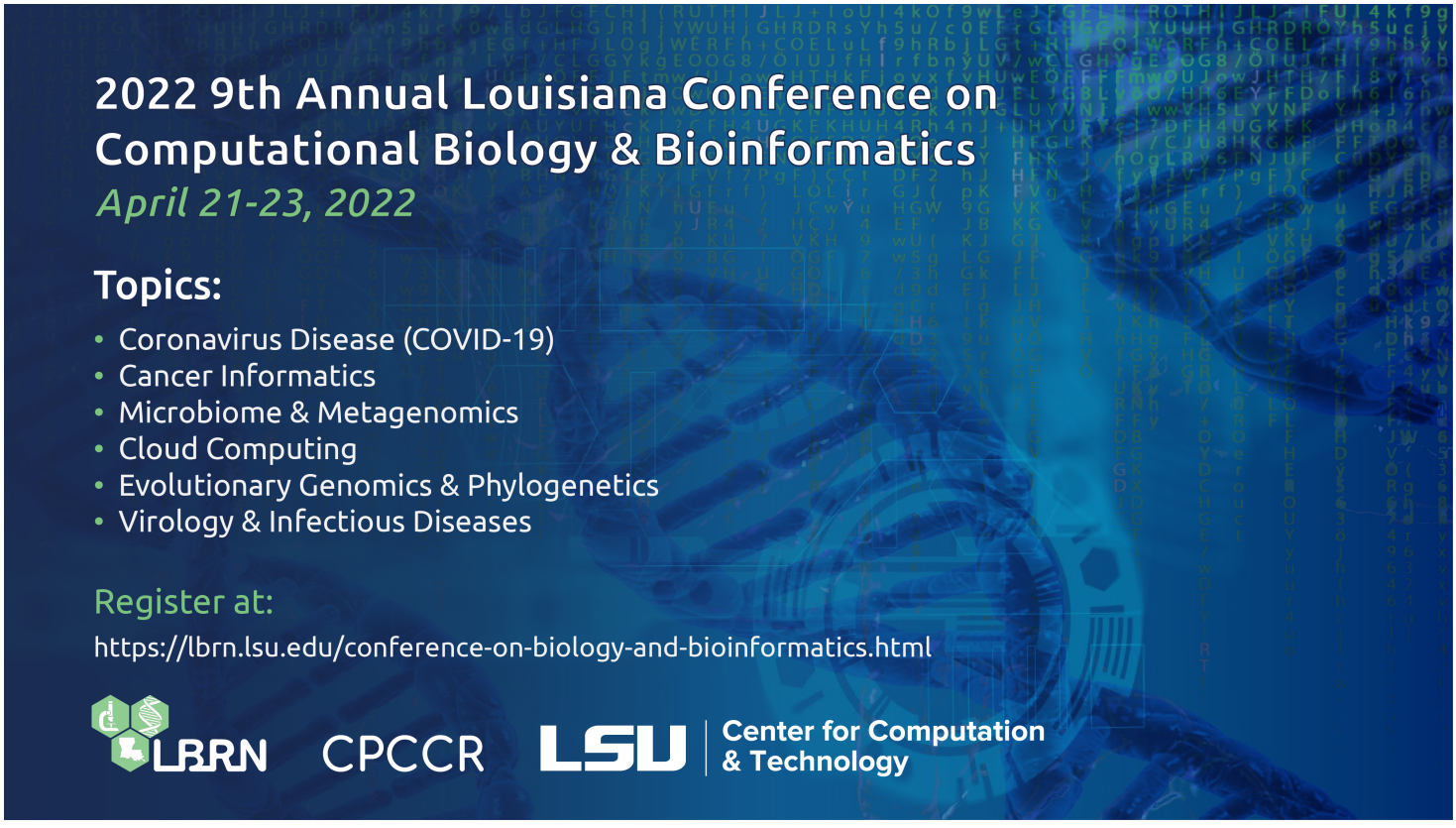
## News, Opportunities and Deadlines for March 2022

# 2022 9th Annual Louisiana Conference on Computational Biology & Bioinformatics

**We are pleased to invite you on April 21-23, 2022 to the**
9th Annual Louisiana Conference on Computational Biology and Bioinformatics

