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News, Opportunities and Deadlines for February 2020

Save the Date - April 3-4, 2020

8th Annual LA Conference on Computational Biology and Bioinformatics

8TH ANNUAL LA CONFERENCE ON
COMPUTATIONAL BIOLOGY & BIOINFORMATICS
April 3-4, 2020 · LSU Digital Media Center · Baton Rouge, LA

- Cancer Informatics and Immunotherapy
- Microbiome and Metagenomics
- Proteomics
- Cloud Computing
- Evolutionary Genomics and Phylogenetics
- Virology and Infectious Diseases

Registration: https://lbrn.lsu.edu/conference-on-biology-and-bioinformatics.html

Alan J. Tackett, PhD
University of Arkansas for Medical Sciences
Professor of Biochemistry and Molecular Biology
Scharlau Family Endowed Chair for Cancer Research
Area: Proteomics/Cancer Immunotherapy

Folker Meyer, PhD
Argonne National Laboratory
Professor of Medicine, University of Chicago
Associate Division Director of Institute for Genomics and Systems Biology
Area: Metagenomics/Microbial Ecology/MG-RAST

Todd Reilly, PhD
NIH/CIT STRIDES Initiative
Chief Scientist, Percipient Consulting
Area: Cloud Computing

Jamie Oaks, PhD
Auburn University
Assistant Professor of Biology
Curator, Museum of Natural History
Area: Phylogenetics

Sanjay Padhi, PhD
Head of AWS Research, US Education
Adjunct Professor at Brown University
Area : Large-scale distributed computing/Data Analytics/Machine Learning

LSU Center for Computation & Technology · LSU Office of Research & Economic Development · LBRN · LSU Center for Experimental Infectious Disease Research, Division of Biotechnology and Molecular Medicine · School of Veterinary Medicine

We are happy to announce that the 8th Annual Louisiana Conference on Computational Biology and Bioinformatics, April 3 and 4, 2020, will take place at Louisiana State University in Baton Rouge.

The conference aims to expose Louisiana to the cutting edge of Computational Biology, Bioinformatics Research and Applications while also providing a platform for exchange of information and technical knowledge among Louisiana-based scientists involved in different aspects of computational biology & bioinformatics.

REGISTER HERE

LBRN Summer Research Program - 2020

LBRN Summer Research Program

for Undergraduate and Graduate students

May 25 — July 31, 2020*

AWARDS

- Undergraduate and Graduate students will receive support of $4,000 and $6,000 respectively
- Housing is provided, if needed

APPLICATION DEADLINE

- If you would like to know more about this program, please go to Research Programs at: https://lbrn.lsu.edu/summer-research-program.html
- If you have any questions, please contact Alexis M. White at lbrn@lsu.edu
- Phone: (225) 578-9683
- Email: lbrn@lsu.edu
- Web: https://lbrn.lsu.edu/
- ** Pending Funding*

LBRN

Louisiana Biomedical Research Network

The Louisiana Biomedical Research Network (LBRN) sponsors a summer research program in support of undergraduate students, graduate students and faculty from any Louisiana institute. We offer qualified participants the opportunity to work in established research laboratories at Louisiana State University, LSU Health Sciences Center in New Orleans, LSU Health Sciences Center in Shreveport, Tulane Medical Center, or Tulane National Primate Research Center. The goal of our program and funding is to support biomedical research through an increase in graduate school admissions in these scientific fields and make Louisiana researchers more competitive in obtaining federal funding for research.

The schedule for undergraduate students covers ten weeks during the summer; the summer program dates are May 25 - July 31, 2020. The schedule for graduate students and faculty is more flexible.

Please see our website for support details and program requirements for each application type, applications are open on our LBRN Summer Program Webpage now. Deadline for applications extended to February 21, 2020.

LOUISIANA CANCER RESEARCH CONSORTIUM SCIENTIFIC RETREAT

LOUISIANA
CANCER
RESEARCH CENTER

-- Call for Abstracts--

The 2020 Louisiana Cancer Research Consortium Scientific Retreat has been scheduled for **Friday, March 13, 2020**, at Xavier University of Louisiana.

