (CAMBERS/PFS), chemical and biomolecular engineering

protecting and developing discoveries beyond the laboratory, and bringing new technologies and services to the marketplace.

Five aspiring entrepreneurs made their final product pitches to a judging panel, and three were awarded tiered funds ranging from \$2,000-\$5,000 to continue to advance their novel innovations.

Han Keun Lee received first prize for EDiVita, a point-of-care diagnostic platform delivering rapid molecular detection to enable cancer diagnoses in under an hour.

Lauana Pereira de Oliveira was awarded second prize for PhotoYield, which uses trait specialization to boost photosynthesis in energy cane and other biomass-capable crops.

Quanhui Ye received third prize for DeResist Bio, a strategy that uses biocatalysts to remove antibiotic resistant genes from wastewater.

Other participants in the pitch competition included Seemesh Bhaskar, who developed a photonic crystal-based diagnostic tool called SteerLight, and Joshua Ye, who proposed natural yeasts that can deliver active skincare ingredients.

Influenza A infection early in life impacts development of gut microbiome and brain gene expression

People Mentioned

Ying Fang (MMG), pathobiology
Christopher Gaulke (MME),
veterinary clinical medicine
Adrienne Antonson (EIRH),
animal sciences

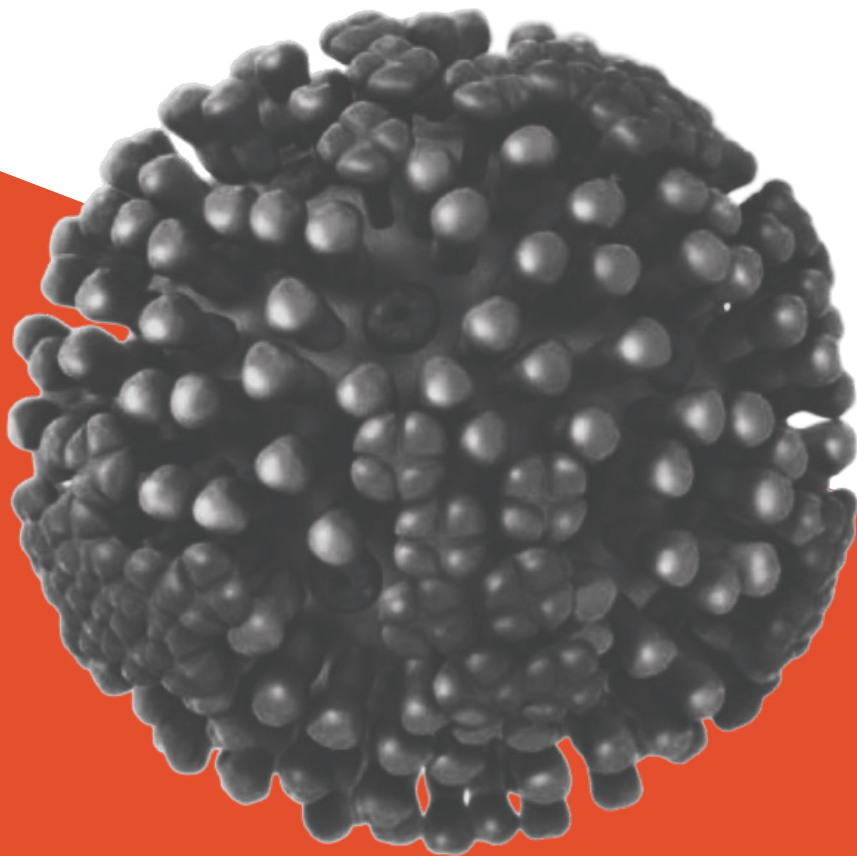
Supported by
NIH

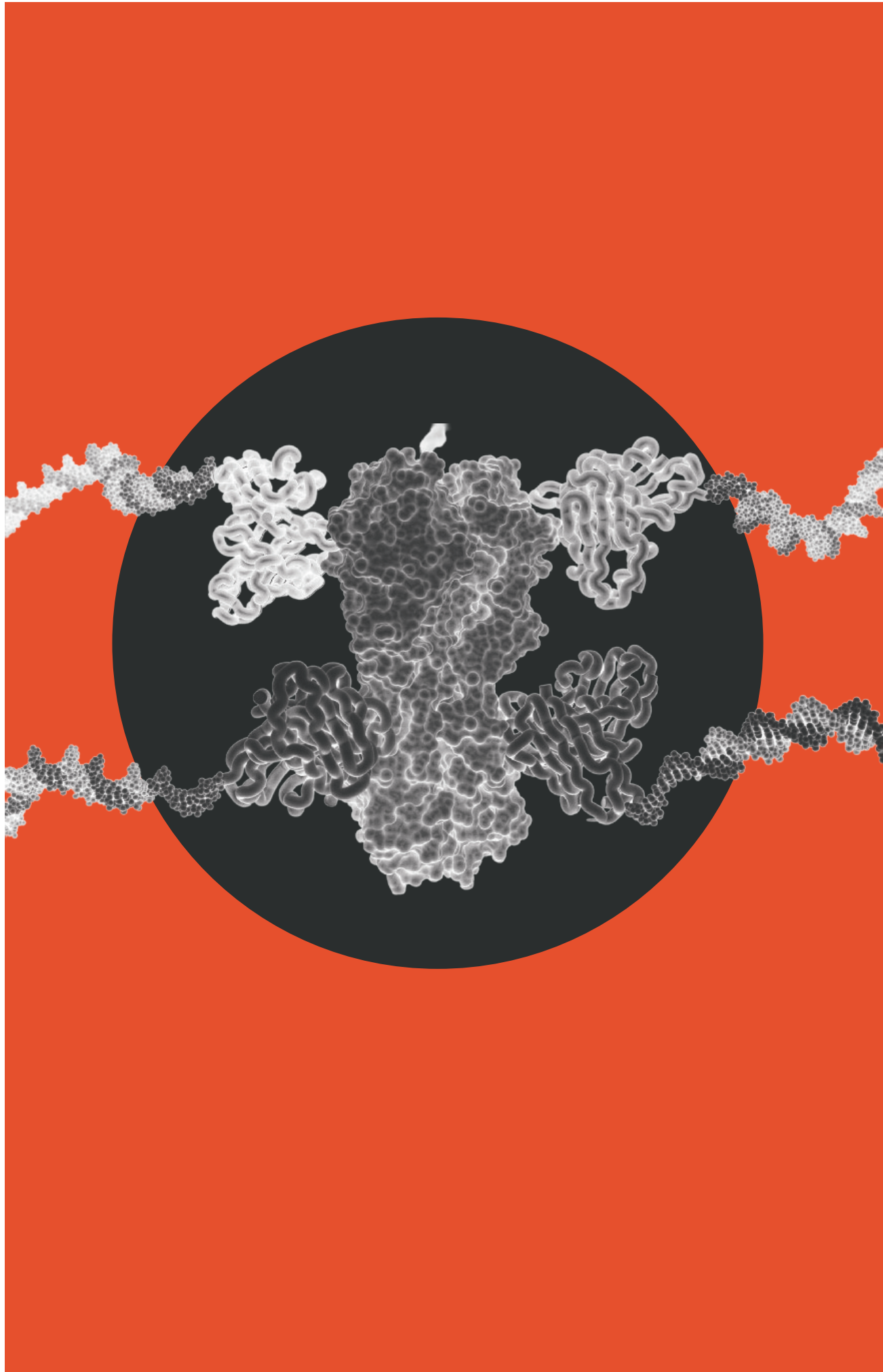
Infants under six months of age are at the highest risk of hospitalization from infection with the influenza A virus and are more susceptible to long-term complications like diabetes, asthma, allergies, and cognitive defects.

“We knew that the microbiome is involved in early brain development, and that influenza can impact respiratory and gut microbiota,” said Christopher Gaulke, who led the research with Ying Fang. “Our study was able to look at how the microbiome may contribute to hippocampal function in the context of this disease.”

The hippocampus is a brain structure that plays a central role in learning and memory, and prior work from collaborator Adrienne Antonson’s lab found that a viral infection during pregnancy can disrupt piglets’ hippocampal development and function. Published in *Veterinary Microbiology*, the study found that infection with influenza A was associated with disruptions in the piglets’ nasal and gut microbiomes, with potentially detrimental changes in gene activity in the hippocampus.

Maternal vaccination against the virus during pregnancy appeared to offer some protection from those changes in the piglets. Further studies are needed to determine the exact mechanisms by which influenza A viral infection leads to these and changes in the microbiome, and whether and how those changes might influence brain health.





High-volume antibody testing platform could accelerate disease research and treatment development

Antibodies are the critical targeting agents of the immune system and the crux of immune therapy and vaccine development, but studying them is slow, expensive and labor-intensive. Now, researchers have developed a new high-volume method, dubbed oPool+ display, that can rapidly build and test large numbers of antibodies at once.

Traditionally, antibodies have been synthesized and studied one at a time – a daunting prospect, considering that the body can make trillions of different antibodies.

“Instead of analyzing one antibody at a time, this approach lets us evaluate thousands of antibody–antigen interactions in just a few days. It not only significantly accelerated the pace of our research but also lowered the cost, both of materials and labor,” said Nicholas Wu, leader of the study.

With the oPool+ display, the researchers built profiles of exactly what each antibody binds, which helps identify the best candidates for treatment development. They also identified features of hemagglutinin antibody activity that were shared across antibodies from many people. The platform could be used to characterize antibodies against many other pathogens as well, whether viruses, bacteria or even cancer. The researchers published their findings in the journal *Science Translational Medicine*.

“If we can search for a potential antibody candidate that’s really good against a certain disease, then it has great potential in becoming an effective therapeutic,” Wenhao Ouyang said.

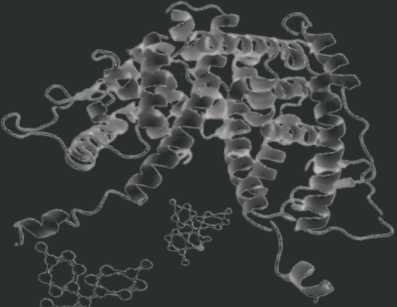
People Mentioned

Nicholas Wu (IGOH/MMG),
biochemistry
Wenhao Ouyang, molecular and
cellular biology

Supported by

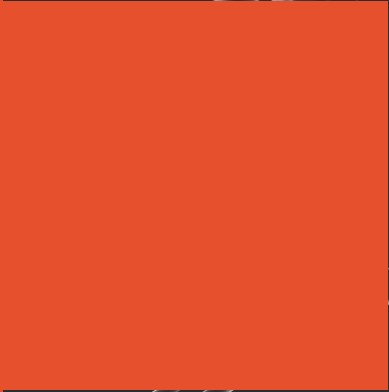
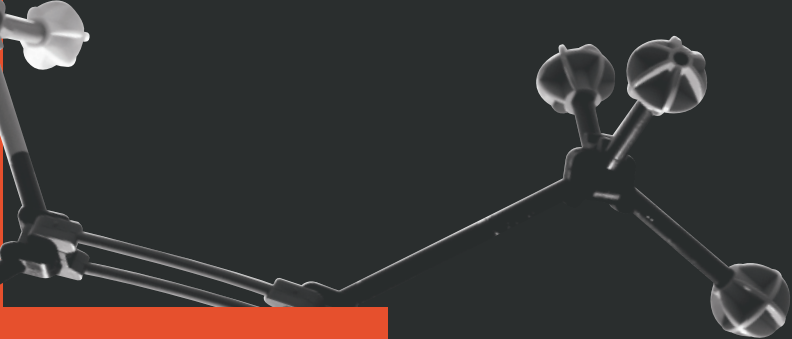
Howard Hughes Medical Institute
Emerging Pathogens Initiative; NIH;
Searle Scholars Program





Some of our most valuable medicines were discovered by chance; a casual observation that a substance alleviates symptoms or kills pathogens ushers it into the pharmaceutical world. Other drugs are discovered through careful study of the process of a disease, which can point to substances that might interrupt that process.

