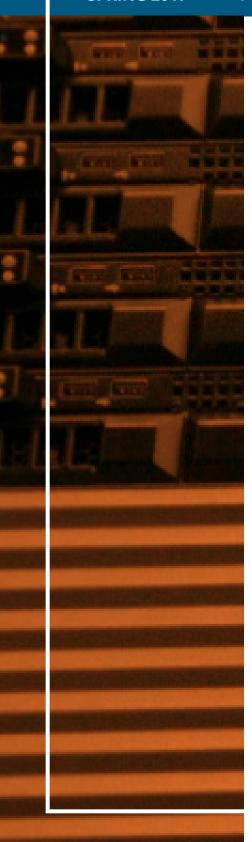


Center for Biomedical Research Support

Enabling Cutting-Edge Research that Changes the World

SPRING 2017 THE UNIVERSITY OF TEXAS AT AUSTIN



Welcome to the new Center for Biomedical Research Support (CBRS) at UT Austin!

It is our great pleasure to (re-)introduce our core facilities, which provide access to cutting-edge technology and expert advice to enhance your research. Whether you need light and electron microscopy or cell sorting; have a sequencing project in mind; require mass-spec expertise, maybe even a crystal structure; or want to custom-create a novel transgenic mouse for your research; we are here to assist and train you. You can also obtain a large

variety of supplies from the BioStore and from our freezer supply core. And you can utilize our new High Performance Computing infrastructure and collaborate with our bioinformatics consultants to turn the data we help you generate into new discoveries and insights that make our world a better place! Read here what we have to offer. We look forward to helping you!

- Hans Hofmann, Director

Proteomics Facility acquires new Fusion mass spec and Digest robot

With support from the Howard Hughes Medical Institute (via HHMI Investigator Tanya Paull) the Proteomics Facility has upgraded the Orbitrap Elite to an Orbitrap Fusion. All LC-MS/MS samples can take advantage of the shorter run times and achieve greater proteomic depth with the Fusion. Thousands of proteins are identified in a two-hour run on a cell lysate, making proteomics experiments routine with pipeline data processing for protein identification. The Fusion has sensitive detection for phosphorylation, acetylation, ubiquitination and other modifications. Quantitative proteomics experiments are enabled with spectral counts, peak area, or isotopic labeling and replicates are encouraged with new low hourly rates. Sample digest is easier, thanks to a new Intavis DigestPro robot. In-gel and solution digests are automated. Visit us in MBB 1.420 or email mperson@austin.utexas.edu to find out how to advance your research with proteomics!



DigestPro robot

TIP

Crosslinking analysis is now possible using Byonic software. Purified samples work best due to the large number of linkages and low stoichiometry. Heterodimer crosslinks were successfully identified for Jessie Zhang to distinguish between molecular conformations.

GSAF'S NEW AUTOMATION TO IMPROVE LIBRARY PREPARATIONS

The Genomic Sequencing and Analysis Facility (GSAF) constantly seeks to improve the services it provides and to deliver innovative new applications. The recently purchased Tecan Freedom Evo system for automated library preparation procedures is an important building block in this effort. Streamlining production of the standard libraries using automated liquid handling is expected to have several immediate benefits. First.



Tecan Freedom Fvo robot

Electronics Shop

Did you know UT has an Electronics Shop (contact: John Goutier at jgoutier@austin.utexas.edu) that can repair laboratory equipment and extend the life of your instruments?

Here's a tip to improve the performance of your centrifuge: periodically (ideally, EVERY day!) remove the rotor and clean mating surfaces with Ethanol. Apply a thin film of vacuum grease to spindle (check with manufacturer). Rotors actually adhere to the spindle when left on too long and if they cannot be removed, the centrifuge may be irreparable. Sounds simple, but is typically overlooked! Safe spinning!

the automated handling will greatly increase our capacity to produce standard libraries, while simultaneously reducing the turn-around time. Because the robotic procedures have excellent volumetric accuracy and pipetting precision, the day-to-day consistency between all the steps of the procedure will also improve, thus increasing the overall quality of our services.

An important indirect benefit of these automated procedures is that it will allow us to focus on helping investigators develop new custom library preparation methods. Since a vital part of the GSAF mission is to help UT researchers stay current with the new applications developed by other researchers in the field, this provides an opportunity to fulfill that mission more consistently and effectively. The research staff in the GSAF have extensive experience with molecular

biology techniques and a nuanced understanding of the different factors that influence successful library preparations for next-generation sequencing.

Email gsaf@utgsaf.org to set up a consultation.

TIP

Helpful tips for faster turn-around and better data for shared runs.

- Avoid using indices that may already be in use. Check the sequencing queues.
- If run types (e.g. SR50 or PE150) can be flexible, note it in the job description.
- Check quality of libraries before submitting them for sequencing.
- Request more reads than needed to complete a job.

BioResCo NEWS

The former ICMB SUPPLY CENTER has a new name! It is now the Biomedical Research Supplies Core (BioReSCo). By popular demand, we will be returning to internal billing for all the vendors. Look for emails to be sent out with more details.

Vendor News for 2017: IDT will be launching Ultramer ® RNA Oligos and Labeled CRISPR RNP and Cpf1, NEB will be offering new real-time PCR reagents Luna® Universal qPCR and RT-qPCR, Sigma will continue its Same Day Oligo service (restrictions apply) and ThermoFisher wants to remind everyone to sign up for an access badge.

For questions or to set up an account, contact Michelle Gadush at gadush@austin.utexas.edu.



