News, Opportunities and Deadlines for February 2021

SAVE the DATE !

2021 ANNUAL LA CONFERENCE ON COMPUTATIONAL BIOLOGY & BIOINFORMATICS

we are pleased to invite you to

2021 ANNUAL LA CONFERENCE ON COMPUTATIONAL BIOLOGY & BIOINFORMATICS

April 15-17, 2021

Further details will be announced soon on the LBRN website

Report : 19th LBRN Annual Meeting

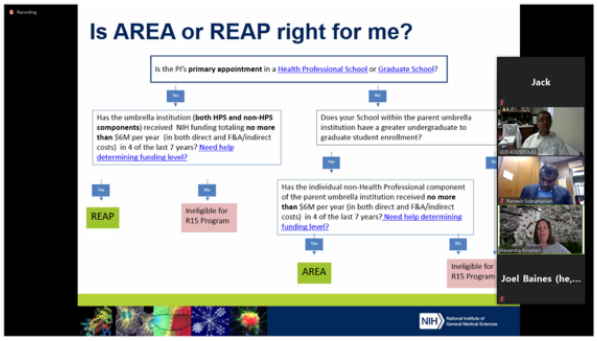
The 19th LBRN Annual Meeting was held for the first time in a completely virtual format on February 12-13, 2021. We had a record number of meeting registrations of 186 for our event and we also navigated setting up a virtual format with 47 submitted posters from our Project PI's, Graduate, and Undergraduate students from our partner and outreach campuses that are part of the LBRN system throughout the state of Louisiana. Below is a sample of the event and images we screen captured. We hope those who participated benefited and appreciated that we were able to hold this in a virtual format considering the pandemic at this time.

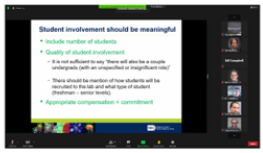
The meeting hosted two invited speakers: On Friday, an Area R-15 grant overview talk by Dr. Alexandra Ainsztein followed by an Area R-15 Panel Discussion. On Saturday, a keynote talk by

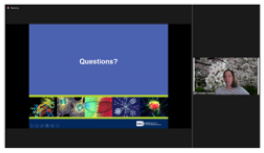
Dr. Ram Samudrala.

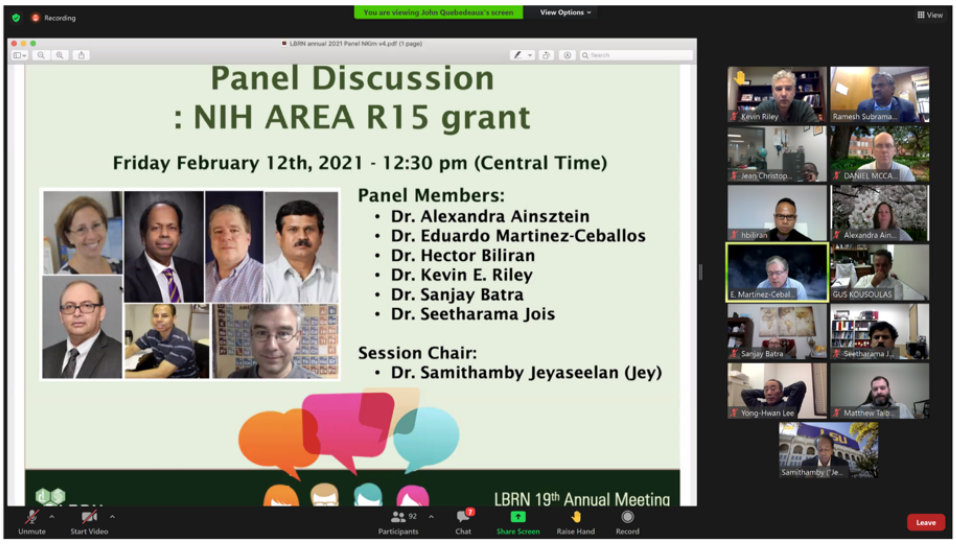
Area R-15 Panel Discussion

Area R-15 grant overview has been presented by Dr. Alexandra Ainsztein followed by its panel discussion. Dr. Ainsztein is a program director in the Division of Genetics and Molecular, Cellular, and Developmental Biology, and administers research grants in the areas of the cytoskeleton, and membrane trafficking. She is the NIGMS point of contact for the Academic Research Enhancement Awards (AREA) (R15) program, and the Collaborative Program Grant for Multidisciplinary Teams (RM1). On the panel discussion we had the following members: Dr. Alexandra Ainsztein, Dr. Eduardo Martinez-Ceballos, Dr. Hector Biliran, Dr. Kevin E. Riley, Dr. Sanjay Batra, and Dr. Seetharama Jois. The panel was chaired by Dr. Samithamby Jeyaseelan (Jey).