These dual pathways place emphasis on the initial discovery. The testing that follows, establishing whether a potential new drug is effective, safe, and scalable, is long and slow. It's also discriminating – early promise is no guarantee of success through all of this experimental work, or of eventual approval.



Delivering on Better Health

Yet each new drug that is conceived of, discovered, developed, tested again and again, represents a hope to cure ailing patients and lessen suffering. Hiding in the genomes of people and pathogens are secrets of disease that point to new treatments.

How do we get from a molecule to a medicine?

'14

Breast cancer is one of the most common types of cancer worldwide. Unfortunately, more aggressive types like metastatic estrogen receptor-positive breast cancer can be insurmountable, even with treatment.

For several years, a research team led by David Shapiro had been exploring how estrogen signaling contributes to ER+ breast cancers, which make up 70% of diagnoses. In 2014, Shapiro's team reported their discovery of a previously unknown mechanism by which estrogen prepares cells to divide, grow and, in the case of ER+ breast cancers, resist cancer drugs.

Estrogen pre-activates the unfolded-protein response, a pathway that normally protects cells from stress, such as when a cell lacks adequate oxygen or nutrients or is exposed to cancer-killing drugs. It wasn't known before this study, however, that estrogen initiates this pathway before such stresses appear. The work revealed the UPR pathway as a promising new target for breast cancer therapy.

'15

Researchers reported that an experimental drug called BHPI rapidly shrinks most tumors in a mouse model of human breast cancer. The key to the drug's potency lies in its unusual mode of action, which targets the UPR pathway.

Because the UPR pathway is overexpressed in therapy-resistant cancer cells, the drug is especially effective in targeting estrogen receptor-positive cells that are resistant to tamoxifen and other anti-cancer drugs.

'16

IGB researchers had successfully made the leap from understanding more about the mechanism of ER+ breast cancers to identifying a compound that could interrupt that mechanism. Now they faced the stage of research that some drug developers call the "valley of death": exploring whether the drug could, with refinement, prove itself in an increasingly stringent series of laboratory experiments and earn a chance at a clinical trial.

During this stage, Shapiro's team examined the performance of several molecules related to BHPI, including a similar molecule called ErSO, hoping to discover one with the best chance of meeting the high standards of drug development.



'20

The pharmaceutical company Bayer AG announced that they had just licensed ErSO based on its promise as a breast cancer treatment. While the full study was not yet published, Shapiro's long-time collaborator Paul Hergenrother disclosed researchers' findings that ErSO rapidly and selectively killed ER-positive breast cancer cells.

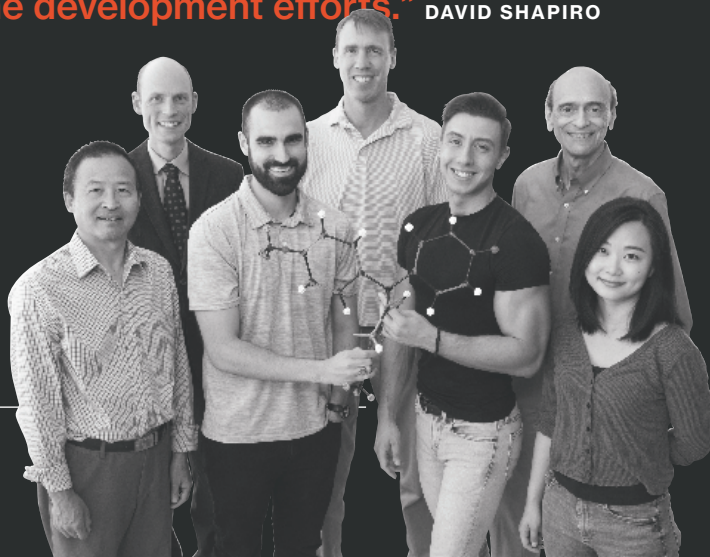
With the license in hand, Bayer AG aimed to explore the molecule's potential for further study in human clinical trials targeting ER-positive breast cancers.

'21

Shapiro and Hergenrother's team published their findings on ErSO compared with their earlier drug prospect, BHPI. While BHPI prevented breast cancer cells from growing, it did not rapidly kill them, and it had undesirable side effects. ErSO, on the other hand, targets the same UPR pathway as BHPI while demonstrating more potent anticancer properties.

"Since the process is estrogen-receptor dependent, ErSO doesn't touch the cells that lack the receptor, and it also doesn't affect healthy cells – whether or not they have an estrogen receptor," Hergenrother said.

"Our Illinois research lab will continue doing what we do best on the research side with the hope that our findings can further empower the development efforts." DAVID SHAPIRO



'21

When they tested the drug in mice models of human ER+ breast cancers and their metastases in the bone, brain, liver, and lungs, the drug killed 95-100% of the cancer cells and shrank large tumors to undetectable levels. The compound was also well tolerated in mice, rats, and dogs.

With these data published and ErSO in Bayer AG's hands to assess its potential for clinical trials, the team was able to turn their focus to further investigating what biological pathways ErSO affects and ways to improve the preclinical drug.

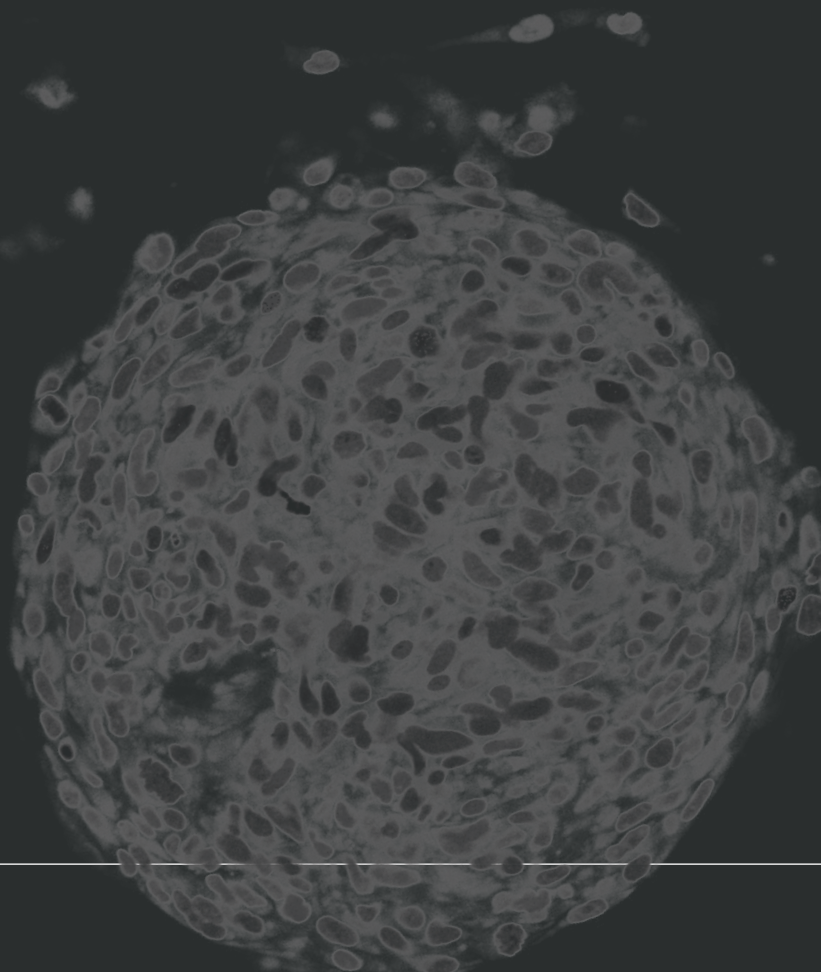
"We've never seen a class of compounds that looks this good. It is really, really remarkable. This is a very promising compound for breast cancer treatment."

PAUL HERGENROTHER

'23

In a study published in the journal *Cancer Research*, the team identified a protein, TRPM4, that was a key driver in the process of necrosis in cancer cells treated with ErSO or BHPI. The study revealed that ErSO-induced changes in the protein led to the movement of ions and water across the cell membrane, causing the cells to swell, leak, and rupture. This in turn attracts immune cells to clean up the debris.

In parallel, Hergenrother's chemistry group was leading the charge in developing an improved version of ErSO, coined ErSO-TFPy. In 2023, this new version of the molecule was licensed to biotechnology company Oncoteq under the name of TEQ103, where it could undergo pre-clinical drug development with the goal of advancing to human clinical trials in late-stage metastatic breast cancer patients.



'25

Further study of ErSO-TFPy showed that in mice, a single dose could achieve the same dramatic tumor eradications observed with multiple doses of ErSO. If the ErSO-TFPy molecule does successfully translate its tumor reducing abilities to human breast cancer, women with the disease could have a much more positive outlook.

The research that began with a fresh insight into how a common type of cancer forms and progresses, after over a decade of careful work, may yet lead to a powerful new treatment. Which research projects beginning today might yield similar results in another decade?



People Mentioned

Paul Hergenrother (ACPP leader/MMG), chemistry; David Shapiro, biochemistry

People Involved

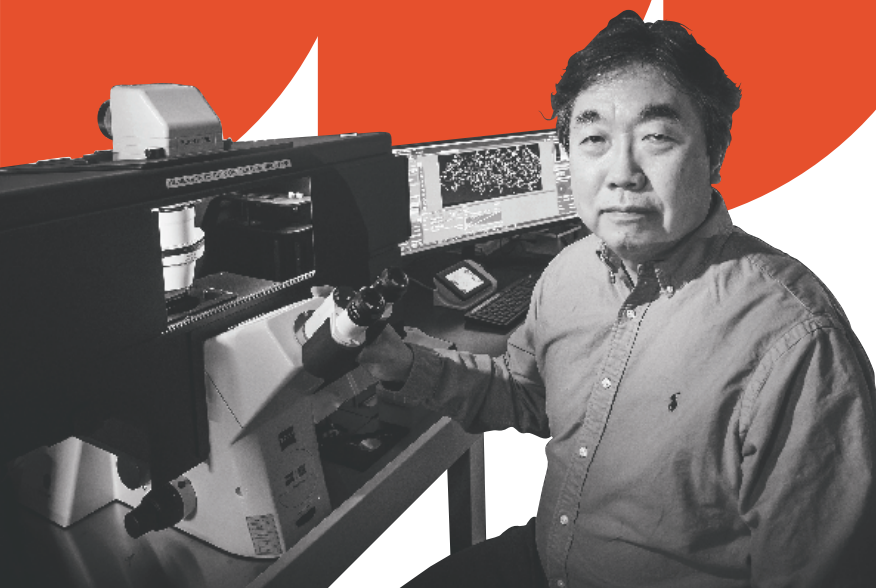
Elaine Alarid (University of Wisconsin), Neal Andruska, Matthew Boudreau, Brooke Bouwens, Elizabeth Bruckheimer (Systems Oncology), Hunter Carrell, Mathew Cherian, Xinyi Dai, Darjan Duraki, Stephanie Ellison (University of Wisconsin), Timothy Fan, Sean Fanning (University of Chicago), Santanu Ghosh, Geoffrey Greene (University of Chicago), William Helferich, Madeline Henn, Paul Hergenrother, Musarrat Jabeen, Xinguo Jiang, Jeffrey Kiefer (Systems Oncology), Ji Eun Kim, Yoongyeong Lee, Mara Livezey, Lily Mahapatra, Chengjian Mao, Ramon Moreno (Systems Oncology), Spyro Mousset (Systems Oncology), Michael Mulligan, Erik Nelson, Ben Ho Park (Vanderbilt University), Edward Roy, David Shapiro, Bingtao Tang, Theodore Tarasow (Systems Oncology), Lawrence Wang, Xujuan Yang, Rachel Yang, Xiaobin Zheng, Junyao Zhu

Publications

Jiang, et al., *Oncogene* 26, 2007; Andruska, et al., *Oncogene* 34, 2015; Andruska, et al., *Proc. Natl. Acad. Sci. U.S.A.* 112 (15), 2015; Boudreau, et al., *Sci. Transl. Med.* 13, 2021; Ghosh, et al., *Cancer Res.* 83 (18), 2023; Mulligan, et al., *ACS Cent. Sci.* 11, 2025

Briefs

Delivering on Better Health



DNA origami guides new possibilities in the fight against pancreatic cancer

One of the challenges of fighting pancreatic cancer is finding ways to define the margins between malignant and normal tissue. A study published in *Advanced Science* used DNA origami structures to selectively deliver fluorescent imaging agents to pancreatic cancer cells without affecting normal cells.

