
Library Resources for Teaching and Research in the Health Sciences

Renaë Barger, Associate Vice Chancellor, HSLS

Ansuman Chattopadhyay, Program Director for
Molecular Biology Information Service

University Libraries



University Library System



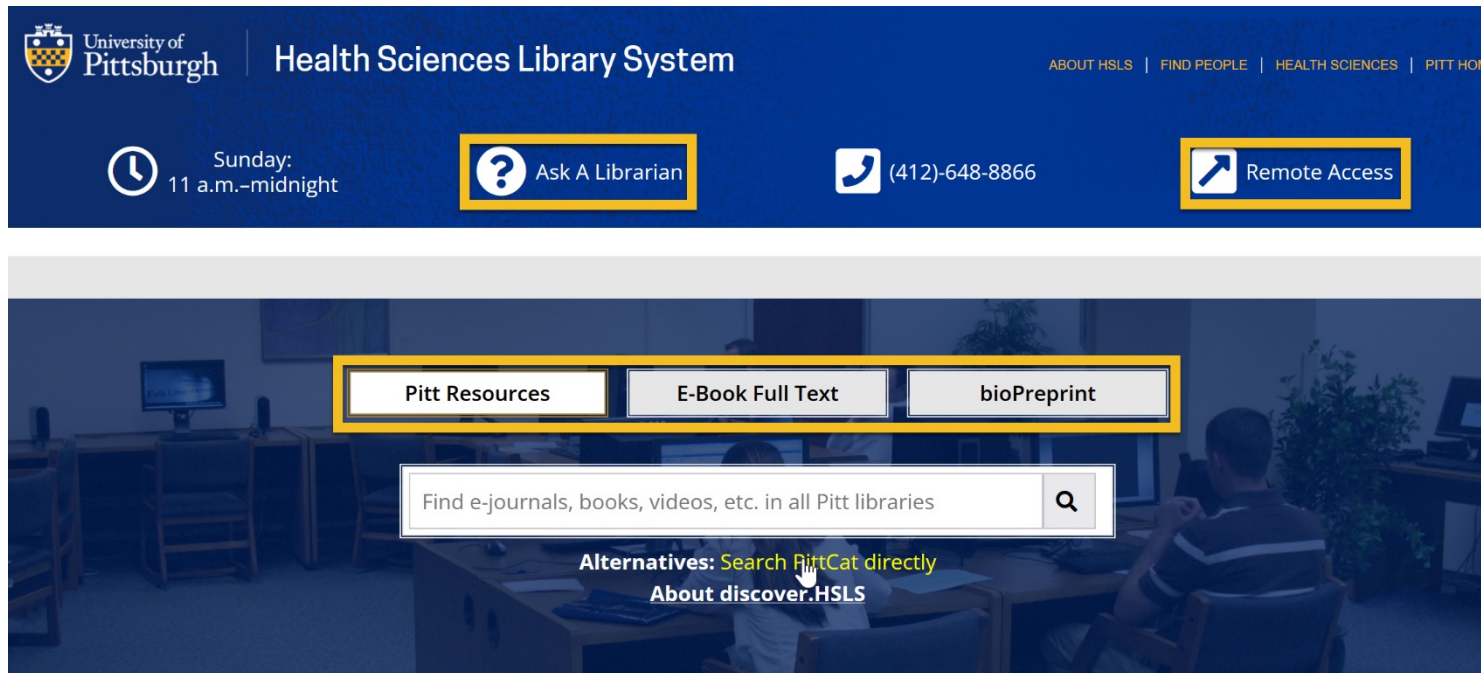
Barco Law Library



Health Sciences Library System

- Falk Library – Level M, Alan Magee Scaife Hall (School of Medicine West Wing)

Virtual Front Door: www.hsls.pitt.edu



The screenshot shows the top navigation bar of the HSLs website. It includes the University of Pittsburgh logo, the text "Health Sciences Library System", and navigation links for "ABOUT HSLs", "FIND PEOPLE", "HEALTH SCIENCES", and "PITT HOME". Below the navigation bar, there are four icons: a clock for "Sunday: 11 a.m.-midnight", a question mark for "Ask A Librarian", a phone for "(412)-648-8866", and a magnifying glass for "Remote Access". The main content area features a search bar with the text "Find e-journals, books, videos, etc. in all Pitt libraries" and a search icon. Above the search bar are three buttons: "Pitt Resources", "E-Book Full Text", and "bioPreprint". Below the search bar, there are two links: "Alternatives: Search PittCat directly" and "About discover.HSLs".

News & Announcements

[HSLs Update Newsletter for August](#)
The August issue of the HSLs Update newsletter

...

[Reserve a Group Study Room](#)

Services

[Instruction](#)
[Consultation](#)
[Liaisons](#)
[MolBio Information Service](#)
[Scholarly Publishing](#)
[Advanced Literature Searching](#)

Resources

[PubMed](#)
[E-journals A-Z](#)
[Databases A-Z](#)
[E-books by Subject](#)
[MolBio Software](#)
[Exam Review](#)

HSLS Liaison Librarians



Resources for Teaching



Customized Instruction for Your Class or Department

<https://www.hsls.pitt.edu/instruction/class-catalog>

Topics:

- Evidence-based searching
- Research data management
- Data visualization
- Research Impact
- Instructional and visual design
- Next generation sequencing

Class Examples:

- Health Equity Research
- Preparing for the NIH Data Management and Sharing Plan
- Visualizing Research Impact
- Scientific Drawing with Illustrator
- Data Analysis using CLC Genomics Workbench
- Citizen Health Science: A Tool for Teaching
- Identifying & Combatting Health Misinformation
- Wikipedia for Health Sciences Students

Citation Management at HSLS

A citation manager can help you store, organize, and cite references.

