

## News, Opportunities and Deadlines for Feb. 2022

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***Save the Date!***

### 2022 9th Annual LA 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](#)



The poster features a dark blue background with a repeating pattern of DNA base pairs (A, T, C, G) in various colors. The text is prominently displayed in the center and right. On the left, there is a small icon of a computer monitor with a calendar on the screen.

**9th Annual LA Conference on  
Computational  
Biology &  
Bioinformatics**

**Save  
the  
Date!**

**Virtual  
CONFERENCE**

**April 21 ~ 23, 2022  
Thursday ~ Saturday**

Further details will be announced soon on the LBRN website:  
<https://lbrn.lsu.edu/conference-on-biology-and-bioinformatics.html>.

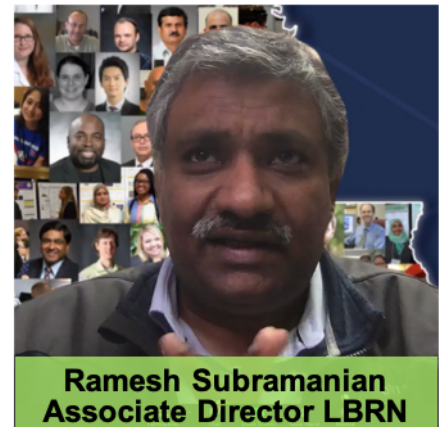
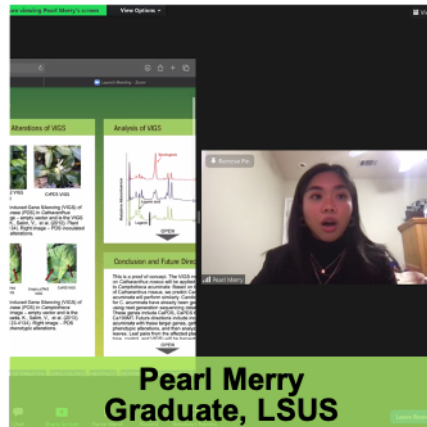
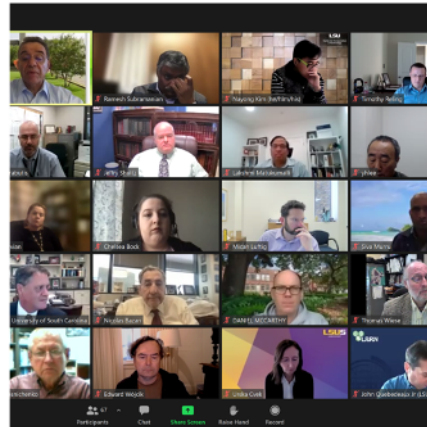
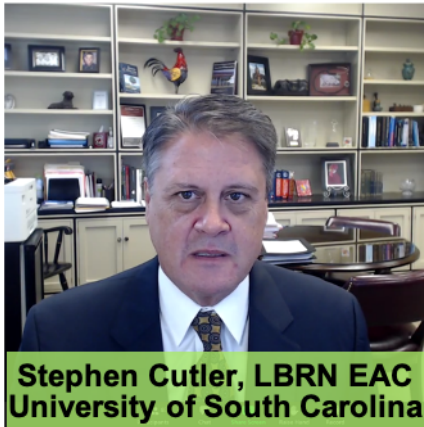
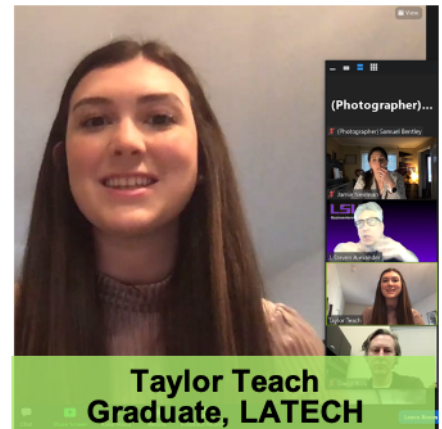
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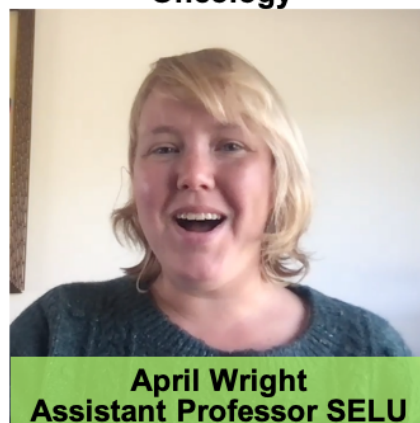
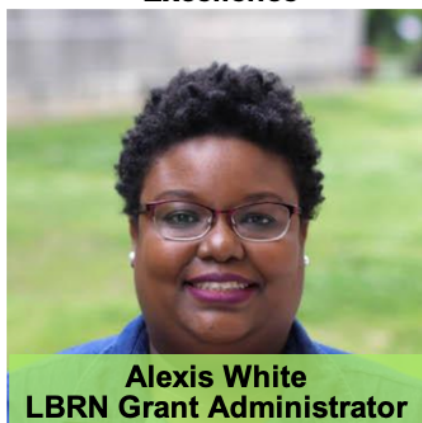
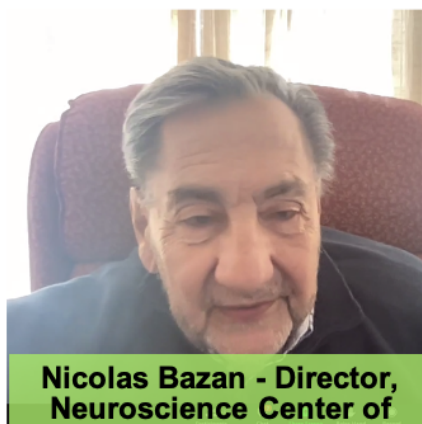
## Report : 20th LBRN Annual Virtual Meeting



The [20th LBRN Annual Meeting](https://lbrn.lsu.edu/annual-meetings.html) was held in a completely virtual format on January 28-29, 2022. We had a record number of meeting registrations of 194 and record number of 58 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.







