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News, Opportunities and Deadlines for January 2021

19th LBRN Virtual Annual Meeting

LBRN is pleased to invite you to
the 19th LBRN **Virtual** Annual Meeting
February 12-13, 2021

We look forward to connecting with you for the 19th Annual Meeting!

Registration deadline : Noon, Monday, January 25, 2021



We are happy to announce that the 19th LBRN Annual Meeting will be held on Friday-Saturday virtually online February 12-13, 2021. All deadlines are NOON January 25, 2021. Click the button below to view all current information.

Please register to join through following link

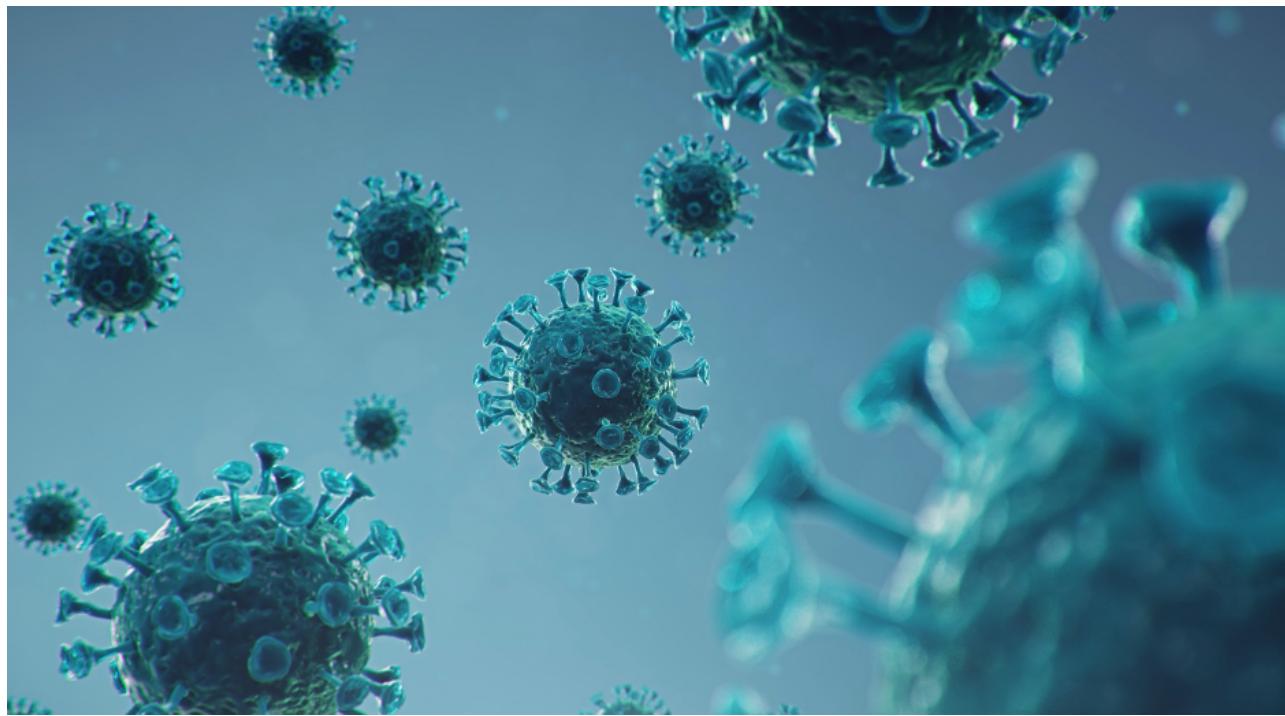
or
please visit LBRN website



Webinar : Genomic Analysis of SARS-COV-2

Genomic Analysis of SARS-COV-2: New Variants and the Vaccine Rollout

This webinar will introduce the upcoming graduate **Bioinformatics for Infectious Diseases Course** at LSU that covers topics, tools and resources developed for infectious disease research.



As the vaccine rollout starts around the world, new variants in the spike protein of SARS-CoV-2 as well as rapid evolution of this RNA virus are raising concerns about the long-term efficacy of the vaccine. In this webinar, we will discuss the ways significant mutations in viral genomes can be identified and studied in the context of evolution, protein structural changes and how to evaluate the significance of such variants for intervention measures

Background: A SARS-CoV-2 variant, referred to as SARS-CoV-2 VUI 202012/01 (Variant Under Investigation, year 2020, month 12, variant 01), has been identified through viral genomic sequencing in the United Kingdom (UK). It is defined by multiple spike protein mutations (deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H) present. Since then, similar mutations have been confirmed in the US and other parts of the world. The emergence of such mutations indicates greater transmissibility and might have other potential impacts, including:

- *Ability to spread more quickly in humans.* There is already evidence that one mutation, D614G, has this property to spread more quickly. In the lab, G614 variants propagate more quickly in human respiratory epithelial cells, out-competing D614 viruses. There also is evidence that the G614 variant spreads more quickly than viruses without the mutation.
- *Ability to cause either milder or more severe disease in humans.* There is no evidence that VOC 202012/01 produces more severe illness than other SARS-

CoV-2 variants.

- *Ability to evade detection by specific diagnostic tests.* Most commercial polymerase chain reaction (PCR) tests have multiple targets to detect the virus, such that even if a mutation impacts one of the targets, the other PCR targets will still work.
- *Decreased susceptibility to therapeutic agents such as monoclonal antibodies.*
- *Ability to evade vaccine-induced immunity.* FDA-authorized vaccines are “polyclonal,” producing antibodies that target several parts of the spike protein. The virus would likely need to accumulate multiple mutations in the spike protein to evade immunity induced by vaccines or by natural infection.