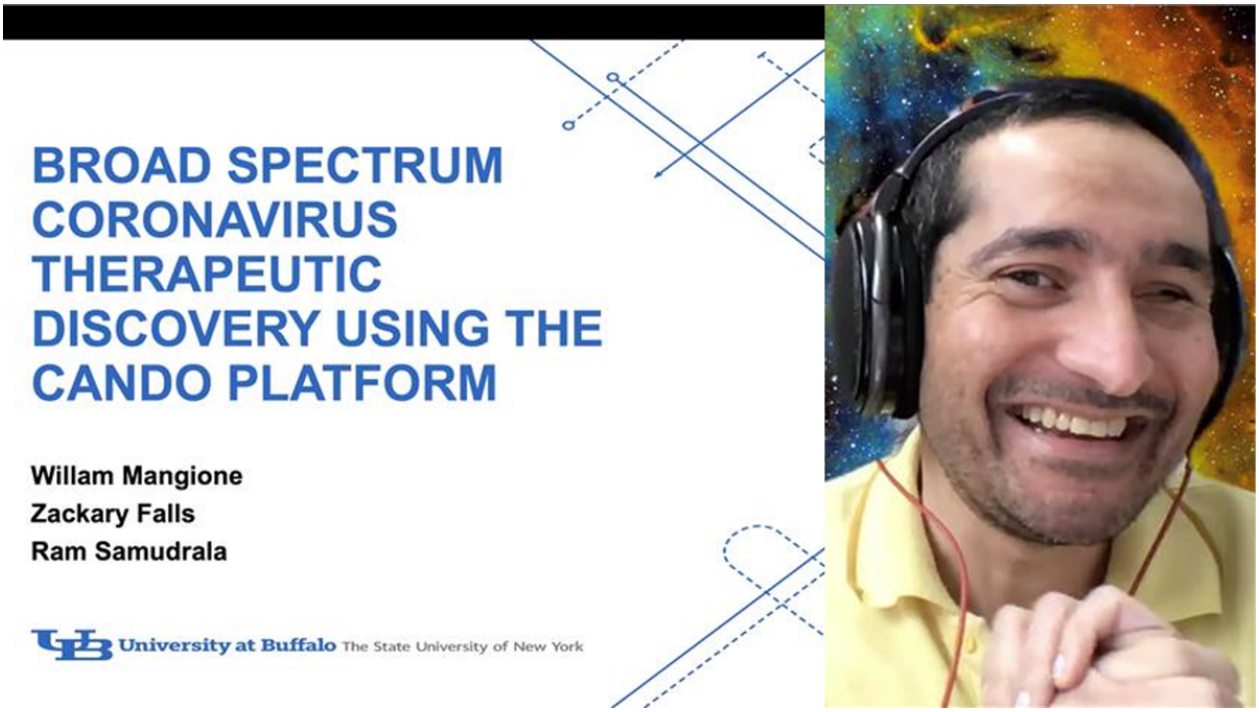




Keynote Speaker

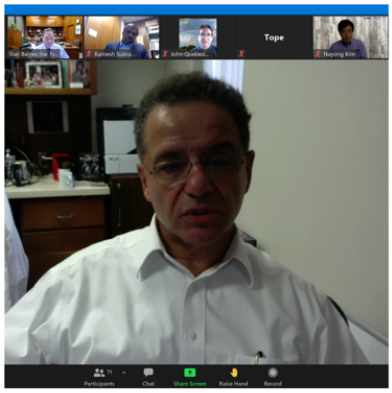
Ram Samudrala, Ph.D.

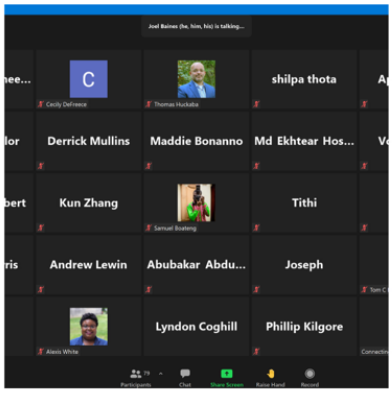
Professor of Computational Biology and Bioinformatics at the University at Buffalo