## Keynote & Invited Speakers

- [Nicolas Bazan, M.D., Ph.D](#)  
Louisiana State University Health New Orleans  
Boyd Professor and Ernest C. and Ivette C. Villere Chair for the Study of Retinal Degenerations at Louisiana State University Health New Orleans
- [Charles Irvin, Ph.D](#)  
University of Vermont Burlington  
Professor of Medicine, Pulmonary Medicine Associate Dean for Faculty Affairs, Director, Vermont Lung Center

- **Krzysztof Reiss, Ph.D**

Louisiana State University Health New Orleans Cancer Center

Professor in the Department Interdisciplinary Oncology, Director of the Neurological Cancer Research Program

### **Oral Presentations**

Fifteen 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 and high schools exhibited a total of 58 posters through a virtual platform, which was especially possible for presentations, conversations and Q&A through 29 Zoom breakout rooms each into 2 one hour sessions. You can explore and search these posters and contact the authors through the iPosterSession platform we utilized for our meeting: [https://lbrn2022am-lsu.ipostersessions.com/Default.aspx?s=lbrn\\_2022\\_gallery](https://lbrn2022am-lsu.ipostersessions.com/Default.aspx?s=lbrn_2022_gallery)

### **LBRN 20th Annual Meeting Poster and Presentation Award Winners**

- **Faculty / PI Poster award winners (tied)**

**Matthew Hayes** – XULA "*Complex Germline Structural Variant Discovery Via Discordant Cluster Normalization*"

**Joseph Chaney** – XULA "*Applying the Brakes: Understanding the Role of the Conformational Changes in the Kinesin-5 on Processivity and Inhibition*"



Complex Germline Structural Variant Discovery Via Discordant Cluster Normalization  
Matthew Hayes, Ph.D.<sup>1</sup>, Derrick Mullins<sup>1</sup>, Angela Nguyen<sup>1</sup>  
<sup>1</sup> Xavier University of Louisiana Department of Physics and Computer Science, <sup>2</sup> Xavier University of Louisiana Department of Biology

**Introduction**  
disease onset. Simple structural variants (SVs) can be found algorithmically using whole genome sequencing read mapped to a reference genome. Complex structural variants are genomic rearrangements with 3 or more breakpoints, they are more challenging to detect algorithmically. This study presents our CleanBreak algorithm that can identify complex structural variants (CSVs) in genomes. The method was compared to SVelter, a state-of-the-art program for this problem, and it generally outperformed it in sensitivity and computational running time. Future development will focus on expansion the

**Methods**  
Figure 4: Deletion normalization. Deletion normalization – four rules:  
1) B0: Move left boundary to next interval boundary  
2) B1: Move right boundary to previous interval boundary  
3) B2: Move left boundary to previous interval boundary  
4) B3: Move right boundary to next interval boundary

**Discussion**  
• Loss of sensitivity in sim data  
– Variants in low-complexity regions  
• Del-dup-inv case  
– CleanBreak only predicts one variant per interval  
• Must extend to account for multiple variants per interval

**Conclusion**  
improve at detecting certain kinds of variants, the following issues will be addressed this year:  
• Extend CleanBreak to detect interchromosomal variants  
• Extend to allow multiple variants per interval to be considered  
• Read depth correction must be

**Complex Structural Variants**  
Fig. 1 CSVs present with three or more breakpoints and are created from adjacent simple structural variants.  
Reference: A B C D  
Del-dup: A C C C D  
Del-inv: A C D D

Algorithm	SV Type	Del-Dup	Del-Inv	Del-Dup-Inv
CleanBreak	Del	0.81/0.99	0.73/0.96	0.38/0.38
	Inv	—	0.74/0.90	<0.05 / <0.05
	Tand. dup.	0.73/0.97	—	0.26/0.96
SVelter	Del	0.70/0.99	0.66/0.98	0.48/0.96
	Inv	—	0.48/0.97	0.33/0.95
	Tand. dup.	0.54/0.98	—	0.30/0.82

**Acknowledgements**  
This work was partially funded by the National Science Foundation Research Initiation Award, grant number HRD-1901258, and startup funding from the Louisiana Cancer Research Consortium.

DISCLOSURES CONTACT AUTHOR GET IPOSTER

Matthew Hayes

Results and Future Direction

ATP Hydrolysis Rates

Rates of ATP hydrolysis of the mutant constructs compared to wild type Eg5 513

- Test effects on ATP hydrolysis rates and motility versus wild-type
- Explore other mutations created using method 2
- Pursue 3-dimensional structure of Human Kinesin-5 and mutant dimers bound to an inhibitor to give greater detail importance of the neck-linker conformation
- Comparing the canonical structure of Kinesin-1 to Kinesin-5

Neck - N L N K P E V N Q I L T K K A  
DAL 1 - D A L N L N K P E V N Q I L T K K A  
DAL 2 - N D A L L N K P E V N Q I L T K K A  
DAL 3 - N L N K P D A L E V N Q I L T K K A  
DAL 4 - N L N K P E V N D A L Q I L T K K A  
DAL 5 - N L N K P E V N Q D A L L T K K A

Joseph Chaney

## • Graduate Poster award winners (tied for first)

**Rizwana Begum** – SUBR Tied for 1st Place *"HSP70 and proteasomes coalesce in lipid rafts to regulate E-cigarette Vapor condensate induced inflammation"*

**Chelsey Jordan** – LSUS Tied for 1st Place *"Assessment of student appreciation for applied bioinformatics and computational drug discovery methods in a project-based course"*

**Prerana Ramesh** – LSUHS 2nd Place *"Improving Patient Outcomes for Inflammatory Bowel Disease through Physician Interactions during Infusion Treatment : Symptomatic Review of Biologic Therapy in IBD (STABILITY)"*

**LBRN** Laboratory of Pulmonary Immunobiology

**INTRODUCTION**

In recent years electronic cigarettes or e-cigs have become the latest trend among adults and youth alike.