Abstracts are now being accepted for participation in this year’s event. The guidelines for formatting and submission can be found at

http://www.louisianacancercenter.org/news-events/guidelines-deadlines/

Please note, the deadline for submitting an abstract is Friday, January 31, 2020.

Other Important Retreat Dates/Deadlines:

January 31, 2020 – DEADLINE to submit abstracts
February 10, 2020 – DEADLINE to submit Core posters ONLY for inclusion in abstract booklet
February 20, 2020 – Notifications will be sent to all poster/podium presenters
February 21, 2020 – DEADLINE to register
March 6, 2020 – DEADLINE for podium presenters to submit slides
March 13, 2020 – 2020 LCRC Scientific Retreat

Additional retreat information is available at http://www.louisianacancercenter.org/news-events/guidelines-deadlines/. Please check in periodically for the latest on the **2020 LCRC Scientific Retreat**.

LSU HPC Training: Introduction to Linux

The schedule for the Spring 2020 HPC Training is available at http://www.hpc.lsu.edu/training/tutorials.php.

Our next HPC training will be held on Wednesday, February 19 at 9:00 AM in 307 Frey Computing Service Center and broadcast online for remote users.

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

Wednesday, February 19, 2020: Basic Shell Scripting
For anyone who works in a Linux/Unix environment, a working knowledge of shell scripting is essential and will boost their efficiency and productivity tremendously. For this tutorial, we will focus on bash as it is one of the most popular shells. This tutorial will include topics such as

creating simple bash scripts, flow control, command line arguments, regex, grep, awk and sed. This is a practical tutorial, so we will provide examples and/or hands-on exercises for most of the covered materials.
Prerequisites: Access to a Linux/Unix based environment, i.e. Linux (VirtualBox images), Mac OSX and Windows with Cygwin or Bash installed.

Next HPC Training:

Wednesday, March 4, 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 who plan on joining remotely 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<https://nam04.safelinks.protection.outlook.com/?url=https%3A%2F%2Fsupport.zoom.us%2Fhc%2Fen-us%2Farticles%2F201362023-System-Requirements-for-PC-Mac-and-Linux&data=02%7C01%7Cfchen14%40lsu.edu%7Cef60da7ddcf740eda2e308d7353499f7%7C2d4dad3f50ae47d983a09ae2b1f466f8%7C0%7C0%7C637036372350179319&sdata=3HjIO9GryZS7tMjTUHyRdoQRxwP4DnLlrKmwokFdeiQ%3D&reserved=0>.

IDeA Co-Funding

NIH National Institute of General Medical Sciences

The IDeA program managed by NIGMS is pleased to announce the 2020 co-funding opportunity for investigators in IDeA-eligible states whose R01 or R15 applications scored well but fall just outside of an IC's funding range. The IDeA program provides a maximum of $320K in total costs for each of the first two consecutive years of a selected award. Nominations are made by the NIH IC that has the primary assignment for the application. PIs wishing to be considered for IDeA co-funding should contact directly the program officer at the IC assigned to the application.

IDeA co-funding is conducted once per year, and the nomination period will close in early April. Final selections will be made in June of 2020. Please visit https://www.nigms.nih.gov/Research/DRCB/IDeA/Pages/IDeA-Co-funding.aspx for further information about this initiative.

GeneLab Launched Two New Illumina Sequencing Machines

GeneLab (School of Veterinary Medicine - Louisiana State University) is a multi-faceted core laboratory directed by the Division of BIOMMED in the School of Veterinary Medicine at Louisiana State University. GeneLab engages in specific research and training projects, which require expertise in Next-Generation Sequencing, traditional DNA sequencing, gene cloning, PCR, gene expression and other molecular methods. The goal of GeneLab is to facilitate the utilization of the state-of-the-art technologies in genomics research by LSU faculty and researchers nationwide at a competitive price and in a timely fashion.

The primary focus of GeneLab is its portfolio of sequencing capabilities. Currently, two Next Generation Sequencing instruments, the Illumina NextSeq, the Illumina MiSeq and 10X Genomics Chromium Controller along with bioinformatics support for NGS data are provided to the research community and offerring will be extended rapidly as NGS and other emerging sequencing technologies are evolving.

