life IN THE lab

PRODUCTS, INFORMATION, AND SCIENTAINMENT

ISSUE 18 | 2018

Inspiring discovery

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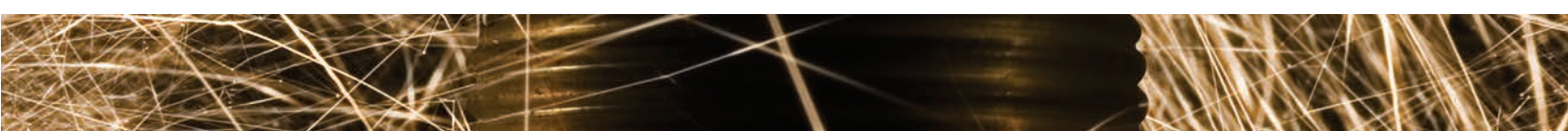
ThermoFisher SCIENTIFIC



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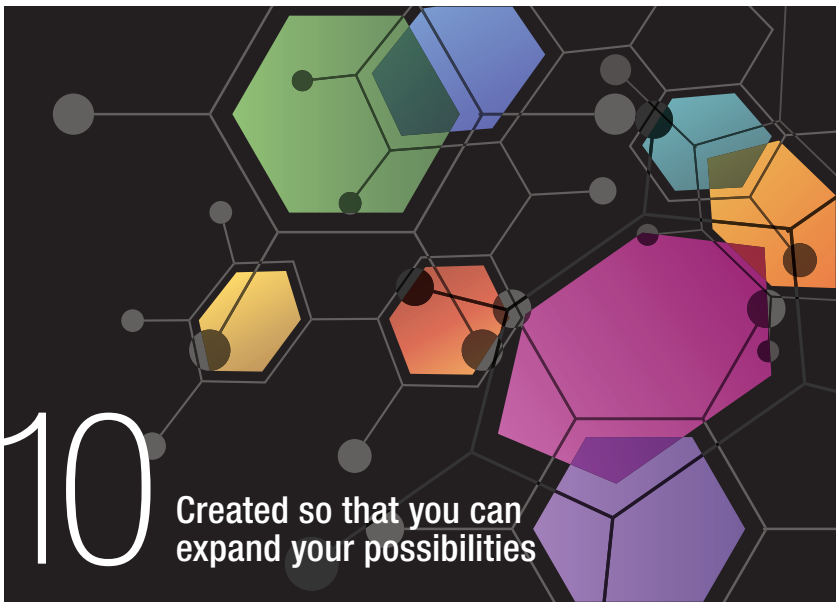

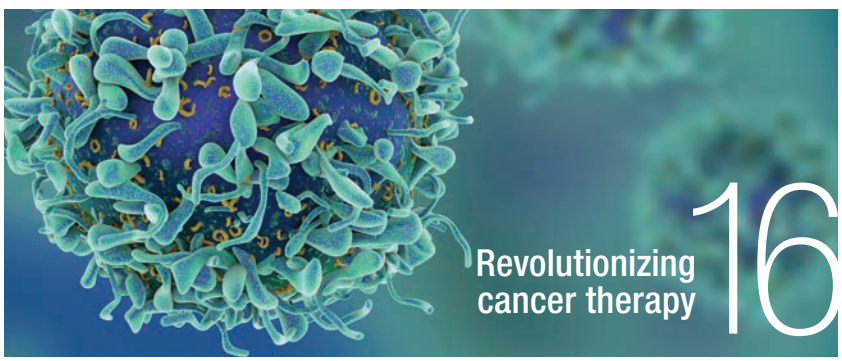

PARTY INSPIRATION

MAKE YOUR HOLIDAY, NEW YEAR'S, OR BIRTHDAY PARTY MORE FUN WITH SCIENCE

Mixology

Gel spheres—Have you ever seen cocktails topped with floating gel spheres? These spheres are created by mixing a liquid with sodium alginate in a syringe. The liquid needs to have a pH range of 4–10 for the liquid to gel. Fruit juices are a popular choice and also add a pop of flavor to champagne or sparkling water.

Cocktail popsicles—For hot days, there is no better way to cool off than with a popsicle. Make it an adult-friendly treat by combining your favorite cocktail with a tasty fruit puree and freezing. The mixers from the cocktail and the fruit puree will blend and help freeze even higher-proofed alcohols.

Nitrogen-chilled cocktails—These are not for the faint of heart. Instantly chill cocktails using liquid nitrogen instead of ice for a great conversation starter at parties. Remember, liquid nitrogen should only be handled when wearing safety glasses, protective clothing, and gloves.

Appetizers

Trail mix test tubes—Fill test tubes (unused, of course) with trail mix or mixed nuts to create a fun snack for your guests.

Cheese molecules—Let partygoers make their own molecules from a plate of cheese cubes, olives, fruit, and veggies.

5 TIPS FOR SUCCESSFUL CRISPR EDITING

Innovative CRISPR technology offers numerous possibilities. Our CRISPR trainer and technical support scientist, Yashashree Joshi, PhD, would like to share the tips she's picked up along the way.

1. Aim for 30–70% confluency.

Optimize cell confluency—seeding density, passage number, and the type of media can impact editing efficiency. Ideal starting confluency when using a Cas9 protein for lipid transfection is 30–70% and 70–90% for electroporation.