Webinar Registration: <https://edu.tbioinfo.com/genomic-analysis-of-sars-cov-2-webinar>

FREE WEBINAR

Genomic Analysis of SARS-COV-2: New Variants and the Vaccine Rollout

January 22, 2021 | 3 p.m. CST



Graduate Course on Bioinformatics for Infectious Diseases

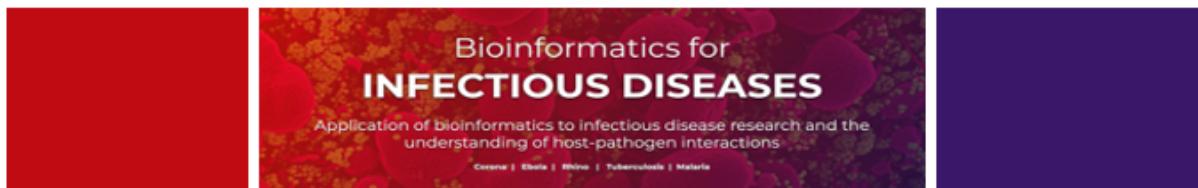
Spring Session Graduate Course on Bioinformatics for Infectious Diseases. Fall session graduate course: LSU PBS 7004 course - 3 credits (Online Coursework and scheduled review sessions via ZOOM).

Faculty: Dr. Gus Kousoulas, Dr. Ramesh Subramanian and Dr. Farhana Musarrat.

Bioinformatics for Infectious Diseases Registration: [Bioinformatics Registration](#)

Flier and all the details of "Bioinformatics for Infectious Diseases"

Information: [Bioinformatics for Infectious Diseases](#)



Spring Session Graduate Course on Bioinformatics for Infectious Diseases. Fall session graduate course: LSU PBS 7004 course - 3 credits
(Online Coursework and scheduled review sessions via Zoom).

Online Materials: This course was prepared as a collaboration between LBRN, BioMMED and Pine Biotech.

Faculty: Dr. Gus Kousoulas, Dr. Ramesh Subramanian and Dr. Farhana Mussarat.

Sessions	Topics	Date
Program overview and Hands-On Workshop	1. Syllabus and Program outcomes: review sessions, practical assignments, and asynchronous resources 2. Bioinformatics analysis of public domain data	Feb 11, 2021
Genomics	First- and Second- Generation Sequencing Data types, approaches and resulting data types	Feb 25, 2021
Analytical Challenges	Pathogen Genome Analysis using examples of viral, bacterial and parasite pathogens	Mar 4, 2021
Sequence Alignment	Pairwise and Multiple Sequence Alignment	Mar 18, 2021
Evolutionary Analysis	Phylogenetic Tree Reconstruction, rate of mutation and association with time	Apr 1, 2021
Association Studies	Genomic Variants and Phenotype: PCA, GWAS, Biological significance of NT and AA variants	Apr 15, 2021
Variant Significance	Working with Protein Structures to map variants, examine properties and match structures	Apr 29, 2021
Host Response	RNA-Seq Data Analysis to study immune response to infection and compare treatment effects	May 6, 2021
Final Exam / Review	Review and Exam	May 14, 2021

Bioinformatics for Infectious Diseases is a course designed to introduce graduate students to the role and the applications of bioinformatics to the study of pathogens that cause infectious diseases of animals and humans and examine their interaction with the host.

Using examples from peer-reviewed publications, participants will learn to apply bioinformatics tools to publicly available genomic and transcriptomic data on Ebolavirus, Sars-CoV-2, *Mycobacterium tuberculosis*, *Plasmodium falciparum* and other pathogens.

Topics we will cover

- Analysis methods and tools for genomic and transcriptomic data analysis of host-pathogen interactions
- Methods to study relationships based on local and global multiple sequence alignment (MSA)
- Phylogenetic analysis and evolutionary studies used for genome ancestry and population fitness
- Chemical and structural implications of sequence variation mapped on PDB models
- Host-pathogen interaction and treatment response



Throughout the course, students will gain access to user-friendly analysis pipelines on the [T-BioInfo platform](#) available through the [Genelab Core Facility of the LSU School of Veterinary Medicine](#), which is supported by the LBRN-INBRE (PI: Kousoulas) and the NIH-funded Center for Lung Disease (CLBD: PI: Jevaselvan). Attendees will learn how to apply statistical analysis to genomic data and visualize it using Excel and R. In addition, attendees will utilize tools like the University of California San Francisco (UCSF) Chimera to explore 3D protein structures to find important features affected by identified genomic variants at the physicochemical level. Curated datasets will be provided for practice with associated tutorials.

LSU HPC Training: Introduction to Linux



The schedule for the Spring 2021 HPC Training is available at <http://www.hpc.lsu.edu/training/tutorials.php>.

Our first HPC training will be held on Wednesday, January 20 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, January 20, 2021: 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, January 27, 2021: HPC User Environment 1, Job Management on HPC Systems

Wednesday, February 03, 2021: HPC User Environment 2, Job Management on HPC Systems

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 January 27 and February 03.

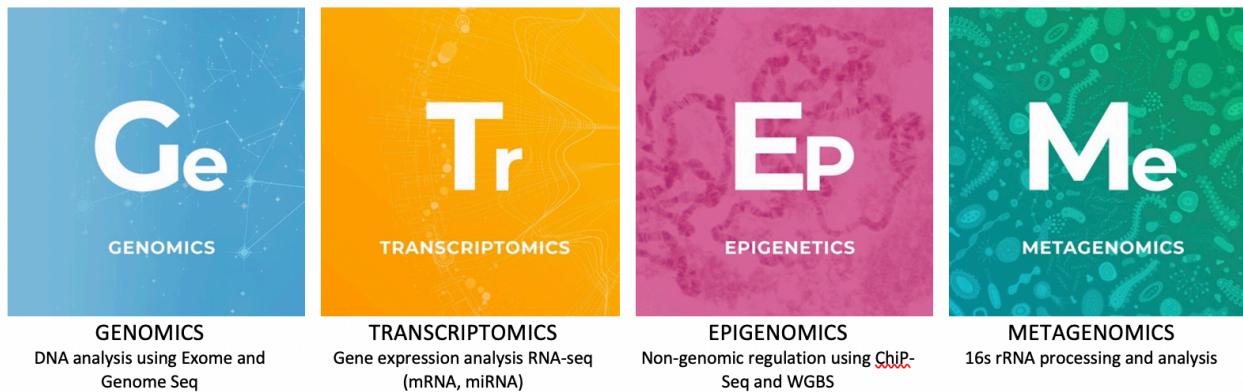
Prerequisite: Familiarity with Linux/Unix commands and editors.