Per a report funded by U.S. FDA and NIEHL, approximately 10.8 million adults currently use e-cigs in the US, with maximum prevalence among the age group between 18-24 years.

**SCHEME, MATERIAL, and METHODS**

**RESULTS**

Figure 2: Data presented as Mean ± SEM. \*p<0.05, \*\*p<0.01, vs Air control as per one-way ANOVA for multiple comparisons.

**ECVC alters the transcription and translation of PRRs**

Figure 3: Data presented as Mean ± SEM. \*p<0.05, \*\*p<0.01, vs Air control as per one-way ANOVA for multiple comparisons.

**ECVC mediated induction of transcription factor NF-κB and MAPKs**

**RESULTS**

Figure 4: Data presented as Mean ± SEM. \*p<0.05, \*\*p<0.01, vs Air control as per one-way ANOVA for multiple comparisons.

**CONCLUSION, FUTURE DIRECTIONS, and ACKNOWLEDGMENTS**

**CONCLUSION**

Our findings indicate a substantial increase in cytokine/chemokine production.

Dr. Rizwana

**LBRN** Assessment of student appreciation for applied bioinformatics and computational drug discovery methods in a project-based course

Chelsey Jordan  
Louisiana State University - Shreveport

**Project Goal**

In this project we evaluated the student learning outcomes for a 100% online project-based course on computer-aided drug discovery (CADD) to identify effective anti-viral drugs against the SARS-CoV-2 virus. This course provides comprehensive inquiry-driven opportunities for students to learn and apply computational drug discovery methods.

**Arbidol: A seed molecule**

Arbidol: A seed compound

- Anti-influenza
- Broad-spectrum antiviral
- Inhibits viral replication
- Inhibits viral assembly

Fig. 1: Chemical structure of Arbidol

**CADD Methodology**

Fig. 2: Compound library design and virtual screening by molecular docking

**Student Survey**

The CADD course was launched in 2020 as a summer LBRN program.

- The participants of this project consisted of a group of 48 students from diverse backgrounds and academic experiences.
- The cohort consisted of undergraduate and graduate students.

**Research Component**

The research component of this course implements a typical computational drug repurposing workflow. This approach includes six major phases: 1) Select a drug to be repurposed (the seed molecule); 2) select a target protein; 3) implement a ligand-based virtual screening workflow; 4) select a class of compounds; 5) select a class of compounds; 6) select a class of compounds.

**SwissSimilarity**

SwissDrugDesign

Don't know where to start? Try with an example Diclofenac, Propranolol or Nilotinib.

1 - Enter a molecule in SMILES format

2 - Select a class of compounds

Please, select a class of compounds here:

**Survey Results**

Students who became 'knowledgeable' are defined as those who gained awareness and understanding from survey responses based on four categories:

I. Changed from strongly disagree to strongly agree (A ↔ D)

II. Changed from strongly disagree to strongly agree (A ↔ D)

Chelsey Jordan

**Background**

Inflammatory Bowel Disease (IBD) includes Crohn's Disease (CD) and Ulcerative Colitis (UC), both of which are characterized by chronic inflammation of the gastrointestinal (GI) tract and extra-intestinal manifestations. At LSUHSC-S, IBD patients who underwent biologic infusion therapy for their IBDs did not routinely meet with a GI physician unless the patient requested this, or upon the infusion nurses' request if the patient was visibly ill. It was observed that many of the IBD patients who did not meet

**Results**

Figure 4: ESR levels were reduced post-STABILITY. The implementation of STABILITY out of the total available paired datasets are as follows: IBD - 41 out of 83 for both males and females, 15 out of 33 for males, and 26 out of 51 for females; CD - 36 out of 75 for both males and females, 11 out of 27 for males, and 25 out of 48 for females; UC - 5 out of 8 for both males and females, 4 out of 6 for males, and 1 out of 5 for females. Normal range for adults is less than 0.01 mg/dL. Statistics were performed by unpaired t-test with Welch's correction.

**ESR levels were reduced post-STABILITY**

Figure 5: Patients who had ESR levels that decreased after the implementation of STABILITY out of the total available paired datasets are as follows: IBD - 18 out of 32 for both males and females, 4 out of 11 for males, and 14 out of 21 for females; CD - 17 out of 30 for both males and females, 4 out of 11 for males, and 13 out of 20 for females; UC - 1 out of 2 for both males and females, and 1 out of 1 for females. Normal range is less than 30 mm/hr for females, and less than 20 mm/hr for males. Statistics were performed by unpaired t-test with Welch's correction.

**Results**

**Infusion Patient Satisfaction Survey Responses**

Following the implementation of STABILITY, Patients felt that their IBD symptoms...	n	%
Improved	24	56
Worsened	1	2
Unsure if there was improvement in symptoms	7	16
No change in symptoms	10	23
Patients' understanding of their IBD improved	36	84
Yes	36	84
No	7	16

**Methodology**

**Patient Demographics:**

The study population was defined as IBD patients at LSUHSC-S with ICD-10 diagnostic coding for Ulcerative Colitis or Crohn's Disease and are currently receiving treatment in our infusion clinic. The sample size was 110 patients total, consisting of 18 Ulcerative Colitis and 92 Crohn's Disease diagnoses (16% and 84%). Mean age was 39.23 years (range 16-67) and male:female ratio was 40:72. Patients in this study had been receiving one of the following medications at the time of assessment: infliximab, vedolizumab, certolizumab or infliximab. Patients on self-selectable biologics were not included as they were not assessed by the GI fellow at the time of each injection. Data spanning from January 2017 to August 2020 was collected to compare disease status prior to and after the initiation of STABILITY.