2. Test 2–3 guide RNAs.

Target the early exon within the gene to disrupt the reading frame. This will identify the gRNA with the highest editing efficiency.
thermofisher.com/trueguide

3. Start with lipid-mediated delivery.

Know what works for your cells, and progress to other methods like electroporation as needed.
thermofisher.com/crisprtransfection

4. Optimize use of controls.

Positive and negative controls help determine gRNA amount and transfection conditions that give optimal efficiency with the highest cell viability.
thermofisher.com/crisprcontrols

5. Confirm gene-editing efficiency.

For robust future screening experiments, verify the control target and select the conditions for optimal editing efficiency.
thermofisher.com/geneeditdetect
thermofisher.com/ngs
thermofisher.com/sangersequencing

Yashashree Joshi, PhD

Technical Applications Scientist
CRISPR Workshop Trainer
Thermo Fisher Scientific

What is your favorite thing about leading this course?
Helping people! Scientists come into this course with their own projects and I get to help them understand the entire workflow. We held our first course in Winter 2016 and I am still in touch with many of the attendees—they tell me about how well their experiments are working!

What is one thing you want everyone to know?
The coolest thing is we have products for the whole genome editing workflow—something none of the other suppliers can say.

Why are you passionate about science?
It is the basis of all advancement and technology that everyone is enefiting from. Basic science research helps unravel the fundamental processes, which can have huge applications. For instance, CRISPR was discovered as the bacterial immune system, but who knew it would have such vast implications in genome editing. It now holds the promise of correcting disease-causing mutations and more.

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For many applications, Sanger sequencing remains the technology of choice due to the simple workflow, quick turnaround time, and cost-effectiveness when running a limited number of samples. It is also an important confirmatory method for NGS results. However, poor quality data can result from not using the right products or the right protocol. Poor-quality data increases the rerun rate, which adds to the overall cost and turnaround time. We have developed a proven protocol that provides a simple and fast Sanger sequencing workflow that can be completed in less than one workday, from sample to answer. The protocol enables high-quality sequencing data using the Applied Biosystems™ BigDye™ Terminator v3.1 or BigDye™ Direct Cycle Sequencing Kits. Visit our page to download our latest protocols for the Applied Biosystems™ products that support every step of our recommended workflow.

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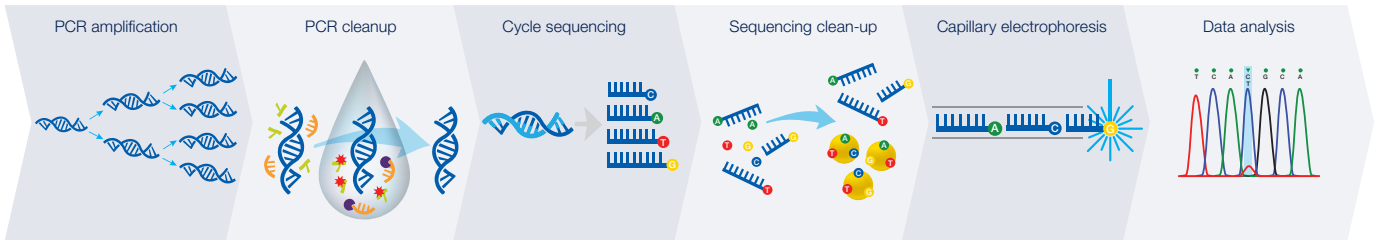

Capillary electrophoresis workflow

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WHY ARE YOU PASSIONATE ABOUT SCIENCE?

I have been passionate about science ever since I was young. Exploring, learning, and understanding the world around me sparked my aspiration for studying science. I was especially fascinated by organism diversity and how their diversity is controlled through the regulation of genetic information during development. I am continuing my passion for science and experience in development and molecular biology to Thermo Fisher Scientific, where I am researching and developing molecular tools and solutions for customers.

Vicki Hurless, PhD, R&D Scientist, Molecular Biology
Thermo Fisher Scientific

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"If I hadn't done this functional study, where, knocking out the *PLK4* gene, resulted in the inhibition of cell proliferation I wouldn't have discovered that *PLK4* is essential for *AT/RT* growth. *PLK4* is only slightly elevated in these tumors. However, this is gene is tightly regulated and slight increases in its expression result in an aggressive tumor phenotype. This overexpression can be targeted by inhibitors opening a new therapeutic prospective for children with *AT/RT*. Significantly, we also found it elevated in other embryonal tumors of the brain, what may have a larger impact in patient care … the fact that we used the Invitrogen™ LentiArray™ Human Kinase CRISPR Library for the functional assay was key."

– Simone T. Sredni, MD, PhD, Associate Professor of Pediatric Neurosurgery at Ann and Robert H. Lurie Children's Hospital of Chicago / Northwestern University Feinberg School of Medicine

thermofisher.com/crisprlibraries

CURIOSITY WITH CRISPR

Olivier Humbert, PhD, Staff Scientist in Hans-Peter Kiem's laboratory, Fred Hutchinson Cancer Research Center

What inspired you to get into science and research?
What inspires you to get up every day? Curiosity about how my surroundings and living things work; I love the excitement of carrying out experiments, the anticipation for results, and the fulfillment of knowing that I am contributing to the development of new medical treatments.

What drives your passion for science? Knowing that I am working with cutting-edge technologies to develop therapies that will become available to patients in the next 5–10 years.

Can you provide an overview of your research? Our goal is to treat hereditary diseases by correcting the underlying mutation in bone marrow stem cells so that these cells will be curative after they are transplanted back to the affected patient. The correction of mutations can be done by means of non-infectious viral vectors or more recently with nucleases that target specific sites in DNA, also known as molecular scissors (such as CRISPR-Cas9). Our laboratory covers a wide range of research, spanning basic science all the way to clinical studies; examples of diseases we work on are blood disorders (sickle cell anemia), severe combined immunodeficiency, and Fanconi anemia (defects in DNA repair).