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>

LBRN Omics LOGIC Bioinformatics Training

Omics LOGIC Bioinformatics Training has been developed by Pine Biotech to give students access to basic introductory to advanced analytical bioinformatics courses. The training is available through an online platform. The training is modeled after undergraduate and graduate course topics at LSU, Georgetown University Medical Center and other universities and was designed by faculty and researchers at the Tauber Bioinformatics Research Center.

Participation of a limited number of approved LBRN students is underwritten by LBRN and the Laszlo N. Tauber Foundation in support of bioinformatics for the Division of Biotechnology & Molecular Medicine, School of Veterinary Medicine, Louisiana State University.



This online training is your opportunity to master BIOINFORMATICS as a supplement to other coursework and receive a certificate of Completion. Bioinformatics is a discipline that combines *Mathematics, Computer Science and Biology*.

By applying for this program, you will gain access to OMICS LOGIC resources on a monthly subscription which provides access to 12 online courses that cover various domains of Big Data Bioinformatics. The same license also enables participants to access the AI guided and user-friendly T-BioInfo platform for hands-on analytical experience and practice.

Many of the courses are introductory and are suited for undergraduate students that are interested to learn about the impact of Big Data and High-throughput Experiments across Life Science Domains, including Biomedical Research,

Biotechnology and Agro-biological Studies. The coursework will be effective for students pursuing undergraduate life sciences degrees and pre-medical students.

The collage includes:

- A research poster titled "Transcriptomic Profiling of normal-like and claudin-low breast cancer cell lines" by Apar Agarwal, Genta Boni Baker, Thuy Van La Ngan, Rida Zainab, Rica Zinsky from Loyola University New Orleans and University of Montana. It features a green LBRN logo at the top left.
- A detailed research poster titled "Leveraging Bioinformatics to Enhance Remote Learning During COVID-19" by Kimberlee Mix¹, Laurie Minns², and Elia Brodsky¹. It includes logos for Loyola University New Orleans, Pine Biotech, and LBRN. The poster discusses leveraging bioinformatics for remote learning during COVID-19.
- A screenshot of a bioinformatics training platform showing course modules like "Introduction to Bioinformatics", "Introduction to Mathematics", and "Introduction to Economics". A user profile for "Waneese C. Dorsey" is shown on the left.
- A central laptop screen displays the "BIOINFORMATICS IN LOUISIANA" portal. The page title is "BIOINFORMATICS IN LOUISIANA". Below it, text reads: "We provide bioinformatics education, training, analytical services, and support for computers and networks used in the analysis of biological data. This portal is a joint effort between the Louisiana Board of Veterinary Medicine, Division of Biotechnology and Molecular Medicine, and Pine Biotech, Inc. The goal of this portal is to expand the statewide infrastructure and facilitate our research network's ongoing interdisciplinary bioinformatics research." Below this is a "Learn More" button.
- User profiles for "Roland Echols" and "LBRN STAFF" are shown on the right side of the laptop screen.

The world of big data is constantly changing as technologies to generate new data open new perspectives for molecular precision and detail in life sciences. This exponential growth in knowledge is accompanied with the need for scientist from all backgrounds to find ways to integrate these concepts to their own research studies and allow them to identify new, meaningful information with either new or old data. This training and associated research resources help students and scientist of all backgrounds to leverage big OMICS data in an efficient way. Many students have applied the learned skills to develop independent research projects after completing this training.

