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News, Opportunities and Deadlines for June 2022

2022 LBRN Summer Bioinformatics Training

LBRN began the 2022 LBRN Summer Bioinformatics Training to undergraduate, graduate, and faculty at institutions across Louisiana. This program replaces regular summer programs canceled due to COVID-19. This program is conducted in virtual/online format with the support of Pine Biotech.

With programs was starting on or after June 6, 2022, LBRN is currently supporting participants from eight PUI campuses includes, **Grambling State University, Louisiana State University in Shreveport, Louisiana Tech University, Southeastern Louisiana University, Southern University and A&M College, University of Louisiana at Monroe, University of New Orleans,** and **Xavier University of Louisiana** and one of our outreach campuses the **University of Louisiana at Lafayette.**

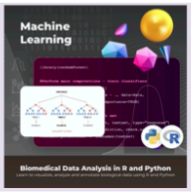
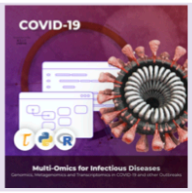
Complete Program List:

- Omics Logic (Basics) Bioinformatics
- *Biomedical Data Analysis in R & Python
- *Bioinformatics for Infectious Diseases
- *Transcriptomics for Chronic Diseases
- *Research Project

2022 LBRN Summer Bioinformatics Training Modules

(for undergraduate, graduate students, faculty and staff of LBRN Institutions)

The Louisiana Biomedical Research Network (LBRN) Summer Program is Supported by the Louisiana Board of Regents and NIH:NIGMS P20GM103424

Program					
	Omics Logic Bioinformatics	Biomedical Data Analysis in R & Python	Bioinformatics for Infectious Diseases	Transcriptomics for Chronic Diseases	Research Project
Duration (months)	3	1	3	3	3
Number of Students	30	10	10	10	4
Difficulty	Beginner	Intermediate	Intermediate	Advanced	All Levels
Description	Getting Started with Bioinformatics	Learn to explore, visualize, and analyze biomedical -omics data using R and Python.	Learn about bioinformatics for COVID monitoring and multi-omics data in infectious disease research.	Master bulk and Single Cell RNA-seq methods used in chronic disease research like cancer.	Work on an independent bioinformatics research project with big data and technical support.

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Louisiana Biomedical Research Network

Program Breakdown:

- Omics Logic Basics. This program is best suited for students interested to learn about various -omics technologies and how bioinformatics is used in biotechnology, healthcare, agriculture and basic research. Program access provides access to all the asynchronous* online courses (basic course certificates only). This can be taken at the same time as ALL the other programs.

*The below projects can be taken at the same time with Omics Logic Basics.

- *Biomedical Data Analysis in R & Python. Getting Started with Bioinformatics in R and Python - As biology is saturated with complex datasets that have to be besorted, explored, and“looked into”, anyone handling data generation, analysis, or decision making based on data has to gain some level of “data science” skills. In most biological and biomedical settings, you will be expected to run or implement programs written by Python, R, and others. R programming offers a complete range of functionality that you can leverage to perform in-

depth statistical analysis, visualization and annotation. The increasing necessity to process big data and develop algorithms in all fields of science means that programming is becoming an essential skill for scientists, with Python the language of choice for the majority of bioinformaticians.

- *Bioinformatics for Infectious Diseases. This program is dedicated to the study of viral diversity and its role in epidemic infectious diseases that keep re-emerging, including zoonotic spillover, transmission between humans, and the process of viral and bacterial disease development. As a result, you will learn to understand relationships between viral strains and haplotypes, find differences in sequence data, and see the implications for drug and vaccine design. This program will provide opportunities to practice analyzing data to gain hands-on experience with curated datasets from public domain collections, guided by experts with bioinformatics experience and knowledge about virology.

- *Transcriptomics for Chronic Diseases An online training program focused on next-generation sequencing (NGS) Data Analysis in application to gene expression data with project examples from infectious diseases, cancer & neuroscience. This online program will introduce real-world applications of RNA-seq data analysis in biomedical research and provide participants with hands-on skills and logical background to extract insights from gene expression data. We will review the methods and history of quantitative and qualitative analysis of mRNA expression. Practical sessions will guide participants to use the methods we review on several project datasets to practice generating a table of expression from raw FASTq files and perform subsequent analysis of this table of gene and isoform expression.

- *Research Project It has been designed to help young researchers and students take advantage of the bioinformatics resources for analysis of complex life science data and become versed in bioinformatics. Research Fellows participate in cutting-edge bioinformatics research led by expert mentors. The program will offer a combination of online resources and mentor guidance to prepare you and help you complete a bioinformatics project. We offer high-grade training and research tools for hands-on analysis for various research fields which includes analysis of Big Data belonging to Multi-Omics fields (Transcriptomics, Genomics, Epigenomics & Metagenomics), Infectious Diseases, Precision Medicine, Neuroscience, Space-Omics, Metabolic Disorders etc.

LBRN Achievement

Caleb Charpentier from Southeastern Louisiana University awarded a Graduate Research Fellowship NSF


Caleb Charpentier from Southeastern Louisiana University was recently awarded a Graduate Research Fellowship from the National Science Foundation to pursue a Ph.D at Virginia Tech starting in the Fall. Only two of these prestigious fellowships were awarded to students from Louisiana last year. Caleb had worked with Dr. April Wright for 5 semesters under an LBRN grant. He is also the first author on a recently published article in the journal Methods in Ecology and Evolution, entitled "Revticulate: An R framework for interaction with RevBayes."

Through his work as a researcher in a computational phylogenetics lab, he has learned to program in three languages and has made a software called RevR that will be very useful to scientists doing phylogenetics research. After graduation he plans to do research as a Ph.D. student.