What are the current challenges you face? One challenge is to correct mutations and engineer DNA in bone marrow stem cells with high efficiency and without affecting the identity of these cells so that they will differentiate into all blood cell types and reconstitute the hematopoietic system of a patient after transplantation. Another big challenge is in the scale-up, where we are looking to engineer the DNA of several hundred millions of cells obtained from patients.

What are the potential solutions? One solution is to find a nuclease platform (such as CRISPR-Cas9) and nuclease delivery method (such as electroporation) that can treat large numbers of cells with minimum toxicity and high efficiency so that they will be therapeutic after they repopulate the patient. Another solution is to refine our definition of true, long-term hematopoietic stem cells, which will decrease the number of these cells that need to be treated.

Describe your results, if you have any. We have so far done two transplant experiments in a preclinical animal model aimed at treating hemoglobinopathies (blood disorders). The results are very encouraging, but we want to follow up on our treatment for over a year to really understand how effective and safe our therapy is.

How are the advances in genome editing enabling you to achieve your research goals? Current gene editing technologies allow us to target virtually any site in the genome in pretty much any cell type. In addition, the improved efficacy of TrueCut Cas9 Protein v2 allows us to reduce the amount used and minimize toxicity.

How are the tools and technologies today allowing you to lead to discovery? Improved efficacy and safety of technology equals more potential to bring an effective therapy to the patient. These reagents are also available in large-scale [quantities] and in cGMP grade for easy translation to the clinic.

What thought do you want to leave us with? I am lucky to be working in such an exciting field with lots of potential to cure a variety of diseases. Nevertheless, researchers need to be vigilant to take all necessary steps to not move this approach too quickly to the patient to avoid any major setbacks.

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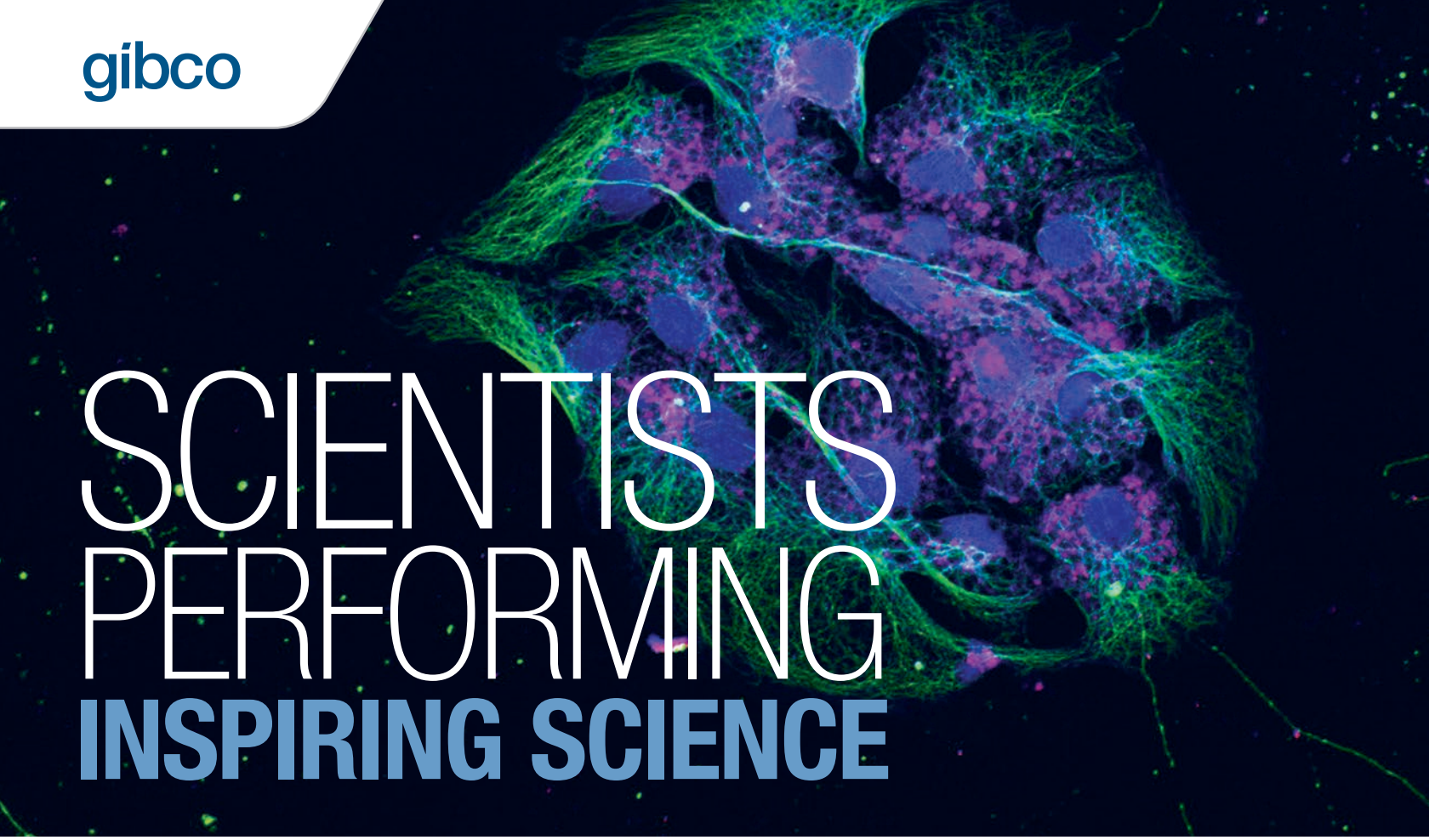