Learn more and register on this link: <https://edu.tbioinfo.com/lbrn-2020-1>

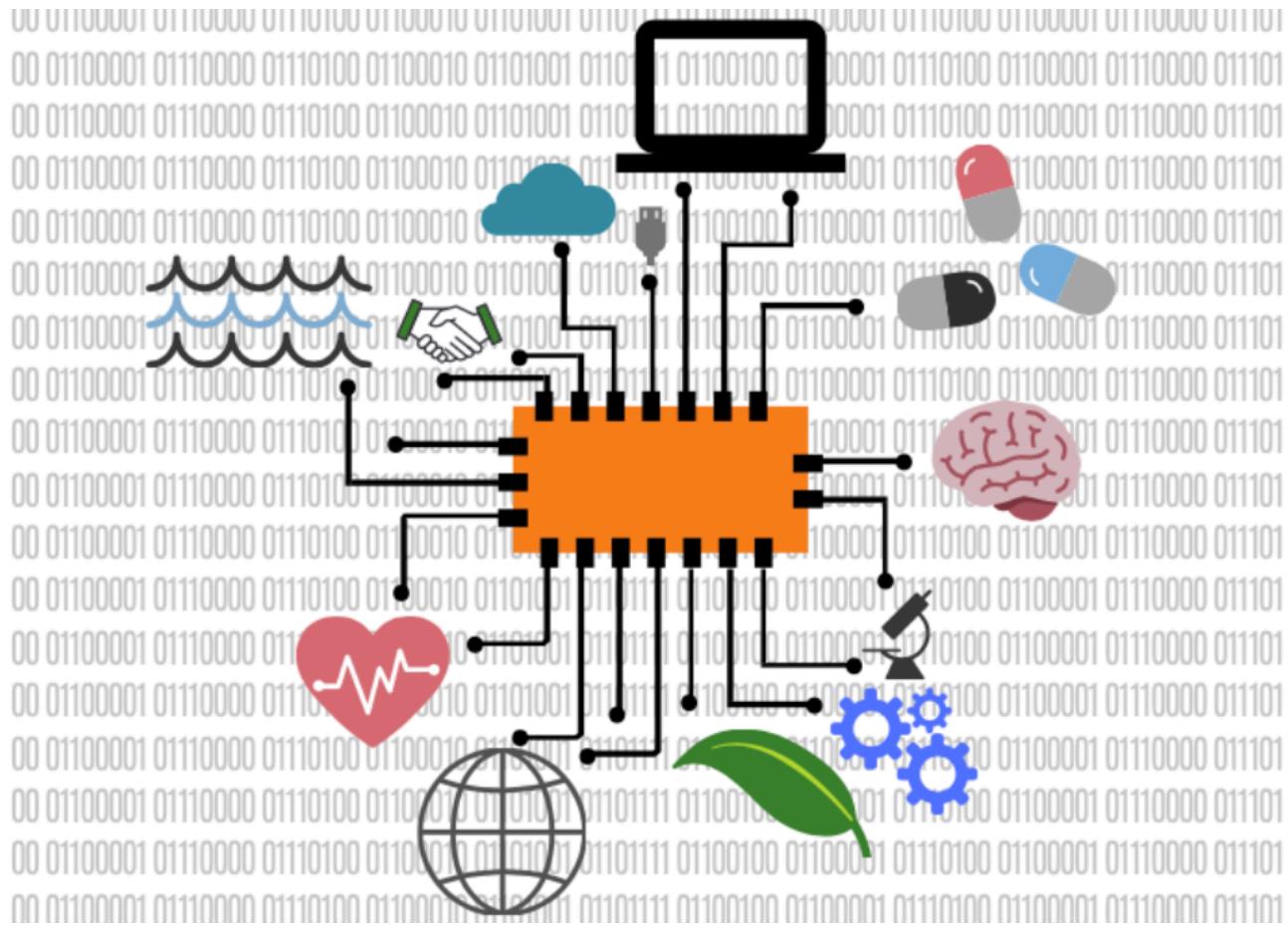
Flier for all the details. OmicsLOGIC Bioinformatics Training: [Omics LOGIC Bioinformatics Training](#)

LBRN Bioinformatics Needs Survey

This survey is conducted by the **Division of Biotechnology & Molecular Medicine**

(BioMMED) of the LSU School of Veterinary Medicine (SVM). The Division operates the core facility **GeneLab** that currently conducts illumina-based Next Gen Sequencing, Single-Cell Gene Expression (10X Genomics) and the **Protein Laboratory** that provides protein production, and purification, and antibody production and characterization. These Core Laboratories are supported by SVM, the Louisiana Biomedical Research Network (LBRN) and the Center for Lung Biology and Disease (CLBD). Current Bioinformatics support is provided through arrangements with **Pine Biotech Inc** through GeneLab. The Pine Biotech proprietary pipelines are available through GeneLab as fee-for-service for a specified time interval. The Illumina BaseSpace Sequence Hub is expected to be available in February, 2021 for all GeneLab clients.

LBRN Bioinformatics Needs Survey: [Take Survey Here](#)



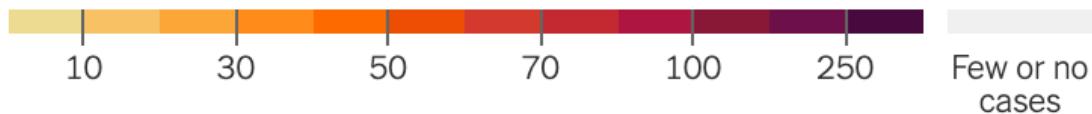
Please fill out and also disseminate to appropriate researchers who are requiring bioinformatics services