Illumina NextSeq

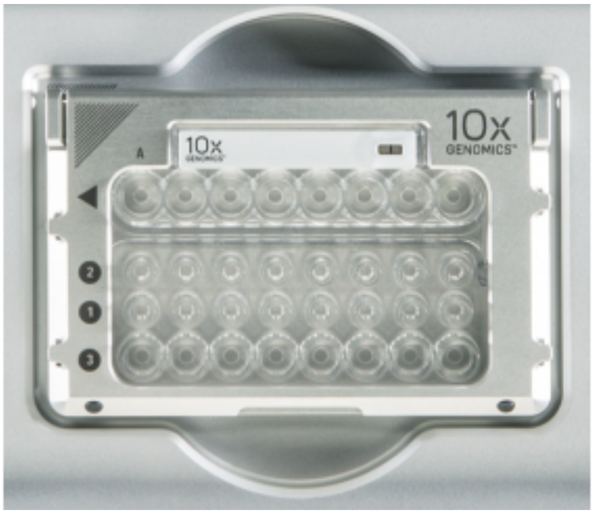
The Illumina NextSeq System is a desktop sequencer with power and flexibility to carry out applications such as whole genome sequencing, exome sequencing, whole transcriptome sequencing, mRNA-Seq, and others. In one run it can sequence a full human genome at 30x coverage. Users can choose between high output or mid output flow cell configurations. At high output, up to 800 million paired end reads can be generated (at 150 bp read length) to produce up to 120 Gb of data in 29 hours. The Illumina sequencing systems utilize a well-established sequencing by synthesis (SBS) method and patented cluster generation technology in which fluorescently labeled nucleotide bases are detected as they are incorporated into DNA template strands. All four reversible terminator-bound dNTPs are present in each sequencing cycle.

Illumina MiSeq

Cluster generation, sequencing, and analysis are all done on a single instrument. The sequencing process takes place on a flow cell with 1 channel. Multiple samples can be run at once by using indices for each sample. 2x300bp reads are supported on the MiSeq and takes ~3 days to run. With v.3 kits the MiSeq can produce >25 million reads or 15GB per run. With v.2 kits the MiSeq can produce >15 million reads or 7.5 GB per run with standard flow cells. There is also the option of using micro and nano flow cells which produce up to 4 million and 1 million reads per run (1.2Gb & 500Mb). Actual output can vary depending on cluster density.

10X Genomics Chromium Controller

Go beyond traditional gene expression analysis to characterize cell populations, cell types, cell states, and more on a cell-by-cell basis. From assessing tumor heterogeneity and stem cell composition, to dissecting neuronal populations—the technological advancements provided by the Chromium Single Cell Gene Expression Solution allow the creation of high complexity libraries from single cells to maximize insight from any sample type.



Services and collaboration can be delivered through the LBRN cores.

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. More details can be found in the attached CFP.

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BBC Core Educational Resource

LBRN Louisiana Biomedical Research Network

The BBC Core provides introductory educational lecture series on informatics topics that are recorded and streamed. Prior offerings that are available for on demand streaming include;

- An Introduction to Computers and Informatics in the Health Sciences

  http://metagenomics.lsuhsc.edu/lectures/introinformatics/

- An Introduction to Microbial Community Sequencing and Analysis

  http://metagenomics.lsuhsc.edu/lectures/intromicrobiota/

On demand streaming links are available by each lecture along with downloadable lecture slides.

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 2019/2020.