**Conclusions and Future Directions**

Since the implementation of STABILITY visits during infusion therapy for IBD patients at LSUHSC-S, there has been a noticeable improvement in the disease management process for these patients.

Clinical findings have shown trends towards improvement in the patient levels of fecal calprotectin, c-reactive protein, and erythrocyte sedimentation rates, but none of these values were statistically significant, likely due to the small sample size under consideration. There has been a significant decrease in the hospitalization rate of IBD patients following STABILITY (p=0.02190).

We are currently working to collect extended clinical data from IBD patient records in order to identify biomarkers that patients had

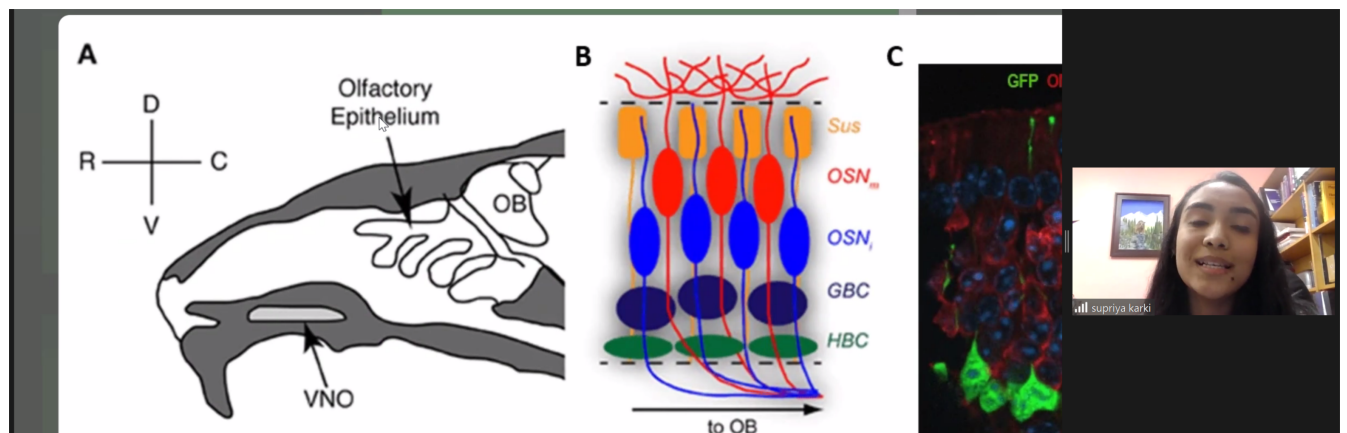
Prerana Ramesh

## • Undergraduate Poster award winners (tied for second)

**Supriya Karki** – LSUS 1st Place *"Developmental Stages of Olfactory Sensory Neurons in Neonatal Life vs. Adulthood"*

**Kalani Myles** – LSUS Tied for 2nd Place *"Computer-aided drug discovery for COVID-19 using virtual screening and molecular docking"*

**Bryan Strong** – ULM Tied for 2nd Place *"Translation initiation factors from early-branching eukaryote Giardia lamblia can form multifactor complex in the absence of 40S ribosome in vitro"*



**Computer-aided drug discovery for COVID-19 using virtual screening and molecular docking**  
Kalani Myles and Elahe Mahdavian  
Louisiana State University - Shreveport

**Introduction**  
The COVID-19 pandemic has negatively affected human health all over the world. This virus, known as SARS-CoV-2, is spreading rapidly and cases are constantly rising every day. People who have contracted the virus have experienced cold-like symptoms or are asymptomatic. Since the pandemic began, over

**Novel SARS-CoV-2 Virion**  
The COVID-19 virus currently has no way of preventing viral entry into the host cell. The virus can enter the host cell and bind to the SPIKE-ACE-2 receptor with no preventative measures. If we create a possible effective drug to treat COVID-19, then the virus would have no way of entering the host cell and would not be able to

**Why Drug Repurposing?**  
•Computer-aided drug discovery (CADD) has expedited drug development for COVID-19.  
•Special emphasis has also been placed on repurposing other anti-viral drugs to reduce the time and cost of drug development. CADD-Repurposing  
•The existing drug has established safety profile therefore the clinical

**Hypothesis**  
Arbidol and certain analogs will bind to spike:ACE-2 interface, disrupt the CoV-2 –specific viral-host recognition/interactions and thus inhibit a key molecular event needed for viral attachment to the host, a crucial step in the viral infectivity mechanism.

**Translation initiation factors from early-branching eukaryote *Giardia lamblia* can form multifactor complex in the absence of 40S ribosome in vitro**  
Bryan Strong, Zachary Wiggins, Francis Kwarteng, Zachary Shaw, Breanna Gottschalk, Srinivas Garlapati  
University of Louisiana at Monroe

**Introduction**  
Initiation complexes are recruited to the initiation codon without a prior scanning mechanism in *Giardia*, apparently due to the short 5' UTRs (2). However, *Giardia* cells have all the initiation factors that are necessary for the scanning process (3). To determine whether the lack of a scanning mechanism is due to the absence of protein-protein interactions between initiation factors eIF1, eIF2, eIF3, and eIF5, GST pull-down assays were performed. These assays were used to not only determine interactions between these factors but also to detect MFC formation.

**Results**  
same protocol as before; however, this time all the MFC initiation factors were tested together with and without the presence of Glet23N. Figure 3 shows the results of these assays.