Louisiana Coronavirus (COVID-19) Information

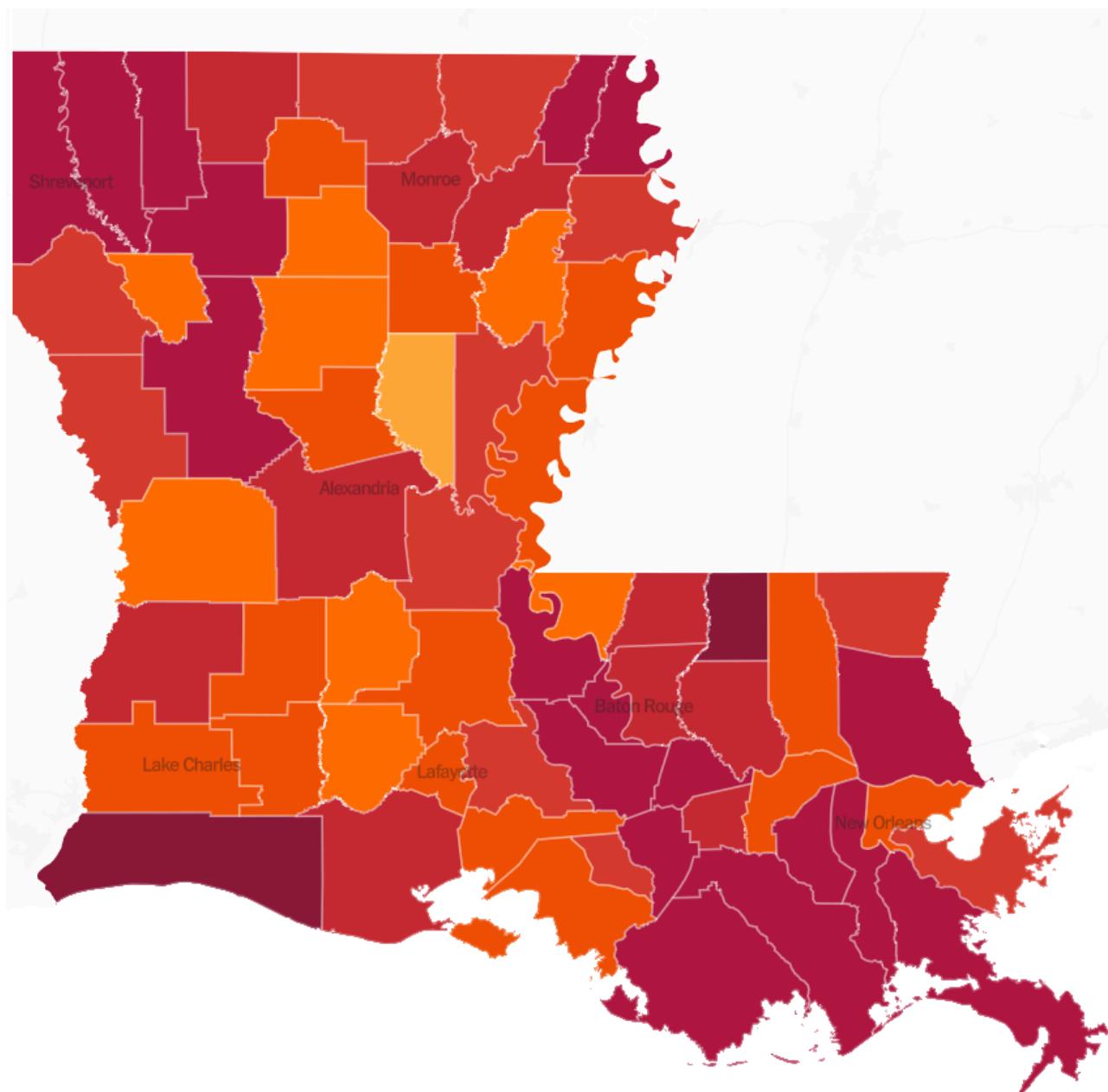
The following information was provided by [The New York Times Interactive Coronavirus website](#).

Average daily cases per 100,000 in Louisiana

Average daily cases per 100,000 people in past week

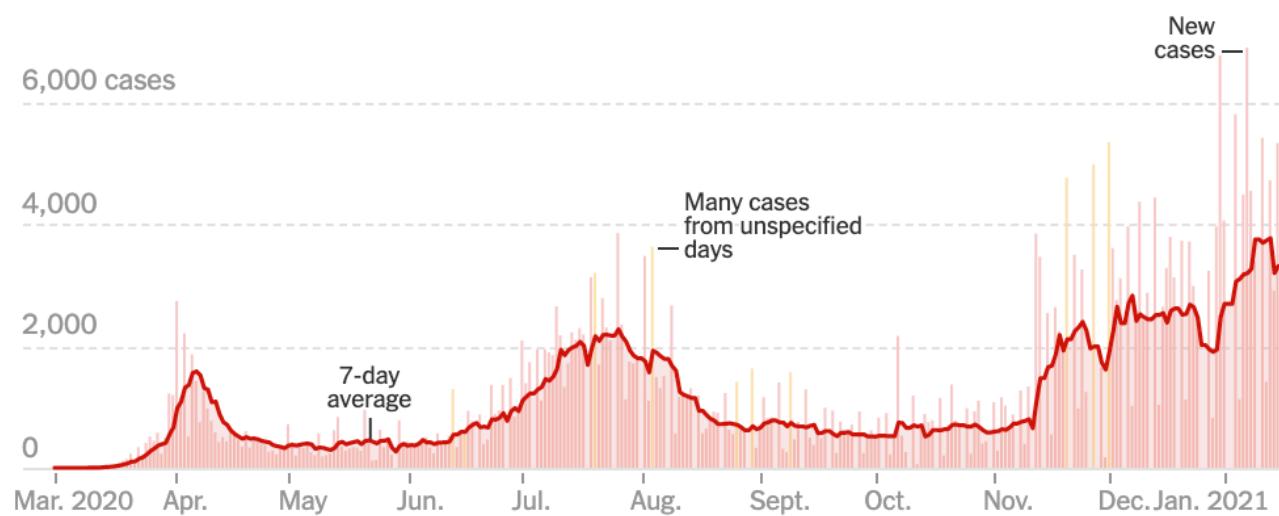


Double-click to zoom into the map.



Daily reported new cases

Updated January 15, 2021, 7:48 A.M. E.T.



	TOTAL REPORTED	ON JAN. 14	14-DAY CHANGE
Cases	361,148	5,313	+23%
Deaths	8,080	58	+63%
Hospitalized		1,975	+22%

We want to remind everyone to continue practicing safety with regards to prevention of spreading and contracting the COVID-19 virus.

We remind everyone of the information provided here on our website: [LBRN COVID-19](#).

The National Research Mentoring Network



Diversity Funding Opportunities

NIH- National Human Genome Research Institute:

NHGRI Training Mission: Prepare a diverse and talented genomics workforce that is operating at the forefront of genomics in order to accelerate scientific and medical breakthroughs to improve human health.

The National Human Genome Research Institute (NHGRI) provides both institutional and individual funding to help scientists develop their skills as researchers and professionals. Our programs offer opportunities at the undergraduate, postbaccalaureate, graduate, postdoctoral and faculty levels.

Mentoring Month Webinars - Thursdays from 11 - 1pm CST

- January 14 – The role of mentoring in promoting DEI in STEM education and research
- January 21 – How to be an effective mentor for Underrepresented STEM trainees
- January 28 – Candid Conversations: Awfulizing & Musturbation during Mentoring
- Register in advance [here](#).

