GEISINGER
Research Connections

Linking the Research Community • Spring 2015

A message from David H. Ledbetter, PhD

This issue of *Research Connections* is devoted to the MyCode® Community Health Initiative, a project with the potential to change significantly health and healthcare. MyCode will uncover new connections between genes and disease, inform and improve the health of Geisinger's patients and re-envision how we approach our own well-being and that of our families.

This project is possible because of Geisinger's specific combination of assets: an established biobank; an extensive and robust electronic health record (EHR); and international expertise in bioethics, medical genetics, genetic counseling and genomics. Our partnership with Regeneron, an innovative biotechnology company with extensive resources for whole exome sequencing, is key to positioning this project to make groundbreaking discoveries. We believe that My Code's successful execution will result in new treatments or more effective ways to manage diseases, as well as new approaches to processing, analyzing and storing huge datasets.

We will also forge new horizons in bioethics as we explore the ways in which patients can be informed of genetic risks that are identified by project, and validated clinically.

So much more than a large scale sequencing program, MyCode Community Health Initiative involves external collaborators as well as clinicians and scientists from across Geisinger, who will work together to define disease cohorts and study the linkages between genes and diseases. We believe that this is an important and defining initiative for Geisinger and fits our goals of putting patients first, continually learning and making Geisinger the best.

MyCode®: Engineering the Perfect Biobank

Geisinger's biobank and the MyCode® Community Health Initiative began in 2004 with a phone call from Glenn D. Steele Jr., MD, PhD, Geisinger's former president and CEO, to David H. Ledbetter, PhD, then at Emory University's School of Medicine. Speaking genetically, not meteorologically, Steele described Geisinger's Pennsylvania footprint and resources to Ledbetter as being, "as close to Iceland as you'll ever find in the United States."*

Ledbetter, now Geisinger's Chief Scientific Officer, found many similarities between Iceland and Geisinger's central Pennsylvania location. Like Iceland, Geisinger's regional population was stable, often with three generations in the area. In addition, Geisinger's healthcare was centralized with a robust electronic health record (EHR) in place since 1996.

According to Ledbetter, the qualities listed above, along with Geisinger's tradition of innovation, creates, "a healthcare laboratory and an ideal model to learn when and how genetic information can improve health." Ledbetter described Geisinger's service area as, "the ideal place in the United States to do longitudinal, large scale, genomic medicine research."

By 2012, genetic research initiatives were launching worldwide. For example, the United Kingdom began the 100,000 Genomes Project, a government-funded initiative to sequence 100,000 whole genomes from National Health Services patients.

What's more, California-based biotechnology pioneer Amgen purchased Iceland's deCODE Genetics, a global leader in analyzing and understanding the link between the genome and disease susceptibility. This collaboration provided access to the genetic and medical data of 140,000 Icelanders as well as an enhanced ability to identify and validate human disease targets. The Amgen/deCODE collaboration prompted Regeneron Pharmaceuticals, Inc., a leading science-based biopharmaceutical company in Tarrytown, NY, to seek a United States-based health partner.

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With an extensive EHR, good clinical data, a rapidly growing biobank, a scientific team in place, and a broad consent process allowing research use of samples and data along with the ability and commitment to return research results, Geisinger's biobank moved to the national forefront.

In 2014, Geisinger and Regeneron announced their human genetics research collaboration.

As part of the Geisinger Regeneron agreement, Geisinger is collecting samples from consented patient participants, while Regeneron sequences the samples to generate de-identified genomic data. This partnership which now anticipates up to 250,000 patients is one of the largest U.S. populations of participants providing genetic material for analysis and comparison in examining long-term health outcomes.

"The combination of Geisinger and Regeneron brings together a unique set of assets and expertise that allows us to conduct research of this size and scope. The long term benefits to human health and patient care will be tremendous. Together, Geisinger and Regeneron offer the expertise, the experience, the reach and financial resources to fulfill this promise," explains Steele.

"For Geisinger, the Regeneron relationship is about the potential to improve individualized patient care," comments Ledbetter.

"We expect that many of our patients will directly benefit from their participation in this research because of Geisinger's ability to validate and return clinically actionable results to them," he says. "This collaboration has the potential to provide Geisinger with tools to transform our ability to anticipate disease before the onset of symptoms, diagnose chronic and potentially fatal conditions before it's too late to intervene, and determine how best to optimize the health and well-being for each of our patients," adds Ledbetter.