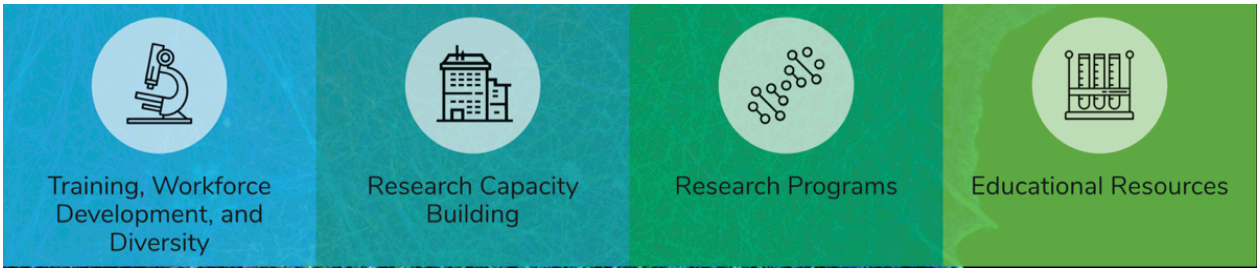



**Further details on the LBRN website:**
https://lbrn.lsu.edu/conference-on-biology-and-bioinformatics.html

# NIGMS News

National Institute of General Medical Sciences

The National Institute of General Medical Sciences (NIGMS) supports basic research that increases our understanding of biological processes and lays the foundation for advances in disease diagnosis, treatment, and prevention. NIGMS-funded scientists investigate how living systems work at a range of levels—from molecules and cells to tissues and organs—in research organisms, humans, and populations. Additionally, to ensure the vitality and continued productivity of the research enterprise, NIGMS provides leadership in training the next generation of scientists, enhancing the diversity of the scientific workforce, and developing research capacity throughout the country.




## NIH Funding Opportunity and/or Policy Announcements

- Research Supplements to Promote Diversity in Environmental influences on Child Health Outcomes (ECHO)- IDeA States Pediatric Clinical Trials Network (ISPCTN) (NOT-OD-22-077).
- Administrative Supplements to Recognize Excellence in Diversity, Equity, Inclusion, and Accessibility (DEIA) Mentorship (NOT-OD-22-057). See FAQs. Due date: April 7.
- RADx-UP - Social, Ethical, and Behavioral Implications (SEBI) Research on Disparities in COVID-19 Testing among Underserved and Vulnerable Populations (RFA-OD-22-005). Due date: May 02.
- RADx-UP Community-Engaged Research on Rapid SARS-CoV-2 Testing among Underserved and Vulnerable Populations (RFA-OD-22-006). Due date: May 02.
- IDeA and NARCH Programs for SARS-CoV-2 Surveillance Studies (NOT-GM-22-026). Due date: March 21.

National Institutes of Health

# NIH's *All of Us* Research Program Releases First Genomic Dataset of Nearly 100,000 Whole Genome Sequences

Nearly 100,000 highly diverse whole genome sequences are now available through the National Institutes of Health's *All of Us* Research Program. About 50% of the data is from individuals who identify with racial or ethnic groups that have historically been underrepresented in research. This data will enable researchers to address yet unanswerable questions about health and disease, leading to new breakthroughs and advancing discoveries to reduce persistent health disparities.

"Until now, over 90% of participants from large genomics studies have been of European descent. The lack of diversity in research has hindered scientific discovery," said Josh Denny, M.D., chief executive officer of the *All of Us* Research Program. "*All of Us* participants are leading the way toward more equitable representation in medical research through their involvement. And this is just the beginning. Over time, as we expand our data and add new tools, this dataset will become an indispensable resource for health research."

The genomic data is available via a cloud-based platform, the *All of Us* Researcher Workbench, and also includes genotyping arrays from 165,000 participants. Whole genome sequencing provides information about almost all of an individual's genetic makeup, while genotyping arrays, the more commonly used genetic testing approach, capture a specific subset of the genome.

In addition to the genomic data, the Workbench contains information from many of the participants' electronic health records, Fitbit devices and survey responses. The platform also links to data from the Census Bureau's American Community Survey to provide more details about the communities where participants live. This combination of data will allow researchers to better understand how genes can cause or influence diseases in the context of other health determinants. The ultimate goal is to enable more precise approaches to health care for all populations. To protect participants' privacy, the program has removed all direct identifiers from the data and upholds strict requirements for researchers seeking access.