Funding for Research Training

NHGRI Training Mission:

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professionals. Our programs offer opportunities at the undergraduate, postbaccalaureate, graduate, postdoctoral and faculty levels.

ASH Minority Recruitment Initiative:

The [ASH Minority Recruitment Initiative](#) (MRI) was created in 2003 to increase the participation of underrepresented minorities training in hematology-related fields and to increase the number of minority hematologists with academic and research appointments.

Additional Opportunities housed on NRMN found [HERE](#).

NIH Extramural Nexus (NIH/OD)

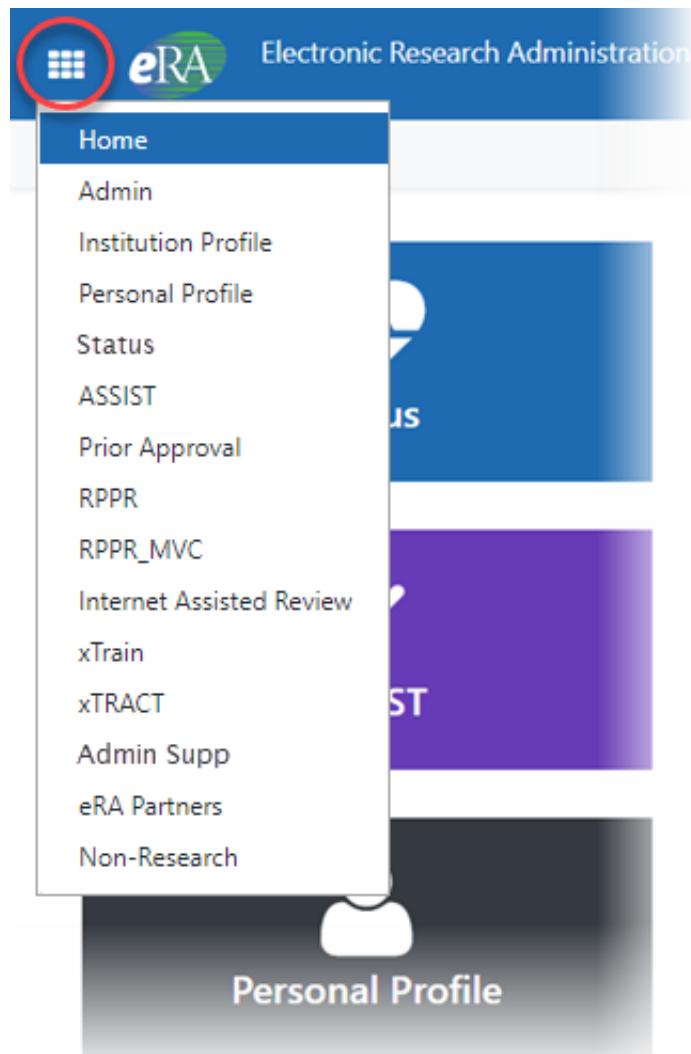


- New eRA Commons Screens Are Almost Here!**

The new eRA Commons home screen (log-in screen) and landing screen (screen when first logged in) are going to be unveiled on **Tuesday, January 12, 2021**.

The screenshot shows the eRA Commons landing page with a new, more modern design. At the top right, there are links for "Contact Us" and "Help". The NIH and OER logos are at the top center. A "System Notification Message" box on the left side contains text about an upcoming standardized layout and a crosswalk for NoA. The main content area has a large "Welcome to the Commons" header. Below it, there's a "Recent News" section, followed by sections for "Register Organization", "How to Create an Account", "Submit a Reference Letter", and "Commons Demo". A "Learn How to Use eRA Systems" section features icons for "Applicants", "Grantees", and "Reviewers". Another section for "Quick Queries" and "iEdison" is also present. At the bottom, there's a "Privacy Act Statement" with a detailed disclaimer.

With the new, streamlined design, navigation to eRA modules within Commons (Status, IAR, XTrain, etc.) will be through the apps icon in the upper left corner of the landing screen.



Need more information? Here are some helpful resources:

- Guide Notice: [NOT-OD-21-028](#)
- Demonstration Video: [New eRA Commons Login and Landing Screens](#)
- Webpage: [Take a Sneak Peek: Redesigned eRA Commons Home Screen Coming in 2021](#)
- [Twitter Video](#)

• Reflections on 2020, Looking Towards 2021

It probably goes without saying, but I'll say it anyways, what a year 2020 was. Our principal focus throughout the year, of course, was on COVID-19 and its disruptions on NIH-supported research and the workforce. Its effect can still be felt, even [many months in](#), and with various [grant flexibilities we put into place](#).

Though the stress it has caused will be with us for some time longer, our response to this public health emergency was not the only story that will continue into 2021. Our work towards [ensuring safe work environments free from harassment](#), [encouraging dialogue on peer review integrity](#), [protecting our nation's intellectual innovation from undue influence](#), [tackling disparities in funding](#), and [staying vigilant online](#) will be with us this new year too.

Last year also saw the roll-out of an exciting [new early-stage investigator program](#) (reminder that applications are due January 26th) . Positive trends, as reported in February, [continued](#) for how many people NIH grants supported in FY 2019, with 2020 data coming soon. And, over 11,000 people attended our first-ever [virtual seminar on grant funding and administration](#)—something we may not have ever tried if it were not for our current situation.