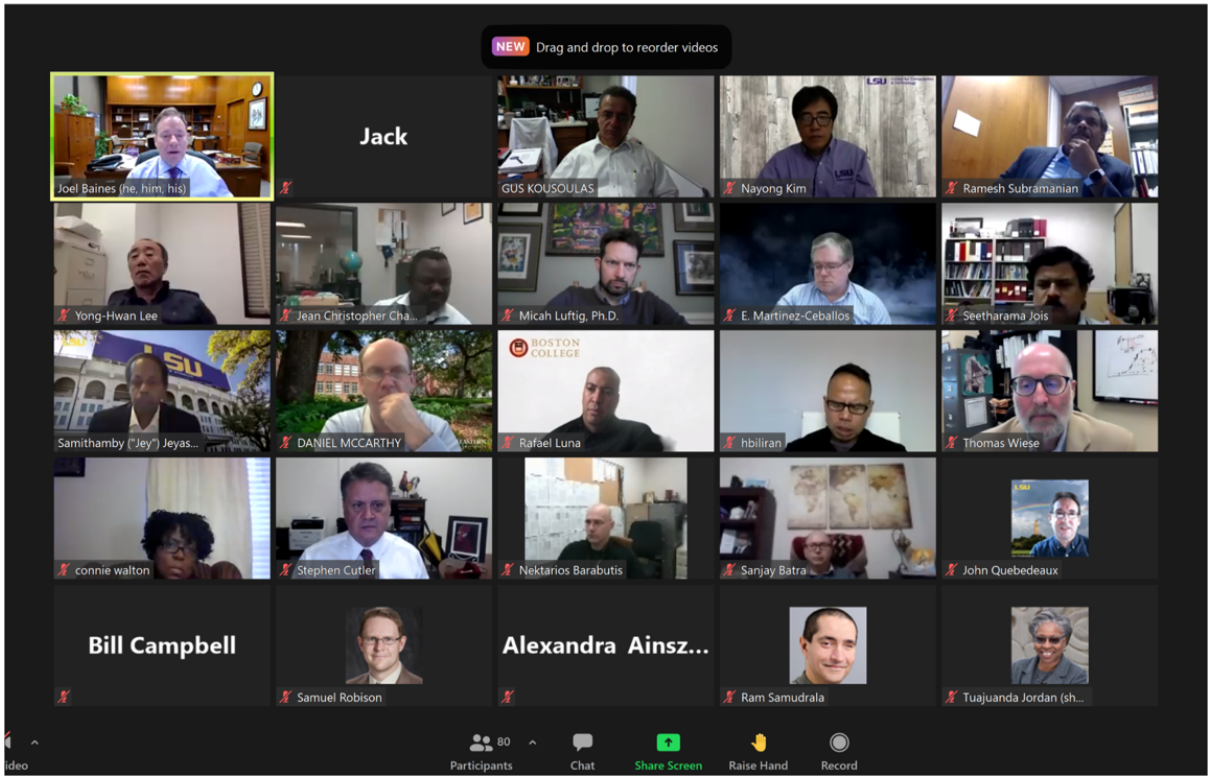


Oral Presentations

Eighteen academic oral presentations were presented by participants from eight different LBRN campuses, our invited speakers, updates from our LBRN Project PI's and the research done by our summer program graduate students.

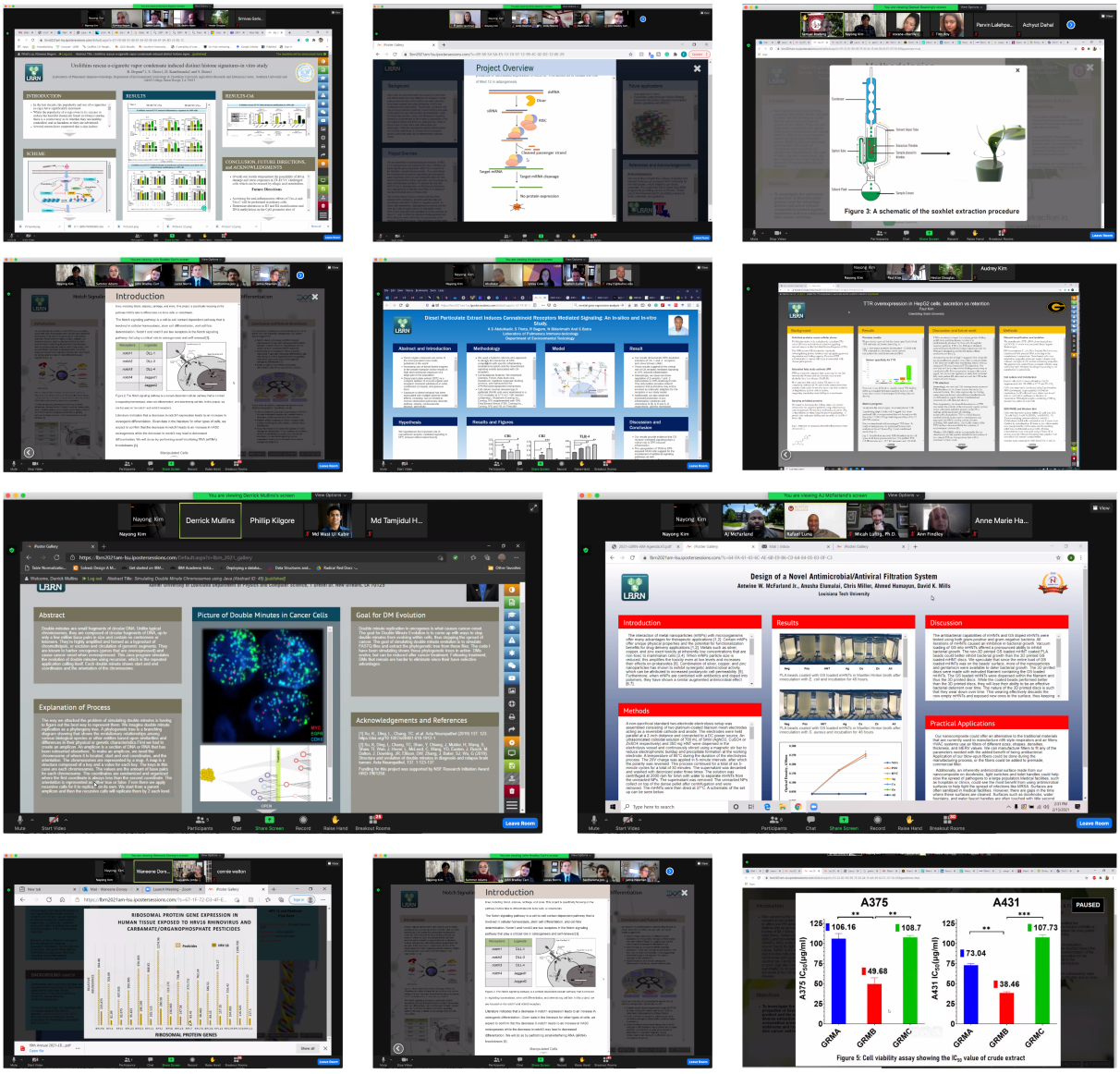






Poster Presentations

Participants from 10 different LBRN campuses exhibited a total of 47 posters through a virtual platform, which was especially possible for presentations, conversations and Q&A through 24 break rooms each in 2 sessions. You can explore and search these posters and contact the authors through the iPosterSession platform we utilized for our meeting: https://lbrn2021am-lsu.ipostersessions.com/Default.aspx?s=lbrn_2021_gallery