“There is a unique depth and dimensionality to the *All of Us* platform that sets it apart from other resources in the field. It’s also designed with team science in mind, allowing researchers to explore topics in an open and collaborative way,” said Gail Jarvik, M.D., Ph.D., head of the Division of Medical Genetics at the University of Washington School of Medicine, Seattle. “As the Researcher Workbench matures, it will create nearly endless possibilities for discovery to understand the role of genes and variants, as well as many other factors that combine to affect health and disease.”

The Researcher Workbench is made possible through the generous contributions of *All of Us* participants. Beyond making genomic data available for research, *All of Us* participants have the opportunity to receive personal DNA results at no cost to them. So far, the program has offered genetic ancestry and trait results to more than 100,000 participants. Plans are underway to begin to share health-related DNA results on hereditary disease risk and medication-gene interactions later this year.

With this release of genomic data, *All of Us* now ranks among other large genomic research efforts worldwide, including the UK Biobank, the Million Veteran Program and the NIH’s Trans-Omics for Precision Medicine (TOPMed) program.

*All of Us* works with a consortium of partners across the U.S. to help reach participants and collect data and samples, including community organizations, medical centers and others. The Researcher Workbench is managed by Vanderbilt University Medical Center in collaboration with the Broad Institute of MIT and Harvard and Verily. The program’s genome centers generate the genomic data and process about 5,000 participant samples each week. These centers include Baylor College of Medicine, Johns Hopkins University, the Broad Institute, the Northwest Genomics Center at the University of Washington and partners. Color, a health technology company, works with the program to return personalized results to participants on genetic ancestry and traits, and the forthcoming health-related genetic results.

To learn more about *All of Us* data and resources for researchers, or to register for access, go to ResearchAllofUs.org. To learn more about getting involved as a research participant, visit JoinAllofUs.org.

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## VIrtual Omics Research Symposium

**Event Date: March 31 - April 1, 2022**


We are glad to announce the upcoming symposium on March 31 & April 01, 2022, bringing together students, researchers, faculty, and industry to discuss recent advances in omics data and bioinformatics. Discussions will highlight challenges involved in research using computational tools for big data, opportunities in this outgrowing field, and applications of the advances in various fields - such as clinical, pharma & biotech, research, and agriculture. The symposium will be accompanied by a poster presentation session and competition, awarding prizes and giving a stage to students, faculty, and research teams to present their research work and get expert feedback.

**Register for the Symposium (Free Event)**


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## LBRN Achievement

Dr. Elahe Mahdavian, Professor of Biochemistry at LSU Shreveport and also LBRN Molecular and Cell Biology Resources Core liaison, recently published "YM155 induces DNA damage and cell death in anaplastic thyroid cancer cells by inhibiting DNA topoisomerase IIα at the ATP binding site" on Molecular Cancer Therapeutics.

**Volume 20, Issue 12_Supplement**
1 December 2021


**Article Contents**

**Abstract**

POSTER PRESENTATIONS - LATE-BREAKING PROFFERED ABSTRACTS | DECEMBER 01 2021

## Abstract LBA033: YM155 induces DNA damage and cell death in anaplastic thyroid cancer cells by inhibiting DNA topoisomerase IIα at the ATP binding site FREE

Ryan Mackay; Paul Weinberger; Elahe Mahdavian; Qinqin Xu



+ Author & Article Information
*Mol Cancer Ther* (2021) 20 (12_Supplement): LBA033.
https://doi.org/10.1158/1535-7163.TARG-21-LBA033



### Abstract

**Introduction:** Anaplastic thyroid cancer (ATC) is among the most aggressive of all human cancers with a median survival of 4.3 months. Currently, there is no effective treatment for most ATC patients - surgery, radiation, and chemotherapy all fail to significantly prolong ATC patient survival. YM155, first identified as a survivin inhibitor, was highlighted in a high-throughput screen performed by the National Cancer Institute, killing anaplastic thyroid cancer cells in vitro and in vivo. However, there was no association between survivin expression and response to YM155 in clinical trials (not including ATC), and YM155 has been mostly abandoned for development despite favorable pharmacokinetic and toxicity profiles. A number of additional mechanisms have been proposed for YM155. The purpose of this study was to investigate the mechanisms underlying YM155-mediated ATC cell death. **Methods:** ATC cell line THJ16T was used as the model for this study. AlamarBlue was used to measure cell viability. Immunofluorescent detection of phosphorylated histone H2AX (γ-H2AX, p-Ser139) foci was used as a surrogate marker for double-strand DNA breaks. siRNA was used to knockdown topoisomerase 2α (Top2α), and Lipofectamine-3000 was used to overexpress Top2α plasmids. In-vivo complex of enzyme assay was used to measure the association between Top2α and DNA. Modeling software Molecular Operating Environment and the crystal structure of human Top2α bound to AMP-