HSLS offers support for citation management in a variety of ways:

- Classes
- Written guides
- Interactive tutorials
- Our citation management librarians are also happy to answer your questions or teach a customized class for your class, lab, or other group

HSLS provides support for three citation managers:



EndNote

- Web and desktop versions
- Free to Pitt students and faculty; \$50 for staff



Sciwheel

- Web-based
- Free for all Pitt affiliates



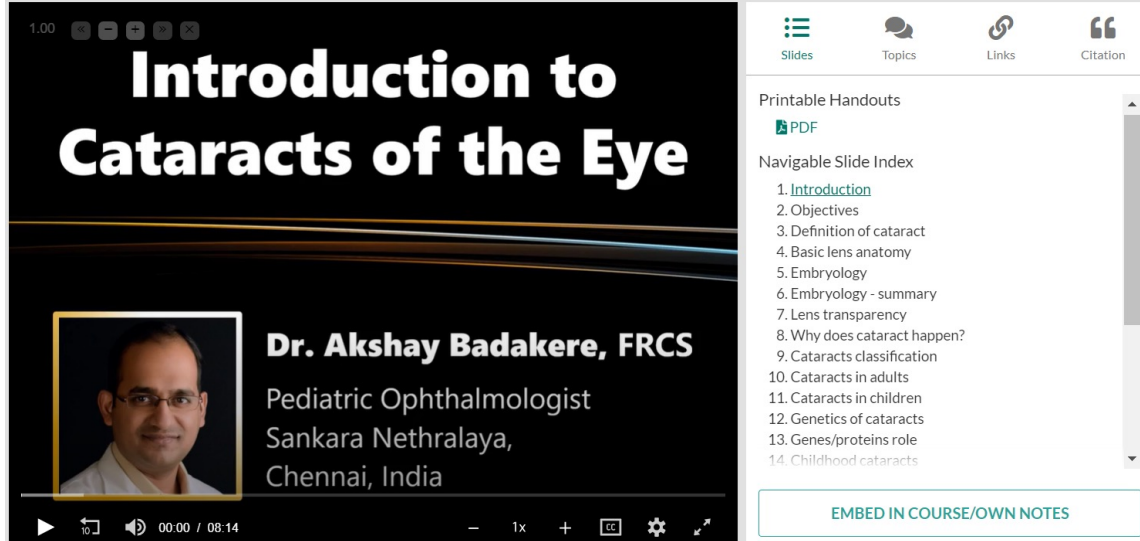
Zotero

- Web, desktop, and iOS versions
- Free and open source

Multimedia Content

<https://www.hspls.pitt.edu/streaming-media>

- Visual guides
- Video protocols
- Documentaries
- Recorded Lectures
- Procedures



Introduction to Cataracts of the Eye

Dr. Akshay Badakere, FRCS
Pediatric Ophthalmologist
Sankara Nethralaya,
Chennai, India

Printable Handouts
PDF

Navigable Slide Index

1. [Introduction](#)
2. Objectives
3. Definition of cataract
4. Basic lens anatomy
5. Embryology
6. Embryology - summary
7. Lens transparency
8. Why does cataract happen?
9. Cataracts classification
10. Cataracts in adults
11. Cataracts in children
12. Genetics of cataracts
13. Genes/proteins role
14. Childhood cataracts

EMBED IN COURSE/OWN NOTES

Sample video from HSTalks with slides and index. Content from HSTalks can be embedded directly into a course LMS.

EXPAND YOUR COURSE CURRICULUM WITH THE **HSLS VR LEARNSPACE**

AVAILABLE APPS INCLUDE:

ANATOMY & PHYSIOLOGY ATLASES

CLINICAL SIMULATIONS

3D MEDICAL IMAGING

AND MORE!

hsls.libguides.com/vr



Health Sciences Library System



ENHANCE YOUR TEACHING WITH HSLS VR LEARNSPACE'S

ANATOMY X

**5,000 DETAILED
ANATOMICAL
MODELS**

**INCLUDES
ANATOMY
FUNCTIONS,
ETYMOLOGY,
AND MORE**

**CUSTOMIZABLE
LEARNING
EXPERIENCES**



Learn more and contact us at
hsls.libguides.com/vr

Resources for Research



Data Services



- **Write** a data management or sharing plan



- **Comply** with data sharing policies



- **Organize & describe** your research data and code



- **Identify** appropriate data repositories



- **Create** effective data visualizations



- **Locate** existing datasets for reuse



- **Preserve** your data and code for long-term access

Measuring Research Impact

- Discovering the impact of your work
- Tools for publication reporting
- Identifying impactful journals in your field
- Increasing your research visibility
- Using research metrics responsibly



Image from [The University of Sheffield Library](#)

Scholarly Publishing and Communication



- Selecting and evaluating journals



- Open access publishing



- Interpreting funder and journal policies



- Promoting your research



- Author rights: copyright, fair use, licensing



- Communicating your research impact

Institutional Animal Care and Use Committee (IACUC) Support

Literature searches for the “3R’s” are required for some IACUC protocols



- **Reduction**—Minimize the number of animals used, without jeopardizing statistical validity



- **Refinement**—Employ techniques that reduce pain & distress



- **Replacement**—Substitute animals with non-animal methods (i.e., computer simulation) or lower animal species

HSLs Systematic Review Program

- Who's eligible?
 - Faculty with primary appointments in schools of the health sciences
 - Residents/fellows affiliated with UPMC Office of GME
- What is required?
 - Submission of a detailed protocol
 - Protocol undergoes scientific review by HSLs librarians
- Be aware – a protocol may be declined due to:
 - Concerns about project feasibility or timeline
 - Limited librarian availability

Create a Document Delivery Account

Home / Services

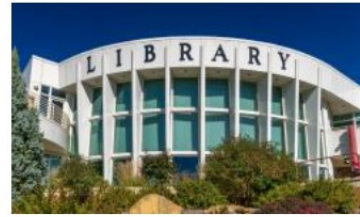

Document Delivery

HSLs Document Delivery Service provides scholarly, health sciences materials including journal articles, book chapters and print based books that are unavailable in our collection.

The Document Delivery Service also facilitates requests for books and journals currently housed off site during Falk Library's [construction project](#)

We serve the faculty, students, and staff of the University of Pittsburgh schools of the health sciences: Dental Medicine, Medicine, Nursing, Pharmacy, Public Health, and Health and Rehabilitation Sciences and UPMC residents and fellows.