NSF Graduate Research Fellowship Program (GRFP) List. (search award year 2022)

Article Reference: https://besjournals.onlinelibrary.wiley.com/doi/10.1111/2041-210X.13852

Our first HPC training will be held on Wednesday, June 29 at 9:00 AM. Due to concern about the COVID-19 pandemic, all training sessions are Zoom online events from 9:00AM to 11:00AM. The sessions will be recorded for later review.

Note that all HPC trainings will start at 9:00AM.

Wednesday, June 29, 2022: Introduction to Linux
The aim of this training is to get users familiar with using Linux systems e.g. the HPC resources. This training will cover basic Linux commands and editors (emacs and vi) on Linux systems. Anyone who is interested in learning about using a Linux based computer is encouraged to attend. If you are not familiar with using a Linux system particularly creating/writing files then this course is a prerequisite for the forthcoming training on HPC User Environment 1 & 2.

This training is *mandatory* for HPC users who are not familiar with using a Linux/Unix system.

Prerequisite: Access to a Linux/Unix based computer i.e. Linux (VirtualBox images), Mac OSX and Windows with Cygwin or Bash installed.

Next two HPC Trainings:

Wednesday, July 13, 2022: HPC User Environment 1, Job Management on HPC Clusters
Wednesday, July 20, 2022: HPC User Environment 2, Job Management on HPC Clusters
This training provides an overview of the HPC/LONI general account and allocation policies, hardware and software environments, queuing system, compiling programs, writing submit scripts, running and monitoring jobs on HPC systems.

This training is a *mandatory* two-day training event for all HPC/LONI new users held on July 13 and July 20.

Prerequisite: Familiarity with Linux/Unix commands and editors.

Please visit http://www.hpc.lsu.edu/training/tutorials.php for more details and register using the link provided. Users will be provided with a zoom link in their registration confirmation email. Please see the system requirements at https://support.zoom.us/hc/en-us/articles/201362023-System-

Requirements-for-PC-Mac-and-Linux.

The schedule for the Summer 2022 HPC Training is available at http://www.hpc.lsu.edu/training/tutorials.php.

NIGMS - Funding Trends

A Closer Look at the NIGMS AREA (R15) Program

Continuing our regular posts detailing funding trends for NIGMS programs, here we provide a closer look at the NIGMS Academic Research Enhancement Awards (AREA) R15 program. AREA grants support small-scale research projects involving primarily undergraduate students at institutions that received no more than $6 million in funding from NIH in 4 of the past 7 years. Awards can be up to $300,000 in direct costs for the entire project period of up to 3 years. Unlike most of our other Research Project Grant (RPG) awards, which have noncompeting renewals on an annual basis, R15 funds are obligated in the first year and last the duration of the project period. Grantees can renew these awards in a competitive proposal process.

NIH offers two different R15 awards: AREA and the Research Enhancement Award Program (REAP). The key distinction between them is that AREA grants are available to undergraduate-focused institutions, while REAP grants are available to health professional and graduate schools. See the FAQs about the programs for a list of common questions. NIGMS participates in only the AREA program.

Figure 1 shows a history of R15 award investments from NIGMS and the rest of NIH on an annual basis from Fiscal Year (FY) 2012 to FY 2021. Because funds for R15s are obligated in the first year, all R15 funding data reflect competing award obligations.