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Louisiana Tech University and Grambling State University co-hosted a health fair from 9:30 a.m.-1:30 p.m. Wednesday, March 16 outside the LATECH Ropp Center, to encourage staff, faculty, and students – as well as the community – to be conscious of their mental and physical health as Spring Quarter begins.  LATECH and GSU are Primary PUI partners of the LBRN. Both Drs. Newman and Kim have been recipients of full project funding from the LBRN. Dr. Kim is the Core Liaison for the BBC Core at Grambling.

News Reference: https://lincolnparishjournal.com/2022/03/16/tech-gsu-partner-for-health-fair/


Dr. Jamie Newman (standing, right), LATECH Associate Professor, Associate Dean for Research and Graduate Studies, College of Applied and Natural Sciences and former LBRN PI.


Dr. Paul Kim (standing, sunglasses), Grambling State University Assistant Professor, Cell Biology and former LBRN PI.

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## LSU HPC Training

Our next HPC training will be held on Wednesday, March 23 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, March 23, 2022: Open OnDemand: Interactive HPC via the Web**

This training will provide an introduction to Open OnDemand, a browser based tool now available to all LSU HPC users on campus. Open OnDemand requires only a web browser (no plug-ins) and an LSU HPC account. It features a file browser, command line shell access, job management, and access to interactive Jupyter notebooks and RStudio servers running interactively on SuperMIC's compute nodes. This training will feature an overview of Open OnDemand, and a demonstration of

all it's features, including Jupyter Notebook and RStudio.

***Prerequisites:*** LSU HPC account, some knowledge of using HPC is assumed but not required

Next HPC training:

- **Wednesday, March 30, 2022: Python package and environment management on HPC**

Python comes with extensive libraries and many of them come in the form of packages that can be installed separately. Given the astounding number of Python packages, it is not sustainable to install all of them system widely under a shared HPC cluster environment. This training tutorial will introduce two popular Python package and environment management tools: The Python Package Index (PyPI) and Conda. Details and examples will be given on how to install different Python packages in user's local directories, and how to create and manage virtual environments for different projects on LSU and LONI HPC clusters.

***Prerequisites:*** Basic understanding of the python programming language is assumed but not required.

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.

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## LBRN Mardi Gras Family Fun

Laissez Les Bons Temps Rouler!

Members of our LSU Veterinary Medicine celebrated in style at the Bacchus Ball inside the New Orleans Convention Center. LBRN was represented!


## NRMN : Upcoming Webinar

NRMN
Mentoring to Diversify the Biomedical Workforce

**How to Leverage the NRMN Network Series**

Every third Monday of the month from 11-11:45am CST, NRMN hosts a new installment of the HTLTNN Webinar Series (How to Leverage the NRMN Network). This series showcases how to utilize existing resources as well as demonstrations of new features both on the NRMN website and within MyNRMN, which is NRMN's virtual community available to NRMN members.

**Apply to the University of Utah's Grant Writing Coaching Group**

- Are you finding it challenging to learn the intricacies of writing NIH-style research proposals?
- Do you struggle with making a compelling case to reviewers for the importance of your research project?
- Are you having trouble getting consistent feedback from experts as you write research proposals?

If any or all of these apply to you, then consider applying for entry into the University of Utah Grant Writing Coaching Group Study.

This study is funded by NIH grant #U01 GM132366. The study protocol was reviewed and approved by the University of Utah IRB (approval #00113440).

**Applications for Cohort 6 are due by March 24, 2022**

- Group coaching for Cohort 6 will take place from August – December 2022.
- You must be targeting an NIH submission deadline of January – March 2023 (preferred) or April – July 2023.
- If you plan to submit your grant proposal before January 2023, you are not eligible to participate in Cohort 6.