One of the cohorts that the partnership plans to look at initially is the "Wellderly" or well elderly. Researchers can often learn the most about diseases from those who do not get sick. "There has to be something interesting we can learn from an active 90-year old smoker with high cholesterol who has not yet had a heart attack," notes H. Lester Kirchner, PhD, director of Biostatistics.

Other areas of early exploration for the partnership include: cardiovascular disease, obesity, and diabetes.

** In 1998 researchers realized that Iceland represented a genetic goldmine. It was a small island nation with only 300,000 genetically and phenotypically homogenous inhabitants. In addition, Iceland had a centralized healthcare system and medical records. A private company, deCODE Genetics, proposed partnering with the Icelandic government to create a biobank that joined biospecimens with health record information.*

Engineering a Partnership: Geisinger and Regeneron

"The collaboration between Geisinger and Regeneron is a perfect match, like peanut butter and chocolate, or perhaps more appropriately, like Watson and Crick," according to Regeneron's Chief Scientific Officer and President of Regeneron Laboratories, George D. Yancopoulos, PhD. Because the partners share common goals, Yancopoulos believes in the potential for the collaboration to make a real difference. Both Regeneron and Geisinger have "a shared commitment and devotion to try to improve patients' lives, and a shared vision in that we both believe in evidence-based medicine, and in particular in this case, in genetic, DNA-sequenced evidence," he says.

From its beginning in 1988, Regeneron has used genetics as the basis for drug discovery. Regeneron's first drug to receive FDA approval was based entirely on genetics. In this instance, Regeneron worked with academic collaborators who identified the gene mutations that are a major cause of a very rare orphan disease -- a cold induced auto-inflammatory syndrome. Once Regeneron and its collaborators understood the gene pathway, they were able to develop a drug to inhibit interleukin-1 (IL-1), the key driver of inflammation in Cryopyrin-Associated Periodic Syndromes (CAPS). Today, most of the drugs in the Regeneron pipeline come from genetics, but the process has been slow and painstaking.

As Regeneron worked to overcome the limitations of efficient sequencing of human genes–on a large scale, they searched for the right partner. "Geisinger was the best potential partner for us in this effort," says Yancopoulos. "Geisinger believed in evidence-based medicine to help drive better optimization of health care. They were leaders in digital medical records and turned that type of data into data that you use to help make decisions, optimize and efficiently deliver the right health care to patients, and get better outcomes."

According to Yancopoulos, the interests of the two organizations were complementary. "Geisinger wants to deliver better health care to their patients; Regeneron wants to use this information to understand how to do drug discovery and drug development in a better way."

MyCode®: Walking through its Development

The creation of a biobank with links to an electronic health record (EHR) has proved to be an important asset to Geisinger research. Even before the Geisinger–Regeneron collaboration, the ability of scientists to access MyCode® samples for research resulted in grant awards in excess of $7 million. What's more, the value of the Geisinger–Regeneron collaboration, based on whole exome sequencing data alone, is in excess of $100 million.

MyCode® Community Health Initiative has grown from its early days with one or two consenters and a part-time manager, to employing:

- 5 full time laboratory technicians
- 3 DNA robots that can process 96 samples at a time
- 20-23 consenters statewide.

MyCode funding has come from a variety of sources including: a State Department of Community and Economic Development grant, internal Geisinger funds, and the current partnership with Regeneron Pharmaceuticals.

Jointly directed by David Carey, PhD, associate chief research officer; W. Andrew Faucett, MS, LGC, director, Policy and Education; and David H. Ledbetter, PhD, chief scientific officer, the project features:

- An integrated process for collecting blood samples
- A broad consent form which allows for future contact
- Dynamic linking of samples and data to the EHR
- Ability to return medically actionable results
- A patient population willing to take part in research

Integrating MyCode into the clinic workflow contributes to patient participation in the study. Before or following regularly scheduled clinic visits, a healthcare provider or consenter briefly educates the patient about the study and asks the patient to consent to have an extra tablespoon or two of blood taken for research at the time of the patient's next clinically necessary blood draw.

The broad consent form explains that the donated blood samples may be used for a wide variety of research studies. It also allows researchers to contact a patient if additional information is needed or to invite a patient to take part in new research studies.

In the near future, MyCode will be launching an online recruiting and consenting process through the MyGeisinger patient portal. "IRB approval to implement online consenting will dramatically scale up our ability to recruit patients," explains Ledbetter.