"This research highlights not only the potential for more accurate cancer imaging, but also selective chemotherapy delivery," said Bumsoo Han, who led the work with Jong Hyun Choi. "The current process of cancerous tissue removal through surgical resection can be improved greatly by more accurate imaging of tumor margins."

People mentioned

Bumsoo Han (M-CELS), mechanical science and engineering

Jong Hyun Choi, Purdue University

Supported by

NIH; NSF

The research team experimented with different sizes of tube and tile-shaped DNA origami nanostructures. Inspired by paper origami, the nanostructures were created by folding DNA – a long, double-stranded molecule – into looping shapes capable of holding fluorescent dye molecules. They tested these dye-packed DNA structures in pancreatic cancer models, imaging the movement of the dyes.

The team found two particular sizes of tube-shaped structures that experienced the greatest uptake by the pancreatic cancer tissue while not being absorbed by the surrounding noncancerous tissue. Other sizes and shapes did not perform as well.

The next step is to explore the use of origami-folded DNA molecules loaded with chemotherapy drugs for selective delivery to cancer cells without affecting normal cells.

Drug-delivering aptamers target leukemia stem cells for one-two knockout punch

Leukemia and other cancers of the blood are difficult to target for treatment because the cancerous cells circulate throughout the body and can't be surgically removed. In a study led by Xing Wang and published in *Advanced Functional Materials*, IGB researchers reported the ability of a nanoscale drug delivery system to precisely target elusive cancer stem cells.

"It's important in leukemia, lymphoma or other blood cancers that we actually target and eliminate these stem cells, because as long as any are remaining, they can cause relapse and secondary cancers," said Abhisek Dwivedy, first author of the paper.

The researchers began by finding DNA aptamers – short single-strand snippets of DNA – that seek out markers found on the surface of acute myeloid leukemia stem cells. The team then paired their aptamers with the leukemia-fighting drug daunorubicin. In mice with leukemia, delivering the drug via aptamer yielded the same efficacy at a dose 10 times smaller than the clinical standard.

"This work demonstrates a way to get to the root of leukemia," Wang said. "Targeted cancer treatments often have problems with toxicity or efficacy. Our aptamers seek out these stem cells specifically and kill them effectively."

People Mentioned

Xing Wang (CGD), bioengineering
Abhisek Dwivedy, structural biology

Supported by

NIH; NSF

Study sheds light on liver maturation, specialization

The human liver performs over 150 specialized functions, including filtering blood, removing waste, regulating blood sugar, and digesting fats. Hepatocytes – the main cell type of the liver – are fully formed by birth but remain dormant for the first few weeks of life. During this time, they gradually mature and develop specialized attributes.

In a study published in *Genes and Development*, researchers identified a key process coordinating liver maturation, a finding that provides insight into hepatocyte specialization that will aid efforts in regenerative medicine. The team, led by Auinash Kalsotra, began by evaluating the gene *ESRP2*. This gene produces a regulatory protein known to control how other proteins are produced in the liver.

"We know [*ESRP2*] is turned on right around the time when liver cells start to mature," Sushant Bangru said. "But is that a coincidence, or is *ESRP2* protein actually involved in liver maturity?"

function. They found that *ESRP2* has a direct effect on liver function that prompts hepatocytes' shift to maturity. The team then worked to find both direct and indirect targets of *ESRP2*, tracing its entire regulatory network.

"Right now, we're learning how we can coax the adult cells to become immature and then back to fully functional," Kalsotra said. "And that will help us tune the regenerative response relative to the need of an organism."

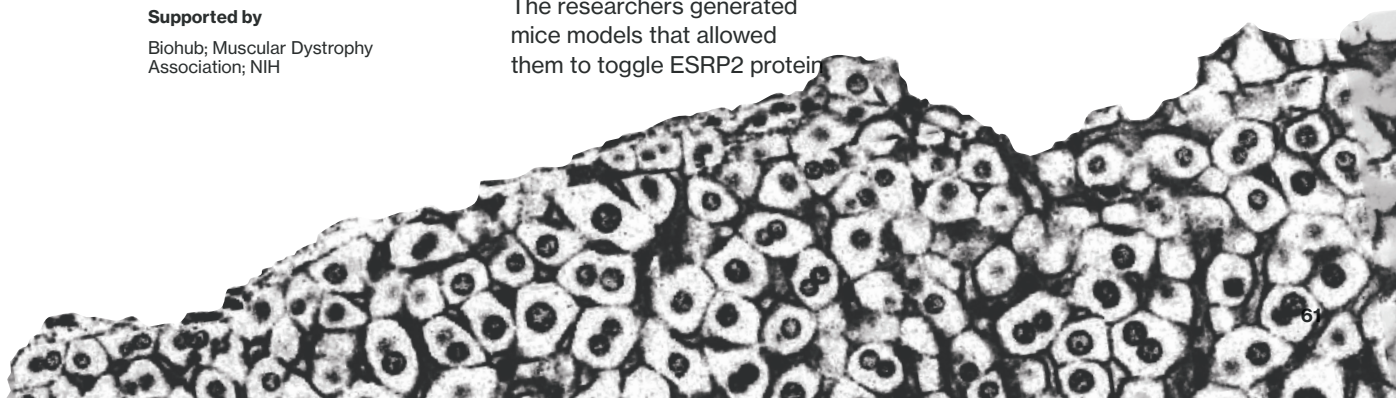
People Mentioned

Auinash Kalsotra (CGD/GNDP),
biochemistry
Sushant Bangru, biochemistry

Supported by

Biohub; Muscular Dystrophy
Association; NIH

The researchers generated mice models that allowed them to toggle *ESRP2* protein



Researchers discover a new type of biomaterial for drug delivery in cancer treatment

Extracellular vesicles, or EVs, are small packages of molecules secreted by cells, budding off from the cell membrane to transmit or offload substances. They have shown promise for the treatment of disease including cancer. In the journal *Nature Communications*, Hua Wang's research group reports a new method to create hydrogels, a material used in drug delivery, made up of EVs.

to minimal incorporation of EV material. The new technique instead uses small amounts of polyethylene glycol polymers to link the EVs together into a larger structure. Through this method, researchers can more easily tune the hydrogel's mechanical properties by changing the EV concentration. Wang's team aims to employ these EV hydrogels for cancer treatment and long-term depot vaccines.

People mentioned

Hua Wang (RBTE), materials science and engineering

Supported by

American Cancer Society; NIH; NSF; Sontag Foundation

"Oftentimes, researchers just physically load EVs into preformed biomaterials," Wang said. "But now they have the choice to fabricate high EV content hydrogel mainly made of EV itself. This new way of use will benefit the whole EV research community."

Common ways to load hydrogels with EVs often lead

"When you inject the hydrogel, it will form a depot at the injection site," Wang said. "This can stay in the body for many weeks, many months, and can generate the immune response for a much longer time. When working with EVs from a tumor cell, that can result in more durable T cell response and anti-tumor efficacy."

Researchers aim to disrupt communication between cells that leads to breast cancer spread

While breast cancer therapies have improved significantly in recent years, many molecular mechanisms involved in disease progression and treatment resistance are still unknown. Led by Erik Nelson, researchers are investigating the relationship between cholesterol and breast cancer progression to inform the development of new therapeutics.

Prior work by the lab identified a cholesterol metabolite called hydroxycholesterol, or 27HC, that suppresses the ability of the immune system to attack cancer. They found that 27HC stimulated immune cells called neutrophils to secrete extracellular vesicles; these EVs are small packages that contain molecular signals to other cells. The lab's latest study, published in *Cancer Letters*, reported new insights into the way that 27HC impacts communication between immune and cancer cells.

'makeup' ... allowing them to become resistant to standard chemotherapies as well as spread to other organs."

Based on these findings, the team will now start working on developing new treatment strategies focused on disrupting this communication in the early stages of breast cancer, with the goal of decreasing the occurrence of breast cancer metastasis.

People mentioned

Erik Nelson (ACPP), molecular and integrative physiology

Natalia Krawczynska, human/medical genetics

Supported by

Beckman; CCIL; DOD; Illinois Postbaccalaureate Research Program; NIH; NSF

"27HC 'tells' neutrophils what to put into EVs before sending them out," said Natalia Krawczynska. "These customized neutrophil-EVs communicate with cancer cells themselves and instruct them to change their



New chemical engineering application expands possibilities for targeted drug delivery

Researchers have proposed a new avenue for targeted drug delivery. Their findings, published in *Materials Today Bio*, represent the first successful application of metabolic labeling in platelets.

Platelets are blood cell fragments that congregate at sites of bleeding and inflammation to form clots. While their unique properties

make them attractive vehicles for targeted drug delivery systems, platelets are notoriously difficult to engineer due to their small size and physiologic simplicity.

“Cells can usually be engineered with a genetic or chemical approach,” lead author Hua Wang said. “But platelets don’t have a nucleus or the typical DNA machinery, which makes them difficult to genetically engineer.”

The researchers turned to a chemical approach called metabolic glycan labeling; Wang’s lab had previously demonstrated successful metabolic labeling in cancer

and immune cells. The researchers began the project by testing their method in a cell culture medium, then shifted to an *in vivo* mouse model. In both cases, the group successfully observed chemical tags on the surface of platelets after addition of the sugar compound.

Scientists are optimistic that specially tagged platelets can be used as drug delivery vehicles for cancer, immune diseases, and blood clotting disorders. Because platelets have a short half-life, their cargo is cleared from the body within days, alleviating concerns over long-term side effects.

People mentioned

Hua Wang (RBTE), materials science and engineering

Supported by

CCIL; NIH; NSF; University of Illinois



Fruit fly study reveals a gene's hidden ability to keep regrowth on the right track

Health research inspired by the remarkable regeneration of animals like axolotls or starfish asks how future therapeutics could promote the regrowth of hard-to-heal tissues, limbs, or even entire organs. A study in *Science Advances* is a step toward clarifying a less visible, yet vital, corollary – how regeneration comes to a successful close when a tissue has healed.

The team, led by Rachel Smith-Bolton, hypothesized that particular genes are responsible for making sure that regeneration ends with the right number and types of cells; they chose to investigate a gene called *Zelda*, known to have important roles in development.

Drosophila fruit fly larvae, the tissue of the developing fly's future wings could not recover from damage. In contrast, if the wing tissue was allowed to develop without disruption, *Zelda* inactivation had no effect on wing growth. *Zelda* was not needed for healthy development, but injured wing tissue couldn't regrow without it.

"During the mid-stages of regeneration, *Zelda* becomes crucial for the wing disc to properly recover," Anish Bose, first author on the publication, said. "This reveals a striking distinction between how tissues grow during development and how they repair themselves after injury."

People mentioned

Rachel Smith-Bolton (GNDP/RBTE), cell and developmental biology

Anish Bose, molecular and cellular biology

Supported by

NIH; University of Illinois

The team found that when *Zelda* was inactivated in

Flightpath Biosciences licenses microbiome-sparing antibiotic developed at Illinois

Flightpath Biosciences, Inc., a clinical stage biotechnology company focused on the development of precision therapeutics targeting bacterial pathogens, has obtained an exclusive global license for all uses of the lolamicin class of antibiotics. This class of drugs inhibits a molecular mechanism exclusive to gram-negative bacteria that cause some of the most difficult bacterial infections to treat.