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## 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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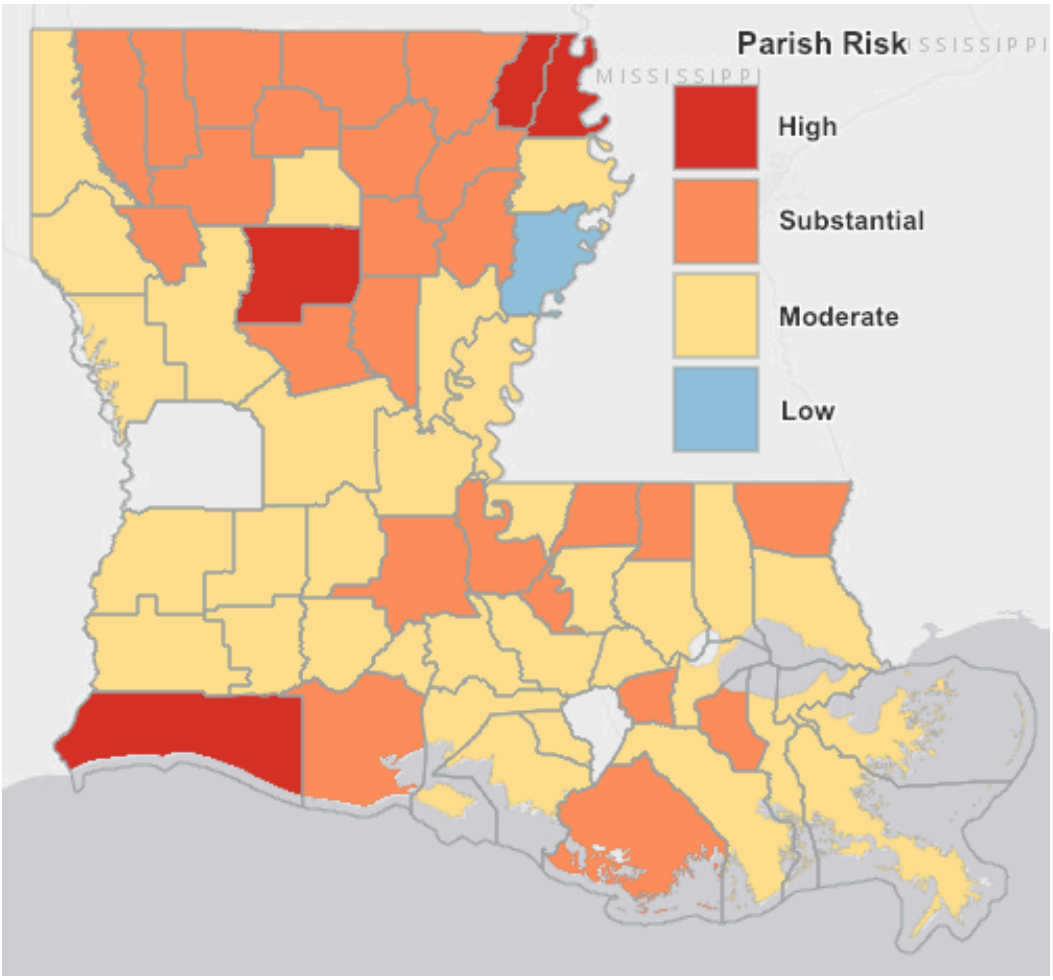
## Coronavirus (COVID-19) Information