DOCUMENT DELIVERY QUESTIONS? PLEASE CONTACT US



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[Ligon to Document Delivery](#)

[Information for other Libraries](#)

Click [Create a Document Delivery Account](#) and follow directions on that page.

HSLs Molecular Biology Information Service

Ansuman Chattopadhyay, PhD

Program Director for Molecular Biology Information
Service

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PowerPoint Slides: t.ly/PPNo1





Software Licensing



Bioinformatics Training Workshops



Web Tools



Consultations



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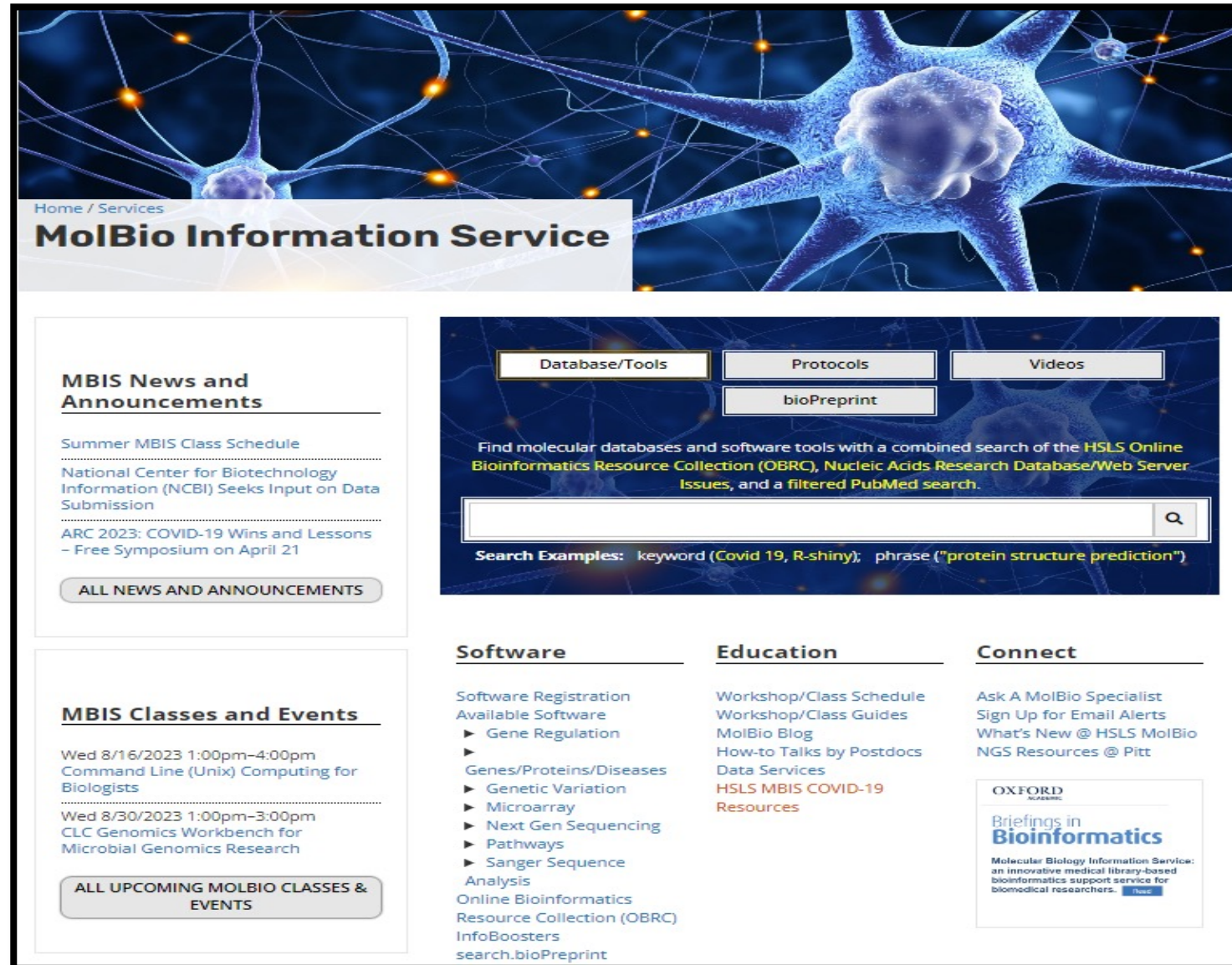


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Web Page



Home / Services

MolBio Information Service

MBIS News and Announcements

[Summer MBIS Class Schedule](#)

[National Center for Biotechnology Information \(NCBI\) Seeks Input on Data Submission](#)

[ARC 2023: COVID-19 Wins and Lessons – Free Symposium on April 21](#)

[ALL NEWS AND ANNOUNCEMENTS](#)

MBIS Classes and Events

Wed 8/16/2023 1:00pm–4:00pm
Command Line (Unix) Computing for Biologists

Wed 8/30/2023 1:00pm–3:00pm
CLC Genomics Workbench for Microbial Genomics Research

[ALL UPCOMING MOLBIO CLASSES & EVENTS](#)

[Database/Tools](#) [Protocols](#) [Videos](#)
[bioPreprint](#)

Find molecular databases and software tools with a combined search of the **HSLs Online Bioinformatics Resource Collection (OBRC)**, **Nucleic Acids Research Database/Web Server Issues**, and a **filtered PubMed search**.

Search Examples: keyword (Covid 19, R-shiny); phrase ("protein structure prediction")

Software

- Software Registration
- Available Software
 - ▶ Gene Regulation
 - ▶ Genes/Proteins/Diseases
 - ▶ Genetic Variation
 - ▶ Microarray
 - ▶ Next Gen Sequencing
 - ▶ Pathways
 - ▶ Sanger Sequence Analysis
- Online Bioinformatics Resource Collection (OBRC)
- InfoBoosters
- [search.bioPreprint](#)

Education

- Workshop/Class Schedule
- Workshop/Class Guides
- MolBio Blog
- How-to Talks by Postdocs
- Data Services
- [HSLs MBIS COVID-19 Resources](#)

Connect

- Ask A MolBio Specialist
- Sign Up for Email Alerts
- What's New @ HSLs MolBio
- NGS Resources @ Pitt

OXFORD
ACADEMIC

Briefings in Bioinformatics

Molecular Biology Information Service: an innovative medical library-based bioinformatics support service for biomedical researchers. [View](#)

Licensed Software

HSL MolBio Available Software

Bioinformatics software available to Pitt researchers.