During last year's MyCode focus groups it became clear that patients trust Geisinger and are willing to help others. "More than half of our focus group participants had been Geisinger patients for 20+ years and 85 percent of them received the majority of their care at Geisinger," notes Faucett. "As a result of patients' long term Geisinger relationship, MyCode participation rates are very high – 80 to 95 percent of patients who are approached agree to participate in MyCode," he adds. "What's more, we have some families with four generations in the system!"

Recent changes to the project include expanding recruitment into Geisinger's northeast and western regions; allowing for collection of blood samples every time blood is collected, instead of annually; and allowing for blood to be collected specifically for MyCode.

"We have the perfect storm for getting very rich longitudinal health data on a very large representative patient population: an integrated system, a stable population, early adoption of electronic health records, and our proven ability to extract and model data," explains Carey.

Lindsay Dunkle, a technician at the Weis Center for Research, pulls a MyCode® sample from storage.

Prominent Geneticist to Lead New Data Integration Program

Marylyn Richie, PhD

Marylyn Ritchie, PhD, a nationally prominent statistical and computational geneticist, was recently hired to lead the new Biomedical and Translational Informatics Program, within Geisinger Research. The program will build expertise in clinical informatics and translational bioinformatics to develop new methods and algorithms to use and integrate data to facilitate complex analysis and research.

Ritchie has extensive experience in all aspects of genetic epidemiology and translational bioinformatics as it relates to human genomics. This includes genome-wide association studies, next-generation sequencing, copy number variations, data integration of meta-dimensional omics data, Phenome-wide Association Studies, and development of data visualization approaches.

In addition to leading the Biomedical and Translational Informatics program, Ritchie also maintains an appointment as a professor in the Department of Biochemistry and Molecular Biology and director for the Center for Systems Genomics at The Pennsylvania State University, State College.

Geisinger is Well-Suited for Precision Medicine Initiative

While precision (or personalized) medicine appears to be the hot new buzzword in health care, the concept isn't new. When Geisinger released its 10-year strategic vision for research (more than six years ago), the Research Advisory Task Force recommended that Geisinger's vision should be to become an "international leader in personalized health research."

The vision stated that Geisinger Research will:

- Answer questions of direct relevance and importance to our patients and clinicians with the aim of creating knowledge and solutions driving improvements in clinical care
- Examine how individual factors and systems, from the molecular to the community level, influence individual health
- Develop and test personalized approaches to treatment and care delivery
- Create value-based solutions to clinical problems

Geisinger's strengths make it uniquely suited to pursue the goal of precision medicine: a strong focus on health care innovation; longitudinal electronic health care records; an integrated comprehensive health care delivery system, a large, non-transitory patient population; and finally, a cutting-edge laboratory for developing and testing new models of personalized health care.

President Announces Precision Medicine Initiative

President Barack Obama announced in the State of the Union Address his intentions to launch a new Precision Medicine Initiative, stating, "I want the country that eliminated polio and mapped the human genome to lead a new era of medicine – one that delivers the right treatment at the right time."

This initiative seeks to upend the medical paradigm of one-size-fits-all medicine, and instead takes into account individual differences in genes, environments and lifestyles. Precision medicine provides clinicians with tools to better understand the mechanisms underlying a patient's health, disease or condition and to better predict which treatments will be most cost effective.

At a January press conference attended by the nation's leaders in genomic medicine (including David H. Ledbetter, Geisinger's Chief Scientific Officer and George D. Yancopoulos, Regeneron President and Chief Scientific Officer), President Obama announced that his 2016 budget will provide $215 million for health information technology to be divided between the National Institutes of Health (NIH), the Food and Drug Administration (FDA) and the Office of the National Coordinator (ONC). His plan is to distribute the bulk of the funds to NIH to finance the development of a national research cohort of one million volunteers to aid in the understanding of health and disease.

Beyond creation of the research database, the initiative focuses in the near-term on cancer and in the longer term to generate knowledge applicable to both health and disease. "This [Precision Medicine Initiative] has the possibility of not only helping us find new cures, but also helping us create a genuine health care system as opposed to just a disease care system," states President Obama.

Driving Research Data and Analytics: the Phenotype Core

An essential component of the MyCode® Community Health Initiative is the Phenotype Core (PC), which is part of the Biostatistics Core. Traditionally, phenotypes are observable characteristics or traits. However, the term has taken on a larger meaning as it now describes a combination of disease attributes as they relate to clinically meaningful outcomes (e.g. symptoms, exacerbations, therapy response, and disease progression rates). This definition allows for classification of patients into distinct groups for both clinical and research purposes.