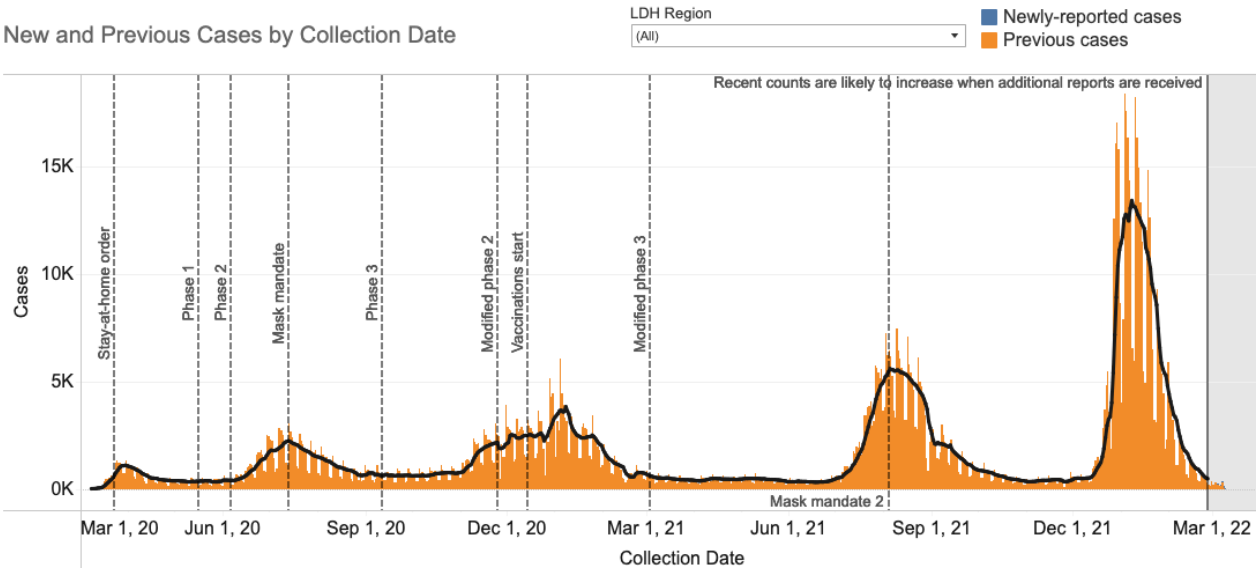
Information from Louisiana Department of Health: https://ldh.la.gov/coronavirus

### Louisiana Covid-19 Information

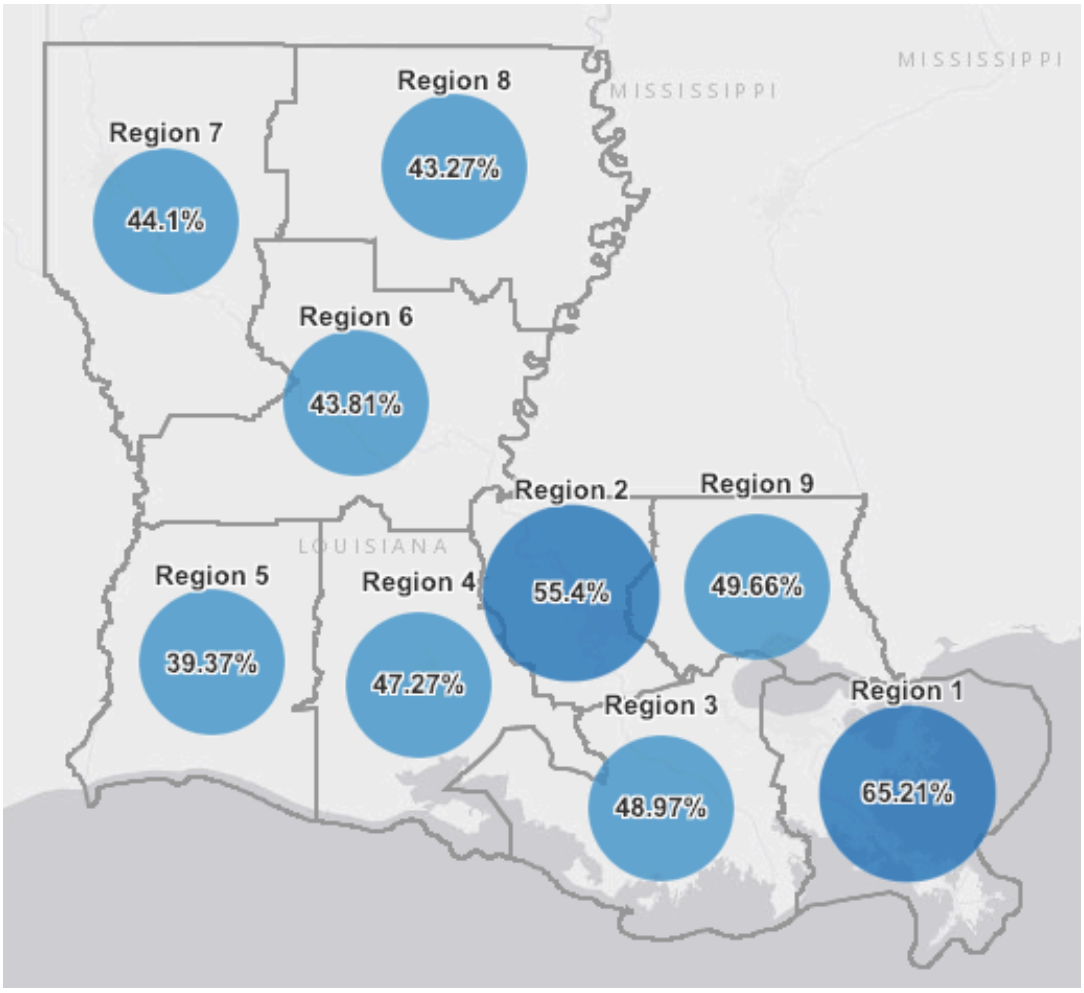
**Community Risk by Parish** (2/24 - 3/02)