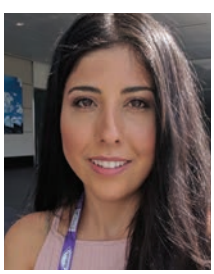
SCIENTISTS PERFORMING INSPIRING SCIENCE

Image courtesy of
Ekaterina Turlova,
University of Toronto

Whether using cells as a model of disease, leveraging cells to make protein, or using cells as therapy, cell biologists inspire us. Scientists like Samantha Yammine and Caitlin Vander Weele are going beyond the bench for public outreach and using science as art.

Samantha Yammine

PhD candidate, Neuroscience and Stem Cell Biology, University of Toronto



What research do you do and do you have any challenges?
I am a PhD candidate in Dr. Derek van der Kooy's neurobiology research lab at the University of Toronto researching stem cell hierarchies in the developing and adult mammalian brain. Our lab studies a variety of different stem and precursor cell populations, including those of the retina, corneal limbus, pancreas, and neural crest, but my thesis has revolved around a very rare population of neural stem cells. And by rare, I mean really rare—after I microdissect the thin stem cell niche surrounding the lateral ventricles in the mouse brain, my stem cells of interest comprise only 0.1% of the total cells dissected at most, and at some ages, they are only 0.01% of the population. But they are phenotypically really interesting cells—we recently published in *Stem Cells* that they act as a reserve pool for the more prominent neural stem cell population, so it's been worth troubleshooting new, sensitive techniques to try to learn more about them.

Have you found a solution? Since our cells are so rare in bulk samples, we knew we'd have to continue improving our purification methods and experiment with new assays that are sensitive enough to detect signals from single cells. Fortunately, single-cell analyses have become more and more popular and I've found a lot of fantastic collaborators in Toronto to help me implement these techniques. After many workshops, literature searches, and planning meetings, we are currently having success studying embryonic precursors with several single-cell transcriptomic platforms thanks to help from technical experts from several other local labs.

What are your next steps? I am excited to combine these new transcriptomics data with previous functional data I've collected on these rare neural stem cells and put forth some new additions to current neural stem and progenitor cell hierarchies. By better understanding the lineage relationships between the earliest cells of the mammalian brain, we will better appreciate how the diversity of the cells of the brain are created during development and homeostasis. Given that the brain has over 170 billion cells and that all of these cells come together to give us the ability to think and do, I find its creation to be one of the most fascinating biological concepts.

What do you want people to know about you? What motivates you to share your story? I created the Instagram account @science.sam so that I could bring more transparency to the process of science research. My goal was to show that there are so many fascinating aspects of science, including the basic biology behind experiments we do in the lab everyday. I share daily updates of research life and new science news through a personal lens to challenge my audience to change their perceptions of scientists and science for the better. I strive for outreach that is interesting and inclusive to everyone, so I use enough analogies and metaphors for the casual science enthusiast, but just enough details to keep fellow scientists interested, too.

A passionate advocate for equity, diversity, and inclusivity, Sam also posts inspiring interviews with people from underrepresented groups in the STEM fields to invite more people into the exciting world of science research. Thank you for inspiring us, Sam!

Instagram: science.sam
Twitter: SamanthaZY
www.samanthayammine.com

Caitlin Vander Weele

PhD candidate, Neuroscience, Tye Lab, Massachusetts Institute of Technology

What research do you do and do you have any challenges? What happens to all the beautiful and interesting images generated from failed science experiments? Typically nothing. Scientists use them to help generate better tools and hypotheses; however, because they will never be published, they get stored away on hard drives for no one to see. I started posting some of the pretty images I gathered from my failed experiments (I'm a PhD student studying the neural circuitry underlying motivated behaviors) on Twitter and other social media outlets. Microscopy images were some of my most viewed and shared media and it struck me how effective they were at communicating science content. I wanted to create a home for these images to be seen and appreciated. On a whim of procrastination, Interstellate was born in May 2016.

Have you found a solution? To start, I made a Twitter account for the project (@interstellate_) and sent over 100 cold emails to neuroscience friends, colleagues, and principal investigators asking for image donations for the project. To be quite honest, I was surprised how enthusiastic and supportive the community was and within six months, I collected over 100 images from ~80 scientists in nine different countries! I tweeted images I collected and started assembling them into an 86-page full gloss magazine. Each page of the magazine features a stunning image generated by scientific research and briefly explains a neuroscience-related concept. For example, the first couple of pages explain the different types of brain cells, how neurons communicate with one another, and how we study them in the laboratory. In October 2016, the digital copy of Interstellate Volume 1 went live (**http://pub.lucidpress.com/Interstellate_Volume1/**) and with help from our generous corporate sponsors, over 1,000 copies have been printed and distributed for free! I think Interstellate provides a platform to celebrate important but often overlooked steps of research. Interstellate's goals are science celebration and neuroscience awareness through art.

What are your next steps? Interstellate is still a really new initiative, so it will be exciting to see what it evolves into! Right now, I'm working on a second volume (and trying to finish my PhD!), which will debut in November 2017, and expanding the social media and outreach presence (you can follow us on Tumblr and Instagram @interstellate_). The whole project is one massive collaborative effort so the future of Interstellate really depends on the network of people who support it. I would love to see Interstellate used as an outreach tool for the public and to recruit the next generation of brain explorers.