**Discussion**  
From our results, we can see that there are significant protein-protein interactions between the initiation factors in the multifactor complex (MFC). Initiation factors Glet1, Glet3CN, and Glet5 all interact with one another. Glet23N interacts with Glet1 and Glet5 outside the complex, but not with Glet3CN. However, Glet23N significantly interacts when the rest of the complex is present. This disproves our hypothesis that the lack of a scanning mechanism in *Giardia lamblia* is due to the lack of protein interactions in the MFC. To examine other possible causes of the lack of scanning mechanism, our lab is currently performing GST pull-down assays between

**Conclusion**  
We have discussed a few of the differences in the translation initiation machinery and process between *Giardia lamblia* and higher eukaryotes. While we were unable to discover new protein-protein interactions in the *Giardia* multifactorial complex, we were able to show that a lack of multifactorial complex formation is not the reason scanning does not occur in *Giardia* translation initiation. Further research examining the pre-initiation multifactor complex could possibly include purifying the 40S ribosomal subunit found in *Giardia* and performing GST-pull down assays to determine what scanning of

**Methods**  
*Giardia* initiation factors eIF1, eIF2L, eIF3CN, and eIF5 were expressed and purified with both a poly-histidine and Glutathione S-Transferase (GST) tag separately for each protein. A GST protein was also purified by fractionation as our control.

**Translation initiation in Mammals**  
eIF4F  
eIF4E  
eIF4G  
AUG  
(A)<sup>3'</sup>

**Translation initiation in *Giardia lamblia***  
Glet1  
Glet3CN  
Glet5  
AUG  
(A)<sup>3'</sup>

**Acknowledgements**  
Research reported in this poster 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 P20 GM103424-01.

## • High School Poster award winners

**Raj Letchuman** – Caddo Parish Magnet High School 1st Place *"Identifying Promising Drug Candidates Against SARS-CoV-2 Using Computational Drug Repurposing Methodology"*

**Devika Dua** – Cedar Creek School 2nd Place *"Investigating Key COVID-19 Questions by Using Natural Language Processing on Scientific Publications"*



	P-value	Inference
Our results vs. GA Tech COVID-19	0.0001	Very statistically significant
Our results vs. CDC	0.0001	Statistically significant
GA Tech COVID-19 vs. CDC	0.0001	Statistically significant

- **Oral Presentation Award Winner**

**Eric Clifford** – Graduate talks winner LSUS *"Drug Screen Trends in Emergency Rooms Among Childbearing-Aged Females"*

- **Full project talk Winners (tied)**

**Kyle Piller** – Tied for 1st Place SELU *"Life in the fast lane: Testing for congruence among transcriptomic signatures"*

**Vonny Salim** – Tied for 1st Place LSUS *"Elucidation of Plant-Derived Drug Biosynthetic Pathways"*

## Drug Screen Trends Among Childbearing-Aged Females


Eric Clifford<sup>1</sup>, Phillip C.S.R. Kilgore<sup>1</sup>, Urska Cvek<sup>1</sup>, Marjan Trutschl<sup>1</sup>, Nadejda Korneeva<sup>2</sup>, Steven A. Conrad<sup>3</sup>, Thomas Arnold<sup>4</sup>

<sup>1</sup> Laboratory for Advanced Biomedical Informatics, Department of Computer Science, Louisiana State University Shreveport, Shreveport, LA 71115

<sup>2</sup> Department of Internal Medicine, Feist-Weiller Cancer Center, Louisiana State University Health Sciences Center, Shreveport, LA 71130

<sup>3</sup> Department of Medicine, Department of Emergency Medicine, Department of Pediatrics, and Department of Anesthesiology, Louisiana State University Health Sciences Center Shreveport, LA 71130


<sup>4</sup> Department of Emergency Medicine, Louisiana State University Health Sciences Center Shreveport, LA 71130




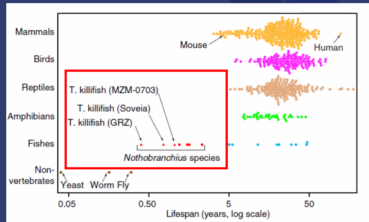
Eric Clifford

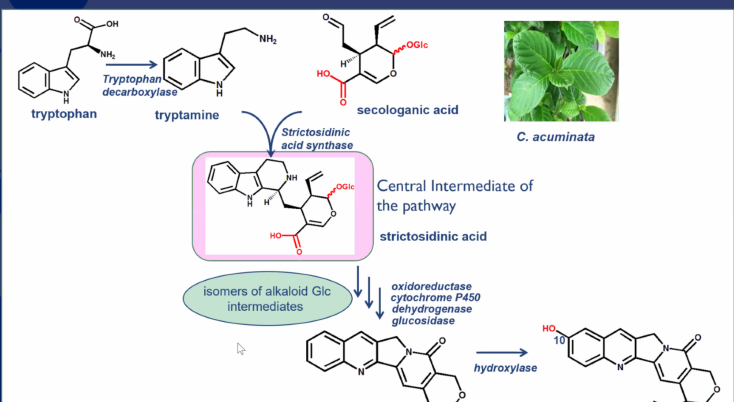
## Why is it a model?

- Complete its entire life-cycle between 10 and 31 weeks
  - Life-span variation among populations (different strains)
- GRZ strain (shortest)
  - Gona-Re-Zhou National Park of Zimbabwe




Kyle Piller



*C. acuminata*



Nonty Salim

The award list and any links to relevant posters is available here: <https://lbrn.lsu.edu/highlights/2022-01-31-LBRN-AM-Awards.html>

### Online

All the major parts of the meeting are available to re-watch here: <https://lbrn.lsu.edu/annual-meetings-2022.html#eventMediaLink>



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## LSU HPC Training



Our next HPC training will be held on Wednesday, February 16 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, February 16, 2022: Version Control with Git**

Version control system is used for tracking changes in computer files and coordinating work on those files among multiple people. It is primarily used for source code management in software development and also used to keep track of changes in any set of files. This tutorial gives an introduction to the Git version control software and will cover the following topics:

- Basic Git usage: create, manage and track changes in git repository
- Working with Git branch
- Remote repository

***Prerequisites:***

A laptop/desktop with Git installed, OR  
LONI or LSU HPC account to access the Git installed on cluster.

Next HPC training:



- **Wednesday, February 23, 2022: Introduction to Python**

Python is a high-level programming language, easy to learn yet extremely powerful. This training will provide an introduction to programming in Python. The subjects include basic Python syntax, Python classes used in object-oriented programming. Basic Python modules for scientific computing and plotting will also be introduced. During the training, simple Python programs will be provided for demonstration.