"We were attracted to Flightpath as a partner because of its past operational and development successes and its stability as a company," said Paul Hergenrother, whose lab produced lolamicin and its derivatives. "Flightpath has the capabilities and resources to advance this exciting new technology for patients."

Published in the journal *Nature* in 2024, the original antibiotic agent, lolamicin, effectively treated bacterial infections in animal models of disease. Importantly, detailed analysis showed that lolamicin had no deleterious effect on the gut microbiome of mice, whereas clinically approved antibiotics killed many of these "good" bacteria, disturbing the gut microbiome. The lolamicin class of drugs is still early in the drug-development process. Additional

preclinical studies must be conducted to demonstrate the lead drug candidate's safety and efficacy.

People mentioned

Paul Hergenrother (ACPP leader/
MMG), chemistry
Matt Tindall, Flightpath Biosciences

Flightpath Biosciences CEO Matt Tindall said, “The novel mechanism of action and resulting targeted drug candidates are potential game-changers in the treatment of infection-driven diseases, preserving, rather than undermining, an intact healthy microbiome and immune system.”

Researchers unlock insights into granular hydrogels for biomedical applications

In a collaborative project led by Brendan Harley and Simon Rogers, researchers have developed a novel framework for understanding and controlling the flow behavior of granular hydrogels – a class of material made up of densely packed, microscopic gel particles. This material has promising applications in medicine, 3D bioprinting, and tissue repair.

“Knowing how well our model works, we could then calculate how the granular hydrogels are going to behave under any flow condition or deformation type, such as being printed into the body or injected into the body,” said Rogers. “Or what would happen once they’re in, say, a shoulder joint or a knee joint, or wherever they’re going to be injected into it.”

Granular hydrogels have a unique ability to mimic the mechanical properties of living tissue, making them ideal candidates for encapsulating and delivering cells directly into the body. In the new study, published in *Advanced Materials*, the team reports a predictive model that captures the essential physics of how these hydrogels deform, reducing a complex problem to a few controllable parameters.

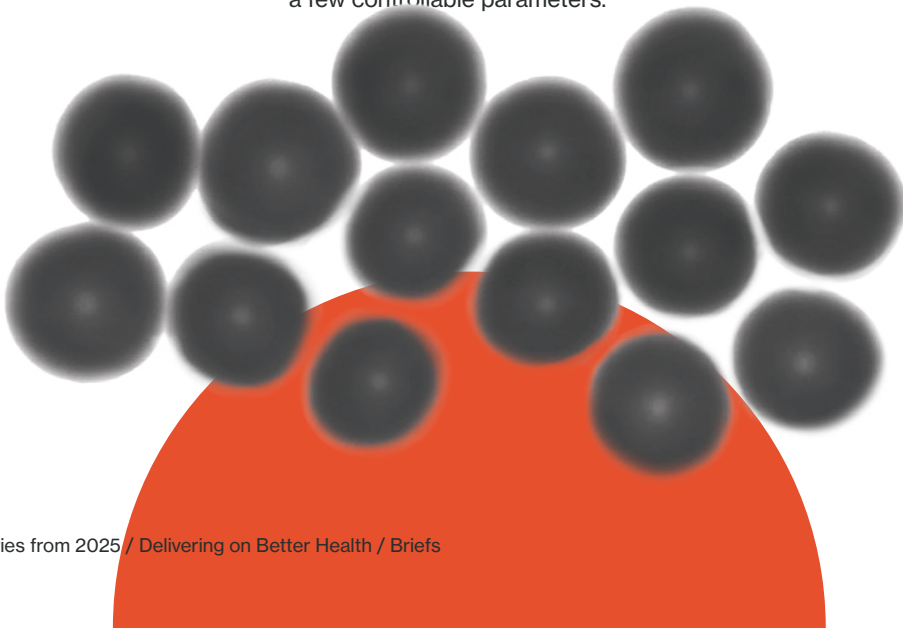
Harley and Rogers agree that bringing together their separate areas of expertise was key to producing the new framework and laying the groundwork for real world application.

People mentioned

Brendan Harley (RBTE leader/EIRH),
chemical and biomolecular engineering
Simon Rogers, chemical and
biomolecular engineering

Supported by

NIH





Harnessing generative AI to expand the mitochondrial targeting toolkit

The mitochondrion, often referred to as the powerhouse of the cell, plays critical roles in cellular function, making it a prime target for biotechnology. Proteins manufactured by the cell are labeled for transport into mitochondria by special molecular tags called mitochondrial targeting sequences. Only a few MTSSs have been discovered in nature; a study led by Huimin Zhao and published in *Nature Communications* demonstrates the utility of generative artificial intelligence for designing new ones.

“Researchers want to study the biology of the mitochondria, which can’t be done efficiently without using targeting sequences,” Zhao said. “But we are currently limited by the availability of these mitochondrial targeting sequences.”

MTSSs found in nature range from 10 to 120 amino acids in length, and they lack predictable patterns in the parts of their sequences that enable mitochondrial targeting. **Generative AI can find patterns in these data**

that are difficult for humans to recognize and extrapolate.

Using an unsupervised deep learning framework called variational autoencoder, the research team identified key features of MTSSs. They then designed a million AI-generated MTSSs and experimentally tested the mitochondrial targeting abilities of 41 of them, achieving a 50 to 100% success rate in yeast, plant cells, and mammalian cells. The team further applied the generated MTSSs for both metabolic engineering and protein delivery.

People mentioned

Huimin Zhao, chemical and biomolecular engineering (BSD leader/CABBI/CGD/MMG)

Aashutosh Boob, chemical and biomolecular engineering

Supported by

DOE

Long-term alcohol use suspends liver cells in limbo, preventing regeneration

The liver has a remarkable ability to regenerate itself after damage or partial removal. However, it loses that ability in patients with alcohol-associated liver disease.

“The only real life-saving treatment option once a patient reaches the liver failure stage in those diseases is transplantation. But if we understood why these livers were failing, maybe we could intervene,” said Auinash

People mentioned

Auinash Kalsotra (CGD/GNDP),
biochemistry

Anna Mae Diehl, Duke University
School of Medicine

Supported by

Biohub; Duke Endowment; Muscular
Dystrophy Association; NIH

Kalsotra, who co-led the study with Anna Mae Diehl.

Their study, published in *Nature Communications*, found that excessive alcohol consumption can disrupt the liver’s unique regenerative abilities by trapping cells in limbo between their functional and regenerative states, even after a patient stops drinking.

To figure out why the cells were getting stuck in this state, the team investigated how the messenger RNA molecules carrying instructions for protein synthesis were pre-processed, or spliced. Errors in splicing can result in the production of dysfunctional proteins within the cell.

“In comparing the samples, we saw RNA was getting

misspliced broadly in alcohol-related liver disease, across thousands of genes, and it was affecting major functions of proteins,” Kalsotra said.

The researchers found a possible driver of the RNA missplicing: alcohol-damaged liver cells had a deficiency of the protein ESRP2, which binds to RNA to splice it properly. Further experiments revealed that liver support cells and immune cells, drawn to the liver tissue damaged by alcohol processing, released high amounts of inflammatory and growth factors. Those factors suppressed ESRP2 production and activity.

Illinois team to lead up to \$28M initiative to build a precision phage platform for promoting public health

IGB researchers are partnering with investigators from industrial and academic institutions, including Ginkgo Bioworks, Baylor University, University of Minnesota, Oregon State University, and Oregon Health & Science University, on a five-year initiative funded by the Advanced Research Projects Agency for Health.

The project, “Microbe/phage Investigation for Generalized Health TherapY (MIGHTY),” aims to harness the natural predators of bacteria – known

as phages – as precision tools to shape the human microbiome and promote health.

Phages have potential transformative uses as precision antimicrobials because they target specific pathogens while leaving beneficial bacteria unharmed. The MIGHTY team will create a platform that enables rapid isolation of bacteria and phages at an unprecedented scale and apply mechanistic modeling and artificial intelligence/machine learning methods to identify effective phage combinations that eradicate harmful bacteria.

As an initial application, the team will focus on the oral

microbiome where bacterial pathogens drive tooth decay and gum disease, and also contribute to chronic illnesses, including cardiovascular disease, Type II diabetes, and oral and colorectal cancers. The researchers aim to develop an easy-to-use, low-cost phage product, such as a chewable gummy, that can improve oral health for everyone.

“Our long-term goal is to usher phage-based therapeutics into mainstream medicine as routine and widely accessible treatments,” said Asma Hatoum-Aslan. “A simple product for oral care is just the start – this platform will support solutions for gut, metabolic, and autoimmune diseases as well.”

People mentioned

Asma Hatoum-Aslan (MME),
microbiology



Computer simulation could light the way to safer cannabinoid-based pharmaceuticals

Novel psychoactive substances, originally developed as potential analgesics but abandoned due to adverse side effects, may still

have pharmaceutical value if researchers can nail down the causes of those side effects.

While synthetic NPS can mimic the effects of classical cannabinoids, Diwakar Shukla's group found that they tend to activate distinct signaling pathways in the human brain compared to classical cannabinoids. Specifically, they often trigger what's called the

"beta arrestin pathway" rather than the "G protein pathway." This switch in signaling can lead to more severe psychological effects.

"New psychoactive substances bind very strongly to cannabinoid receptors in the brain and are slow to unbind, making them difficult to observe and simulate in standard laboratory or

People mentioned

Diwakar Shukla (BSD/CAMBERS/MMG), chemical and biomolecular engineering

Supported by

NIH; NSF

computer experiments,” Shukla said. “It can take a huge amount of computer time to see these rare binding and unbinding events.”

The team used a new simulation approach called the Transition-Based Reweighting Method to

predict the dynamics of slow molecular processes. They also took advantage of the Folding@Home platform, which enables millions of volunteers worldwide to donate computing power. The combination of these methods allowed the researchers to uncover new

physical insights into how NPS interact with receptors. The study’s findings are published in the journal *eLife*.

Continued support builds momentum for a unique interdisciplinary training program

Last year, with support from Mark Tracy, the IGB established a program to help train a new generation of interdisciplinary researchers. After a successful first year and with the help of a new gift from Tracy, the Tracy Undergraduate Team Science Training Program continues to build momentum and extend its reach.

Tracy was inspired to extend his support after seeing the program and the trainees in action. Students in the program engaged in a variety of training activities throughout the year, including seminars, participatory workshops, and a biotechnology industry site visit. The program content also specifically emphasized interdisciplinary teamwork skills.

“I learned those skills in the workplace, in multi-disciplinary collaboration...if you get that as an undergrad, I think that helps you not only with the scientific process, but as an individual,” Tracy said.

Rene Mohammadi, who participated in the program’s inaugural year, found that the program offered her a unique training opportunity as she considered how to integrate her academic and research interests.

People mentioned

- Mark Tracy, Tracy BioConsulting, LLC
- Tracy Parish, external relations and strategic partnerships
- Rene Mohammadi, mechanical engineering

“As someone who’s studying mechanical engineering while researching biomolecular engineering, the concept of ‘interdisciplinary research’ felt intuitive,” Mohammadi said. After obtaining her bachelor’s degree, she now has a graduate position at the Mayo Clinic investigating early cancer detection methods. “By joining this program, I was investing into my future as an engineer-scientist.”





Automation revolutionized societies. Machines replaced human workers in performing tasks that required precision and tedious repetition. Does this capability, so valuable in industry, have a place in scientific research?

Synthetic biology has provided a clear answer. In the last two decades, the emergence of this field has brought about its own revolution in the life sciences.

Synthetic biologists apply the principles of engineering to living systems, editing and adding to microbial genomes or growing tissues to address challenges in medicine, agriculture, and industry.