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 Extramural Nexus (NIH/OD)

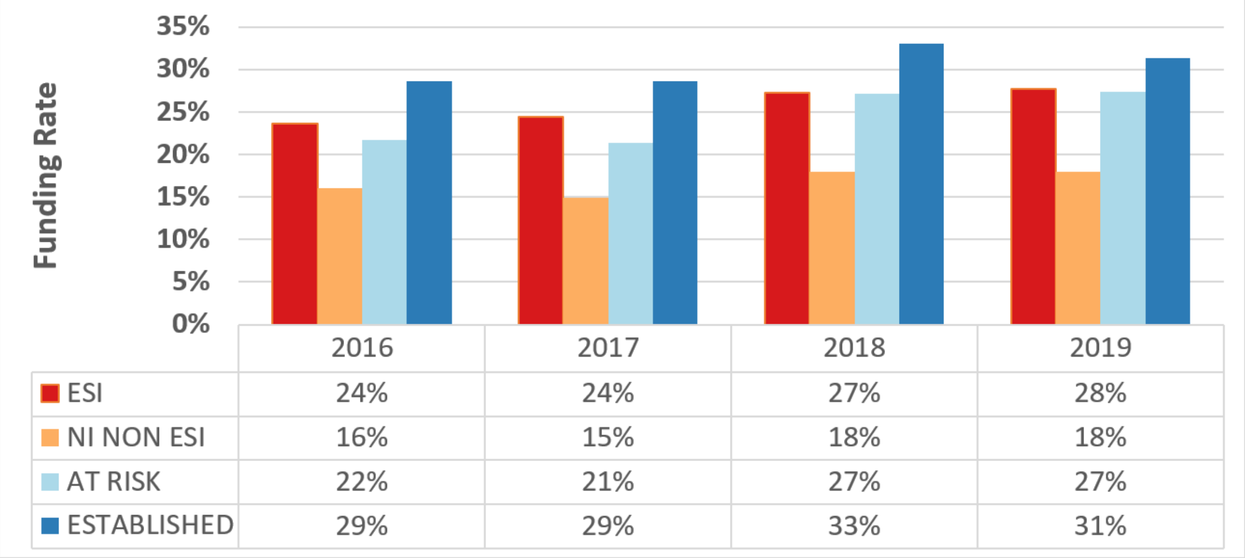
What’s Happening With “At-Risk Investigators?”

In December 2018, the NIH Advisory Committee to the Director (ACD) offered a number of recommendations to NIH on the “Next Generation Researchers Initiative.” Among those: The Committee recommended “special funding consideration for “at-risk” investigators. These are researchers who developed meritorious applications who would not have significant NIH research funding if the application under consideration is not awarded. We plan to draw more attention this year, both inside and outside NIH, to outcomes for at-risk investigators, to ensure those submitting meritorious ideas to NIH are not lost to the system.

We agree with the ACD on the need to support these researchers and are identifying strategies to call attention to both early-stage investigators and at-risk investigators who are designated on a meritorious grant application that did not get funded.” Here’, we present some data on our progress towards achieving this goal.”

To answer this question, we will focus on the “funding rate.” This is a person-based metric, as described before, representing the proportion of those scientists who are successful among those applying for an NIH grant.

Funding Rate = (Number of Unique Awardees in Fiscal Year)/(Number of Unique Applicants in Fiscal Year)



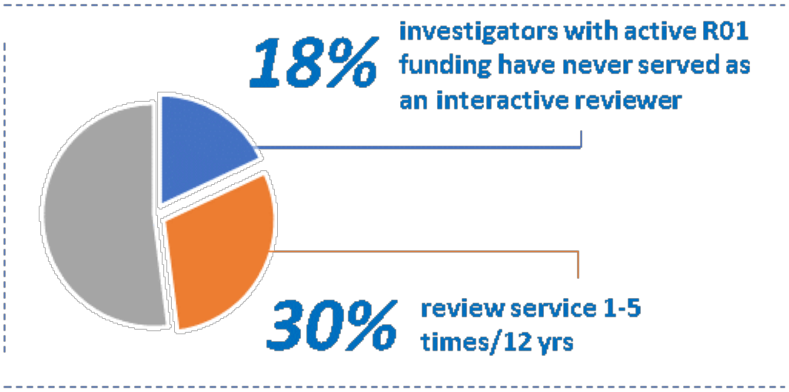
	2016	2017	2018	2019
🟥 ESI	24%	24%	27%	28%
🟧 NI NON ESI	16%	15%	18%	18%
🟦 AT RISK	22%	21%	27%	27%
🟦 ESTABLISHED	29%	29%	33%	31%