***Prerequisites:***

Basic understanding of a 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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## NRMN : Upcoming Webinar



**BLACK HISTORY MONTH  
WEBINAR SERIES**

*A Time For Healthy Change in STEM  
for Black Scientists Through Allyship*

**Thursday, February 24 from 11a - 12p CT**

Join us for our Black History Month Webinar Series as we will be joined by Drs. Antentor Hinton, Tam'ra-Kay Francis, Zer Vue, Brittany Taylor and Arnaldo Diaz Vazquez, discussing allyship and the benefits and impact it can provide for black scientists.

**NRMN**  
Mentoring to Diversify the  
Biomedical Workforce

**VANDERBILT**  
School of Medicine  
Basic Sciences

**#NRMNmentoringMatters**

We are excited to announce that we will be hosting a new webinar in our Black History Month webinar series with Drs. Antentor Hinton, Tam'ra-Kay Francis, Zer Vue, Brittany Taylor and Arnaldo Diaz Vazquez!

In this webinar, our speakers will be discussing allyship and the benefits and impact it can provide for black scientists.

Join us on February 24 at 11am CST for an important discussion about the importance of allyship for black STEMM professionals.



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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 proflin 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 CDC: <https://www.cdc.gov/coronavirus/2019-ncov/index.html>

# Self-Testing At Home or Anywhere

## What is a Self-Test or At-Home Test?

**Self-tests** for COVID-19 give rapid results and **can be taken anywhere**, regardless of your vaccination status or whether or not you have symptoms.

- They detect **current** infection and are sometimes also called “home tests,” “at-home tests,” or “over-the-counter (OTC) tests.”
- They give your **result in a few minutes** and are different from laboratory-based tests that may take days to return your result.
- Self-tests along with [vaccination](#), [wearing a well-fitted mask](#), and physical distancing, help [protect you and others](#) by reducing the chances of spreading COVID-19.
- Self-tests **do not** detect antibodies which would suggest a previous infection and they do not measure your level of immunity.

## When To Take an At-Home COVID-19 Test

Test Yourself If...	Timing
You have any <a href="#">COVID-19 symptoms</a>	Immediately
You were exposed to someone with COVID-19	At least 5 days after your exposure  <b>If you test negative</b> for COVID-19, consider testing again 1 to 2 days after your first test
You are going to an indoor event or a gathering	Immediately before the gathering, or as close to the time of the event as possible  <b>This is especially important before gathering with <a href="#">individuals at risk of severe disease</a>, <a href="#">older adults</a>, those who are <a href="#">immunocompromised</a>, or people who are not <a href="#">up to date on their COVID-19 vaccines</a>, including children who cannot get vaccinated yet.</b>

Learn what to do if you [test positive](#) or [test negative](#).

## How to Get an At-Home COVID-19 Test

- **Order free tests** at [COVIDtests.govexternal icon](#). Free tests are also available through [local health departments](#).
- **Buy tests** online or in pharmacies and retail stores. Private health insurance may reimburse the cost of purchasing self-tests. Visit [FDA's websiteexternal icon](#) for a list of authorized tests.
- If you're not able to obtain a self-test when you need it, you might also **visit a community testing site, or call your local health department** for more options.

## How to Use an At-Home COVID-19 Test

**Read the complete manufacturer's instructions** for use before using the test.

- To use an at-home test, you will collect a nasal specimen and then test that specimen.
- If you do not follow the manufacturer's instructions, your test result may be incorrect.



- Wash your hands before and after you collect a nasal specimen for your test.
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## What Your Test Results Mean



IF YOUR TEST IS

### Positive

- The test detected the virus and **you have an infection.**
- Stay home for at least 5 days and [isolate](#) from others in your home.
- Tell your [close contacts](#).
- Wear a [well-fitted mask](#) when around others. If available, a N95 or KN95 respirator is recommended.
- Watch for [symptoms](#). If you have any [emergency warning signs](#), seek emergency care immediately.
- Tell your healthcare provider. Contact them as soon as possible if:
  - Your symptoms get worse.
  - You are more likely to get very sick because you are an [older adult](#) or have an [underlying medical condition](#). [Possible treatment](#) may be available for you.
  - You have questions about your isolation.