One advantage of these carefully designed living systems is their potential to obviate the need for automated manufacturing. Instead, it is their development that requires cycles of labor-intensive, repetitive laboratory tasks. Despite decades of study and

Designing Stronger Systems

incredible advances, our understanding of the full complexity of a genome's function is limited. Synthetic biology requires trial and error on a genomic scale; laboratory automation is moving this work from extraordinary to everyday.

How can we work on robots to make them work for us?

'09

This year brought the first example of automating synthetic biology workflows.

A Harvard University research group reported a new method called multiplexed automated genome engineering. Using a prototype autonomous device to help carry out the MAGE workflow, the researchers could generate 4.3 billion different genetic variants of *E. coli* per day, enabling rapid screening for strains with useful traits.

For many years, Huimin Zhao's research group worked to develop new biosynthetic tools and use these for applications like drug discovery and sustainable biomanufacturing of industrial products. Following in the footsteps of MAGE, and aided by continuously advancing technology and computational capabilities, the team set out to bring laboratory automation to Illinois.

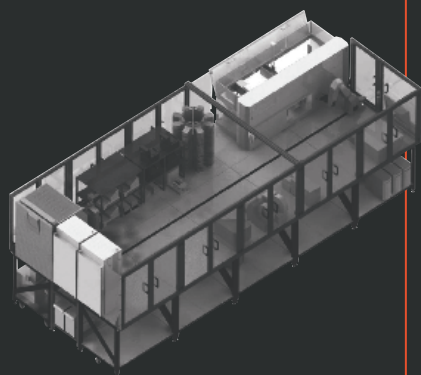
'14

Zhao's team reported their development of FairyTALE, an efficient platform for making TALE proteins, a required component for some gene editing processes. The platform took advantage of an automated robotic liquid handling system that can process samples more accurately and hundreds of times more quickly than humans.

Building on this work, the Illinois Biological Foundry for Advanced Biomanufacturing



'17



was established in 2014. Conceived and led by Zhao, the iBioFAB expanded past just liquid handling, bringing together physical infrastructure and computational tools to perform the laboratory work needed for complex synthetic biology lab processes. With a robotic arm that moves the samples between different instruments and modules, the platform supported the efficient design, fabrication, validation, and analysis of genetic constructs.

With access to the iBioFAB, Zhao's team fully automated the synthesis of TALEs, as well as TALENs, a related protein-based gene editing tool. Rather than developing a customized platform specific for TALEN synthesis, which is not efficient or economical, the researchers chose to instead use generalized workflows implemented on the iBioFAB. With its modular design and components, the biofoundry's infrastructure was more adaptable, allowing researchers to use it for a diverse range of applications.

Another 2017 publication demonstrates this versatility: Zhao's group showed that multiplex genome-scale engineering in *Saccharomyces cerevisiae* could also be carried out with the iBioFAB.

In a single step, multiple gene edits were made to the yeast cells. These were combined in random permutations, generating many different strains, each with its own unique sets of modifications. These strains were then subjected to selection processes to identify those with desirable traits.

"A hundred years ago, people built cars by hand . . . Now, that process is much more economical and efficient thanks to automation, and we imagine the same for biomanufacturing of chemicals and materials."

HUIMIN ZHAO



'19

IGB researchers reported the first autonomous experimentation paradigm for biosystems; iBioFAB was integrated with artificial intelligence to form a closed-loop, fully automated system called BioAutomata. Employing machine learning algorithms, the system designed, built, tested, and learned complex biochemical pathways to produce lycopene, a red pigment found in tomatoes and commonly used as a food coloring.

BioAutomata runs experiments, generates data, and learns from the results to inform the next round of experiments, updating its predictive models as it goes. Through this process, the AI can minimize the number of experiments required to reach its programmed objective, while also saving costs. Continued improvements to the robotic hardware of iBioFAB also improved the speed and accuracy of complex biosynthetic and genomics lab processes.

'22

Prior innovation mainly focused on automating laboratory processes to build biosynthetic constructs. New research aimed to improve other steps in the workflow to create a robust and reliable end-to-end pipeline.

The team led by Zhao developed PlasmidMaker – an automated, computational platform to design and construct small pieces of DNA called plasmids – as a proof of concept. DNA assembly is a key step in molecular and synthetic biology that is often a bottleneck in the process. This platform for building DNA fragments features a user-friendly web interface on the front end and back-end software accessible to technicians who perform quality checks before sending the plasmid to be built by the iBioFAB.

'24

The NSF awarded \$15 million to Illinois to establish the iBioFoundry. One of five new NSF facilities in the United States, each with a different focus, the iBioFoundry aims to expand the use of automated systems, machine learning, and AI to promote and optimize advances in synthetic biology, biotechnology, and genomics.



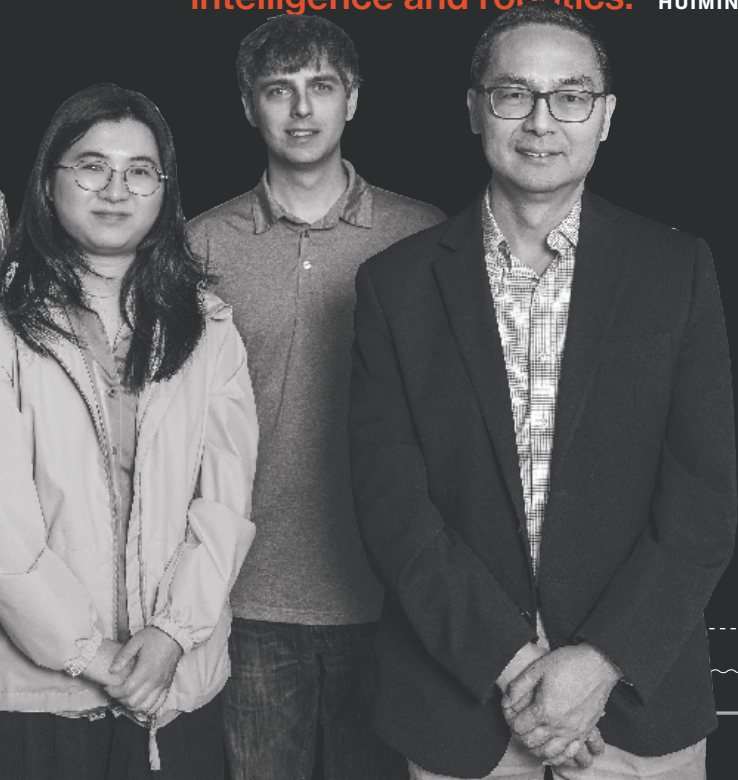
'25

Publishing in *Nature Communications*, Zhao's group showcased the iBioFoundry's capacity for generalized autonomous experimentation by extending the paradigm to enzyme engineering, a pursuit that is often time-

consuming, labor-intensive, and not straightforward. The researchers were able to improve performance of two important industrial enzymes, and created a user-friendly, fast process to improve many more.

Moving forward, a key focus is to democratize the capabilities of the platform, offering a grant proposal program and remote access for external users to work on their own scientific problems. As the applications of synthetic biology continue to expand, the time invested in developing automation frees researchers to work swiftly to find solutions to societal challenges.

"It also will be an open ecosystem of disruptive thinking, education and community engagement that will revolutionize the way biology is taught and train the next generation workforce in biology, artificial intelligence and robotics." HUIMIN ZHAO



People Mentioned

Huimin Zhao (BSD leader/ CAMBERS/CGD/MMG), chemical and biomolecular engineering

People Involved

Zhanar Abil, Zehua Bao, Aashutosh Boob, Ran Chao, Haiyang Cui, Behnam Enghiad, Emily Gaither, Mohammed Hamed Rad, Linyang Ju, Stephan Lane, Jing Liang, Jiazhong Lian, Roy Liu, Jingxia Lu, Yuhao Min, Vassily Petrov, Adrianna Ramos, Wen Ren, Chengyou Shi, Tong Si, Nilmani Singh, Saurabh Sinha, Siddhartha Suryanarayana, Ipek Tasan, Scott Weisberg, Yuying Wu, Pu Xue, Tianhao Yu, Huimin Zhao

Publications

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Briefs

Designing Stronger Systems



Team awarded \$2M to develop new separation membranes inspired by biological cells

People mentioned

Jessica Schiffman, UMass Amherst

Charles Sing, chemical and biomolecular engineering

Cecilia Leal (M-CELS), materials science and engineering

Supported by

NSF

For more than 60 years, synthetic separation membranes – manufactured barriers that selectively filter out unwanted substances – have been made the same way, using the same chemicals. But researchers at Illinois, along with collaborators at the University of Massachusetts Amherst, aim to create new, biological-based membranes that can be made without the use of toxins.

“The current generation of membranes is an amazing technology, but as emerging contaminants are present in our waste streams, we need new technologies that can separate them out and keep our water safe,” said Jessica Schiffman, co-investigator of the project.

The full team also includes Charles Sing and Cecilia Leal, along with researchers from the University at Buffalo and the Air Force Research Lab. Their project takes inspiration from how human cells allow some small molecules to enter through the cell wall while filtering others out. Ultimately, the team aims to create a foundational platform that would support development of a membrane specifically tuned to filter out the desired material, with a broad range of applications. Within water purification, such membranes could be used for desalination and water treatment of various pollutants.

“We are taking on a massive challenge, but that is the thrill of doing collaborative research,” Sing said.

Automated method increases the efficiency of bioactive natural product discovery

Natural products derived from bacteria, fungi, and plants have a variety of valuable applications, and in particular have led to the development of many lifesaving medicines. Identifying potentially useful compounds from among the tens of thousands found

People mentioned

Huimin Zhao (BSD Leader/CAMBERS/CGD/MMG), chemical and biomolecular engineering

Yujie Yuan, chemical and biomolecular engineering

Supported by

NIH

in nature can be difficult, especially when organisms produce them in low quantities. To overcome this, researchers developed FAST-NPS, an automated method to accelerate the discovery and scale up of bioactive natural products found in *Streptomyces*.

“In the past we developed the CAPTURE method, which allows us to clone large biosynthetic gene clusters from microbial genomes with high efficiency. Although the process is very efficient, it is tedious and involves a lot of manual work,” said Huimin Zhao, who led the study published in *Cell Systems*. Biosynthetic gene clusters are groups of genes located together that encode all the enzymes to make a natural product.

“We are using the self-resistance genes as markers to prioritize BGCs of natural products with bioactivity,” said Yujie Yuan. Self-resistance genes evolve to shield organisms from any negative effects of their own natural products. The presence of self-resistance genes in BGCs therefore serves as a predictor of bioactivity for the corresponding natural products.

This proof-of-concept platform demonstrated a 95% success rate, allowing the researchers to identify five promising BGCs. All five proved to produce bioactive compounds. Yuan’s concerted effort to automate the process and express BGCs from about ten to several hundred at a time.

Bioengineers create revolutionary new nanocrystals

From medical imaging to solar panels, many technologies of the future rely on nanocrystals. Nanocrystals are tiny particles of material, often only a few nanometers (one billionth of a meter) across. Their microscopic size gives them unique properties, such as the way they interact with light, conduct electricity, or react with chemicals. Nanocrystals are key components in drug delivery devices, medical tests, and even everyday products like sunscreen.

However, the traditional way in which these crystals are manufactured has a drawback: it leaves them unstable in water. Most nanocrystals are synthesized in oils, which naturally separate from water – picture oil and vinegar in salad dressing. This makes them unsuitable for many biological applications.

To solve this problem, Andrew Smith’s research lab developed a novel technique to generate stable, water-soluble nanocrystals, outlined in a paper published in *Nature Synthesis*. Instead of using more traditional hydrocarbon ligands, Smith’s team coated the exterior of the nanocrystal in alkoxy ligands.

“Alkoxy ligands contain oxygen atoms interspersed throughout the molecule,” Smith said, “which makes them interact strongly with water through hydrogen bonds. This makes nanocrystals synthesized using alkoxy ligands compatible with water, and therefore, with biology.”