...Continue reading

Broadening the Pool of NIH Reviewers

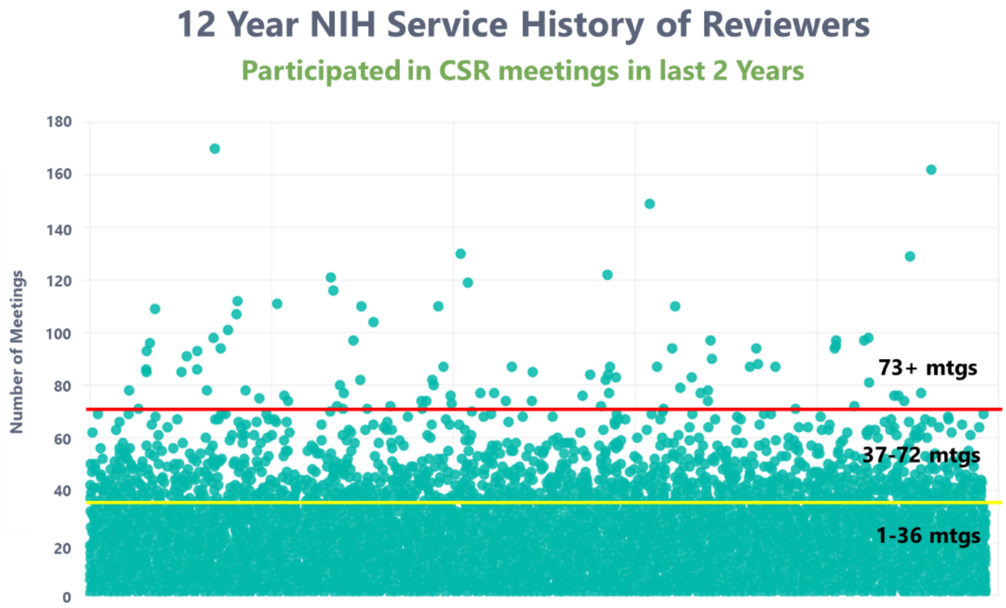
The scientific peer review process benefits greatly when the study section reviewers bring not only strong scientific qualifications and expertise, but also a broad range of backgrounds and varying scientific perspectives. Bringing new viewpoints into the process replenishes and refreshes the study section, enhancing the quality of its output.

In this context, CSR recently removed the requirement to have at least 50% full professors on committees. This had sometimes led to a misguided attempt to “do better than the metric” by aiming for a committee of all full professors. We are now encouraging scientific review officers (SROs) to focus on scientific contributions (demonstrable in a range of ways, e.g. recent publications, R01 or equivalent extramural funding from other sources, etc.), expertise, and breadth instead of trying to meet a career-stage metric. Our goal is to achieve a balance of perspectives by including a mix of qualified senior, mid-career, and junior scientists on study sections.Our data show that this can be achieved, as we have not exhausted the pool of eligible reviewers. Using R01 grant funding as a rough indicator of “qualified to review” we looked at interactive (i.e. excluded mail review) review service records of R01 awardees. As of January 1, 2020, there were 22,608 individuals with active R01 funding. Of these, 30% (6715) have served one to five times, and 18% (4074) have never served as a reviewer in the last 12 years. Of those who have served only one to five times over 12 years, 26% are assistant professors and 34% are associate professors.



In an effort to facilitate broader participation in review, we are making these data available to SROs and encouraging them to identify qualified and scientifically appropriate reviewers, who may not have been on their radar previously. In another step to broaden the pool of reviewers, we will launch a web page this spring through which scientific societies can recommend qualified reviewers.

We greatly appreciate the generosity of reviewers who contribute to the scientific community by freely giving their time to review NIH grant applications. However, one aspect of broadening the pool of reviewers is to avoid excessive review service by a small fraction of people, which can lead them to have a disproportionate effect on review outcomes. We are looking into issue of undue influence, or the “gatekeeper” phenomenon, where a reviewer has participated in the NIH peer review process at a rate much higher than their peers, and thus has had a disproportionate effect on review outcomes in a given field. Below is a plot examining the service records of all 24,642 reviewers who served as reviewers (in a capacity other than as a mail reviewer) for CSR within the past two years. Each dot represents a reviewer's number of meetings for the NIH over the last 12 years.