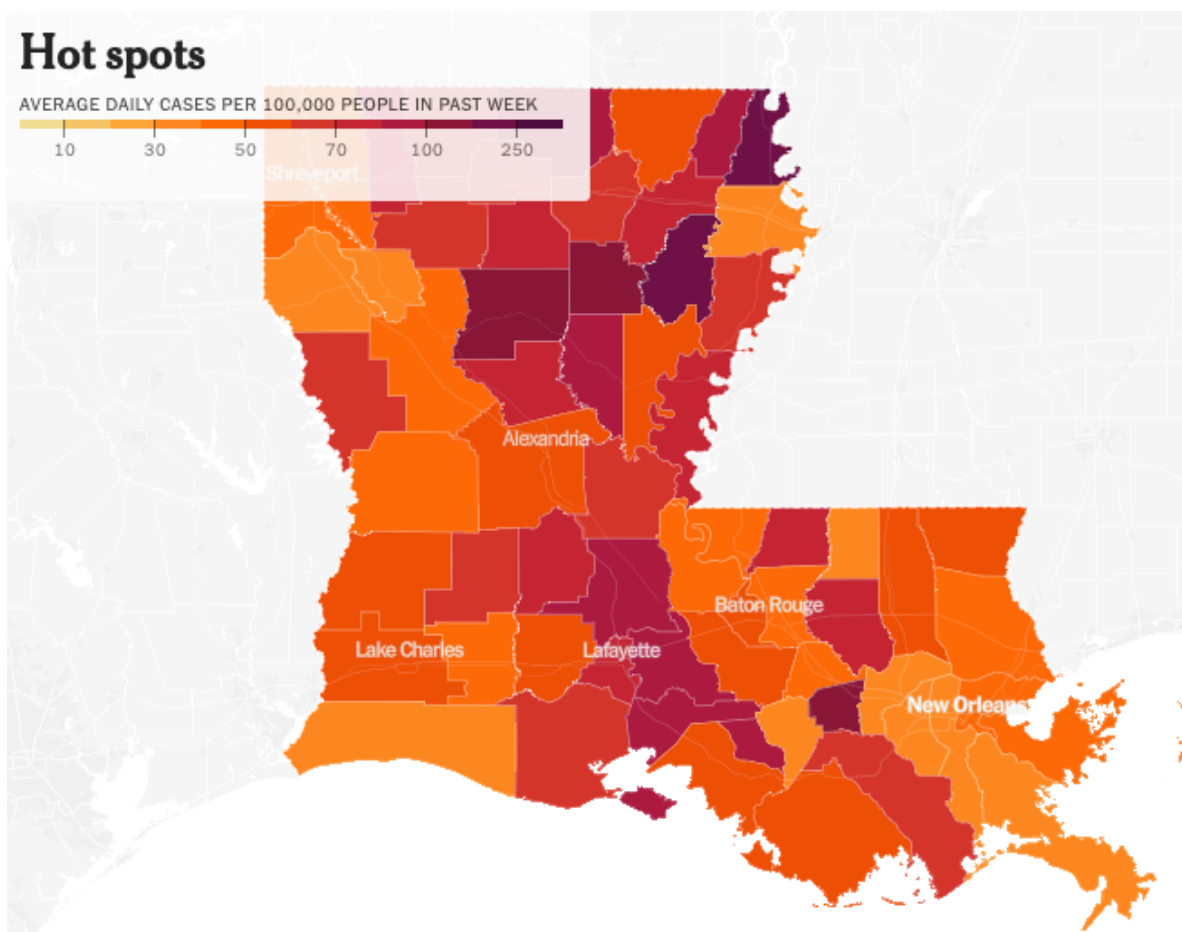
IF YOUR TEST IS

### Negative

- The test did not detect the virus, **but doesn't rule out an infection.**
- Some self-tests are designed to be used in a series (also known as serial testing). Consider repeating the test 24 to 48 hours later. Multiple negative tests increases the confidence that you are not infected with the virus that causes COVID-19.

## COVID-19 in Louisiana

Information from New York Times: <https://www.nytimes.com/interactive/2021/us/louisiana-covid-cases.html>



## NIH Extramural Nexus

## • New NIH Administrative Supplements Available to Support Diversity Mentorship

Qualified investigators can now submit proposals in response to the Chief Officer for Scientific Workforce Diversity (COSWD)-led [Notice of Special Interest \(NOSI\) NOT-OD-22-057: Administrative Supplements to Recognize Excellence in Diversity, Equity, Inclusion, and Accessibility \(DEIA\) Mentorship](#). **Proposals are due by April 7, 2022.**

Mentorship is a critical part of recruiting and retaining an inclusive scientific workforce. Evidence suggests [mentorship helps foster scientific identity](#) and [career progression](#) in science, technology, engineering, mathematics, and medicine (STEMM) disciplines. For example, research shows that grant-writing mentorship for early-career biomedical investigators from underrepresented groups [can foster increased publication productivity](#), a key contributor to scientific career advancement.

Based on this evidence, [one goal of my office](#) is to support and amplify the impact of programs that develop scientific talent through training and mentorship. Thus, this new NOSI is part of our commitment to enhancing mentorship within NIH-supported research, with an emphasis on scientists from underrepresented groups.

The [participating NIH Institutes and Centers](#) will supplement the existing awards of scientists who have demonstrated a commitment to exceptional training and mentorship, especially to individuals from groups identified as [underrepresented in the biomedical sciences](#).

Supplements are available for various grant types, including career development, training, cooperative, and Research Project Grants (R01). They will provide up to \$250,000 in [direct costs](#), not to exceed the direct costs of the parent award. Investigators may use the funds to perform additional research within the parent grant's scope, develop curricula or training activities to strengthen mentor training, or help foster the research career development of additional students, post-doctorates, or other trainees.

The NIH [has an array of mentorship initiatives and resources](#), and I am excited about this addition to the agency's offerings. I encourage all eligible investigators to take advantage of this opportunity to be recognized for outstanding mentoring, and for promoting inclusive excellence.

## • All About Grants Podcast – How to Find Help

Have questions about funding opportunities, developing an application, or managing a grant award? Unsure to whom you should reach out for help? Check out this [NIH All About Grants](#) podcast to get a refresher on the ins and outs of what to do when seeking assistance from NIH extramural staff ([MP3](#) / [Transcript](#)). Sheri Cummins, with the NIH Office of Extramural Research's communications group, explains where to find answers to many [frequently asked questions](#) and other information online, deciphering program, review, and grants administrative [staff roles at NIH](#), when to reach out and when not to, and much more.

“...[I have] asked: Have you ever wanted to reach out to NIH but decided not to and why? And I was floored to see how many people said fear. Fear of looking stupid or uninformed, feeling that their questions were somehow unworthy of NIH attention...It’s literally our job to help. We all want the same thing...to advance our scientific understanding and ultimately improve the nation’s health...the pandemic has shown us all how truly vital that NIH mission is for everyone and we really just need to help each other to get there.” – Sheri Cummins

Please also visit our [Help page](#) for more information.

## • Feedback Sought on the NIH-Wide Strategic Plan Framework for Diversity, Equity, Inclusion, and Accessibility

We are pleased to announce that the framework for the NIH-Wide Diversity, Equity, Inclusion, and Accessibility (DEIA) Strategic Plan was released earlier this week ([NOT-OD-22-061](#)). Your input on the framework as the plan is developed is encouraged. Feedback will help us ensure that DEIA principles continue to be embraced and integrated across NIH going forward.