People mentioned

Andrew Smith (CGD), bioengineering

Supported by

NIH; NSF

The new method also eliminates hazardous waste, instead producing biodegradable byproducts that can be decomposed and used by microorganisms.

How baby pigs are shaping science

People mentioned

Ryan Dilger (GNBP), animal sciences

Kaitlyn Sommer, animal sciences

When piglets don't get enough milk in the first weeks of life they struggle to thrive. A study, published in the *Journal of Animal Science*, asks a deceptively simple question: what is the best way to feed artificially reared pigs?

A nutritional study led by Ryan Dilger compared the growth of piglets allowed to feed freely, or *ad libitum*, on a complete milk replacement with the growth of those fed scheduled doses comparable to regular nursing sessions.

After 15 days, pigs in the *ad libitum* group gained more weight and drank more milk overall, although their soft tissue composition was comparable to the scheduled eaters.

"This suggests that *ad libitum* pigs are simply growing faster, possibly due to differences in insulin production," said Kaitlyn Sommer. Piglets in the *ad libitum* group ate larger, less frequent meals, leading to prolonged periods where their insulin levels were above the threshold needed to trigger muscle growth.

"What really stood out in this work is just how much the way we feed pigs can influence everything else we're trying to measure," said Ryan Dilger. These insights have potential applications for human nutrition, as pigs are a relatively close model for human biology.

Researchers discover a way to reduce waste and save energy in making an industrial chemical

People mentioned

Scott Denmark, chemistry

Matthew Albritton, chemistry

Supported by

NIH; NSF

Polypropylene is the second-most used plastic, and the clarified form is driving a global increase in production that is expected to top 100 million metric tons per year by 2030. Consequently, there is increasing demand for production of clarifying additives, which give polypropylene near-glass-like clarity and lower processing temperatures.

For decades, the most prevalent polypropylene clarifying chemical has been produced using a complex, costly, and environmentally unfriendly process that results in a large amount of toxic tin byproducts. Research led by Scott Denmark and published in *Nature* has developed a production method that is more efficient and earth friendly.

The crux of the chemical challenge was figuring out how to form a carbon-carbon bond to a glucose molecule, in aqueous solution. "Making

[carbon-carbon] bonds usually requires reagents and conditions not compatible with water," Denmark said.

The crucial piece to the new approach turned out to be a small amount of indium metal that catalyzes the reaction. "If you use a lot – and by a lot, I mean like only 5% of the soluble indium salt – you get moderate yields. You have to use a very, very small amount in order for it to work best," said Matthew Albritton.

Working with collaborators at MIT, the team also optimized the reaction for a flow system, which has smaller manufacturing footprint than typical, large batch reactors.

CABBI team deploys robotic lab to revolutionize plant bioengineering

While traditional breeding takes years to develop more resilient crops, plant bioengineering offers a faster, more precise way to improve traits for higher yields and better stress tolerance. But engineering plants to enhance their helpful traits is still a complex process demanding significant time and labor.

"If we can use robots for plant bioengineering, that is a game changer. Automating plant transformation will allow us to develop better bioenergy crops and do it more quickly," said Matthew Hudson.

Hudson and his collaborators described FAST-PB, a fast, automated, scalable, high-throughput pipeline for plant bioengineering, in a publication in *The Plant Cell*. The team used FAST-PB to engineer plants with enhanced production of vegetative lipids, a promising avenue to improve global plant oil production without the need for increased fertilizer or land use.

Researchers created three automated processes to speed up the design and testing of genetic changes in plants. One of these included combining iBioFAB with single-cell metabolomics to engineer plant genomes and

characterize cellular effects, which has never been done before. Overall, this research accelerates the development of bioenergy crops with enhanced oil production, resilience, and efficiency, paving the way for more resilient and scalable biofuel production.

"Profiling the chemical differences between individual plant cells allows us to measure desired plant characteristics such as lipid production without the confounding impact of using populations of cells," Jonathan Sweedler said.

People mentioned

Matt Hudson (BSD/CAMBERS/GNDP), crop sciences

Jonathan Sweedler (BSD/CAMBERS/MMG), chemistry

Supported by

DOE



Researchers capture nanoparticle movements to forge new materials

People mentioned

Qian Chen (M-CELS), materials science and engineering

Supported by

DOD; NSF; Office of Naval Research

Some forms of energy, like light, move in invisible waves. Phonons can be thought of as discrete quantities of energy waves that move through the building blocks of material – whether atoms, particles or 3D-printed hinges – causing them to vibrate and transfer energy. Some materials are designed to move phonons along specific paths, imparting specific mechanical attributes. Researchers can now observe the phonon dynamics in self-assembled nanomaterials.

“Using the liquid-phase electron microscopy technique developed in our lab at Illinois, the new study marks the first time we’ve been able to observe phonon dynamics in nanoparticle self-assemblies, acting as a new type of mechanical metamaterials,” said Qian Chen.

Published in the journal *Nature Materials*, the multi-institutional study combined nanoparticle assembly with mechanical metamaterial principles, enabling the engineering of mechanical properties through structural design. To develop a new framework for metamaterials design, the team employed theoretical modeling in conjunction with experimental and observational techniques.

“With nanoparticle assembly, we can design structures with very controlled geometry, and then with mechanical metamaterials, adapt the theoretical framework in material design,” Chen said. This advance will enable researchers to incorporate desired mechanical properties into metamaterials that can be reconfigured in different situations; these materials have wide-ranging applications, from shock absorption to devices that guide acoustic and optical energy in high-powered computer applications.



NSF reinvests in Molecule Maker Lab Institute, AI tools to solve chemistry's challenges

With a five-year, \$15 million award, the NSF renewed its support of the Molecule Maker Lab Institute, a research collaboration focused on developing AI tools for quick, accessible discovery and synthesis of molecules for applications in medicine, energy, industry and more.

"Functional molecules such as drugs, chemicals, enzymes and materials play a critical role in addressing many grand challenges facing society today. However, the process of discovering and manufacturing such molecules has remained slow, expensive, and highly specialist-dependent," said Huimin Zhao, who directs the NSF-MMLI.

In its first five years, the NSF-MMLI has made advances in developing AI models, demonstrating their utility to predict the function of

molecules based on their structures or suggest how to improve a molecule's performance. The institute also integrates those models with automated molecule-building systems and user-friendly interfaces to make the AI-driven solutions accessible even to researchers who are not chemists or biochemists.

Over the next five years, the NSF-MMLI plans to continue developing foundational AI agents for discovery and synthesis of functional molecules, as well as advancing AI-enabled discovery and development of catalysts, drugs and materials. In addition, the NSF-MMLI will refine and scale up the innovative education and workforce development tools and programs that were developed in its first five years, such as the Digital Molecule Maker and Lab 217 Escape Room.

People mentioned

Huimin Zhao (BSD leader/CAMBERS/CGD/MMG), chemical and biomolecular engineering

Supported by

NSF

Ready for market: new process boosts clean, cost-efficient chemical production

Building on their past innovations in cleaner organic acid production, CABB researchers have pushed one particular product closer to commercialization with a major upgrade in yield. The team re-engineered the metabolism of the yeast *Issatchenkia orientalis* to supercharge its fermentation of plant glucose into succinic acid – an important industrial chemical used in food additives and a diverse array of other products.

This natural fermentation process, relying on yeasts and renewable plant material, is more environmentally friendly than conventional production using petrochemicals. But cost remains a barrier for commercial adoption, according to Huimin Zhao, a lead author on the study. Improving the yield – the amount of succinic acid produced from a gram of glucose – would make the process more economically viable.

In the study, published in *Nature Communications*, the researchers used a metabolic engineering strategy on *I. orientalis*

called decompartmentalization, moving a key cellular process from an enclosed structure within the cell to a larger and more central area.

Decompartmentalization boosted succinic acid yield to 85%, and this increase in succinic acid yield to 0.85 grams per gram of glucose reduced the minimum product selling price to 97 cents per kilogram, down from \$1.30 previously. Zhao said, "For those industrial chemicals, even a few cents is a big reduction."

People mentioned

Huimin Zhao (BSD leader/CAMBERS/CGD/MMG), chemical and biomolecular engineering

Supported by

DOE; NSF

IGB celebrates opening of iBioFoundry, National Institute for Biofoundry Applications

People mentioned

Huimin Zhao (BSD leader/CAMBERS/CGD/MMG), chemical and biomolecular engineering

Supported by

NSF

Scientists, government officials and participants from around the world gathered for the grand opening of the NSF's Illinois BioFoundry, or iBioFoundry, and the National Institute for Biofoundry Applications. The ribbon-cutting ceremony took place at the IGB, where the new facilities are housed.

The iBioFoundry builds on more than a decade of research at Illinois to integrate synthetic biology, laboratory automation, and artificial intelligence to advance protein and cellular engineering. It is one of several biofoundries established in the U.S., each of which has its own focus and mission.

"The NSF iBioFoundry serves as a hub for innovation, bringing together researchers, industry experts, and policymakers to foster collaboration and accelerate

the development of sustainable biomanufacturing processes," said iBioFoundry director Huimin Zhao. "By centralizing resources and expertise, it will streamline the creation of new bio-based products and technologies, ranging from renewable chemicals to advanced medical treatments."

The grand opening coincided with the Global Biofoundry Alliance annual meeting, which welcomed approximately 150 participants from more than 30 biofoundries in 14 countries. Attendees included leaders from academia, industry, national laboratories, nonprofit organizations, and U.S. government agencies such as NSF and the DOE.

Atom-scale stencil patterns help nanoparticles take new shapes and learn new tricks

Inspired by an artist's stencils, researchers have developed atomic-level precision patterning on nanoparticle surfaces, allowing them to "paint" gold nanoparticles with polymers to give them an array of new shapes and functions. Described in the journal *Nature*, the "patchy nanoparticles" can be made in large batches, then used for a variety of electronic, optical, or biomedical applications.