[*...Continue reading*]()

- ## Case Study in Review Integrity: Asking for Favorable Treatment

What happens when a former colleague contacts you, a reviewer, out of the blue to ask if the application on which he is a principal investigator could be treated favorably at the review meeting? Do you brush off the investigator and figure you will not let the contact influence your review of that application? Or do you instead immediately notify NIH?

Intrigued? We have a case for you (based on true stories, details have been changed slightly and names have been fictionalized). Read on.

Dr. Miller, a reviewer recently appointed to an NIH study section, was surprised to get an email from a former lab colleague, Dr. Johnson. They had not kept in touch over the years. As it so happened, Johnson was designated as a PI on one of the applications Miller was reviewing. Johnson mentioned their common scientific interests and went on to ask if any of the other applications on the study section involved members of the 'old gang.' Perhaps, he suggested, those applications could get favorable consideration from Miller and other reviewers.

[*...Continue reading*]()

- ## FY 2020 Ruth L. Kirschstein National Research Service Award (NRSA) Stipends, Tuition/Fees, and Other Budgetary Levels

Looking for the latest on Kirschstein National Research Service Award (NRSA) stipend levels, tuition/fees, and training related expenses? Check out NOT-OD-20-070 for full details.

- ## New “All About Grants” Podcast on Notices of Special Interest (NOSIs)

When dutifully scanning the weekly Table of Contents email for the NIH Guide for Grants and Contracts every Friday afternoon, have you found yourself wondering where all the Notices of Special Interest (NOSI) came from? And, what is a NOSI anyways?

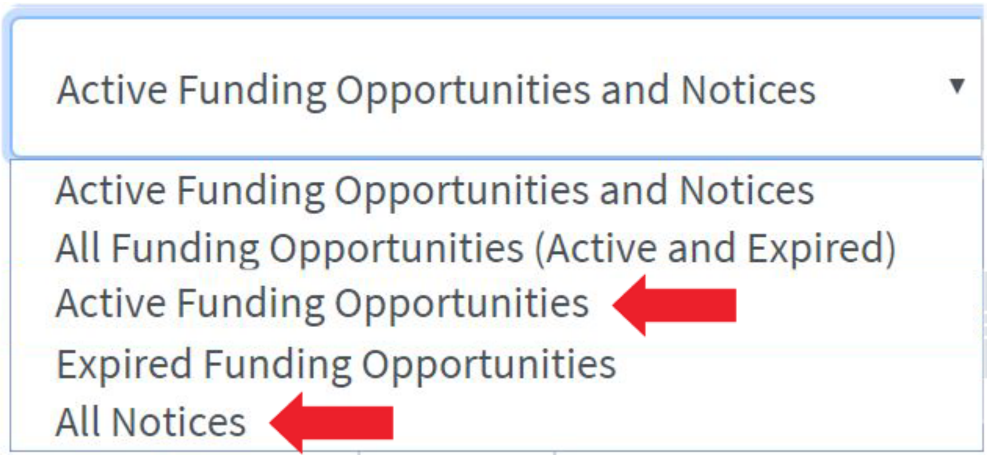
Dr. Jodi Black, Deputy Director of NIH’s Office of Extramural Research, joins us in this next installment of the NIH’s All About Grants podcast series to break down NOSIs (MP3 / Transcript). We discuss what they are and why NIH is using them, what you should know about them when putting together an application, who you should go to for questions, and why it is so important to include that NOSI number in Box 4B of your application.

Need a refresher on the alphabet soup of funding opportunity types touched on in the discussion? Check out our Understand Funding Opportunities page or listen to this classic 2011 All About Grants podcast to learn the difference between PAs, PARs, PASs, RFAs and parent announcements.