We strongly believe that an inclusive and diverse pool of highly talented individuals is key for the country to remain a global leader in scientific discovery and innovation (see [these posts for more](#)). This means we must actively consider factors that address DEIA principles and appropriately embed them within NIH and the wider scientific community. Embracing this DEIA vision will enhance our ability to drive biomedical innovation and serve an increasingly diverse US population.

The NIH-Wide DEIA Strategic Plan strives to clearly communicate our DEIA vision. It will align with the [NIH-Wide Strategic Plan](#) released last year, and encompass our ongoing initiative to address [structural racism in biomedical research](#) as well as build on the wider [federal effort](#) to expand DEIA across the workforce.

The scope of the plan covers accomplishments, needs, opportunities, and challenges related to DEIA within the NIH workforce, its structure and culture, and our supported research. The main objectives are to:

- Implement organizational practices to center and prioritize DEIA in the workforce
- Grow and sustain DEIA through structural and cultural change
- Advance DEIA through research

What are the potential benefits or drawbacks to this framework? Are there priority areas missing? Which best practices and policies are likely to foster positive culture change? What barriers stand in the way? How should DEIA be defined for the purposes of this effort? What metrics measure progress?

We welcome your comments and feedback on the framework. Please send them [electronically](#) by April 3, 2022.



## • Gearing Up for 2023: Implementing the NIH Data Management and Sharing Policy

*Guest post by Dr. Lyric Jorgenson, Acting Associate Director for Science Policy and Acting Director of the NIH Office of Science Policy, originally released on the [Under the Poliscopes blog](#).*

Frequent readers of this blog will remember that back in October 2020, NIH issued its [Data Management and Sharing \(DMS\) Policy](#) to further our commitment to making the research we fund available to the public. Our strategic decision to make the effective date for the Policy approximately two years later led some to ask NIH “why wait so long?” while others asked “why not give us more time?” Fortunately, the answer to both these questions is the same. Our goal is to lead a [cultural shift](#) that makes data sharing the norm. The degree of that shift, for some, may vary. For example, many data sharing policies are already in place and researchers currently sharing data will likely not need to significantly alter their approach. But prospective planning for how to share data (i.e., developing plans, requesting NIH funds) may be new for some. As such, it seemed reasonable that two years was the right balance of time to lay the groundwork for implementation. Today I am excited to provide an update on what NIH is doing to make our data management and sharing efforts a success on the one-year mark prior to the Policy’s effective date.

Since the Policy’s release, NIH has continued its approach of meeting and seeking feedback from its stakeholders. For example, in April 2021, NIH supported a two-day National Academies [workshop](#) to share strategies for successful data management and sharing and identify areas of additional need for seamless policy implementation. Thanks to the success of this workshop, we were able to continue engaging the public on multiple related resources and issues, such as [consent for data sharing](#), [harmonizing the NIH Genomic Data Sharing Policy](#) with the DMS Policy, and the [discoverability of our data resources](#). We also have been partnering with our colleagues in the NIH Office of Extramural Research to provide implementation updates at extramural-focused meetings such as last year’s [Virtual Seminar](#).

As you may recall, when the DMS Policy was released, we asked the community what other types of information would be of value to help with implementation. Based on the feedback we received, we are releasing additional resources today and have plans for continuing to release more throughout 2022.

Today, NIH is:

- Publishing a new set of [FAQs](#) that respond to questions we have heard since the release of the DMS Policy. We plan to update these FAQs throughout the year, as necessary
- Issuing a request for public comments on draft [Supplemental Information to the NIH Policy for Data Management and Sharing: Responsible Management and Sharing of American Indian/ Alaska Native Participant Data](#) to continue our partnership with Tribal communities by promoting responsible management and sharing of AI/AN participant data

Over the course of 2022, you can expect to hear more from us regarding resources, including:

- Helpful tips for developing budgets in Plans describing data management and sharing
- Updated information on principles for protecting research participant privacy and de-identification to help guide sharing of research participant data
- Educational resources including webinars and potentially sample Plans
- Plans for further harmonizing NIH's data management and sharing expectations, particularly with reducing duplicative plan submissions

In addition to the above, during 2022 NIH will also continue providing supplemental funding for grantees to:

- Improve the FAIR and Artificial Intelligence/Machine Learning-Readiness of their NIH-Supported Data
- Align existing data repositories with FAIR and TRUST principles and evaluate usage, utility, and impact

This is definitely an exciting year for NIH, and we look forward to continuing our engagement with the stakeholder community throughout 2022. Make sure to stay tuned –there is plenty more to come as we work together to accelerate scientific discovery through effective data management and sharing.

## • Extending Existing Guidance for Preparing Applications During COVID-19

For Spring 2022 due dates, NIH recently [extended the guidance](#) that while grant applications should not include contingency or recovery plans for problems resulting from the COVID-19 pandemic, investigators may address effects due to the pandemic on productivity or other scoreable issues in the personal statement of the biosketch. Reviewers will be instructed to take these pandemic-related circumstances into account when assessing applicants' productivity and other score-driving factors. If needed, NIH staff will request and assess plans to resolve specific problems arising from the COVID-19 pandemic prior to funding.

NIH also [extended the special exception for post-submission material](#) to applications submitted for the August/October 2022 Council rounds. For applications submitted for the August/October 2022 Council rounds (beginning with applications submitted for the January 25, 2022 due date), the NIH, AHRQ, and NIOSH will accept a one-page update with preliminary data as post-submission materials for applications submitted under all activity codes, ONLY if the Funding Opportunity Announcement (FOA) used for submission allowed preliminary data in the application. One page of preliminary data will be accepted for single component applications or for each component of a multi-component application.

The deadline for submitting all post-submission materials, including preliminary data, will be 30 days before the study section meeting, unless specified otherwise in the FOA. Because applications for

emergency competitive revisions and urgent competitive revisions undergo expedited review, post-submission materials will not be accepted for those applications.

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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.*

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