Poster Presentation Award Winners

Graduate Poster award winners

- # 37 Achyut Dahal – ULM “Conformationally Constrained Multicyclic Grafted Peptidomimetic as an Immunomodulator in Rheumatoid Arthritis”
- #25 Tithi Roy – ULM “Data-Driven Evaluation of New Synthetic Fisetin Analogs Identify Kinase Inhibitors with Anti-Skin Cancer Activities”
- #40 Jafrin Jobayer Sonju – ULM “Novel pH-Sensitive Liposome Formulation of Peptidomimetic-Doxorubicin Conjugate for Enhanced, Site Specific and Targeted Delivery of Anticancer Conjugate on HER2 Positive Lung and Breast Cancer”

Undergraduate Poster award winners

- #45 Derrick Mullins – XULA 1st “Simulating Double Minute Chromosomes using Java”

- #27 Remmington Bishop LSUS – 2nd "Computational-Aided Drug Discovery of Anti-Viral Therapeutics for COVID-19 "
- #23 Emily Meaney LATECH – 3rd "The Influence of MED12 Knockdown on Adipogenesis"

Oral Presentation Award Winners

- Graduate talks winner – Shilpa Thota – SUBR – "Pentachlorophenol mediated regulation of cannabinoid receptor-mediated signaling (in vitro)"
- Full project talks winner – Kun Zhang – XULA – "Detecting Race-Relevant Molecular Biomarkers with Clinical Utilities using Multi-omics Data across Tumor Types"

Online

All the major parts of the meeting are available to re-watch here: 2021 LBRN 19th Annual Meeting Media.

LSU HPC Training: Interactive HPC via the Web

HPC Training: Introduction to Singularity: Creating and Running Containers on HPC

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

Wednesday, March 3, 2020: 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 SuperMike-II's compute nodes. This training will feature an overview of Open OnDemand, and a demonstration of all its features, including Jupyter Notebook and RStudio.

Prerequisites: LSU HPC account, Some knowledge of using HPC 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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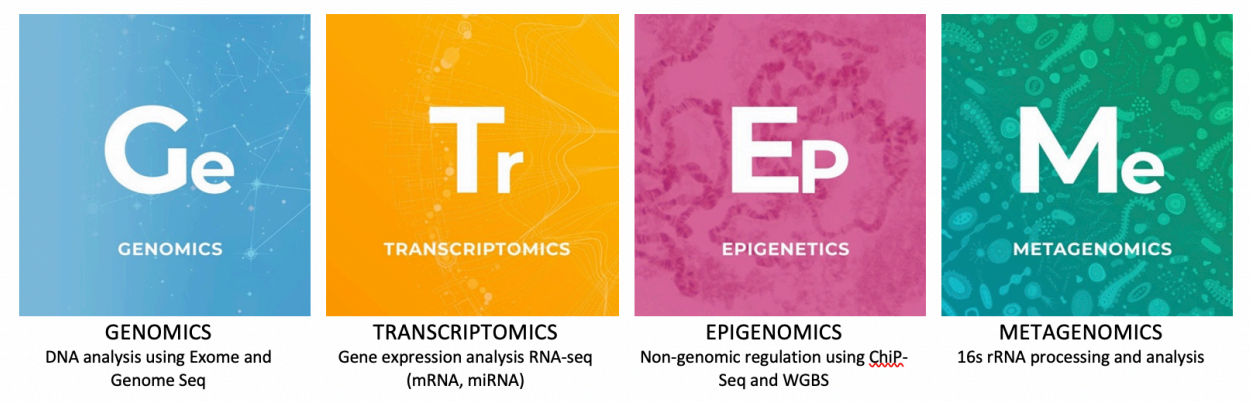
LBRN Omics LOGIC Bioinformatics Training

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 Laszio 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 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.