Home

Resources by Topic

Resources A - Z

Which Tool Should I Use To...

Registration

CLC Genomics Workbench

CLC Main Workbench

Correlation Engine

HGMD

Ingenuity Pathway Analysis (IPA)

Lasergene

Partek Flow

Partek Genomics Suite

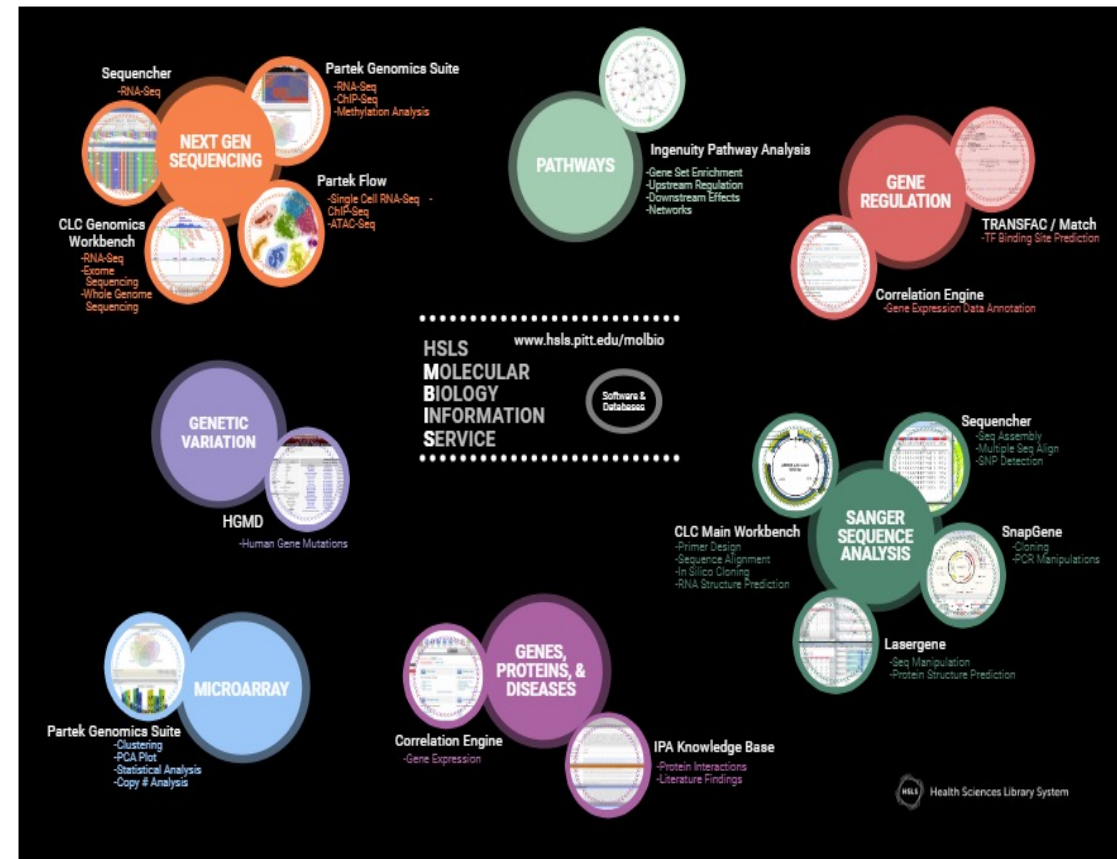
Sequencher

SnapGene

TRANSFAC/Match

For additional information, contact:

Resources by Topic



Bioinformatics Workshops

scRNA-Seq Data Analysis using PartekFlow

- Wed 5/31/2023, 1:00pm to 3:00pm

IPA and Correlation Engine – A Comprehensive Approach to Pathway Enrichment Analysis

- Wed 6/7/2023, 1:00pm to 3:00pm

Data Wrangling in R

- Tue 6/13/2023, 12:00pm to 1:00pm

All of Us Researcher Workbench – Terminology and Data Models Training

- Tue 6/13/2023, 1:00pm to 3:00pm

Data Visualization in R using ggplot2

- Tue 7/11/2023, 12:00pm to 1:00pm

All of Us Researcher Workbench – EHR and Survey Data Analysis

- Tue 7/11/2023, 1:00pm to 2:00pm

Single cell Multiomics Analysis with Partek Flow

- Wed 7/12/2023, 1:00pm to 3:00pm

Transcriptome Analysis – From GEO Data Mining to Submission

- Wed 7/26/2023, 1:00pm to 3:00pm

Command Line (Unix) Computing for Biologists

- Wed 8/16/2023, 1:00pm to 4:00pm

CLC Genomics Workbench for Microbial Genomics Research

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Bioinformatics Workshops Guide Pages