[... Continue reading to learn more](#)

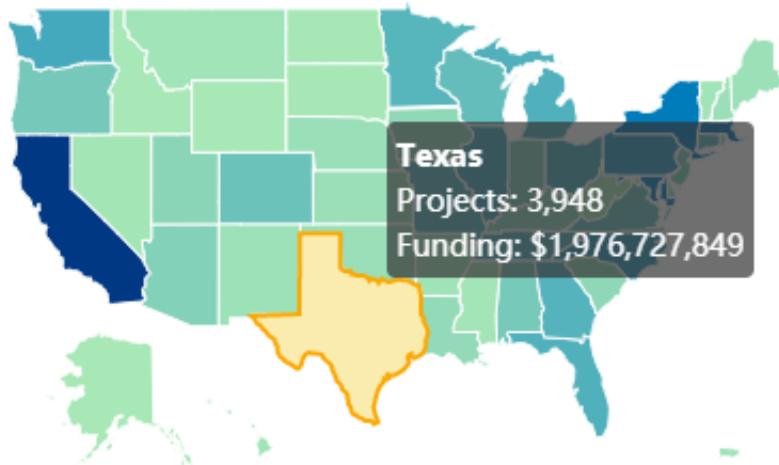
• Explore RePORTER’s State Map Visualizations

Ever find yourself wondering what and how much research NIH supports near you? Check out what the [modernized RePORTER site](#) has to offer in three easy steps!

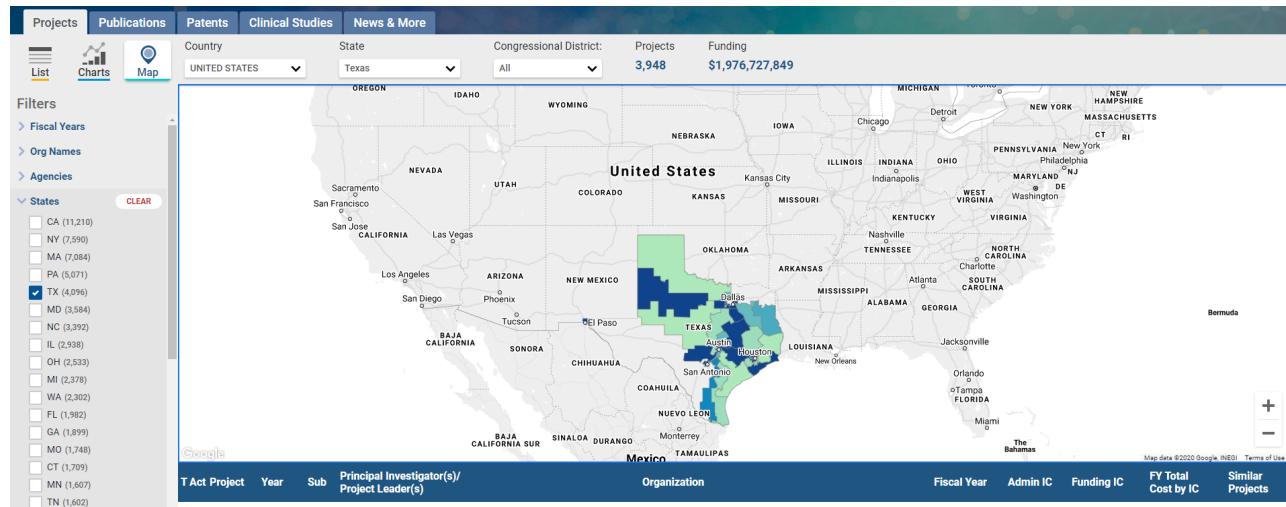
RePORTER’s main search page offers a new map visualization, highlighting active NIH projects by state. As first mentioned in [this NIH Open Mike post from October](#), these maps are fast and interactive so you can dive into the results in your local area. Let’s take Texas as an example. Hovering your mouse cursor over the state, it shows 3,948 projects are active, totaling \$1,976,727,849 in funding

Active Funding by State

Select a state to view projects



Going deeper, if you click on Texas, you can filter results for Congressional district, principal investigator, awardee organization, fiscal year, or administering NIH Institute(s) or Center(s). Darker colors (compared to lighter shaded areas) indicate more funding in that district



Focusing on central Texas, we can learn even more about its 21st Congressional district and the organizations NIH is supporting. From there, you can scroll down to read the project titles and learn more about individual projects.



• Case Study in Review Integrity: Sharing an Application Being Reviewed

A series to raise awareness, encourage dialog and inspire creative problem solving of the challenges in maintaining integrity in peer review

Sharing an application with anyone who has not been officially designated to participate in the peer review process is a big no-no. It undermines the integrity of peer review. It disregards the confidentiality that is required of peer reviewers, who specifically sign a confidentiality agreement before accessing the applications. And it is specifically prohibited by NIH peer review policy.

We have a case for you where this sharing occurred (based on a true story; details have been changed slightly and names have been fictionalized). Read on to see how it ended.

Researcher A had been invited by Researcher Z to collaborate on an upcoming project by providing expertise for a new grant application where Researcher Z was a Principal Investigator. Researcher A gave suggestions for an imaging protocol in the application. During the back and forth, Researcher A learned that Researcher Z was reviewing a grant application with an imaging protocol that might be helpful. Researcher Z then shared a screen shot of the protocol, copied it and emailed it to Researcher A.

[... Continue reading to learn more](#)

• eRA Will Require the Use of Login.gov to Access eRA Commons, ASSIST, IAR and Commons Mobile in 2021

Users will be required to use two-factor authentication (2FA) through login.gov to access eRA Commons, ASSIST, Internet Assisted Review (IAR), and Commons Mobile by September 15, 2021. This secure 2FA allows users to log in to four different grants systems (eRA, Grants.gov, GrantSolutions.gov and Payment Management System) using the same login.gov credentials.

We first shared information about [eRA initiating the use of 2FA](#) as part of HHS' Reinvent Grants Management Initiative in April 2020.

eRA is first phasing in the requirement for reviewers using IAR. The new requirement started being phased in December 14, 2020, for reviewers, meeting by meeting, effective for review meetings February 1, 2021 and beyond. As reviewers are enabled for meetings, their accounts will be transitioned to require login.gov to access IAR.