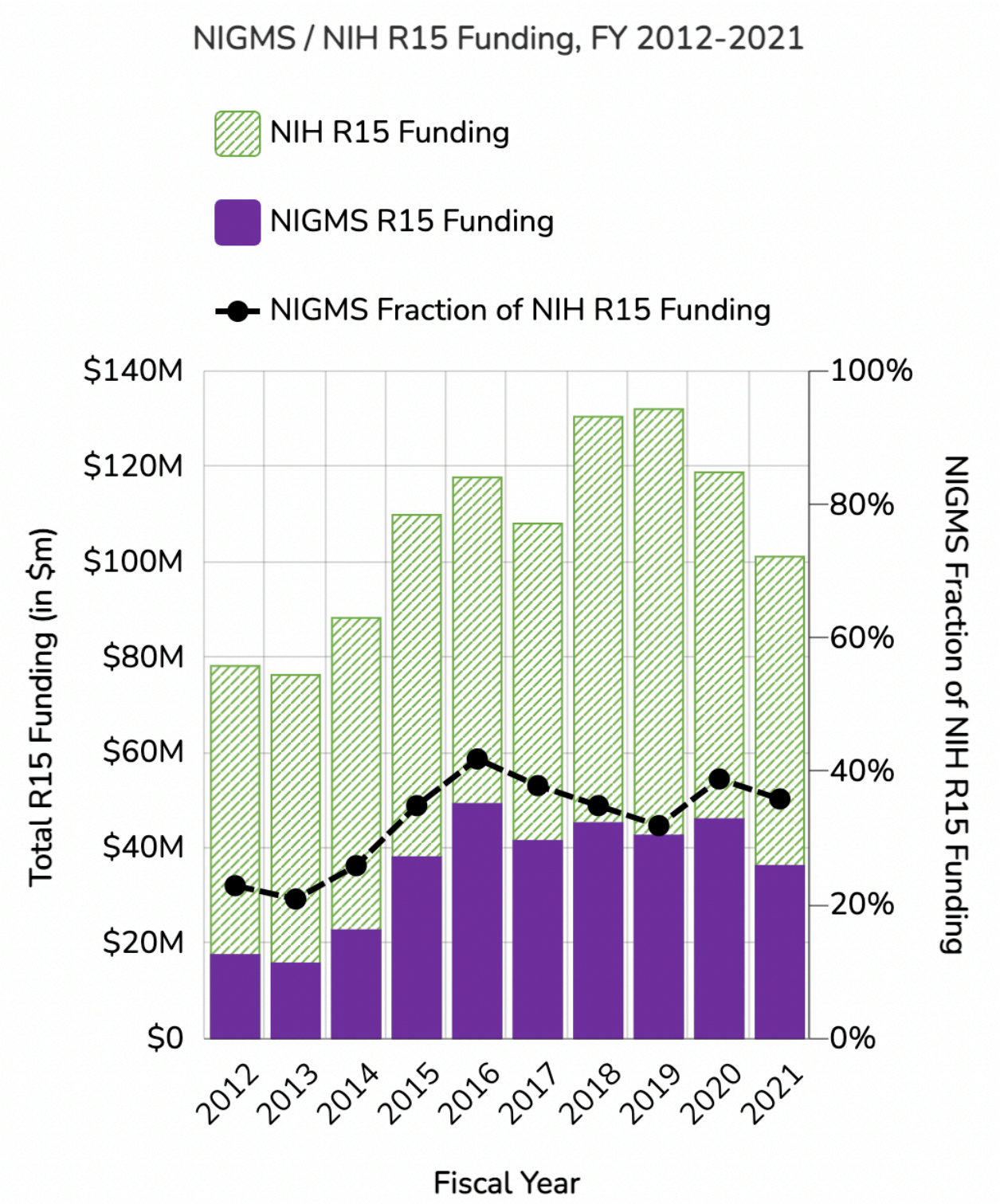

Figure 1. NIGMS and NIH Funding of R15 Awards, FY 2012-2021. Illustrated is the total funding for R15 awards by NIGMS (solid purple bars; left axis), NIH as a whole (green-striped bars; left axis), and the fraction of NIH R15 funding provided by NIGMS (black dashed line with circles; right axis). NIGMS has provided 30% to 40% of all funds awarded to R15 grants over the past 7 years.

Continue Reading.....

NIGMS - High School and Undergraduate Programs

- **High School**

Research Supplements to Promote Diversity in Health-Related Research (Admin Supp)

PA-21-071; Shakira Nelson; Zuzana Justinova

This program employs the research project grant as the platform for intensive mentored research experiences within the scope of the grant during the continuum from high school to the postdoctoral level and investigators developing independent research careers. The goal is to increase the nation's pool of students from underrepresented groups by preparing them to continue their training and career advancement in biomedical research.

- **Community College Student**

Bridges to the Baccalaureate (T34)

PAR-22-125; Shakira Nelson; Laurie Stepanek

The goal of the program is to provide structured activities to prepare a diverse cohort of community college students to transfer to and complete a bachelor's degree in biomedical research fields. The program supports institutions that develop and implement effective, evidence-informed approaches to biomedical training and mentoring. This program requires partnerships between two-year post-secondary educational institutions granting the associate degree with four-year colleges or universities that offer the baccalaureate degree.

NIH Common Fund Initiative: The Diversity Program Consortium - Enhancing the Diversity of the NIH-Funded Workforce, Building Infrastructure Leading to Diversity (BUILD)(U54)

RFA-RM-13-016; Edgardo Falcón-Morales; Sydella Blatch; Laurie Stepanek; Consortium contact: Alison Gammie

BUILD awards are designed to implement and study innovative approaches to engaging and retaining students from diverse backgrounds in biomedical research, potentially helping them on the pathway to become future contributors to the NIH-funded research enterprise. BUILD awards differ from other NIH-funded training grants in that they aim to achieve simultaneous impact at the student, faculty, and institutional levels.

NIH Common Fund Initiative: The Diversity Program Consortium - Enhancing the Diversity of the NIH-Funded Workforce, National Research Mentoring Network (NRMN)(U24)

RFA-RM-18-002; RFA-RM-18-003; RFA-RM-18-004; Michael Sesma; Consortium contact: Alison Gammie

The National Research Mentoring Network (NRMN) resource center provides mentoring and networking opportunities for biomedical researchers from diverse backgrounds, including those from underrepresented groups, from the undergraduate level through early career faculty. The NRMN coordination center brings together the NRMN awardees, including the resource center and the research on mentoring, networking and navigating critical transition points.

- **Undergraduate Student**

Maximizing Access to Research Careers (MARC) (T-34)

PAR-21-147; Patrick Brown; Sydella Blatch

The goal of the program is to develop a diverse pool of undergraduates who complete their baccalaureate degree, and transition into and complete biomedical, research-focused higher degree programs (e.g., Ph.D. or M.D./Ph.D.). MARC is an undergraduate student training program for institutions with research-intensive environments. Eligible institutions must have a 3-year average of NIH research project grant funding greater than or equal to $7.5 million in total costs per year.

Undergraduate Research Training Initiative for Student Enhancement (U-RISE) (T34)

PAR-21-146; Kenneth Gibbs; Baishali Maskeri

The goal of the program is to develop a diverse pool of undergraduates who complete their baccalaureate degree, and transition into and complete biomedical, research-focused higher degree programs (e.g., Ph.D. or M.D./Ph.D.). U-RISE is an undergraduate student training

program for institutions with research-active environments. Eligible institutions must have a 3-year average of NIH research project grant funding less than $7.5 million in total costs per year.

National Resesarch Mentoring Network

The NIH Common Fund's High-Risk, High-Reward Research (HRHR) program issues annual funding opportunities for exceptionally creative scientists with highly innovative research ideas. The NIH remains committed to encouraging diversity in the workforce while funding the best science and so encourages applications from individuals of diverse backgrounds, scientific areas, and institutions. This webinar will share four funding opportunities within the HRHR program - the NIH Director's Pioneer, New Innovator, Transformative Research, and Early Independence Awards, supporting high-impact research from scientists at all career stages.

Join us on July 7 at 1pm CST for an important discussion.

Weekly Update from DRCB / NIGMS

Weekly Update from DRCB/NIGMS

Issue 86

PIs who receive the update are expected to forward to researchers, students, and staff on the awards

NIH Funding Opportunity and/or Policy Announcements

• Small Business Innovation Research (SBIR) program (PA-22-176 and PA-22-177).