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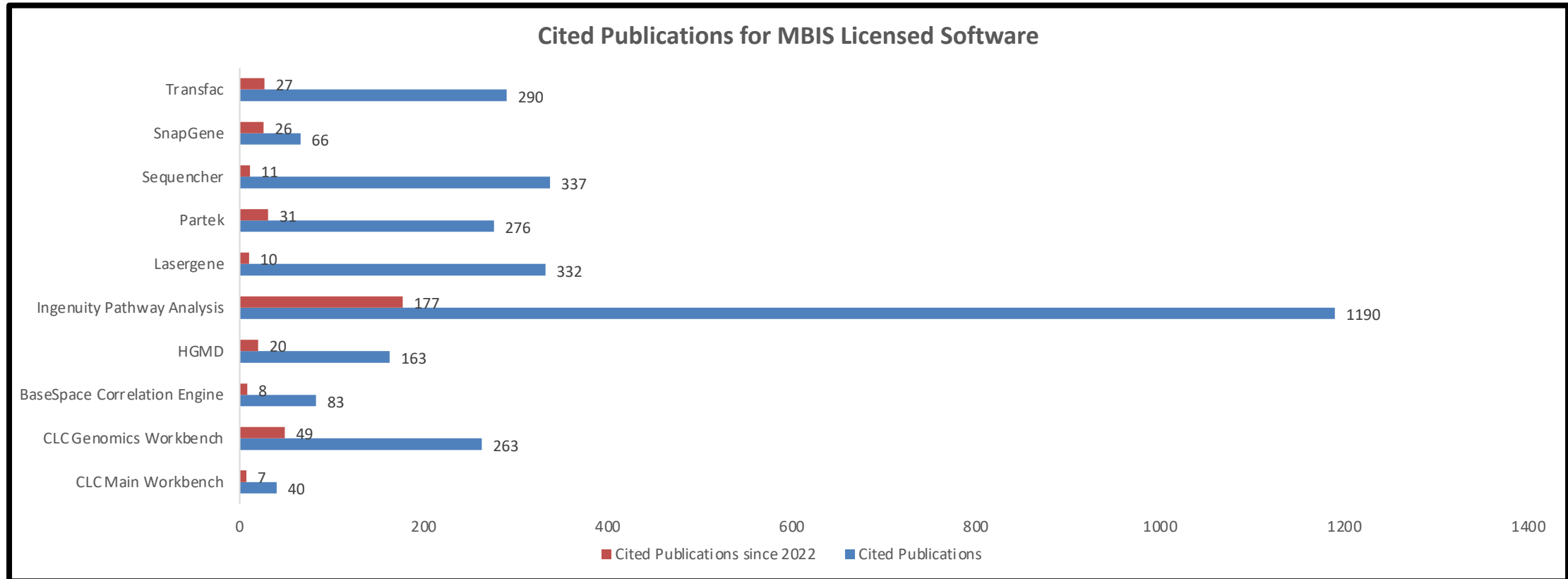
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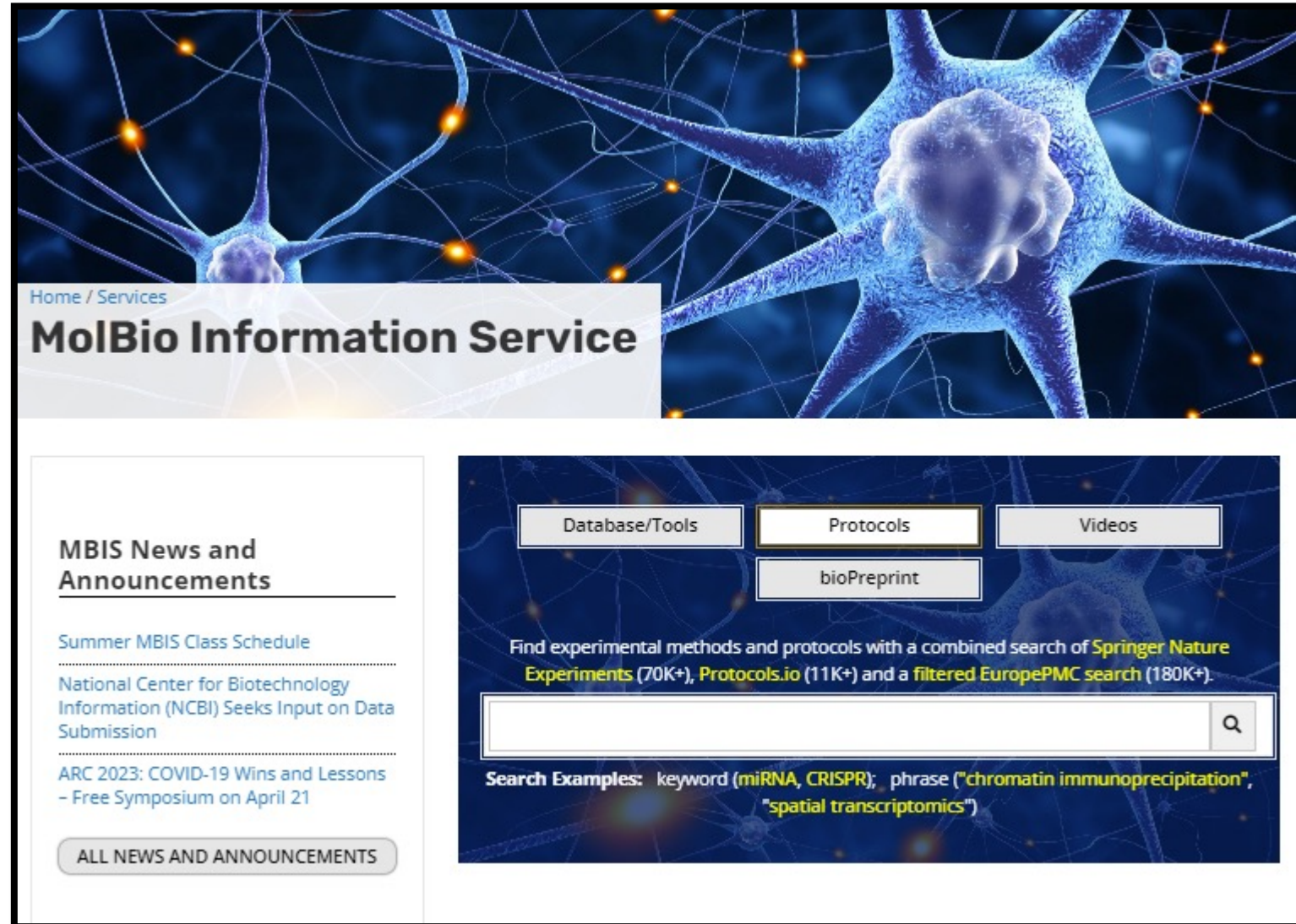
- Wed 8/30/2023, 1:00pm to 3:00pm

Since 2022, University of Pittsburgh researchers have referenced HSLS-licensed commercial software in

313 papers, as tracked by Google Scholar.



Life Sciences Search Engine



Home / Services

MolBio Information Service

MBIS News and Announcements

- Summer MBIS Class Schedule
- National Center for Biotechnology Information (NCBI) Seeks Input on Data Submission
- ARC 2023: COVID-19 Wins and Lessons - Free Symposium on April 21

ALL NEWS AND ANNOUNCEMENTS

Database/Tools Protocols Videos bioPreprint

Find experimental methods and protocols with a combined search of **Springer Nature Experiments** (70K+), **Protocols.io** (11K+) and a **filtered EuropePMC search** (180K+).