All users of eRA Commons, ASSIST, IAR and Commons Mobile are encouraged to switch to 2FA through login.gov now, before the mandatory deadline of September 2021.

For more information on making 2FA a requirement, please see Guide Notice [NOT-OD-21-040](#).

Resources

- Web page: [Two-Factor Authentication: Accessing eRA Modules via login.gov](#)
- [Two-factor authentication video tutorials:](#)
 - [Two-Factor Authentication: Accessing eRA Modules via login.gov](#)
 - [What to Do If You Already Have a login.gov Account](#)
 - [What to Do If You Want to Switch to a Different login.gov Account](#)
- [One-page flyer](#)
- [Two-Factor Authentication FAQs](#)
- [eRA Commons Online Help](#)
- [ASSIST Online Help](#)

Help

- If users run into issues with login.gov or associating your login.gov account

with their eRA account, they contact the eRA Service Desk at <https://grants.nih.gov/support/index.html> .

- Users can also refer to login.gov for additional help at <https://www.login.gov/help/>

• All About Grants Podcast: Human Subjects' Research Post-Award

So you have confirmed that you are doing human subjects' research after [listening to the first podcast in our human subject mini-series](#). And you have a clear human subjects' protection and monitoring plan developed for your application after tuning in to [the second episode in the series](#). Now, what should you keep in mind after the award is made?

The latest [NIH All About Grants](#) podcast episode delves into just this issue ([MP3](#) / [Transcript](#)). Lyndi Lahl, R.N., an NIH Human Subjects' Officer, joins us (and her dog too!) in this final episode of this human subjects' research mini-series. Tune in for tips about important post-award requirements, what's needed for annual progress reporting, engaging your IRB and NIH when a protocol change is needed, the difference between adverse events and unanticipated problems, and much more.

The National Association of IDeA Principal Investigators



The National Association of IDeA Principal Investigators (NAIPI) is the collective voice of all of us in the IDeA community.

Dr. Gus K. Kousoulas, the LBRN PI, will serve NAIPI as a president for 3 years.

NAIPI aims to protect and promote the IDeA programs. It fosters interactions, promotes resource sharing, enhances the national visibility of the INBREs, COBREs, and CTRs, develops consensus on priorities, identifies and disseminates best practices, identifies opportunities and develops strategies.

NAIPI's mission is to protect and promote the INBRE, COBRE, and CTR programs within the IDeA states. NAIPI provides leadership and communication across the IDeA community. As a Principal Investigator, Project Coordinator, Project Investigator, or Project Leader on an NIH IDeA award or an award co-funded by IDeA, you are a member of NAIPI.

The NAIPI represents you and the interest of your state in biomedical research education and infrastructure building. Our goals are to become stronger by:

- Sharing best practices
- Connecting researchers to facilities, collaborations, and colleagues
- Collecting and highlighting our IDeA successes
- Developing a consensus on priorities important to the IDeA community
- Identifying opportunities within the IDeA community

In addition to NAIPI members, this site helps the lay public, state and federal legislators, higher education administrators, and business communities learn about health-related research and education in their state, region, and across the nation.

Nationwide Voucher Program



Purpose: The IDeA National Resource for Quantitative Proteomics provides subsidized access to sophisticated proteomics services for investigators performing biomedical research within the mission of NIGMS

(<http://idearesourceproteomics.org/>). In addition to providing cost effective access to a variety of proteomics services, the resource supports a competitive voucher program that provides fully subsidized access at no cost to the user. The goal of the voucher program is to provide pilot scale data to investigators that will create new hypotheses, support publications, and support on-going research studies within the mission of NIGMS. This voucher program supports discovery proteomics workflows limited to 10 sample Tandem Mass Tag (TMT) or 20 sample data independent acquisition (DIA) quantitative proteomic platforms. For example, a 10-plex TMT could be 5 biological replicates of a control versus 5 biological replicates of a treated cell line, while a 20 sample DIA could be 10 control vs 10 experimental tissue/plasma samples. Interested applicants may contact the resource prior to applying to discuss the proposed sample analysis and determine eligibility for the voucher program.

Voucher application due dates: 5:00pm on October 15, February 15, June 15.

Earliest start date: November 1, March 1, July 1. Anticipated number of awards: 100

annually

Award budget: Fee-free voucher for 10-plex TMT (>7,000 proteins) or 20 sample DIA Award Period: Samples must be submitted within 4 months from award date

Eligibility: One awarded voucher per laboratory Principal Investigator per year. Priority will be given to researchers funded by NIGMS, funded through the NIGMS-IDeA Program, and early-stage/new investigators working within the mission of NIGMS. Only one submission per laboratory Principal Investigator per due date.

Pre-submission consultation: Interested applicants may contact the resource at IDeAproteomics@uams.edu to discuss the proposed sample analysis and determine voucher eligibility.

Content and form of application submission: Applications are limited to 2 pages (11pt font, single spaced, 0.5 inch margins) and should include the following sections: Project Overview (outlining the specific research question), Preliminary Studies (providing example data to support the proposed proteomics analysis), Quality Control Data (provide evidence of sample quality such as a gel image, verification of 50 micrograms of protein or 25 microliters of plasma/serum, and details on sample homogenization including buffer components), and Data Utilization (discussing how the proteomics data will be used to support work within the scope of NIGMS). An optional pre-submission consultation may be used to determine whether TMT or DIA proteomics would be most appropriate for the study. Applications are to be submitted as a PDF file at <https://is.gd/IDeAVoucher>.

Other documents for submission: Principal Investigator NIH Biosketch and NIH Other Support documents.

Other requirements: For eligibility, recipients will be required to participate in pre- and post-award surveys.

Contacts: For general questions, contact IDeAproteomics@uams.edu. For administrative questions, contact Ms. Sonet Weed (SWeed@uams.edu)

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 2020/2021.

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:

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