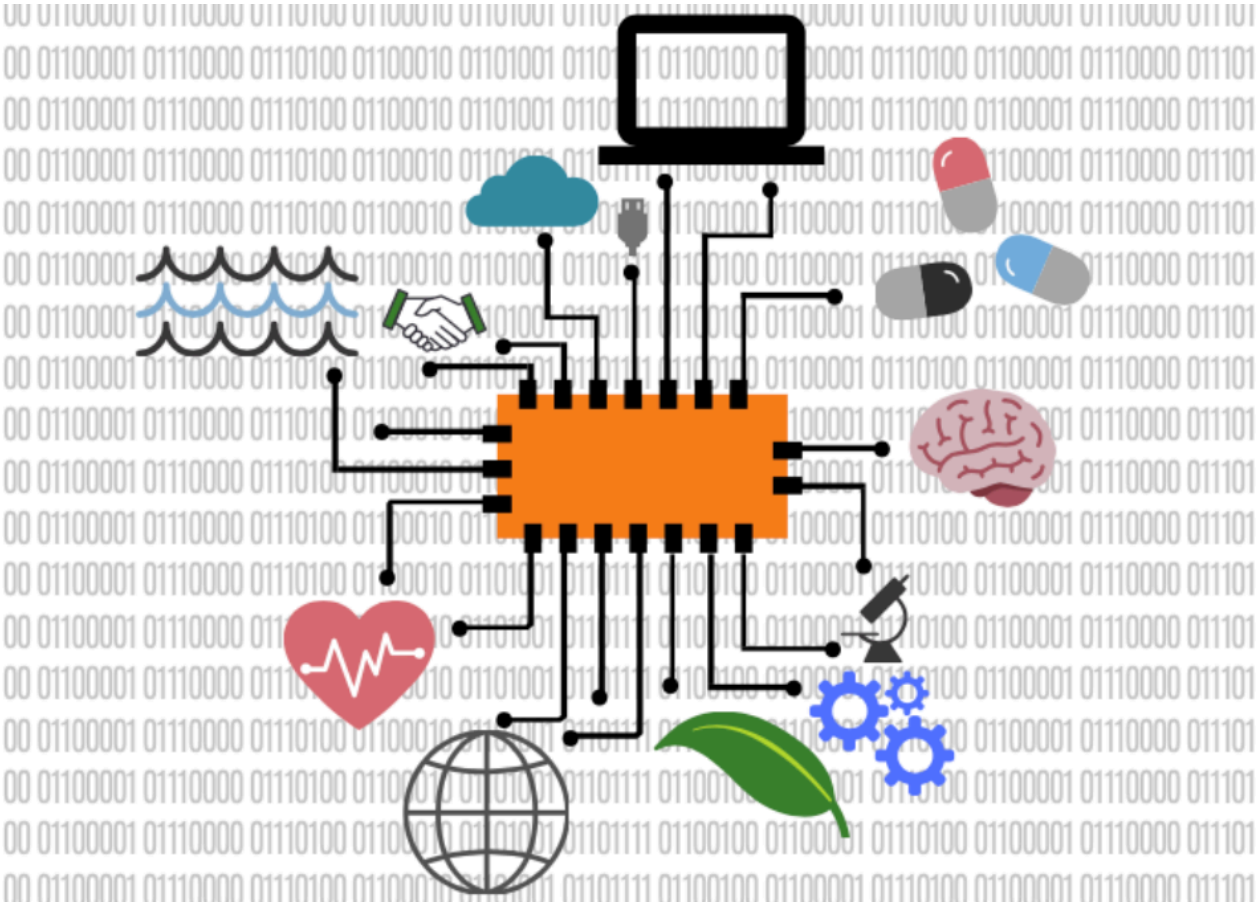
Learn more and register on this link: https://edu.tbioinfo.com/lbrn-2020-1