A brain explorer that collects images of pretty neurons along the way, Caitlin is showing us the beauty in science. Thank you, Caitlin!

*Instagram: interstellate_*
*Twitter: interstellate_*
www.caitlinvanderweele.com
www.interstellate.com

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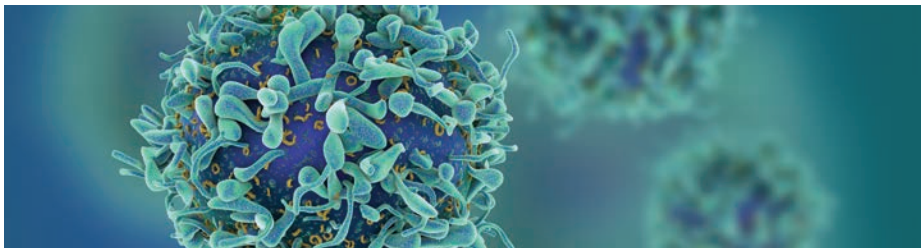
REVOLUTIONIZING CANCER THERAPY



For several decades, scientists have been studying ways to use the immune system to help fight cancer. Exciting new discoveries have shown that immuno-oncology (I-O) research can provide potential anticancer therapies to patients who previously had very few treatment options available to them. I-O therapies represent a breakthrough in cancer treatment and have the potential to revolutionize the way we treat many forms of cancer.

A HUGE STEP FORWARD FOR IMMUNOTHERAPY: FIRST EVER FDA-APPROVED CAR-T CELL THERAPY

August 30, 2017 marked the start of an exciting new era in personalized medicine. On that day, the US Food and Drug Administration (FDA) approved a therapy that genetically alters a patient's own cells to fight leukemia. Novartis™ KYMRIAH™ therapy, also known as tisagenlecleucel, is a treatment for pediatric acute lymphoblastic leukemia (ALL), and is now the first FDA-approved chimeric antigen receptor T (CAR-T) cell therapy to be commercially available. This historic approval brings awareness to emerging immunotherapies and their potential to transform cancer treatment, and even cure specific cancers.

Emily Whitehead, 12, was the first child ever to receive this type of "living drug." She was one of 63 patients whose cases were used as evidence showing that the treatment had an 83% remission rate at the 90-day mark.

Read the full blog post at thermofisher.com/ctsblog

Read the press release and find out how Gibco™ CTS™ products played a role at thermofisher.com/ctspr

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FINDING INSPIRATION

Words to spark the imagination

What's your favorite inspiring science quote?

Learn the art of science and the science of art and you'll find everything is connected. – Leonardo da Vinci

10

Science and everyday life cannot and should not be separated. – Rosalind Franklin

5

What's the best lab or science career advice you've ever received?

Career advice: Never stop asking questions. Lab advice: Never forget the controls.

9

The only dumb question is the one you didn't ask.

11

To achieve greatness in the lab you must have an unlimited imagination to question everything.

2

WHAT BOOKS DO YOU READ TO INSPIRE YOU?

THINKING, FAST AND SLOW
by Daniel Kahneman

WHEN BREATH BECOMES AIR
by Paul Kalanithi

BIG MAGIC
by Elizabeth Gilbert

WHAT IF?: SERIOUS SCIENTIFIC ANSWERS TO ABSURD HYPOTHETICAL QUESTIONS
by Randall Munroe

LAB GIRL
by Hope Jahren

IMAGINE
THE BEAUTY IN
SIMPLIFIED CELL ANALYSIS

SEE IT TO BELIEVE IT

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We have developed the Thermo Scientific™ CellInsight™ CX7 LZR HCA Platform that uses laser technology and its On-Stage Incubator to give you both the sensitivity and speed you need for imaging your live cells, along with the quantitative tools you need to measure the phenotypic changes in your sample in real time. New live-cell imaging capabilities are now available across all of our HCA instruments to enable you to better understandthe dynamics of your cells in context.

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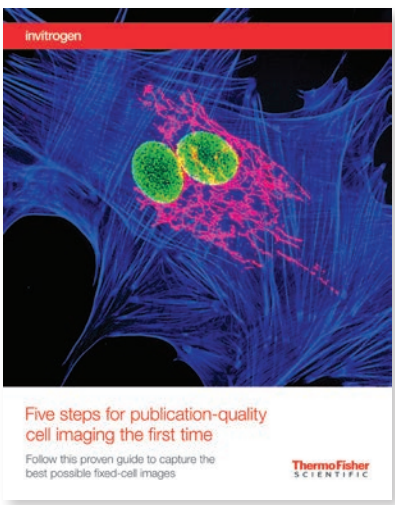
- **Simplified workflow**—save protocols easily via the adjustments screen
- **Modified profile indicator**—shows that the gating settings have been changed

Learn more about these features or download the software to upgrade your existing Countess II or Countess II FL Automated Cell Counter at
thermofisher.com/countessupdate
thermofisher.com/countessii



5 STEPS TO PUBLICATION-QUALITY IMAGES

Want to get the most out of your fixed-cell imaging experiments? From preparing your cells for labeling to imaging, this brochure will help you obtain publication-quality images in just 5 steps. Download the brochure at **thermofisher.com/5steps**

Check out our 5-steps promotion on the back cover!