## New Cases by Lab Collection Data




## Louisiana Covid-19 Vaccination Information




## COVID-19: Safe Travel Guidance

The Louisiana Department of Health (LDH) and the Centers for Disease Control and Prevention (CDC) recommend delaying all travel until persons are fully vaccinated. While vaccination efforts are underway, safe travel is of utmost importance to prevent introduction of variant strains into Louisiana — particularly because travel itself (especially the use of shared spaces in planes, buses, railways or boats) can increase a person's chance of spreading and/or infecting themselves with COVID-19.

### Travel Requirements

- All travelers should follow CDC Travel Guidance for Domestic Travel and International Travel, as well as follow state and local guidance including CDC public health recommendations.
- Masks are required for travelers 2 years of age or older and should be worn over the nose and mouth in indoor areas of public transportation (including airplanes) and indoors in US transportation hubs (including airports).
- International air passengers must show a negative COVID-19 viral test result taken no more

than 1 day before travel to the United States or proof of recovery within the last 90 days.
- Do not travel if you have been exposed to COVID-19, you are sick, or if you test positive for COVID-19.
- All travelers should self-monitor for symptoms of COVID-19; isolate and get tested if you develop symptoms.

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## NIH Extramural Nexus

National Institutes of Health
*Office of Extramural Research*

- # Coming Soon – New Scientific Data Sharing Website

If you're working on NIH-funded research, you probably know the new NIH Data Management and Sharing (DMS) Policy goes into effect January 25, 2023. Don't worry — there are several resources in the works to help you prepare! In April we are launching a new NIH Scientific Data Sharing website, a one-stop shop for all the information you need to know about NIH sharing policies.

Check out a sneak peek of the new website.

There's much more on the horizon for NIH data sharing. We invite you to explore the new site beginning in April 2022 to find the latest news and updates, especially as we prepare for the new NIH Data Management and Sharing Policy. Stay tuned for more information as we work together to accelerate scientific discovery through effective data management and sharing.

## Designing Analyses by Sex or Gender, Race, and Ethnicity in NIH-defined Phase 3 Clinical Trials

NIH-defined phase 3 clinical trials are required to conduct and report analyses by sex or gender, race, and ethnicity for each primary outcome. These analyses, referred to as "valid analyses" are unbiased assessments that on average, yield the correct estimate of the difference in outcomes between two groups of participants. One can think of valid analysis as a stratified analysis that explores how well an intervention works among sex or gender, racial and ethnic groups.

Investigators may ask, "how do I conduct an 'unbiased assessment' as stated in the definition of valid analysis?" Bias can be reduced in several ways. For example, bias in the evaluation can be reduced by using objective measures, and blinding study staff to the treatment assignment of participants. Statistical bias can be reduced by adjusting for potential confounders. When it comes to comparing the intervention effects, one way to achieve this includes reporting intervention effects and their confidence intervals separately for each sex or gender, racial, and ethnic group. It is important to note that simply adjusting the primary analysis for sex or gender, race, or ethnicity is generally insufficient.

Still have questions? Review the resources found on the Analyses by Sex or Gender, Race and Ethnicity for NIH-defined Phase III Clinical Trials (Valid Analysis) website or check with your Program Officer.

## Updated Resources for Registration in eRA Commons

Simplified wizard-like screens will greet signing officials who are completing the one-time registration for their organization in eRA Commons. The updated Registration screens accommodate SAM-issued Unique Entity Identifiers (UEIs) and will pre-populate institutional information based on available active registration data in SAM.gov.

Note that assignment of a UEI is sufficient to register in eRA Commons while your full SAM.gov registration is being processed, though pre-population of SAM.gov data is not available.

While the registration process remains the same, the link to the registration screens has changed to https://public.era.nih.gov/commonsplus/public/registration/initRegistration.era. A temporary redirect is in place.