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

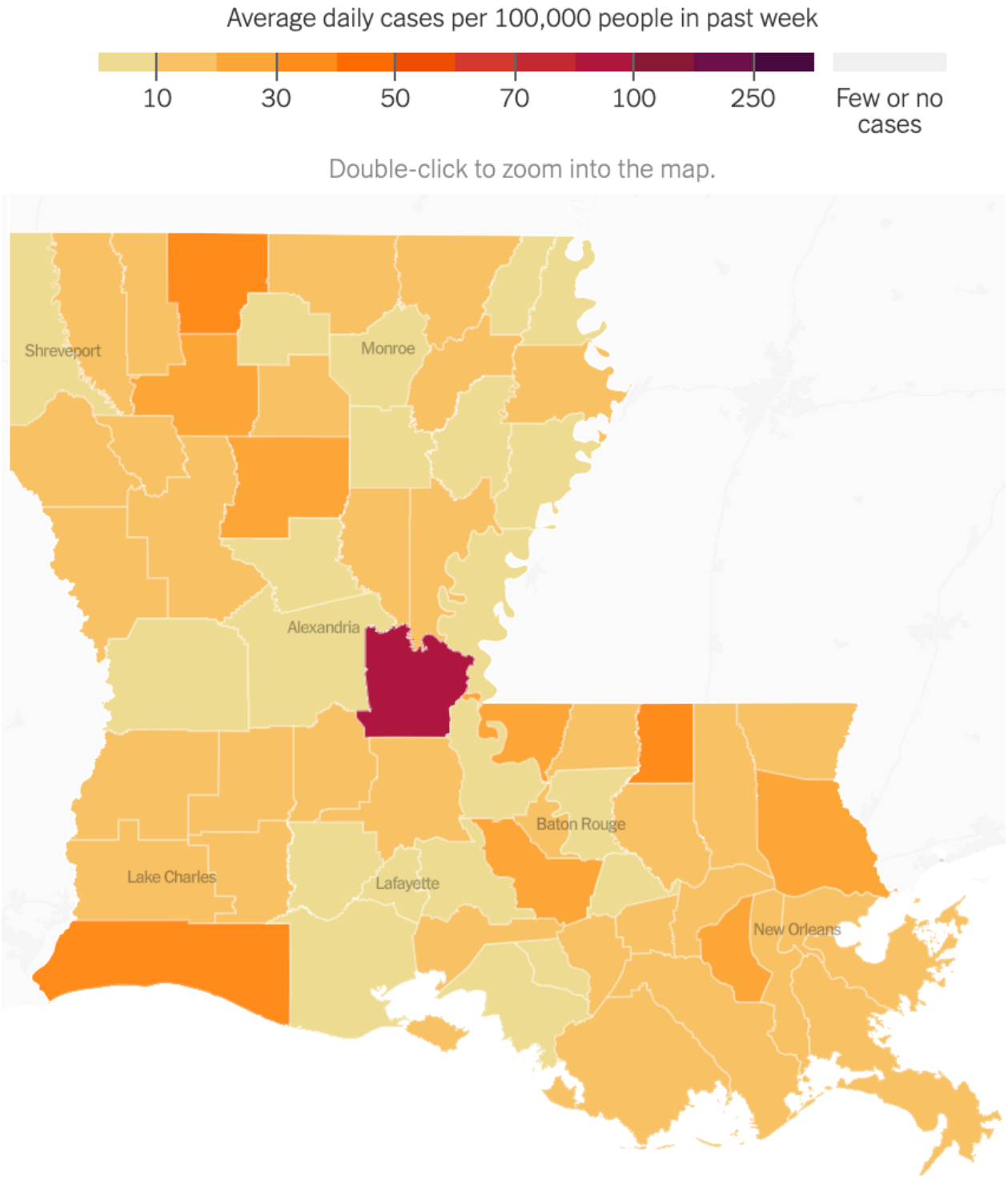


Please fill out and also disseminate to appropriate researchers who are requiring bioinformatics services

Louisiana Coronavirus (COVID-19) Information

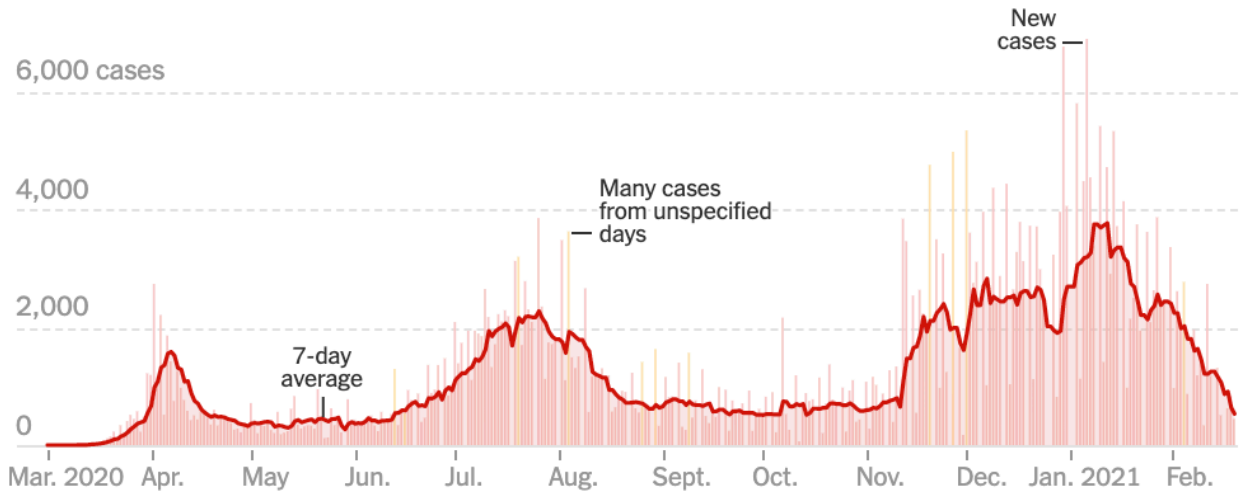
The following information was provided by [The New York Times Interactive Coronavirus website](#).

Average daily cases per 100,000 in Louisiana



Daily reported new cases

Updated February 20, 2021, 12:09 A.M. E.T.



	TOTAL REPORTED	ON FEB. 19	14-DAY CHANGE
Cases	422,287	441	-71%
Deaths	9,440	34	-40%
Hospitalized		806	-38%

Day with reporting anomaly. Hospitalization data from the Covid Tracking Project; 14-day change trends use 7-day averages.

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

NRMN
Mentoring to Diversify the Biomedical Workforce

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.

Funding for Research Training

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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.

Intramural NIAID Research Opportunities (INRO)

Intramural NIAID Research Opportunities (INRO) promotes biomedical research training opportunities in allergic, immunologic, or infectious diseases. Applicants for INRO should be talented senior-level undergraduate students, those who have recently completed a master's degree, or those who are in their final year of a master's degree program. Through INRO, the

NIAID training office sponsors postbac trainees from U.S. populations underrepresented in the biomedical sciences and those dedicated to promoting diversity and inclusion — as defined by Notice of NIH's Interest in Diversity Notice. Individuals from underrepresented populations and/or disadvantaged backgrounds are strongly encouraged to apply.