COUNT ON EFFICIENCY

Learn how you can use the Countess II FL Automated Cell Counter with your CRISPR experiments to optimize measurements of transduction efficiency. Download the application note at **thermofisher.com/crisprcountess**

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THE INGENUITY BEHIND IMPACTFUL ASSAYS

Gerald BW Wertheim, MD, PhD
Assistant Professor
Children's Hospital of Philadelphia

DEVELOPING AN ASSAY THAT MEASURES DNA METHYLATION, AN INDEPENDENT PREDICTOR OF LEUKEMIA

Background: Acute myelogenous leukemia (AML) is generally a disease of older people, although it is also the second most common blood cancer in children. In AML and other leukemias, alterations in DNA methylation are well recognized, and the aggressiveness of AML tumors can be determined by studying methylation. Mutations in the genes that regulate DNA methylation have been shown to cause different forms of leukemia. Studies have also demonstrated that the prognosis of patients with AML can be predicted by this altered DNA methylation pattern with as few as 17 loci. However, tests that directly measure multiple-locus DNA methylation are typically expensive and technically challenging, making them difficult to perform in a routine setting. Gerald Wertheim and his colleagues have developed a novel approach to simultaneously analyze DNA methylation patterns at the 17 target loci by integrating multiplexed branched DNA technology from Thermo Fisher Scientific and fluorescent microsphere technology from Luminex. The method uses techniques that are inexpensive and can be easily performed in a routine

setting. The technique is called expedited microsphere HpaII tiny fragment enrichment by ligation-mediated PCR, or xMELP. It accurately reflects the methylation levels at each analyzed locus and enables segregation of individuals with acute myeloid leukemia into prognostic subgroups. Dr. Wertheim and his colleagues have published papers in *The Journal of Molecular Diagnostics* and the journal *Clinical Chemistry* [1,2].

Tell us about your studies of DNA methylation.

My primary interest has been on developing methods to better diagnose leukemia and lymphoma and to assess their prognosis in patients. Ultimately, we hope that clinicians can use our findings to help guide their therapy choices. We have known for some time that mutations are present in leukemia tumor cells, but we have not had the information to risk-stratify patients optimally. So I have been focusing on DNA methylation, which is thought to control transcription in certain numbers of genes. There are a number of pieces of evidence demonstrating that differential DNA methylation is important for AML prognosis. Many researchers have shown that genes that regulate DNA methylation are mutated in different types of leukemias, and some have directly shown that looking at DNA methylation alone can predict the outcome in patients with AML. Our goals are to find a set of genetic loci that vary in their DNA methylation patterns among patients, which can predict who will do well and who will do poorly with therapy, and to then develop a clinically relevant assay to detect levels of methylation at these loci.

How did you develop your analysis method?

With an ultimate goal of taking our assay to the clinic, we wanted to find a technique that was relatively inexpensive and could be multiplexed. We wanted to be able to look at multiple methylated regions to improve robustness, and we needed an assay that was highly reproducible. Because we use microsphere technology in the clinical lab, I initially tried a microsphere assay without branched DNA, and it did not have the appropriate analytical sensitivity. One of my collaborators was aware of the Invitrogen™ QuantiGene™ Plex Assay from Thermo Fisher Scientific and suggested that we look at it for our work. The QuantiGene Plex Assay uses branched DNA (bDNA) to amplify the signal rather than amplifying the target, and it sufficiently improved our sensitivity. Having the branched DNA amplification signal has been critical. We found that this QuantiGene Plex Assay was remarkably quantitative, with the results obtained by the QuantiGene Plex Assay and qPCR being virtually identical. Thus, this looked like the robust, multiplex assay program that could ultimately be used in high-throughput clinical lab settings. Evaluation of methylation is done through the measurement of microspheres and does not require custom-made, solid-phase oligonucleotide microarrays or high-throughput sequencing. The examination of methylation levels is performed by flow cytometric analysis of fluorescent microspheres, alleviating the need for high-throughput sequencing. This assay format can be easily expanded for the evaluation of 80 loci without an increase in reactions; the simultaneous assessment offers advantages, including a streamlined workflow and relatively fast turnaround time. The technical staff from Thermo Fisher taught us how to set up the instruments and run the assay. They were readily available by phone to help when I had questions. We were also able to have Thermo Fisher run some of our samples so we could compare runs and rapidly troubleshoot problems. I think that going forward, the diagnostic field is going to have to look at some of these other aspects, such as RNA expression analysis or epigenetic events. Hopefully, our assay will give clinicians a more accurate indication of prognosis and will help guide their decisions.

References

1. Wertheim GB et al. (2015) Validation of DNA methylation to predict outcome in acute myeloid leukemia by use of xMELP. *Clinical Chemistry* 61(1):249–258.
2. Wertheim GB et al. (2014) Microsphere-based multiplex analysis of DNA methylation in acute myeloid leukemia. *Journal of Molecular Diagnostics* 16(2):207–215.

* Internet access required.