In addition to its many duties, the PC has two main functions:

- Develop phenotype algorithms
- Model electronic health record (EHR) data

One example of a phenotype algorithm created by the Core is metabolic health and obesity. To create this algorithm, the PC staff looked beyond basic ICD-9 codes for obesity or metabolic diseases, searching patient records for sustained periods of obese and lean measurements. According to H. Lester Kirchner, PhD, senior investigator and director, Biostatistics Core, studying this phenotype "allows us to understand the genetics that protect individuals with prolonged obesity from development of obesity-related co-morbidities."

The phenotype algorithms and data model created by the PC are not only essential to the success of the project, but also benefit all Geisinger research. Often experts base phenotypes on simpler algorithms, primarily using ICD-9 codes. "Other institutions don't have the depth and breadth of our data to create detailed phenotypes," explains Joe Leader, associate director, Biostatistics Core.

In addition to data in the Clinical Decision Intelligence System (CDIS), the PC extracts disparate clinical and departmental data for use in their activities. They also use metrics, such as frequency of visits, laboratory results, procedures, diagnoses, etc. to enrich phenotype algorithms. Once a phenotype is created; it is then validated through chart review.

Another important responsibility for the PC is to ensure that Geisinger data follows standard clinical nomenclature when available (e.g., LOINC, SNOMED CT, RxNorm) so that data can be shared broadly with collaborators. For example, Geisinger's EHR uses Medispan, a proprietary classification system, for medication orders. To enable cross-institution sharing of the data, the PC is mapping all of the historical Medispan information to RxNorm, a publicly available data standard that provides links to drug vocabularies commonly used in pharmacy management and drug interaction software.

Headed by Kirchner and Leader, the team includes six programmers, a project manager, an ETL developer/Database Administrator, and a biostatistician. "So far we've been fortunate to hire folks who are experienced both in the healthcare setting and as programmers," notes Leader. "We train our team in multiple disciplines and they routinely work with multiple programming languages and databases and they must understand clinical care and workflow processes."

The Core Team: The Phenomic Analytics and Clinical Data Core of Geisinger's Biostatistics Core, includes, left to right (seated): Brandon Geise, manager, research data; Joe Leader, associate director, Biostatistics Core; Dustin Hartzel, data analyst, Phenomics; (standing) H. Lester Kirchner, PhD, director, Biostatistics Core. Missing from photo: J. Neil Manus, John Snyder and Lance Adams.

Advancing Ethical Issues Raised by Biobanks, Genomics

Throughout history, scientific breakthroughs are often met with debate and discussion about their ethical and moral implications. Whole genome or exome sequencing and the creation of biobanks have followed this well-worn path. Some of the questions raised include:

- Is it ethical to ask patients to provide only a broad, general consent for the use of their specimens, or can "informed consent" only occur with a detailed, study-specific consent?
- Are researchers obligated to return results to study participants on genomic findings discovered during the research process?
- If genomic findings have familial implications, do researchers have a duty to warn and care for family members?

Dan Davis, PhD, director of Bioethics, spends a lot of time exploring and investigating these issues and is excited about the unique position Geisinger now enjoys at the nexus of genomics and ethics. "We're really on the ground floor of moving genomics into the clinical realm," he says. "If anyone has a chance to advance the development of evidenced-based standards for addressing these issues, I think it's us."

Geisinger began grappling with consent questions in part by engaging patients and participants, through surveys and focus groups. Patients overwhelmingly responded that initially they would like to be asked if their blood could be used for research, but said that they did not need to be contacted for each specific study. Davis described the process as "a wonderful example of patient engagement whose results were used to inform institutional policy."

In general, institutions conducting whole genome sequencing using biobank specimens do not return results. Sequencing is considered a research activity whose purpose is to advance knowledge, not to advance the care of specific patients.

Geisinger rejected this argument. "We doubt that Geisinger patients make any big distinction between Geisinger as a conductor of research and Geisinger as a provider of care," explains Davis. As a result, Geisinger has committed itself to returning clinically actionable findings to patients (see page 7, Return of Genomic Results).

The issue of familial implications is also on the agenda. "If we embrace the duty to warn and care for the individual patient, we also have to embrace that duty for the patient's family," says Davis. To help Geisinger sort through these and future ethical issues, an Ethics Advisory Committee has been established under the chairmanship of Kevin FitzGerald, SJ, PhD, a Georgetown University-based expert in genomics and bioethics.