POP-UP INSTITUTE NEWS: UNDERSTANDING INDIVIDUAL AND POPULATION VARIATION IN BIOLOGY, MEDICINE, AND SOCIETY

The Vice President for Research recently funded three Pop-Up Institutes in an effort to foster interdisciplinary research and collaborations across campus. CBRS Director Dr. Hans Hofmann leads one such Institute, called Seeing the Tree and the Forest, which will pursue the fundamental question: what are the causes and consequences of individual variation? Individuals differ in a myriad of ways, from their genetics to their lifetime health. Understanding this variation is critically important for promoting the success of individuals and the populations within which they live. The Seeing the Tree AND the Forest Pop-Up Institute brings together faculty and trainees from

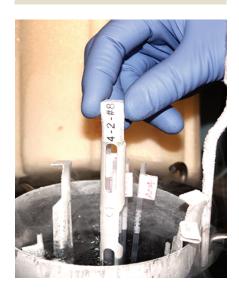
the Natural Sciences, Liberal Arts, Dell Medical School, and other institutions to collaborate across traditional research boundaries. Together, they aim to identify fundamental similarities and shared research goals across disciplines; establish a unique, integrative, and collaborative and research plan; and develop solutions to shared problems that currently limit progress.

The Pop-Up Institute will take place May 8-26, 2017. Contact Institute Coordinator Dr. Tessa Solomon-Lane with questions or for information on getting involved: (tksolomonlane@utexas.edu)

TIP Mouse Genetic Engineering Facility

The MGEF does both sperm cryopreservation and embryo cryopreservation. One advantage of sperm cryopreservation over embryo cryopreservation is that it requires fewer mice: 2 proven males of reproductive age for sperm freezing versus 15-20 or more male and female mice for embryo freezing.

For more information contact Dr. Bill Shawlot at wshawlot@austin.utexas.edu.





GET INVOLVEDS INDIVIDUAL & POPULATION VARIATION POP-UP INSTITUTE 2016

THE UNIVERSITY OF TEXAS AT AUSTIN

Biomedical Research Computing Facility

You probably already know what the CCBB bioinformatics consulting group (http://ccbb.utexas.edu/consultants.ht-ml) and our training program (http://ccbb.utexas.edu/training.html) can do for you. But did you know that we have just completed a major IT standarization project, with many significant accomplishments to celebrate? A vast hodge-podge of legacy IT equipment has been replaced with a standardized hardware and software architecture that can be efficiently and centrally managed.

The resulting Compute POD systems provide local compute and storage capabilities suitable for research computing workflows not addressed by TACC. POD compute servers offer a wide variety of pre-installed bioinformatics software (with flexibility for additions), in an interactive non-batch environment without execution time limits. POD storage servers offer high-capacity storage for research artifacts, coupled with automated backup and archiving processes.

We have now implemented 6 compute PODs, consisting of 18 compute servers, over 500 TB of local storage, and more than 400 TB of spinning disk backups. For information about how to participate in this architecture, contact Hans Hofmann (hans@utexas.edu) or Anna Battenhouse (abattenhouse@utexas.edu). For more technical information on the new POD architecture, visit https://wikis.utexas.edu/display/RCT-Fusers

Welcome our new light microscopy specialist!

Please join the Microscopy Facility in welcoming Anna Webb! Anna has over 10 years of experience helping users on high-end imaging instruments and is a welcome addition to our team.

Please stop by and say hello to Anna in MBB 1.426K anytime!



MICROSCOPY

The Microscopy and Imaging Core is a dynamic place where researchers from across campus analyze a variety of experimental samples using a suite of imaging technologies. Our goal is to support the research endeavors at The University of Texas by offering high-end, versatile imaging equipment and easy access to knowledgeable and helpful staff.

2016 was an exciting year at UT Austin and within the Microscopy facility. The inaugural year of the Dell Medical School opened the doors for an expanded research community as well as core facilities to support them. We are excited to announce that Facility Director Julie Hayes now serves in a joint role between the College of Natural Sciences and the Dell Medical School, as Director of the Microscopy and Imaging core and Director of Dell Med Cores.

An exciting new addition is coming to our FACS facility; a BD FACS Fusion Cell Sorter. Richard Salinas, our FACS

specialist, has worked hard to coordinate the addition of this instrument, which will be housed within a Bio-safety hood and will allow users to conduct BSL-3 experiments (our previous cell sorter was limited to BSL-2 experiments). The new instrument will be up and running in March!

We welcome your feedback on how the Microscopy core is serving your research needs or how we might better be able to support you. Please reach out anytime to Julie Hayes at juliehayes@utexas.edu

Bio Store Room

The Biostore provides many necessary lab and office supplies and is located in the Norman Hackerman Building in room 1.502.

Macromolecular Crystallography: When Structure is Needed

Would knowing the structure of a particular protein enhance your research? The Macromolecular Crystallography Facility (MCF) is staffed to carry out structural analysis on a service basis and to train and assist interested users in crystallization and collecting, processing, and interpreting X-ray diffraction data.

Obtaining quality crystals that diffract well in the X-ray beam is key to solving a crystal structure. Crystallization plates can be set up easily in the Facility using the Art Robbins Instruments Phoenix crystallization robot. Each plate contains from 96 to 288 crystallization experiments.

Our facility features two complete X-ray crystallography systems for collecting crystal diffraction data.

We also coordinate data collection from beamlines at the Advanced Light Source synchrotron at Lawrence Berkeley National Laboratory. Once a month, crystals are shipped to the synchrotron, and users here conduct their diffraction experiments remotely, taking advantage of the powerful synchrotron radiation.

To discuss your project, contact MCF manager Art Monzingo at art.monzingo@mail.utexas.edu.

Big Data Short Courses and Summer School are here!

ccbb.utexas.edu/ training.html