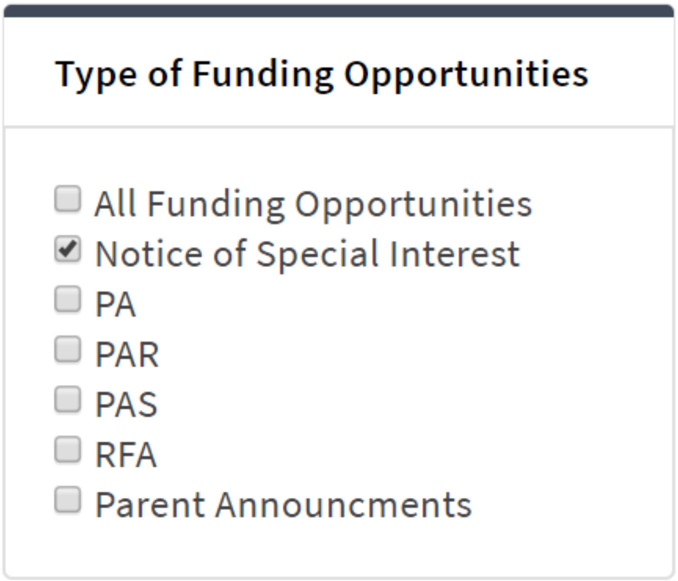
- ## Searching for Funding Just Got a Little Easier

What’s new with the NIH Guide for Grants and Contracts? In addition to faster, more precise search results, a few key filtering features have been updated.

Notices of Special Interest (NOSIs) are displayed in the results when searching either “Funding Opportunities” or “Notices.”

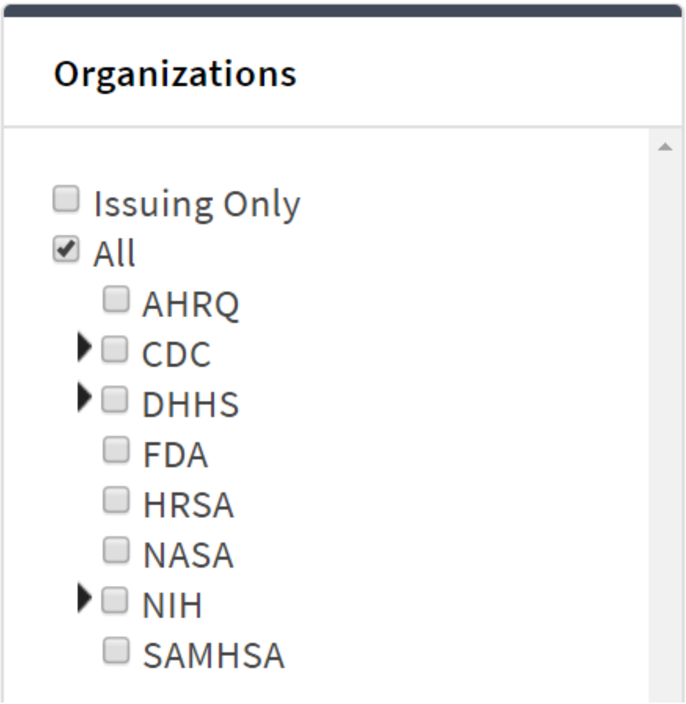


The “Type of Funding Opportunities” filter now includes “Notice of Special Interest.”


Type of Funding Opportunities

☐ All Funding Opportunities
☑ Notice of Special Interest
☐ PA
☐ PAR
☐ PAS
☐ RFA
☐ Parent Announcments

Quickly find notices by organization.



Organizations

☐ Issuing Only
☑ All
  ☐ AHRQ
  ☐ CDC
  ☐ DHHS
  ☐ FDA
  ☐ HRSA
  ☐ NASA
  ☐ NIH
  ☐ SAMHSA

NIH publishes funding opportunities and notices in the NIH Guide daily and recaps the week's postings every Friday afternoon via a Weekly NIH Funding Opportunities and Notices email to the NIH Guide LISTSERV. **Subscribe to receive the weekly updates or to follow us on Twitter today**!

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:

Funded by an Institutional Development Award (IDeA) from the National Institutes of Health.
or
*Funded by the LBRN (*P20 GM103424-18*) an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health.*

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