Candidates must demonstrate a strong commitment to the promotion of diversity and inclusion in the biomedical sciences and be actively pursuing a postbaccalaureate (postbac) research training position – also called an Intramural Research Training Award (IRTA) – in NIAID at the time of their INRO application. If selected to attend the visit, and if offered a position, candidates should be prepared to confirm a laboratory by March 1, with a start date of June 15 of the visit year.

Additional Opportunities housed on NRMN found **HERE**.

NIH Extramural Nexus (NIH/OD)

- ## Extensions for Early Career Scientists Whose Career Trajectories Have Been Significantly Impacted by COVID-19

The COVID-19 pandemic, along with extensive mitigation measures, has adversely affected progress in many biomedical research settings. Evidence from multiple sources, including a survey NIH issued to its supported extramural research workforce last fall, indicates legitimate concerns about career trajectory for early career scientists, including those with caretaker responsibilities. An article by Dr. Erin Gibson and her colleagues argued for a "reset" with focus on early career investigators. One point I took away from this paper is that a reset does not necessarily mean for us to go "back to normal" after the pandemic is over, because that time may have favored certain investigators and disfavored others (something I reflected on in this video and this blog).

Hearing your concerns, NIH issued a Guide Notice last week detailing our approach to support early career scientists whose career trajectories may have been significantly affected by the pandemic as funding will allow). Specifically, NIH is providing an opportunity for recipients in their last year of NIH Fellowship ("F") and NIH Career Development ("K") awards who have been impacted by COVID-19 to request extensions. Such extensions will be considered on a case-by-case basis, within the existing constraints of available funding. We encourage you to read the Guide Notice and if appropriate reach out to NIH staff as directed.

We hope these opportunities will provide some help for some of our researchers whose careers have been adversely affected by the effects of the pandemic. If you are in the last year of an F or K award, consider whether an extension would be helpful.

- ## Keeping on Top of NIH-Funded Research You Care the Most About Just Got Easier

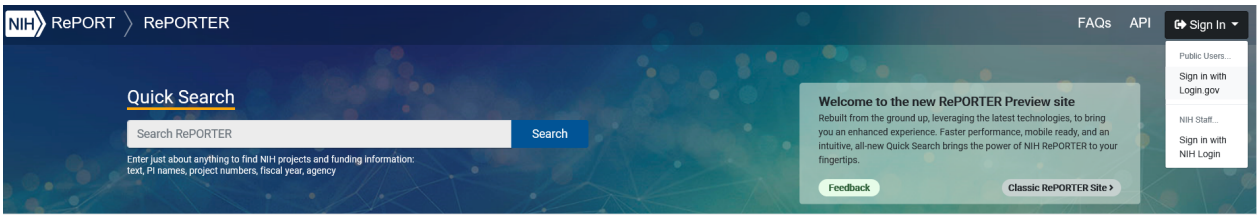
Last fall, we launched our newly revamped RePORTER site which made it easy to find information about specific NIH supported grants, investigators, and institutions. Today, we are adding to RePORTER's functionality with a modernized version of MyRePORTER so you can stay on top of the research you care the most about.

With MyRePORTER, you can save searches and set customized weekly email alerts that are sent

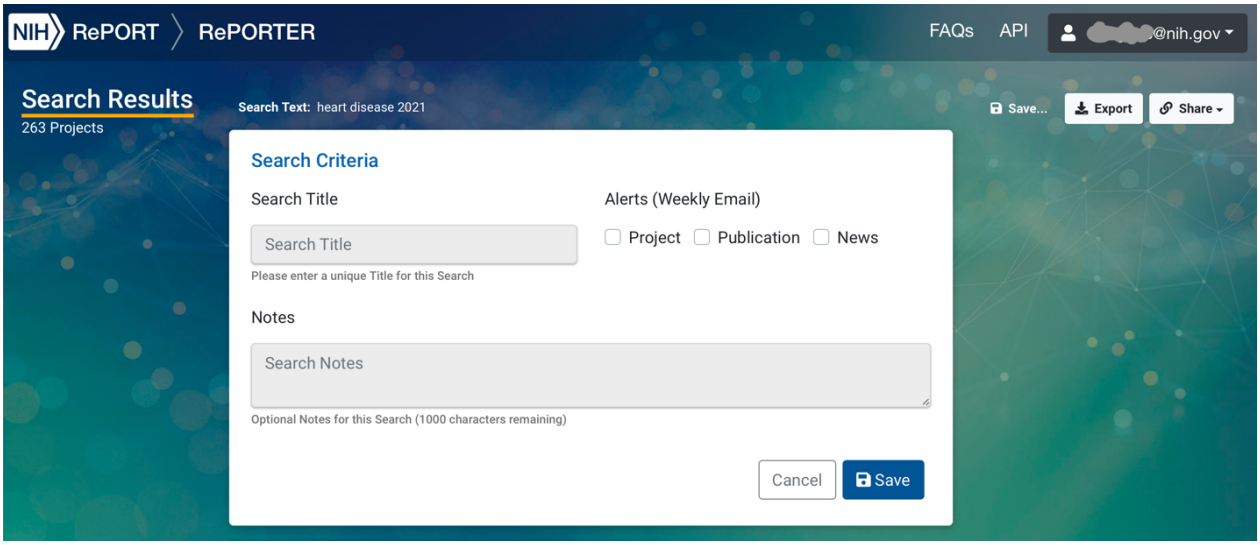
when new projects are funded or new publications are linked to projects in your search. Email alerts will provide a summary listing of the new items, with hyperlinks to bring you back to MyRePORTER to get more information about the projects and publications.