• Small Business Technology Transfer (STTR) program (PA-22-178 and PA-22-179).

• Needs Assessment Program for NIH SBIR/STTR Awardees (NOT-OD-22-133).

Reports/News/Program Messages

• COBRE Phase 2 Informational Webinar video and slides are now available here.

***See previous Weekly Updates at DRCB website**: https://www.nigms.nih.gov/Research/DRCB/Pages/weekly-updates-from-DRCB.aspx*

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Weekly Update from DRCB/NIGMS
Issue 85

- SEPA Pre-Submission Webinar for PAR-20-153 via Zoom, June 16, 2:30 pm – 4:00 pm ET.
- Evaluation Workshop, hosted by Division of Training, Workforce Development and Diversity at NIGMS, June 21, 1:00 pm – 4:00 pm ET. More information and the agenda are available

on the webinar registration webpage.

NIH Funding Opportunity and/or Policy Announcements

- Small Business Innovation Research (SBIR) program (PA-22-176 and PA-22-177).
- Small Business Technology Transfer (STTR) program (PA-22-178 and PA-22-179).
- Needs Assessment Program for NIH SBIR/STTR Awardees (NOT-OD-22-133).
- Maximizing Investigators' Research Award (R35) (PAR-22-180).

Reports/News/Program Messages

- COBRE Phase 2 Informational Webinar video and slides are now available here.

Weekly Update from DRCB/NIGMS
Issue 84

NIH Funding Opportunity and/or Policy Announcements

- Small Business Innovation Research (SBIR) program (PA-22-176 and PA-22-177).
- Small Business Technology Transfer (STTR) program (PA-22-178 and PA-22-179).
- Needs Assessment Program for NIH SBIR/STTR Awardees (NOT-OD-22-133).
- Maximizing Investigators' Research Award (R35) (PAR-22-180).
- Administrative supplements to advance precision medicine using the All of Us Research Programs Data (NOT-PM-22-002). Due date: July 6. Eligible programs include, but not limited to, IDeA-CTR, COBRE, INBRE, NARCH, SuRE and SCORE.

Reports/News/Program Messages

- COBRE Phase 2 Informational Webinar video and slides are now available here.
- The NIH Office of Research on Women's Health (ORWH) issues new resources on the Maternal Morbidity and Mortality (MMM) Web Portal.

LBRN "Core Bucks"

The BBC Core and MCBR Core offer researchers the opportunity to earn “Core Bucks” to support faculty and students upto $1500. Requests for Core Bucks from Member Institutions must be initiated through the respective Core Contact on campus.

- The Bioinformatics, Biostatistics, and Computational Biology Core (BBC Core)

The BBC Core serves to train and support project investigators and their teams across Louisiana. It works to enable Louisiana Biomedical Research Network project PIs and their teams to employ Louisiana cyberinfrastructure (especially high performance computing), and to provide bioinformatics services, training, and educational support.

The core provides bioinformatics training, conducts workshops, and provides bioinformatics analysis services. The core also provides access to the IBM Delta Cluster and has a dedicated BBC allocation for the high performance computing resources at LSU. The BBC Core maintains software licenses and access to Ingenuity Pathway Analysis (IPA), Partek Flow, DNASTAR, and Ion Torrent analysis software. In addition, several open source tools for bioinformatics such as bowtie, tophat, cufflinks, samtools, GATK, QIIME, DADA2, Phyloseq, etc. are installed and maintained.

Some examples of standard bioinformatics workflows that can be supported through core bucks

requests:

- Gene Pathway Analysis
- RNA-Sequencing Processing and Analysis
- 16S rRNA Microbial Community Analysis
- ITS2 Fungal Community Analysis

Other workflows can be developed or adapted from existing software on an as needed basis.

For more information, see: https://lbrn.lsu.edu/cores.html#corebucks

- The Molecular and Cell Biology Resources Core (MCBR Core)

MCBR Core Services include both one-on-one training for faculty and students as well as workshops on topics like bioinformatics and protein purification.

Sample services:
1. Molecular Biology Reagent Equipment and Services

- GeneLab provides conventional and next generation nucleic acid sequencing (NGS), and recombinant DNA Service. NGS equipment includes Torrent PGM, Ion Proton etc
- NGS Services provides a reliable connection between NGS experiments and the analysis of NGS data

2. Protein Production, Purification and Characterization Laboratory

- Protein Purification and Characterization includes semi automated Bio-rad profinia affinity chromatography system, AKTA Explorer FPLC system, and HPLC and ultracentrifugation equipment
- Peptide Synthesis and purification
- Protein-protein interactions are investigated using primarily Surface Plasmon Resonance (SPR) implemented on Biacore and ForteBio SPR equipment. Additional physicochemical characterization of protein-protein interactions is available through collaborations with the LSU Department of Chemistry.
- Gene-to-Protein-to-Antibody Services – you provide the gene, we return an antibody

3. Molecular Immunopathology Laboratory Services

- Pathology Services including necropsy procedures, gross and histopathological examinations and interpretation of immunohistochemistry and special stains performed by veterinarians and histology specialists
- Flow Cytometry and immunophenotyping Services
- Multiplex/Luminex complements immunophenotyping services for rapid and standardized analysis of soluble factors e.g., lymphokines, using bead based array technology.
- Microscopy – contains transmission and scanning electron microscopes, a laser dissection microscope, a Leica TCS SP2 for 3D fluorescence microscope, and a high-throughput digital slide-scanner.

For more information, see: https://lbrn.lsu.edu/cores.html#corebucks

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NIH Extramural Nexus

- # Action Required for In-Progress RPPR Budget Forms By or Before June 22

The Research Performance Progress Report (RPPR) module in eRA Commons is moving June 23 to the new visual appearance of other eRA modules. This is part of a required technology upgrade that will enhance the security and stability of the module. The release will include the addition of the new unique entity identifiers (UEI) where applicable as well as required FORMS-G changes, including updated budget forms.