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System comparison

	 SeqStudio Genetic Analyzer	 310 Genetic Analyzer	 3130 Genetic Analyzer
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Calibration	Auto calibration	Autosampler must be calibrated when capillary is replaced. Syringe calibration required when replaced.	Spatial calibration required when you install or replace array. Spectral calibration required when changing array length or polymer type.
Number of capillaries	4	1	4
Interactive touch screen with easy-to-use interface	Yes	No	No
Consumable tracking (RFID)	Yes	No	No
Capillary/array length	28 cm (in click-in cartridge)	47 cm, 61 cm	22 cm, 36 cm, 50 cm, 80 cm
Polymer type	POP-1 universal polymer	POP CAP, POP-4, POP-6	POP CAP, POP-4, POP-6, POP-7
Instrument size	49.5 x 64.8 x 44.2 cm (W x D x H)	61.0 x 55.9 x 86.4 cm (W x D x H)	149 x 55 x 81 cm (W x D x H)
Minimum sequencing run time	30 min	38 min	35 min
Minimum analysis run time	25 min	30 min	20 min
Sample capacity	96-well plate and 8-tube strips	1–96 sample tubes	2 sample plates (96- or 384-well)
Number of dyes	6	5	5
Applications	Sequencing and fragment analysis on same run	Sequencing, fragment analysis	Sequencing, fragment analysis
Sequencing read length	Up to 800 bp	Up to 600 bp	Up to 950 bp
Maximum sequencing throughput (base pair reads/day)	67K	15K	78K
Maximum fragment throughput (samples/day)	230	48	288
Connectivity	Wi-Fi and RJ-45 Ethernet ports	No	No
Remote monitoring and data storage	Yes	No	No
Configuration	Stand-alone, optional desktop or laptop computer	Computer required	Computer required
SmartStart orientation	Yes	No	No

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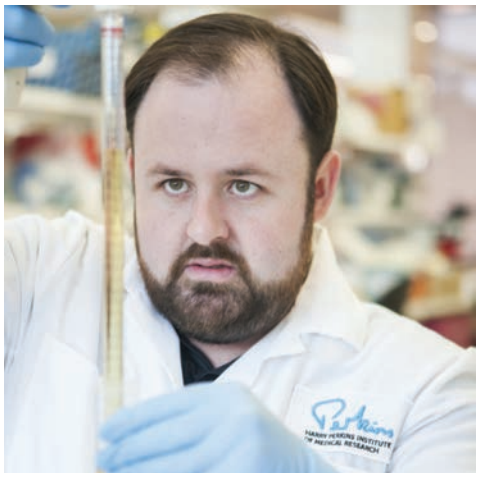
Kieran Mulroney, BSc



Biomedical Science Honors, PhD candidate at the Harry Perkins Institute of Medical Research, Faculty of Health and Medical Sciences, The University of Western Australia

Describe the importance of your work.
My research focuses on rapid diagnostics in severe bacterial infections, specifically looking at the antibiotic resistance profile. Using the correct antibiotic is essential for a patient to survive.

Tells us how the Attune NxT cytometer helps your research.
We are looking for the effects of the antibiotic drug on individual cells in a very rapid manner. Traditional antibacterial sensitivity testing can take 1–3 days depending on how difficult the bacteria are to grow, isolate, and then test for sensitivity. The Attune NxT cytometer allows us to tell whether or not the drug is effective within 1 hour, and gives inhibitory concentrations within 3 hours.

What do you hope to achieve with the Attune NxT cytometer?
We aim to characterize and test a full suite of drugs and bacterial combinations in order to move into the clinical space. We want to create a portable diagnostic and bring it to the areas of the world that need it the most.

Learn more by watching Kieran's interview at **http://bit.ly/2vEKVtn**

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NGS CHANGES COURSE FROM TRADITIONAL GENOMICS TO WATER TREATMENT

While NGS is commonly used in hospitals for cancer and genetics research, and in labs focused on forensic analysis, a group of researchers in Australia is using a simple water sample to determine which organisms, including vertebrates, native fish, and bacteria, have been in contact with that water sample. The end result is an improved process and improved outcomes for customers in the form of cleaner water.

The innovators at the Australian Water Quality Centre (AWQC) are the first in the Australian water industry to apply NGS for more efficient and targeted water treatment.

"It's very useful to know the diversity and abundance of aquatic life in water sources, as they can be indicators of a healthy water system and the Ion Chef™ and Ion S5™ technology are helping us do just this," said Karen Simpson, senior manager of laboratory services at the AWQC.

Conventional methods for detecting fecal contamination require days for culturing, and are limited because these methods target specific bacteria; parasites can be missed even after hours under microscopy. Use of NGS technology cuts down on the time to result for these scientists, enabling them to implement a rapid, targeted response to contaminants, and notify the public when applicable.

"Knowing more about what's in water sources enables better informed decisions on how to treat the water before it's supplied to customers," said Ian Hunter, minister for water and the River Murray.

The AWQC has been able to verify the data it is generating against curated databases and is developing its own unique curated database to match new samples against, to ensure accuracy and consistency of testing. By enhancing traditional testing with NGS DNA technology, one intelligent sample will provide more information, enabling better water quality–management directions and risk assessments.

INTRODUCING THE ION GENESTUDIO S5 SERIES

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The Ion GeneStudio™ S5 Series, a new line of benchtop next-generation sequencing (NGS) instruments, provides unmatched flexibility and scalability enabled by five Ion S5 chips, including the new Ion 550 chip, to facilitate wide-ranging experiments on a single platform. The new series also provides low cost per sample for small and large projects across multiple research applications. The Ion GeneStudio S5 Series delivers the highest level of dynamic range and read lengths of up to 600 base pairs to drive more powerful and cost-effective experiments in multiple areas, including cancer research, inherited disease, and microbial and infectious disease applications. With the flexible chip format, the Ion GeneStudio S5 platform can accommodate two sequencing runs per day with data analysis, delivering between 2-260 million reads and a total output between 0.5 GB to 50 GB.