Advisory Committee Provides Ethics Oversight

Kevin FitzGerald, PhD, SJ is a man at the crossroads – the intersection between science (PhD in molecular genetics), and religion (Jesuit priest with a PhD in bioethics). "It is more helpful to operate at this crossroads if you have a Union card for both," notes FitzGerald.

With these credentials, FitzGerald is the ideal person to chair the eight member Ethics Advisory Committee –four members from the world of genomics and ethics and four who are Geisinger patients. In addition to FitzGerald, Advisory Committee members include:

- Kyle Brothers, MD, a pediatrician with an interest in Genomics at the University of Louisville
- Joan Scott, MS, genetic counselor, Chief, Genetic Services Branch in the Maternal and Child Health Bureau of the Health Resources and Services Administration
- Sylvia Mann Au, MS, director of the Hawaii Department of Health Genetics program
- Geisinger patients: Thomas Shannon, Sarah Kirkland, Mary Louise Schweikert and Raven Rudnitsky

FitzGerald believes that this committee has the opportunity to influence the dialogue on genomics and bioethics on a national and international level. "What is going on right now at Geisinger is unique in terms of the size of the project, ways in which the public is being engaged, and the ethical issues being addressed. I think there is an opportunity here to set a precedent, for other health systems, other biobanks, other research projects," he says. "When other organizations get to the point that Geisinger is now, they can look at the Geisinger experience and learn from it."

"I think there is an opportunity here to set a precedent, for other health systems, other biobanks, other research projects."

Kevin FitzGerald, PhD, SJ,
Chair, Ethics Advisory Committee, Geisinger Health System

The patient-facing report provides patients and their clinicians with genomic testing results in a clear concise manner.

"This project will help set the standard for using this kind of genomics approach to inform patient care."

Michael Murray, MD
Director, Clinical Genomics

Return of Genomic Results to MyCode® Community Health Initiative Participants

For about two percent of the MyCode® Community Health Initiative participants whose genes are sequenced – as many as 5,000 individuals – participation could be truly life changing for them and their families. This is because they will receive clinically important information on findings from the sequencing of their genes.

Geisinger is the first such program on this scale committed to returning medically important genomic test results to research participants when those results are judged clinically valid and actionable. "This project will help set the standard for using this kind of genomics approach to inform patient care," says Michael Murray, MD, director, Clinical Genomics, who leads the "Return of Results" program.

The list of conditions that trigger a return of results includes the 25 conditions recommended in the 2013 guidelines from the American College of Medical Genetics and Genomics (ACMG) for research participants who have had clinical exome or genome sequencing. Both Marc Williams, director, Genomic Medicine Institute, and Christa Martin, director, Autism and Developmental Medicine Institute, served on the original ACMG committee that recommended the guidelines. Martin now chairs that committee.

Building on the ACMG list, Geisinger plans to return results for 76 genes related to 27 different conditions. "The bulk of these genes are related to cardiac disease and cancer predisposition," explains Monica Giovanni, director, Clinical Genomics Strategy, Northeast.

The Geisinger program will return clinical results to research participants only after confirming the research result via a different methodology in a clinical laboratory and in accordance with CLIA (Clinical Laboratory Improvement Amendments) requirements. In addition, an established workflow facilitates the return of results to patients in the most effective manner possible. For example, the Geisinger provider as well as the patient will receive direct communication about the genomic finding with detailed recommendations for next steps. Providers will be offered educational resources and expert guidance to assist them in meeting a patient's needs regarding the genetic finding.

Cloud-Based Storage Provides Data Opportunities

During a tour of the Regeneron facility, Jeffrey Reid, Regeneron's director Genome Informatics, advised the Geisinger group, "We'll save the data center for last."

Reid showed the group the millions of dollars spent on high-throughput DNA sequencing technology. When the tour group approached the "data center", Reid opened the door to a completely empty room. A picture of a cloud was taped to the wall. Reid explained that instead of investing additional millions to create a center to analyze and store the data generated from the project, Regeneron is contracting with DNAnexus (a software company specializing in genome informatics & data management) and storing all the data on the cloud.