Here is how it works (check out this short tutorial video too).

Users outside NIH will need a login.gov account to access MyRePORTER (Figure 1). The system will allow you to create a new account with login.gov if you do not have one, or to use your existing login.gov credentials, as you can now do with eRA systems. Of note, please clear your browser's cache if you do not see the sign-in option on initial launch.



Once logged in, you can create a saved search after conducting either a Quick Search (which is new to modernized RePORTER) or an Advanced Search. A "Save" button appears on pages with search results, which opens a save window when clicked (Figure 2), allowing you to name the search, add detailed notes, and select desired email alerts. These alerts include newly funded projects, new publications, or related news.



... Continue reading to learn more

- ## Progress Towards a Modernized ClinicalTrials.gov

Guest post by Rebecca Williams, PharmD, MPH, acting director of ClinicalTrials.gov at the

National Library of Medicine, National Institutes of Health. Originally released on the Musings from the Mezzanine blog.

In 2019, NLM introduced a multi-year effort to modernize ClinicalTrials.gov, the world's largest publicly accessible database of privately and publicly funded clinical trials. This effort was launched with a commitment to engage with and serve the millions of users who rely on this essential resource — with a focus on delivering an improved user experience on an updated platform that will accommodate growth and enhance efficiency.

In keeping with that promise, NLM has embarked on several stakeholder activities as part of the roadmap for modernization that we want to highlight in this post. We will also continue to share opportunities for involvement and invite you to join us for an upcoming webinar on February 18, 2021 at 3 pm ET to learn more about our modernization efforts.

Starting Out

Early in the process, our modernization team reached out to stakeholders through a request for information (RFI) to solicit input on topics around website functionality, information submission processes, and use of data standards. We received nearly 270 responses, which were summarized and discussed during a virtual interactive public meeting held in April 2020, and attended by nearly 400 participants. This robust feedback from the stakeholder community, along with input gathered from leaders and stakeholders across the NIH, provided the foundation to identify high-impact user-driven goals and set priorities. Currently, to advance the crucial next step of setting modernization goals and priorities, the team is working closely with NLM's Board of Regents Public Service Working Group on ClinicalTrials.gov Modernization. Members in this group represent a range of stakeholder perspectives and provide input to ensure the continued integrity and utility of ClinicalTrials.gov.

Serving Stakeholders

Feedback received in response to last year's RFI revealed several themes for modernizing ClinicalTrials.gov including ways to improve the management of search results, study records, and plain language information for the website, as well as enhancements to support structured and unstructured data, the quality control review process, and workflow management for information submission.

... Continue reading to learn more

- ## 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

- ## Help Us Understand How You Use Common Data Elements in NIH-Supported Research

The NIH Data Science Strategic plan drives us towards having accessible, well-organized, secure, and efficiently operated data resources to maximize the value of data generated from NIH funding. To meet the mark as we move forward, data need to be interoperable, interconnected, harmonized, standardized, and shared where and when appropriate. One way we hit the mark is through encouraging researchers to adopt Common Data Elements (CDEs).

CDEs foster rigor, facilitate data sharing, and allow multiple datasets to be integrated. They also help make data more FAIR (Findable, Accessible, Interoperable, and Reusable). Many different CDEs are currently in use and can vary across research disciplines, so we would encourage researchers check out databases like the NIH CDE Repository for examples, tools, and other related resources.

Through a recently released Request for Information (NOT-LM-21-005), we seek your thoughts on how you use CDEs, potential challenges to their adoption, and how NIH might facilitate and incentivize their use to help us plan future CDE-related efforts.

Do you use CDEs? How have they benefited your work? Did you face any barriers, and how were they overcome? What resources or tools would make it easier for you to use CDEs? Can the NIH CDE Repository be enhanced? Please tell us.

We seek general feedback on CDEs regardless of the research topic or disease area. That said, we are especially interested in their use in COVID-19 research. Systematic and consistent data on study participants, for instance, could be collected across multiple COVID-19 sites with CDEs. And since CDEs allow data to be pooled, strengthen their statistical power, and facilitate reuse, we might learn more about coronavirus disease as a result.

We look forward to hearing your thoughts. Comments are being accepted electronically here until May 10, 2021.

- ## FY 2021 Fiscal Policies for Grant Awards: Funding Levels, Salary Limits, and Stipend Levels

NIH issued guidance for NIH Fiscal Operations for FY 2021 including the following policies:

- **FY 2021 Funding Levels:** Non-competing continuation awards made in FY 2021 will generally be issued at the commitment level indicated on the Notice of Award.
- **Ruth L. Kirschstein National Research Service Awards (NRSA):** NIH will increase NRSA stipends by approximately two percent for predocs and two percent for postdocs.
- **Next Generation Researchers Initiative Policy:** NIH will prioritize meritorious R01-equivalent applications from Early Stage Investor (ESI) PD/PIs.
- **Salary Limits:** Salary limit is set at $199,300.

For additional guidance and details, see NOT-OD-21-058.

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 verses 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:

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 GM103424-18 and 3 P20 GM103424-15S1.

• 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 P20GM12345.

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

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