Flexibility on the Ion GeneStudio S5 Series is achieved simply by switching between Ion S5 chips, not another sequencer, to match the appropriate throughput requirement for each project. The interchangeable chip format enables users to cost-effectively process samples in increments, eliminating the need to delay experiments by waiting to batch samples. The Ion GeneStudio S5 Series includes the Ion GeneStudio S5, Ion GeneStudio S5 Plus and the Ion GeneStudio S5 Prime systems. Formatted for ease of upgradability, each delivers increasing levels of speed, throughput and scalability and is designed to easily integrate with Ion AmpliSeq technology and the Ion Chef System for automated library preparation and amplification, as well as Ion Torrent downstream bioinformatics and reporting tools for a seamless sequencing workflow.

When combined with the expanded Oncomine portfolio of assays for liquid biopsy and immuno-oncology announced today, the new series of instruments offers the industry's most comprehensive, end-to-end oncology solution based on a single platform for applications ranging from research to preclinical.

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"In my institute, many customers outsource for exome and whole genome studies. They come to me for speed and flexibility for different gene panels tailored to disease areas of interest," said Morten Dunoe, laboratory director, Molecular Genetic Laboratory at the Juliane Marie Centre, Rigshospitalet, Copenhagen University Hospital. "This is the most elegant workflow on the market today. I can now offer a range of applications and deliver the data in the fastest turnaround time at costs that are competitive."

Ion GeneStudio S5 Series systems and Ion 550 Chip are for research use only. Not intended for diagnostic procedures.

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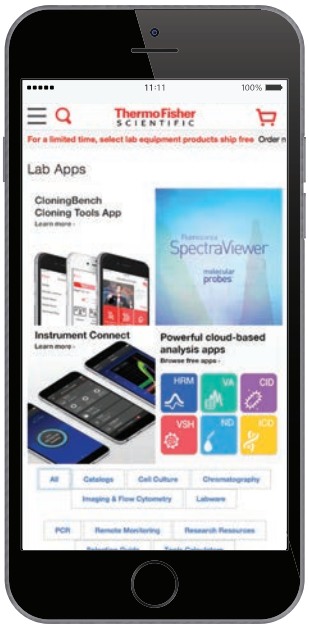

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– Kay Nicholson, Medical College of Wisconsin

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Rebecca Sinnott-Devaux,
Postdoctoral Associate,
University at Albany, SUNY, New York

What are you researching and how has the iBright system helped your lab?

In Dr. Herschkowitz's lab at the Cancer Research Center at the University at Albany, I am focused on the study of long noncoding RNAs and how they function in breast cancer progression. Over the past 30 years, advances in imaging technology and increased emphasis on early detection have led to a dramatic increase in the diagnosis of ductal carcinoma *in situ* (DCIS), a precancerous growth in the breast. Although only 40% of diagnosed DCIS cases are predicted to progress into breast cancer, we currently cannot distinguish between those DCIS cases that would remain harmless, and those that require immediate attention. Therefore, a DCIS diagnosis results in a cancer diagnosis, surgery, potentially radiation therapy, and potentially hormone therapy as well. This has created a current state of overdiagnosis and overtreatment, impacting tens of thousands of women every year. The only way to truly combat overtreatment is to gain a better understanding of the biology underlying breast cancer progression to better inform patient treatment, or nontreatment, options.

Long noncoding RNAs (lncRNAs) are relatively new players in both normal biology and in impacting disease. Our studies focus on the expression of lncRNAs that are misregulated in breast cancer progression. Recently, we purchased the Invitrogen™ iBright™ CL1000 Imaging System from Thermo Fisher Scientific. This instrument was critical to our lab environment as it not only replaced older, less efficient technology, but also combined white light, UV, and chemiluminescence imaging in one unit. For my studies, this instrument has been wonderful for developing southern and western blots to look at RNA:protein interactions, but in reality the entire department uses this instrument, taking advantage of its versatility. It has been a great addition to our platform.

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#IAmAScientist

If you're reading this, a scientist somewhere at some moment of time has impacted your life. Scientists working hard toward advancing discovery have a shared passion for the work that they do, but who exactly are these scientists? We've created a space for scientists, like you, to share their stories and explore personal journeys of other scientists around the world to learn more about the people behind the science.

Why did you choose to pursue science?
"I always had an interest in science, but the enthusiasm of my instructors and undergraduate research adviser really solidified my path. Ultimately I hope to be able to give younger students the same opportunities and investment I was given." – Krista Armbruster

If you could change society's perception about science, what would you say?
"The scientific community is working to advance science! Scientists do not go to work every day to prove conspiracy theories, harm the general public, or destroy the world. Most things that scientists do are overwhelmingly helpful to the general public. Look around at everything you interact with in your daily life and there is a scientist behind it! That food you ate? Tested for safety by a scientist. That car you drive? The fuel was tested to be the least harmful to the environment by a scientist. That toy that your child is playing with? The material was developed to be nontoxic and safe to play with by a scientist! We are good people and want to see the world evolve to become a better, safer place!" – Heather Hanson

Do you have any advice for the next generation of scientists?
"Quit focusing on the negatives. If you want to do it, start the journey. A journey can take as long as it needs to. So what if yours is longer than someone else's. It's the destination that counts." – Lisa Ramey

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However, I know that it is also a constant balance of business and science, and the business of science. It is my responsibility to ensure that I contribute to the success of our business. Our technologies and our business have to be sustainable to allow for further evolution and advancement to ultimately enable our customers to succeed. Twenty years ago, I chose this path ... and 20 years ago, I chose to keep going no matter how exhausted I am. I am passionate. I am dedicated. #IAmAScientist."
– Mary Ann Santos, Senior Technical Specialist for Synthetic Biology, Thermo Fisher Scientific

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