This is a heads up that since the budget forms (applicable to non-SNAP awards only) will be updated to the new Forms-G version, recipients with in-progress RPPRs will need to redo their

budget forms if their RPPR is not submitted by June 22, a day before the release. See NOT-OD-22-130 for details.

RPPRs submitted on or before June 22 will reflect the FORMS-F budget forms. Due dates for submission of the RPPR remain unchanged. See https://grants.nih.gov/grants/rppr/index.htm.

See also: Updated RPPR Instruction Guide Available.

• Top 5 eRA Resources You Should Know

As you apply for or manage an NIH award, check out these 5 resources to help you navigate our grants systems:

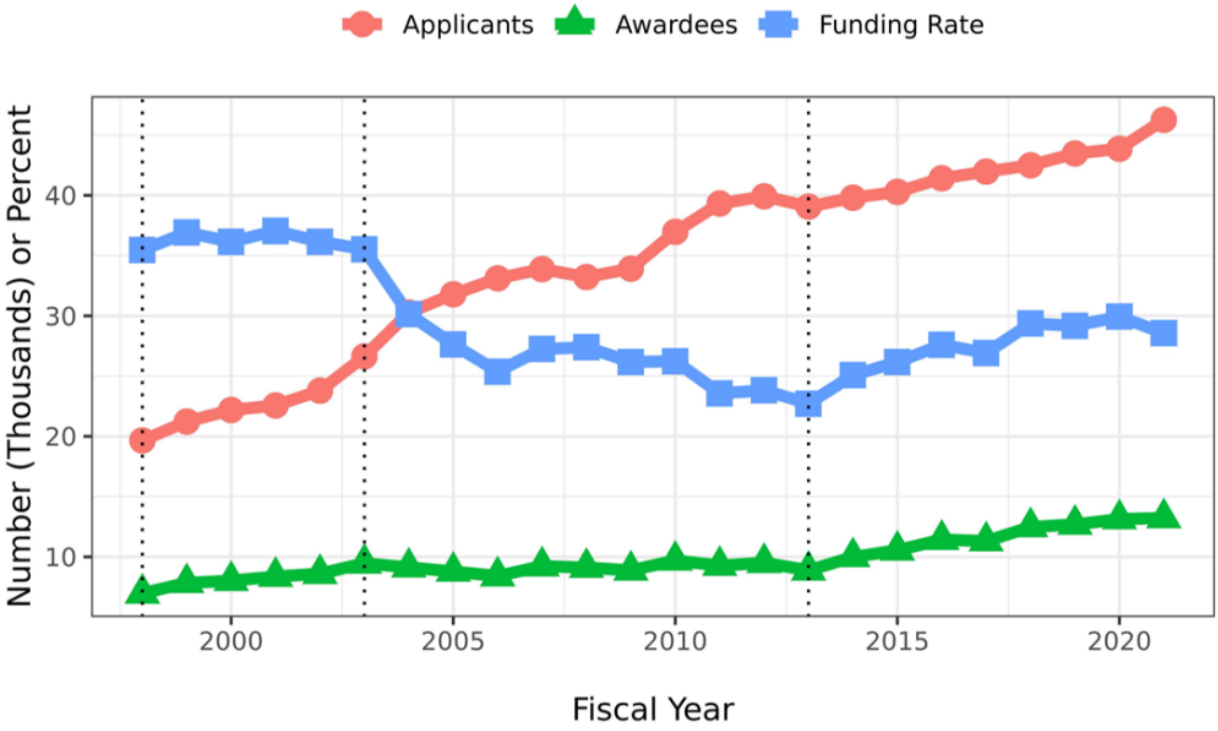
1. New to eRA Commons? **Start here!**
   Get to know NIH grant systems with a high-level overview of the steps taken by applicants/grantees in eRA Commons over the grants lifecycle.
2. eRA Commons Online Help **for step-by-step instructions**
   eRA Commons Online Help can be accessed throughout the eRA Commons modules by clicking the question mark icon in various places on the screens. But did you know the online help is also available outside of the eRA Commons modules? Using the link above, you can get to the complete online help content. It provides information from passwords to ORCID iDs, status to closeout and everything in between.
3. Two-Factor Authentication **for logging in securely**
   To make eRA user accounts more secure with two-factor authentication, eRA is offering its users two ways to comply: use Login.gov and/or use an InCommon Federated account that supports NIH's two-factor authentication standards to log in to eRA modules. If you need additional help, contact the eRA Service Desk.
4. eRA Video Tutorials **for quick overviews**
   Sometimes you just want to see how something works and we have an ever-growing library of videos (currently at 50+) to help you. Designed to be short and sweet and to the point, most videos are less than 5 minutes and demonstrate key functionality of the different modules that make up eRA Commons.
5. eRA Commons Frequently Asked Questions **for helpful answers**
   FAQs are kind of the unsung hero of this list. Developed from real user feedback, the FAQs are constantly being updated with new content and improved information. Divided into 25 different categories, eRA FAQs cover a wide range of topics to help you find the answers that you are looking for.

- ## Research Project Grant Funding Rates and Principal Investigator Race and Ethnicity

NIH has long collected self-designated demographic information on scientists designated as Principal Investigators (PIs) or Key Personnel and used this information to gain insights into the NIH-supported biomedical research workforce. Just over 10 years ago, Ginther and colleagues used these data to publish a seminal paper that showed that Black/African American PIs were less likely than whites to receive funding on R01 applications. Since that publication, NIH embarked on efforts to enhance the diversity of the biomedical research workforce; these efforts include establishing the Chief Officer for Scientific Workforce Diversity, the Diversity Program Consortium as well as numerous other trainee-focused interventions to enhance the scientific workforce.