People mentioned

Qian Chen (M-CELS), materials science and engineering

Ahyoung Kim, materials science and engineering

Supported by

DOE; NSF

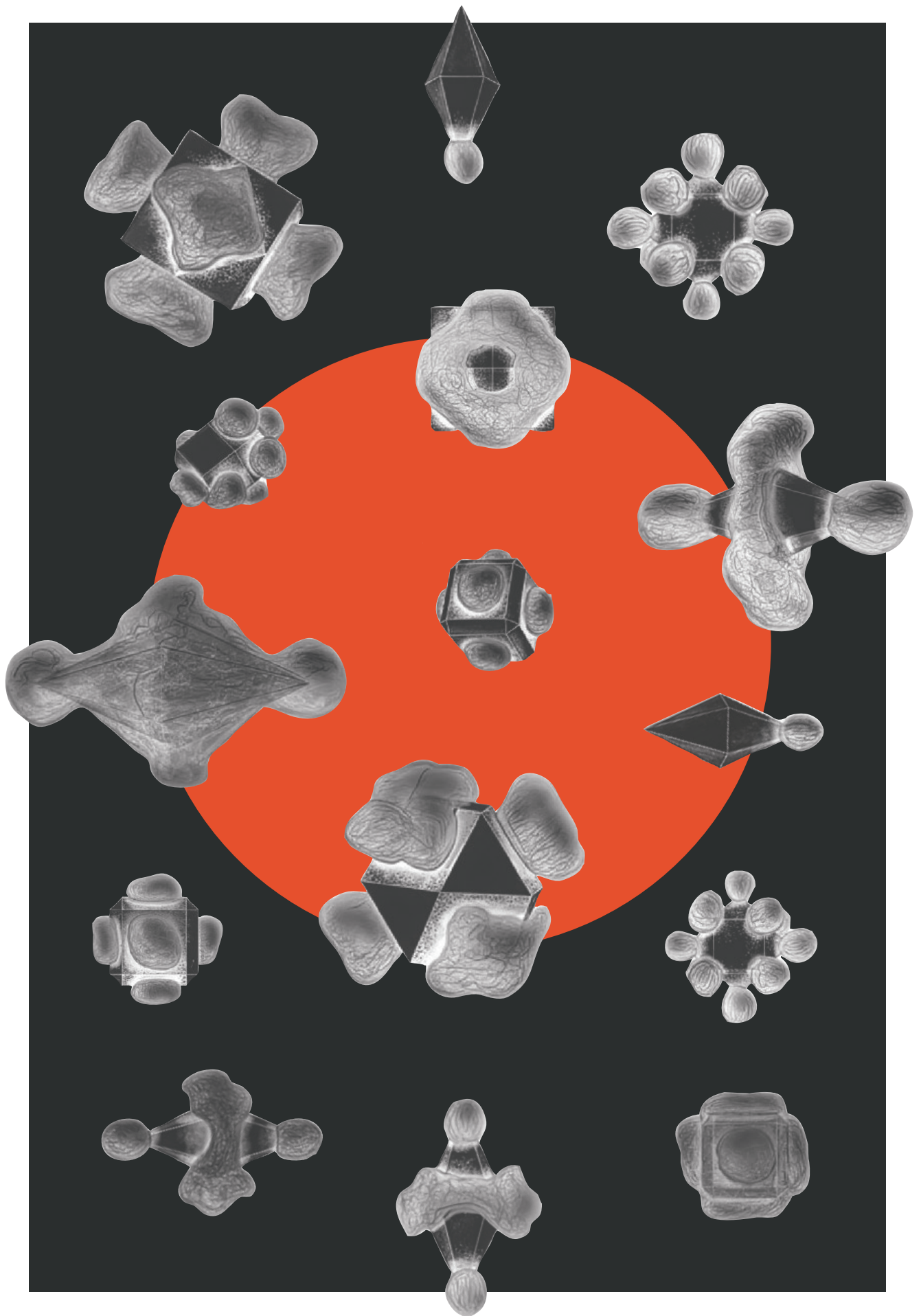
"One of the holy grails in the field of nanomaterials is making complex, functional structures from nanoscale building blocks. But it's extremely difficult to control the direction and organization of each nanoparticle, especially in achieving materials beyond simple close packing," said Qian Chen.

The team also drew inspiration from nature's complex biomachinery, proteins whose multiple substructures each perform a different function. However, applying this design to nanoparticles is not straightforward. Co-first author of the study Ahyoung Kim found a solution in a pottery class, where she learned

about a stenciling technique that used a mask to paint a complex design on a curved piece of pottery.

"We can coat some surfaces of a gold nanoparticle in just one layer of iodide, and others in an organic primer. Then we can bring in the polymer, and it sticks just to the facets with the organic primer. The iodide masks the other facets," Kim said.

With collaborators, the team used computer simulations to predict how the process would work. Chen's group then validated the simulations experimentally, successfully making more than 20 distinct patchy nanoparticles.



DNA nanostructures get a major upgrade

DNA nanostructures are exciting new biomedical tools with great potential in treatment, diagnosis and disease prevention. Made of folded DNA, these nanostructures are highly programmable, enabling many applications including viral detection and therapeutics.

Despite their promise, these structures degrade quickly in biological environments, limiting their potential. Though necessary for their assembly, magnesium ions can render DNA nanostructures unstable within most organisms, causing them to quickly

degrade. Researchers in Xing Wang's group investigated ionic liquids such as choline dihydrogen phosphate as a more stabilizing alternative.

"Ionic liquids have traditionally been used in petrochemical, electrochemical, and battery applications," Wang said. "We wondered if we could assemble DNA nanostructures in ionic liquids and utilize their properties for potential therapeutic applications."

The results, published in the *Journal of the American Chemical Society*, exceeded the researchers' expectations. Though Wang's lab only set out to verify that the nanostructures

would retain functionality when assembled in this new way, the data indicated the structures' ability to bind to protein biomarkers on a cell's surface had improved, allowing for more precise targeting. The nanostructures even showed particular affinity when binding to cancer cells, something that had been difficult in previous magnesium-based assembly systems.

"We're now translating this platform toward cancer therapy and understanding how these ionic liquid-based DNA nanostructures perform in targeting and delivery payloads to cancer cells," Wang said.

People mentioned

Xing Wang (CGD), bioengineering

Supported by

NIH; NSF





New IGB theme aims to boost the bioeconomy through the revitalization of an ancient biological partnership

Since the dawn of agriculture, our societies have been powered by the sunlight captured by plants and supplied by microbes that tap into the resources of those plants that we cannot. A new research theme at the IGB pulls together cutting-edge methods across an array of fields – genomics, biotechnology, remote sensing, automation, biogeochemistry, technoeconomic analysis, and artificial intelligence – to leverage our modern

bioeconomic partnership with plants and microbes to the fullest.

The research theme, Crops And Microbes for BioEconomy Resilience and Sustainability, is led by Andrew Leakey. CAMBERS, which has 29 faculty members and affiliates, expands upon the ongoing activities of CABBI, also directed by Leakey.

"I am very excited about establishing CAMBERS,"

Leakey said. "It provides a pathway and meeting point for a transdisciplinary team of scientists from across campus to accelerate progress on developing the scientific understanding and technological innovations needed for the agricultural bioeconomy to be more profitable, while also delivering net environmental benefits."

CAMBERS is supporting investment and innovation in new cutting-edge methods upstream of the work performed within CABBI. Another key effort is to expand campus access to cutting-edge research facilities, such those found in the Plant Biology Innovation Greenhouse, opened in 2024. CAMBERS is also building partnerships to make sure innovations from its fundamental science projects are refined and scaled up so that they will be adopted at farms and biorefineries.

People mentioned

Andrew Leakey (CAMBERS leader/PFS), plant biology

The image is a full-page architectural rendering. It features a modern building with large glass windows and a brick base at the bottom. A large, solid red circle is positioned in the center-left, partially overlapping the building and a large, stylized architectural detail on the right. The detail on the right consists of dark, angular structural elements and a grid of fine vertical lines. The text 'FY25' is prominently displayed in a large, bold, black sans-serif font within the red circle. Below it, 'IGB Numbers' is written in a smaller, bold, black sans-serif font. The page number '86' is located in the bottom left corner.

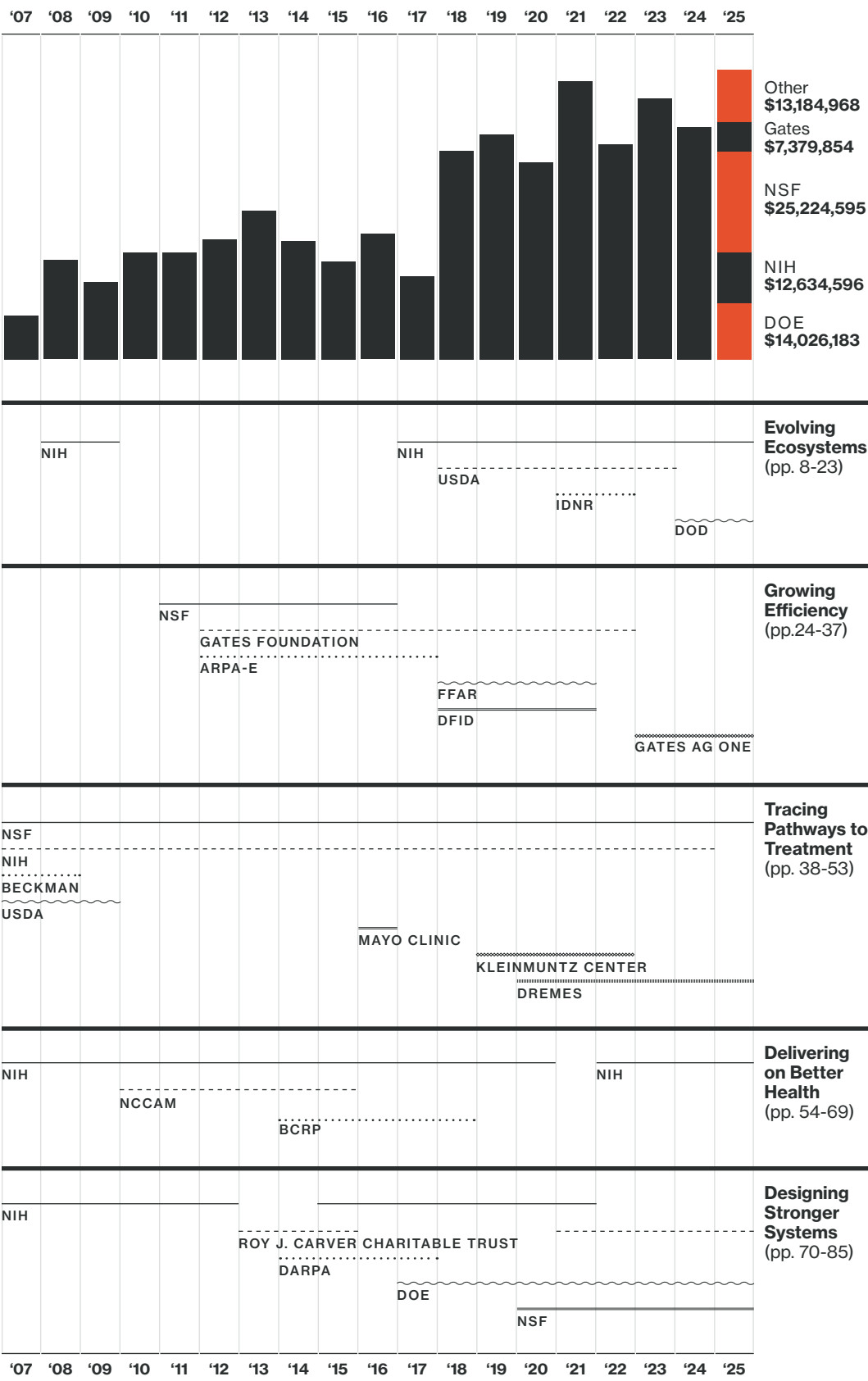
FY25

IGB Numbers



Grant Funding FY25

\$72,450,197



Economic Development FY25



U.S. Patents Issued

- Stephen Long** Overexpression of PsbS Improves Water Use Efficiency

Yong-Su Jin Whole Cell Biosynthesis of a Functional Oligosaccharide, 2'-Fucosyllactose, and its Precursor, L-fucose, using Engineered *Saccharomyces Cerevisiae*

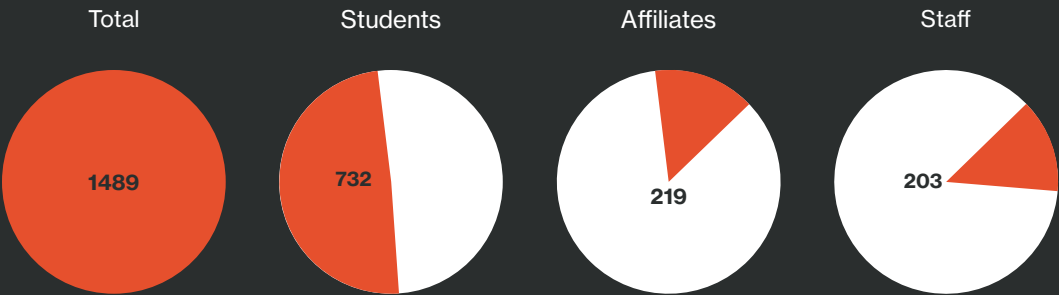
Huimin Zhao A CRISPR/Cas9-Based Tool for Genome Editing in *Issatchenkia orientalis*

Taekjip Ha Bio-Engineered Hyper-Functional Super Helicases
- Hyunjoon Kong** Catalytic Microgelators for Decoupled Control of Gelation Rate and Rigidity of the Biological Gels