Search Examples: keyword (**miRNA**, **CRISPR**); phrase ("**chromatin immunoprecipitation**", "**spatial transcriptomics**")

Search.BioPreprint

Refine your preprints search via Topic Clusters to discover cutting edge, yet-to-be published or peer-reviewed biomedical research articles retrieved from Europe PMC.

Search Examples: keyword ([COVID-19](#)); phrase ("[Coronavirus disease](#)")

Use quotation marks for searches with 2 words or more.

Results are sorted by date of publication (most recent on top; maximum of 1000; 25 per page). Resources include: [AAS Open Res](#), [bioRxiv](#), [ChemRxiv](#), [F1000Res](#), [Gates Open Res](#), [HRB Open Res](#), [medRxiv](#), [MNI Open Res](#), [PeerJ Preprints](#), [Preprints.org](#), [Research Square](#), [Wellcome Open Res](#).

Results 1-2 of 2 in Enabled Large Language Models

Topic Clusters

Top 400 Results remix

- + SARS-CoV-2 (125)
- + Protein complexes (28)
- + Protein design (25)
- Language Model (18)
 - + Single (8)
 - **Enabled Large Language Models (2)**
 - Existing Sequence-Based Methods Have Limited (2)
 - Esmfold, Omegafold (2)
 - SARS-CoV-2 (2)
 - Other Topics (2)
- + Human proteins (17)
- + Model quality assessment (19)
- + Distance prediction (22)
- + Annotation (11)
- + Graph neural networks (11)
- + Cryo, Electron microscopy (11)
- + Homology search (7)
- + RNA structure (6)
- + Mutations On Protein (8)
- + Contact Map (11)
- + Protein-ligand complexes (6)
- + NMR data (9)
- + Cancer (6)
- + Residue-residue contact prediction (10)
- + Accurate contact predictions (9)

1. [ProtT5: Bilingual Language Model for Protein Sequence and Structure](#) new window

Advanced Artificial Intelligence (AI) enabled large language models (LLMs) to revolutionize Natural Language Processing (NLP). Their adaptation to protein sequences spawned the development of powerful protein language models (pLMs). Concurrently, AlphaFold2 broke through in protein structure prediction. For the first time, we can now systematically and comprehensively explore the dual nature of proteins that act and exist as three-dimensional (3D) machines and evolve in linear strings of one-dimensional (1D) sequences. Here, we leverage pLMs to simultaneously model both modalities by combining 1D sequences with 3D structure in one generic model. For this, we encode protein structures as token sequences using the 3Di-alphabet introduced by Foldseek. The resulting "structure-sequence" representation is processed by a pLM to extract features and patterns. Toward this end, we constructed a non-redundant dataset from AlphaFoldDB and fine-tuned an existing pLM (ProtT5) to translate between 3Di and amino acid sequences. As a proof-of-concept for our novel approach, dubbed Protein structure-sequence T5 (ProtT5), we showed improved performance for subsequent prediction tasks, and for "inverse folding", namely the generation of novel protein sequences adopting a given structural scaffold ("fold"). Our work showcased the potential of pLMs to tap into the information-rich protein structure revolution fueled by AlphaFold2. It paves the way for the development of tools optimizing the integration of this vast 3D structure data resource, opening new research avenues in the post AlphaFold2 era. We released our model at <https://github.com/mheininger/ProtT5>.

Date: 2023-07-25

Authors: Heininger M, Weissenow K, Sanchez JG, Henkel A, Steinegger M, Rost B.

Ref: bioRxiv

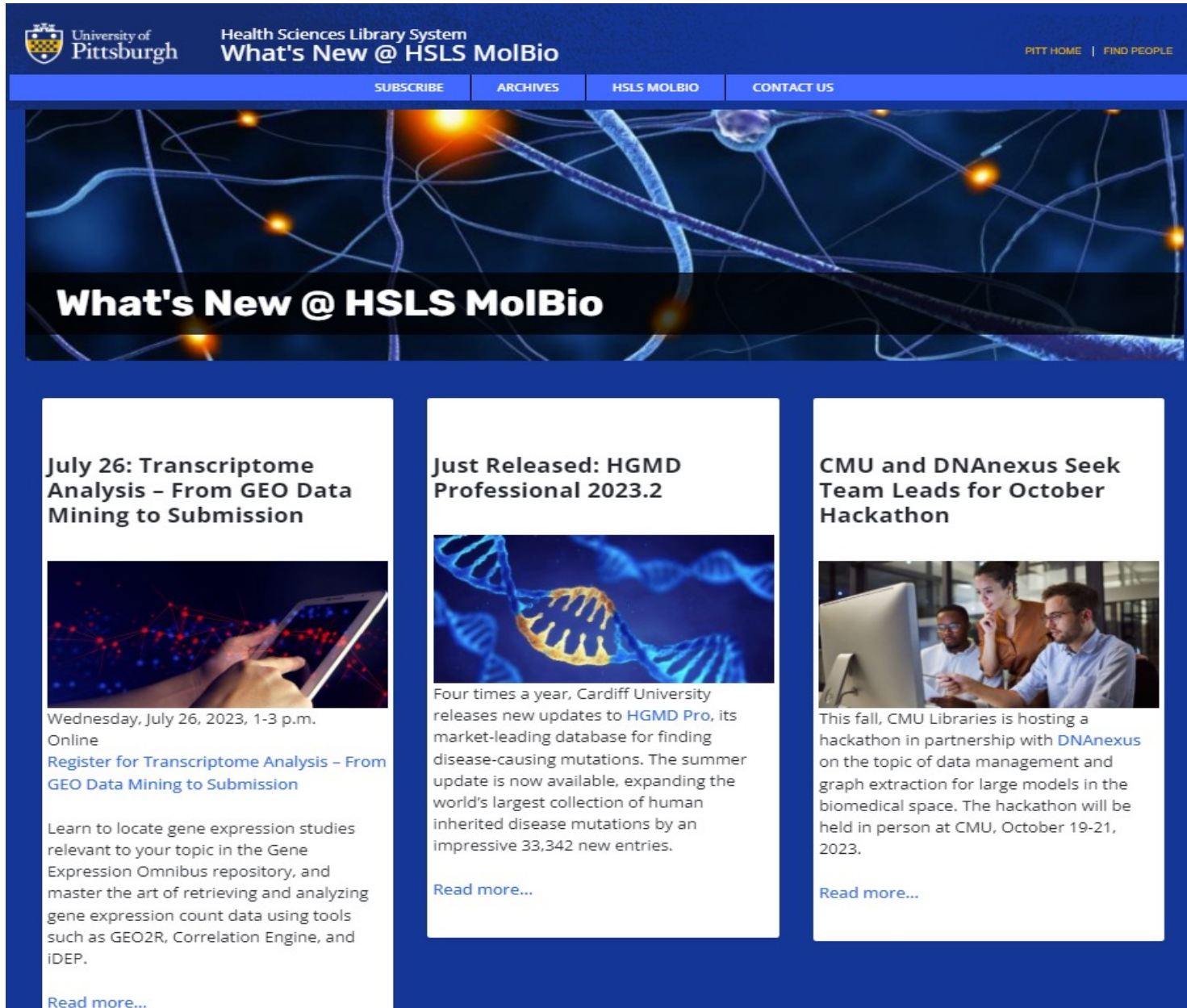
<https://doi.org/10.1101/2023.07.23.550085> - Europe PMC