New screens call for updated resources. Here are some that will be handy for those planning to register (please spread the word):

- Register in eRA Commons webpage
- Register webpage on the Grants & Funding website
- Registering Institutions & Organizations in eRA Commons (video tutorial)
- Register Your Organization/Institution (online help)
- DUNS to Unique Entity ID (SAM) Transition (from SAM.gov)

Effective April 4, 2022, the UEI will become the official identifier for an organization through the federal award lifecycle and will replace DUNS. For those organizations already registered in eRA Commons, your SAM-issued UEI is automatically reflected in your eRA Institution Profile and there is no action needed to update your registration.

## Check Your Application for Completeness Before Submitting

We really care about the details. It is important to a fair review that all applicants competing together for funding have adhered to the same rules. It is also important that your application is submitted in a way that allows us to efficiently process your application and make it available for funding consideration. Consequently, your application will be checked at Grants.gov, by our eRA systems and finally by our staff before it is referred for review.

This may sound daunting, but the key to getting through this series of application checks is simple:

- Follow the application guide and funding opportunity announcement instructions
- Submit early enough to allow time to address any system identified errors and submit a corrected application prior to the deadline

Here are some examples of both system validations and manual checks we perform on your application after you submit:

- Does the topic of the application fit NIH's mission and the mission of one of the participating institutes/centers?
- Is the applicant eligible to apply?
    - For example, if applying to the AREA (R15) program do the applicant organization and

PI meet the eligibility requirements specific to that program?

- Do you already have an application with essentially the same content under review?
  - You can't have overlapping applications under review at the same time (NOT-OD-18-197).
- Are all your attachments in PDF format?
- Did you follow the page limits documented in our Table of Page Limits (unless otherwise specified in the announcement)?

Learn more on our page, How We Check for Completeness.

## Strengthening Efforts to End Harassment and Discrimination at NIH-Supported Conferences

A year ago, we began requiring plans to enhance and strengthen diversity in applications seeking funding for scientific conferences and meetings. Our guide notice NOT-OD-21-053 reiterated the long-standing expectation that recipients maintain a safe and respectful environment, free from harassment and discrimination. Building on these efforts, we are now asking recipients to proactively show how they will address safety and harassment.

Conferences, unfortunately, may present increased risks for harassment compared to campus environments. Increased harassment risks at off-campus events have been linked to a lack of awareness regarding codes of conduct, unavailability of reporting mechanisms, and power imbalances among attendees (see this 2019 report from the National Academies). The same standards and expectations of behavior must be upheld at meetings, conferences, and other off-campus environments to allow all individuals to fully participate and feel comfortable in exchanging their scientific ideas.

As a funder and organizer of scientific conferences, NIH is in a position to enable culture change at conferences. Following recommendations from the Advisory Committee to the NIH Director (see #1.7 in their 2019 report), all NIH R13/U13 conference grant applicants that are recommended for funding must submit a pre-award Plan to Promote Safe Environments (NOT-OD-22-074). Conference organizers are required to describe strategies that communicate "safety plans" to attendees, to describe how they will document allegations and resulting actions, and to describe information on steps to ensure a safe and respectful environment. These requirements are effective for R13/U13 applications submitted for the April 12, 2022 receipt date and beyond. And, as we feel strongly in these principles to promote culture change, we at NIH are planning to implement similar strategies to bolster safety at conferences and meetings that we organize.

Safety plans, unlike Diversity Plans, are not submitted with the application. Instead, they will be

requested as Just-In-Time materials. Nevertheless, applicants should consider resources that may be needed to maintain a safe and respectful environment as they are preparing an application. The guide notice identifies a minimum set of required elements to be addressed, which include:

- Statement of commitment to provide a safe environment
- Expectations of behavior
- Instructions on how to confidentially report alleged violations of the expectations of behavior to conference organizers
- Description of how the organizers will assess allegations and the consequences for those who are found to violate the expectations of behavior

Through steps like these and other related efforts, we will continue creating meaningful reforms to end harassment in biomedical and behavioral science. We hope that attendees will feel welcomed at NIH-supported conferences to share their scientific ideas, perspectives, and points of view without concerns about harassment and discrimination.

For more on conference safety plans, please review our R13/U13 conference page and FAQs.

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## 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.

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## 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.

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## 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.*

***Please do not use the NIH or NIGMS logo to acknowledge funding, as these logos are only to be used for material produced by NIH and its components.***