NIH tracks the success of applicant PIs (that is scientists designated by their institutions as PIs on applications for funding) with a metric called the “funding rate,” which is the ratio of the number of unique applicant PIs who are successful on at least one application to the number of unique applicant PIs who submitted at least one application. Thus, if in a given fiscal year there were 40,000 unique PIs and 10,000 who were successful in securing funding at least once the funding rate would be 10,000 / 40,000 or 25%. Figure 1 shows funding rates for PIs who sought funding on NIH Research Project Grant applications.

Figure 1: Funding rates for Research Project Grant (RPG) Principal Investigators (PIs) 1998-2021.



Now we focus on data derived from the voluntary collection of personal demographic information. Table 1 shows selected characteristics of FY2021 applicant PIs according to race-ethnicity. It is important to note that nearly 12% chose not to provide their race-ethnicity. There were differences: for example, self-designated Black/African American PI, who constituted 2.6% of applicants, were less likely than whites to submit an application proposing animal research, but more likely to submit an application proposing human participant research.

Table 1: RPG PI Characteristics FY2021. Characteristics of scientists designated as Principal Investigators (PIs) on at least one Research Project Grant (RPG) application submitted to NIH in FY2021 according to self-designated race-ethnicity.

Characteristic		White	Asian	Unknown	Hispanic	Black
Total N (%)		25728 (55.6)	11129 (24.1)	5408 (11.7)	2219 (4.8)	1219 (2.6)
Female		9824 (38.2)	3555 (31.9)	732 (13.5)	900 (40.6)	574 (47.1)
Age (years)	Median (IQR)	43 (38 to 51)	41.0 (38 to 47)	42.0 (37 to 49)	41 (37 to 48)	41 (37 to 47)
Degree	MD	3862 (15.0)	1320 (11.9)	427 (7.9)	317 (14.3)	207 (17.0)
	MD-PhD	2270 (8.8)	1409 (12.7)	255 (4.7)	211 (9.5)	104 (8.5)
	Other	1231 (4.8)	586 (5.3)	2772 (51.3)	159 (7.2)	131 (10.7)
	PhD	18365 (71.4)	7814 (70.2)	1954 (36.1)	1532 (69.0)	777 (63.7)
Submitted an R01E		22868 (88.9)	9629 (86.5)	3734 (69.0)	1877 (84.6)	951 (78.0)
Submitted multi-PI		19107 (74.3)	7473 (67.1)	3665 (67.8)	1551 (69.9)	762 (62.5)
Submitted animal app		14974 (58.2)	7569 (68.0)	2348 (43.4)	1287 (58.0)	453 (37.2)
Submitted human app		17884 (69.5)	6933 (62.3)	3476 (64.3)	1458 (65.7)	968 (79.4)

Continue Reading.....

- ## DataWorks! Prize – Incentives for building a culture of data sharing and reuse

A $500,000 prize purse, rewarding data sharing and reuse in biomedical research, is a new, innovative strategy for supporting the research community. The DataWorks! Prize highlights the role of data sharing and reuse in scientific discovery while recognizing and rewarding researchers who engage in these practices. This prize, which launched on May 11, 2022, is a partnership between the NIH Office of Data Science Strategy and the Federation of American Societies for Experimental Biology (FASEB).

The future of biological and biomedical research hinges on researchers' ability to share and reuse data. Sharing and reuse had a sizable, catalytic impact on the development of COVID-19 vaccines and treatment protocols. The DataWorks! Prize is an opportunity for the research community to share their stories about the practices, big and small, that lead to scientific discovery.

To participate, research teams share their stories through a simple two-stage application. Through narrative prompts, teams share details of the practices they used, the scientific impact of their achievements, and the potential for replicating their practices for further scientific research. This year, the DataWorks! Prize purse is up to $500,000 across 12 monetary awards including two $100,000 grand prize awards.

Beyond monetary awards, the DataWorks! Prize is an opportunity for the research community to

learn from peers and apply those lessons to their research practices. The innovative approaches and tools from prize winners will be highlighted in a symposium 2023 and made available to support community learning.

As implementation of the NIH Data Management and Sharing Policy draws near, consider the broader intent of this policy: building a culture of data sharing and reuse in the biomedical research community. Incentives are a major part of culture change and we are excited to provide a space for the community to share their achievements and learn together. Through initiatives like the prize and the launch of the new sharing.nih.gov website, we are taking new steps to support the future of biological and biomedical research at the center of the NIH's Data Management and Sharing Policy.

The DataWorks! Prize is currently open for submissions. Participants must register to participate by June 28, 2022. – visit *Challenge.gov* for more information and to apply.

• A Reflection on Impact

Some of you may have heard me quote a thoughtful essay by Daniel Shapiro and Kent Vrana (both of Pennsylvania State College of Medicine) that is critical of research institutions promoting what funds they've received over what scientific progress those funds have supported. The authors argue that instead of using a ranking system to measure success that favors number of grants and dollars, we should consider a new system that focuses on the efficiency by which the science was conducted and how the research contributes to answering questions that are meaningful to science.

With that in mind, it's worth reflecting that it has been more than two years since the COVID-19 pandemic began. Let's look back to the months of early to mid-2020 when the nation (and the rest of the world) faced a "novel" coronavirus, one which we knew could be fatal and for which there was little knowledge about how it spreads and no known effective treatment, limited diagnostic tests, and no vaccine. How did NIH make fast and meaningful contributions to respond to the pandemic?