2. [Evolutionary-scale prediction of atomic level protein structure with a language model](#) new window

Artificial intelligence has the potential to open insight into the structure of proteins at the scale of evolution. It has only recently been possible to extend protein structure prediction to two hundred million cataloged proteins. Characterizing the structures of the exponentially growing billions of protein sequences revealed by large scale gene sequencing experiments would necessitate a break-through in the speed of folding. Here we show that direct inference of structure from primary sequence using a large language model enables an order of magnitude speed-up in high resolution structure prediction. Leveraging the insight that language models learn evolutionary patterns across millions of sequences, we train models up to 15B parameters, the largest language model of proteins to date. As the language models are scaled they learn information that enables prediction of the three-dimensional structure of a protein at the resolution of individual atoms. This results in prediction that is up to 60x faster than state-of-the-art while maintaining resolution and accuracy. Building on this, we present the ESM Metagenomic Atlas. This is the first large-scale structural characterization of metagenomic proteins, with more than 617 million structures. The atlas reveals more than 225 million high confidence predictions, including millions whose structures are novel in comparison with experimentally determined structures, giving an unprecedented view into the vast breadth and diversity of the structures of some of the least understood proteins on earth.

Date: 2023-07-21

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What's New @ HSLs MolBio

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What's New @ HSLs MolBio

July 26: Transcriptome Analysis - From GEO Data Mining to Submission



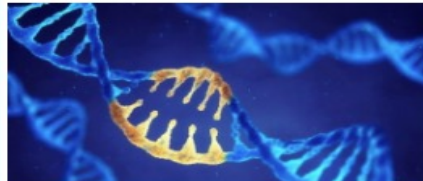
Wednesday, July 26, 2023, 1-3 p.m.
Online

[Register for Transcriptome Analysis - From GEO Data Mining to Submission](#)

Learn to locate gene expression studies relevant to your topic in the Gene Expression Omnibus repository, and master the art of retrieving and analyzing gene expression count data using tools such as GEO2R, Correlation Engine, and iDEP.

[Read more...](#)


Just Released: HGMD Professional 2023.2



Four times a year, Cardiff University releases new updates to **HGMD Pro**, its market-leading database for finding disease-causing mutations. The summer update is now available, expanding the world's largest collection of human inherited disease mutations by an impressive 33,342 new entries.

[Read more...](#)

CMU and DNAnexus Seek Team Leads for October Hackathon



This fall, CMU Libraries is hosting a hackathon in partnership with **DNAnexus** on the topic of data management and graph extraction for large models in the biomedical space. The hackathon will be held in person at CMU, October 19-21, 2023.

[Read more...](#)

One-on-One Consultations

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Ansuman Chattopadhyay
Program Director
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[ALL UPCOMING MOLBIO CLASSES & EVENTS](#)

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Search Examples: keyword (Covid 19, R-shiny); phrase ("proteomics")

Software

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- Available Software
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 - ▶ Genes/Proteins/Diseases
 - ▶ Genetic Variation
 - ▶ Microarray
 - ▶ Next Gen Sequencing
 - ▶ Pathways
 - ▶ Sanger Sequence Analysis
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- InfoBoosters

Education

- Workshop/Class Schedule
- Workshop/Class Guides
- MolBio Blog
- How-to Talks by Postdocs
- Data Services
- HSLs MBIS COVID-19 Resources**

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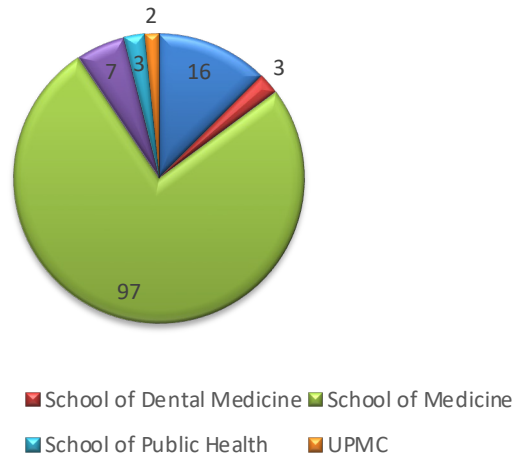
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Briefings in Bioinformatics