Whole exome sequencing is extremely data intensive. While the exome coding region represents only about 2 percent of the whole genome, it contains about 60 million base pairs. To map the exome accurately, overlapping regions are sequenced multiple times. Regeneron plans on conducting a minimum of 20 reads of each base for about 90 percent of the base pairs in order to reduce errors. Seven to ten gigabytes of data are needed per each whole exome sequence. To put that into context, one gigabyte of data is equivalent to 894,784 pages of text. The use of cloud computing not only will allow for one copy of the data to be shared by both companies (Regeneron and Geisinger), but cloud storage saves millions of dollars that would have been spent to accommodate the computers needed to store the vast amount of data. In addition, those computers would require upgrading every 3 to 5 years. Instead, leasing space on the cloud, removes the cost of hardware updates.

Cloud computing holds promise for a wide variety of applications in the future. Not only will cloud storage allow Geisinger to store large volumes of data from a myriad of sources: EHR, imaging, and patient reported data, among others, but the cloud will provide a base for the integration of these diverse data streams. Researchers such as Marylyn Ritchie, PhD, Director, Biomedical and Translational Informatics, are exploring ways to leverage the power of cloud computing. Ritchie is currently developing methods and algorithms that will allow her to conduct phenome wide association studies (PheWAS) in the cloud.

"Seven to ten gigabytes of data are needed per each whole exome sequence. One gigabyte of data is equivalent to 894,784 pages of text."

MyCode® Program Director Samantha Fetterolf (at right) explains the MyCode® process to employees and advisory committee members.

Geisinger Staff Publications

From June 2014 through April 2015 Geisinger authors published more than 270 publications. The list below is a selection of those publications. The Geisinger author's name is bolded.

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Recent Awards

This list includes new awards and competitive renewals from external agencies, including new awards from the Bucknell Geisinger Research Initiative from August 2014 through April 2015. To protect sponsors' confidential information, we omit dollar amounts for clinical trials and industry-sponsored agreements and some clinical trial listings. If an award is inadvertently overlooked, please forward the information to Richard Fogaley (rafogaley@geisinger.edu) for inclusion in the next issue.

William Azeredo, Geisinger Health System
Jenna W. Briddell, Geisinger Health System
Donna Ebenstein, Biomedical Engineering, Bucknell University
Otolaryngology
Analysis of the Effect of Saliva on the Degradation Rate of Absorbable Sutures
Bucknell Geisinger Research Initiative grant
$25,747

David J. Carey
Weis Center for Research
Genomic diagnosis and individualized therapy of highly penetrant genetic diabetes
University of Maryland/National Institutes of Health
$162,828

Brenda Finucane, Geisinger Health System
Aaron Mitchel, Psychology, Bucknell University
Autism & Developmental Medicine Institute
Multisensory Integration in Klinefelter and Turner Syndromes
Bucknell Geisinger Research Initiative grant
$149,829

Edward Gorak
Hematology/Oncology
National Cancer Institute Community Oncology Research Program (NCORP) Community Sites
National Institutes of Health
$880,000

Brian Irving, Geisinger Health System
David Rovnyak, Chemistry, Bucknell University
Obesity Institute
NMR Metabolomic Characterization of Human Serum
Bucknell Geisinger Research Initiative grant
$40,955

Adam K. Lee, Geisinger Health System
James Widmaier, Geisinger Health System
Sarah Manoogian, Mechanical Engineering, Bucknell University
Orthopaedic Surgery
Determining the Influence of Surgical Drilling Procedures on Thermal Osteonecrosis
Bucknell Geisinger Research Initiative grant
$36,852

Robert McQuillan
Diversified Services
FTA Section 5310 Elderly & Disabled Specialized Transit
Pennsylvania Department of Transportation
$48,000

Andrew Michael, Geisinger Health System
Richard Kozick, Electrical and Computer Engineering, Bucknell University
Autism & Developmental Medicine Institute
Method Development to Characterize Functional Brain Networks: Application to Autism and Other Neurodevelopmental Disorders
Bucknell Geisinger Research Initiative grant
$49,991

Tooraj Mirshahi, PhD and Janet Robishaw, PhD (Multi-PI)
Weis Center for Research
An integrated approach to study GPCR variants associated with complex diseases
National Institutes of Health
$2,083,322

Janet Robishaw
Weis Center for Research
Novel Aspects of Golf Signaling in Brain
National Institutes of Health
$1,452,000

Heinric Williams, Geisinger Health System
Mitchell Chernin, Biology, Bucknell University
Urology
Mechanisms of Bladder Cancer Growth Inhibition Using Dual HSP70 Inhibitors
Bucknell Geisinger Research Initiative grant
$23,108

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