On February 21, 2020, weeks *before* many of us were sent home from workspaces, the international Adaptive COVID-19 Treatment Trial (or "ACTT-1") began enrolling patients into a definitive randomized trial on remdesivir in hospitalized patients. The trial was largely (though not completely) funded by NIAID and NCI through existing large-scale contracts and cooperative agreements. The trial stopped enrolling patients on April 19, 2020, *only 1 month after* we were sent home, and published a preliminary report of its main results on May 22, 2020. The trial, which enrolled 1,062 patients, showed positive results, meaning that remdesivir improved clinical outcomes safely. NIH-funded researchers leveraged extensive existing infrastructure to respond

rapidly to the public health emergency and identify, in a definitive manner, an effective treatment *within a matter of a few months*.

Also in early 2020, NIH intramural researchers as well as NIH-supported extramural researchers leveraged years – decades even – of research discoveries to develop and test a candidate COVID-19 vaccine. Figure 1 (taken from a December 10, 2020, presentation given by Dr. Anthony Fauci to the NIH Advisory Committee to the Director) shows the timeline of their efforts. A Phase 1 trial began within 65 *days* from when the virus sequence became known; the definitive Phase 3 trial, which enrolled over 30,000 volunteers, began 198 *days* after sequence release. The trial was led and supported by the HHS Office of the Assistant Secretary for Preparedness and Response, Biomedical Advanced Research and Development Authority and by NIAID through large-scale contracts and cooperative agreements. Like ACTT-1, the trial was positive, with the vaccine showing 94% efficacy for symptomatic COVID-19 infection and high levels of safety. The vaccine itself, based on an mRNA platform, was itself quite novel. The time from virus sequence to FDA Emergency Use Authorization submission was only 325 *days.*

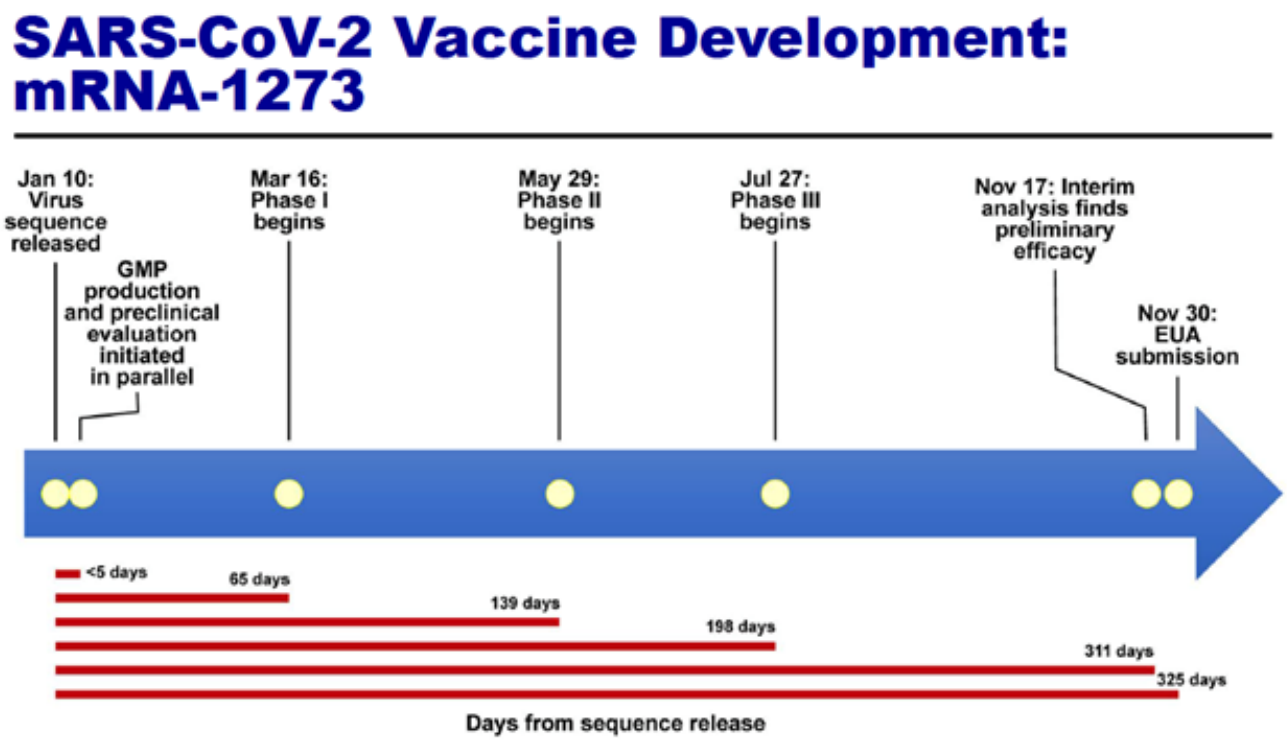


Figure 1: *Timeline for development of the NIH-Moderna mRNA 1273 COVID-19 vaccine. From Dr. Anthony Fauci, presentation to the NIH Advisory Committee to the Director on December 10, 2020.*

To put this in perspective, see Figure 2, also taken from Dr. Fauci's presentation. The Figure shows the duration between the discovery of a microbiologic cause of disease and development of a vaccine. For typhoid, that was 105 years. Polio: 47 years. HPV: 22 years. Measles: 10 years. But for COVID-19 in 2020, *only 11 months*.