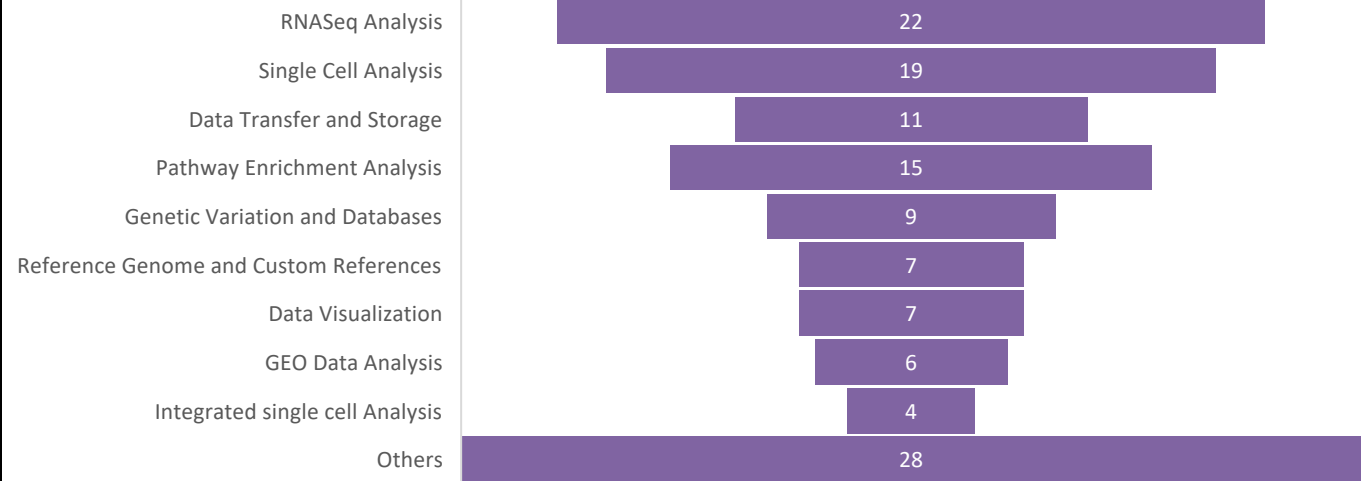
Molecular Biology Information Service: an innovative medical library-based bioinformatics support service for biomedical researchers. [Read](#)

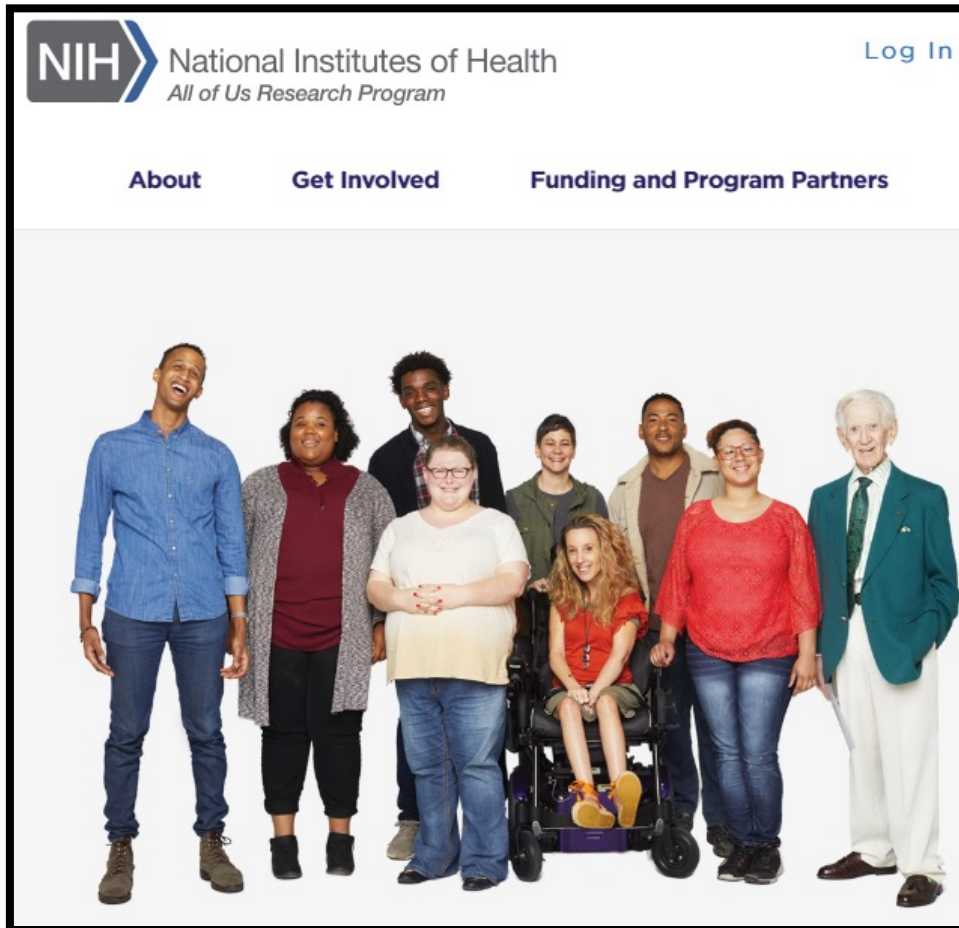
In FY2023, MBIS conducted 128 individual consulting sessions for 144 researchers.

MBIS Consultation Sessions by Schools



MBIS Consultation Sessions by Topics





Training Initiatives for *All of Us Research Workbench*

Workshops

- Introduction to AoU Research Workbench
- Terminology and Data Models Training
- EHR and Survey Data Analysis

Summer Course for MD/Ph.D. students

- Translational Biomedical Analytics:
- Exploring, Analyzing, and Innovating with the All of Us (AoU) Research Program

Code templates

In-person Consultations
Friday Office Hours

Mission: Providing bioinformatics resources via software procurement, implementation, and training to assist biomedical scientists with solving their research questions.

Review > [Brief Bioinform.](#) 2020 May 21;21(3):876-884. doi: 10.1093/bib/bbz035.

Molecular Biology Information Service: an innovative medical library-based bioinformatics support service for biomedical researchers



Ansuman Chattopadhyay¹, Carrie L Iwema¹, Barbara A Epstein¹, Adrian V Lee¹, Arthur S Levine¹

Affiliations + expand

PMID: 30949666 DOI: [10.1093/bib/bbz035](https://doi.org/10.1093/bib/bbz035)

FULL TEXT LINKS

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