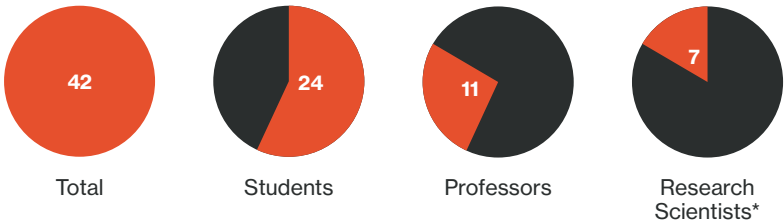
Timothy Fan | Paul Hergenrother New Compounds for Treatment of Cancer, Including Intracranial Tumors

William Metcalf A Novel Natural Product Herbicide from the *Pantoea ananatis* LMG 5342 Hvr Biosynthetic Gene Cluster

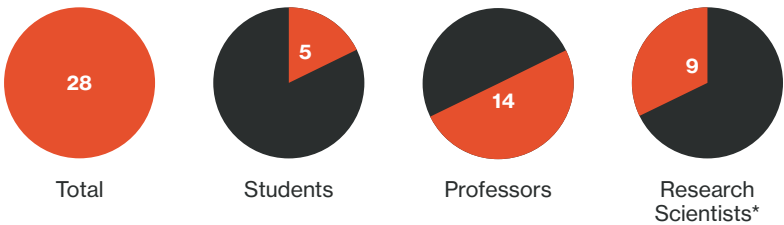
People



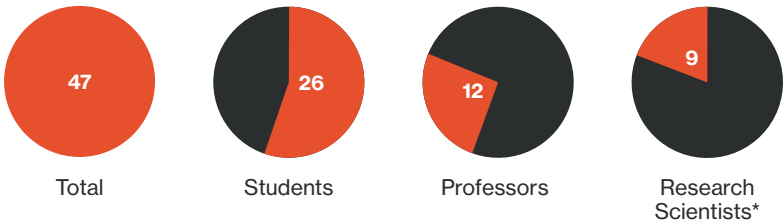
Evolving Ecosystems
(pp. 8-23)

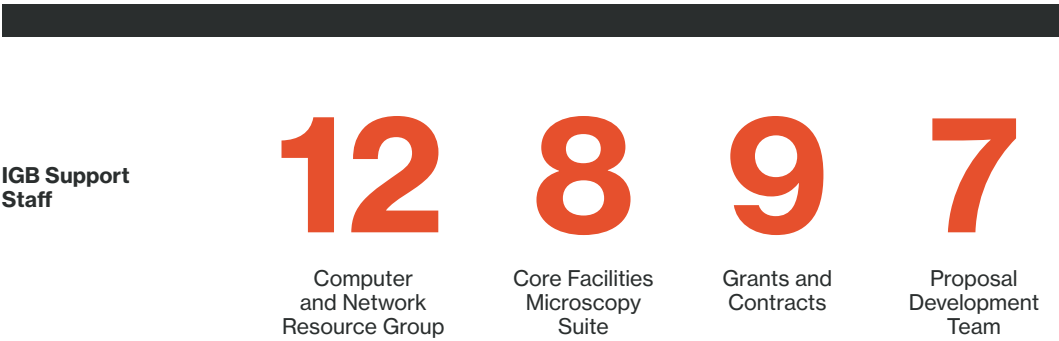
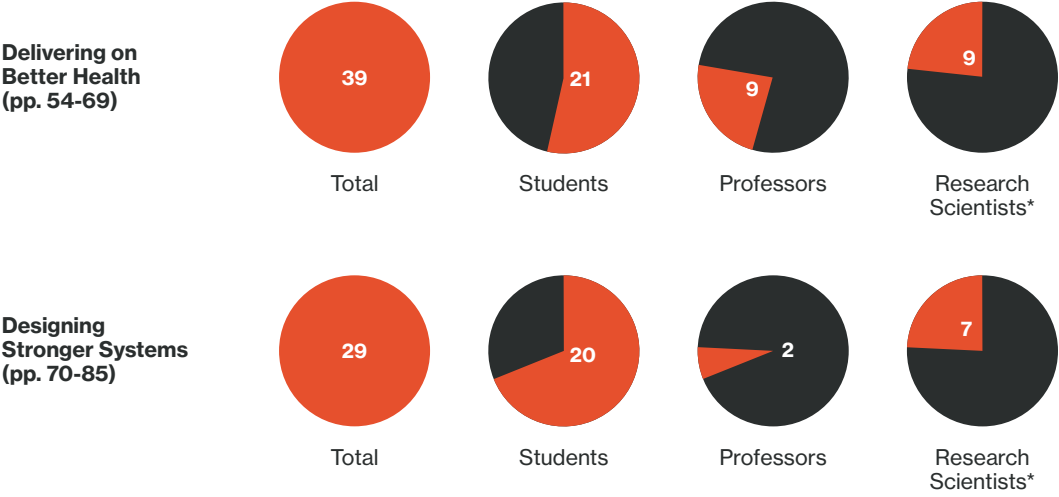
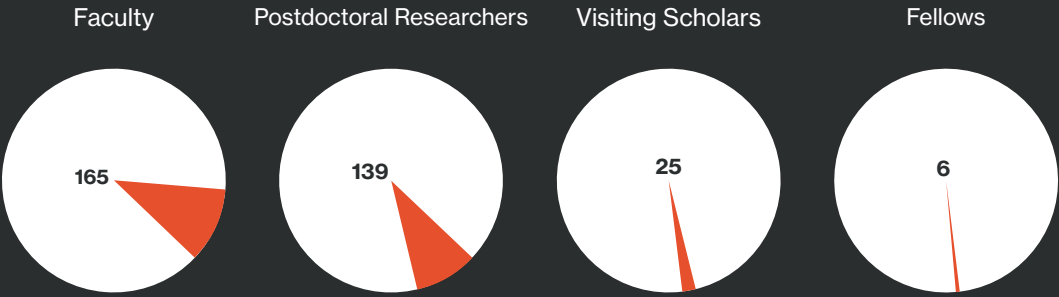


Growing Efficiency
(pp.24-37)



Tracing Pathways
to Treatment
(pp. 38-53)





*Postdoctoral researchers are included in research scientists

FY25 Publications

893

Papers published

6

Science and
Nature papers

Closed-loop transfer enables artificial intelligence to yield chemical knowledge, Angello, N. H., Friday, D. M., Hwang, C., Yi, S., Cheng, A. H., Torres-Flores, T. C., Jira, E. R., Wang, W., Aspuru-Guzik, A., **Burke, M. D., Schroeder, C. M., Diao, Y. & Jackson, N. E.**, *Nature* 633, 8029, p. 351-358

Thread, read, rewind, repeat: towards using nanopores for protein sequencing, **Aksimentiev, A.**, *Nature* 633, 8030, p. 533-534.

Catalytic allylation of native hexoses and pentoses in water with indium, Adak, T., Menard, T., Albritton, M., Florit, F., **Burke, M. D.**, Jensen, K. F. & **Denmark, S. E.**, *Nature* 640, 8057, p. 94-99

New antifungal breaks the mould, Maji, A. & **Burke, M. D.**, *Nature* 640, 8059, p. 606-607.

Asymmetric photoenzymatic incorporation of fluorinated motifs into olefins, Li, M., Yuan, Y., Harrison, W., Zhang, Z. & **Zhao, H.**, *Science* 385, 6707, p. 416-421

Safeguarding crop photosynthesis in a rapidly warming world, **Bernacchi, C. J., Long, S. P. & Ort, D. R.**, *Science* 388, 6752, p. 1153-1160

Core Facilities

Users

400+

Research groups

145

Outreach

14,284

People reached

12,187

Participant hours

115

Events

174

Volunteers

45

Community partners

33

Campus partners

63 in 24

Locations

Cities

In 2025, the IGB mobile lab visited Arthur, Bement, Broadlands, Champaign, Chicago, Decatur, Fisher, Georgetown, Henry, Homer, Louisville, Macon, Martinsville, Monticello, Oblong, Oglesby, Paxton, Paris, Petersburg, Princeton, Quincy, Springfield, Taylorville, and Urbana in Illinois



Awards

Rohit Bhargava,
Engineering (CGD)

*Fellow, Biomedical
Engineering Society*

Marni Boppert, Health and
Kinesiology (RBTE); **Ying
Diao**, Chemical & Biomolecular
Engineering (BSD)

*Presidential Early Career Award
for Scientists and Engineers,
White House Office of Science
and Technology Policy*

Isaac Cann, Animal
Sciences (MME); **Matthew
Wheeler**, Biotechnology and
Developmental Biology (RBTE)

*Fellows, American Association
for the Advancement of Science*

Qian Chen, Materials Science
& Engineering (M-CELS)

University Scholar

Kaiyu Guan, Natural
Resources & Environmental

Sciences (CAMBERS);
Tracy Lawson, Plant Biology
(CAMBERS/PFS); **Donald
Ort**, Plant Biology and Crop
Sciences (PFS leader/BSD/
CAMBERS); **Brent Roberts**,
Psychology (GNBP); **Boxuan
Zhao**, Cell & Developmental
Biology (GNBP); **Huimin Zhao**,
Chemical & Biomolecular
Engineering (BSD leader/
CAMBERS/CGD/MMG)

*2025 Clarivate Analytics
Highly Cited Researchers*

Kaiyu Guan, Natural
Resources & Environmental
Sciences (CAMBERS)

*Levenick Professor
of Sustainability*

*Excellence in Agricultural
Research Innovation,
agInnovation*

Jeremy Guest,
Civil & Environmental
Engineering (BSD/CAMBERS)

*Levenick Professor and
Director of the Levenick Center*

*for a Climate-Smart
Circular Bioeconomy*

Rochelle Gutiérrez,
Curriculum & Instruction (CIS)

National Academy of Education

Brendan Harley, Chemical
& Biomolecular Engineering
(RBTE Theme Leader/EIRH)

*Board of Directors, American
Institute for Medical and
Biological Engineering*

Katy Heath, Plant Biology (IGOH)
University Scholar

Paul Hergenrother, Chemistry
(ACPP leader/MMG)

*American Chemical
Society Fellow*

Laura J. Hetrick,
Art Education (GNBP)

*Center for Advanced
Study Associate*

**IGB Communications
and Outreach group**

*Campus Excellence in Public
Engagement Team Award,
Office of the Provost*

Heng Ji, Computer Science
(BSD/CAMBERS)

*Fellow of the Association for
Computational Linguistics*

Tracy Lawson, Plant Biology
(CAMBERS/PFS)

*Highly-ranked scholar in
photosynthesis research,
ScholarGPS*

Deborah Leckband,
Chemical & Biomolecular
Engineering (M-CELS/RBTE)

*Fellow of the
Biophysical Society*

Liviu M. Mirica,
Chemistry (MMG)

*Center for Advanced
Study Associate*

Doug Nelson, BodyWork
Associates President

*Distinguished Service
Award, University of Illinois
Alumni Association*

Erik Nelson, Molecular
& Integrative Physiology
(ACPP)

*Keith W. and Sara M. Kelley
Endowed Professor of
Immunophysiology*

Helen Nguyen, Civil
& Environmental
Engineering (IGOH)
*GeoHealth Section
Award, AGU Advancing
Earth and Space Sciences*

James Slauch,
Microbiology (IGOH)
*Deb & Tim Paul Chair
in Human Infectious
Disease & Immunology*

Andrew Suarez,
Entomology and Evolution,
Ecology, & Behavior (GNBP)
*Fellow, Entomological Society
of America*

Jonathan Sweedler,
Chemistry (BSD/CAMBERS/
MMG)

*American Academy of Arts
and Sciences*

Amy Wagoner Johnson,
Mechanical Science &
Engineering (EIRH/RBTE)
*Richard and Hinda Rosenthal
Emerging Leaders in Health
and Medicine Forum, National
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Hua Wang, Materials Science
& Engineering (RBTE)
*Rising Star Junior Faculty
Award, Biomedical Engineering
Society Cellular and Molecular
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