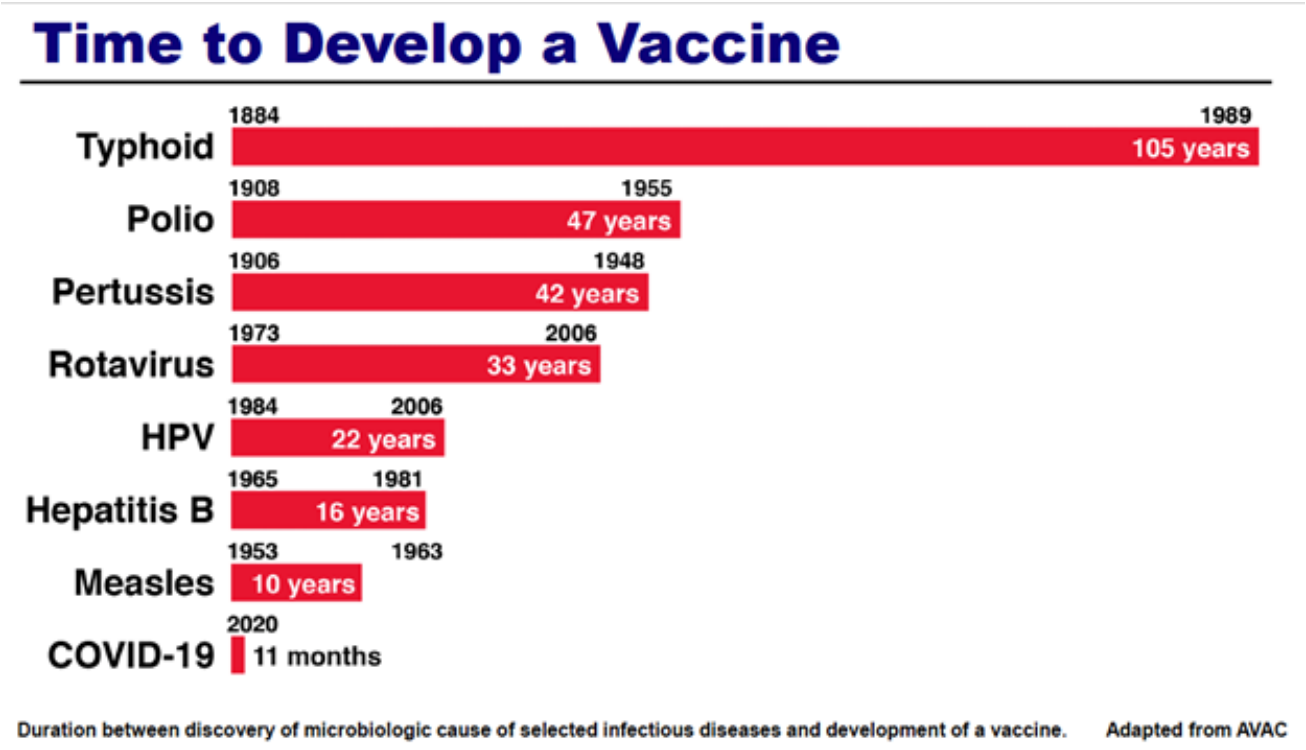


***Figure 2**: Time from discovery of a microbiologic cause of selected infection diseases to development of an effective vaccine. From Dr. Anthony Fauci, presentation to the NIH Advisory Committee to the Director on December 10, 2020.*

There were other important developments in early 2020 for which NIH and its partners leveraged resources, existing and new (e.g., through Congressional supplemental allocations), to respond to the pandemic. These included the establishment of the "Accelerating COVID-19 Therapeutic Interventions and Vaccines (ACTIV)" program, described as "an unprecedented partnership for unprecedented times." ACTIV projects have led to important discoveries about treatments that work and, equally important, treatments that do not work. Another was the Rapid Acceleration of Diagnostics (RADx®) initiative, which employed a shark tank-like approach and other approaches to support and stimulate development of diagnostic tests. In two years, companies supported by RADx have added approximately 2 billion tests and test products to the U.S. capacity.

I have only summarized a few of the events of 2020, but nonetheless some key themes emerge. First, NIH worked closely with partners in and out of government to leverage existing infrastructure and newly available funding to pivot rapidly (on a scale of days to weeks to months) in response to the pandemic. And second, these efforts (and many others) reflect more than grants, contracts, and dollars; they led to meaningful *results* – effective diagnostic tests, treatments, and vaccines – within a remarkably short time.

CFA for Short Term Core Projects

Molecular Cell Biology Research Resources Core (**MCBRC**) and Bioinformatics, Biostatistics, and Computational Biology Core (**BBCC**) are calling for proposals to carry out short term projects in collaboration with the Cores. All LBRN researchers can submit a proposal for a defined project that can be carried out in collaboration with the Core facilities listed in the attached Call for Proposals (CFP) on a competitive basis. Each selected project will be allocated $1,500 to fully or partially offset Core expenses. Please contact your LBRN Steering Committee Member.

LONI HPC Allocation for LBRN

To support the LBRN / BBC Core community on LONI HPC systems, we have renewed our high-performance computing allocation for 2021/2022.

This can be utilized in lieu of individual investigators having to apply for and acquire their own allocations to access the HPC resources. If any of your campus members need access to high performance computing, please have them interface with Dr. Nayong Kim.

NIH LBRN Acknowledgement

So that we can most effectively communicate the scope and results of our funding support, we would like to know when you are planning news announcements about IDeA awards or program activities and achievements…

When you produce such material, please be sure to identify the IDeA program, not just the INBRE, COBRE or sub-program, and to provide context about the program's goals along the lines of:

The University of _____ has received $XXX from the National Institutes of Health (NIH) to support an Institutional Development Award (IDeA) Center of Biomedical Research Excellence. The IDeA program builds research capacities in states that historically have had low levels of NIH funding by supporting basic, clinical and translational research; faculty development; and infrastructure improvements.

In journal articles, news releases, or other materials about your program's activities or achievements, please use funding acknowledgement language such as:

Research reported in this {publication, release} was supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number 5 P20 GM103424-20.

• In journal articles, oral or poster presentations, news releases, news and feature articles, interviews with reporters and other communications, acknowledge the IDeA program's full or partial support of the research. The citation in scientific publications should use the following format:

Research reported in this publication was supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number P20GM103424-20.

• If you wish to acknowledge NIH/NIGMS funding on your Web site or other communication product, you may use wording such as:

Funded by an Institutional Development Award (IDeA) from the National Institutes of Health.
or
*Funded by the LBRN (*2P20GM103424-20) *an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health.*

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