

The Human BioMolecular Atlas Common Fund Program (HuBMAP)

Pre-Application Webinar

October 1st, 2021, 12:00 - 1:00 PM EDT

To submit questions during the webinar please use the Q&A box. We will address questions at the end of the presentation. Following the webinar, questions can be sent to HuBMAP@mail.nih.gov



Agenda

- Common Fund & HuBMAP Program — 5 mins
- Tissue Mapping Center RFA— 15 mins
- Demonstration Projects RFA — 10 mins
- Q&A — 30 mins

What is the NIH Common Fund?

- Supports a set of **trans-NIH** scientific programs;
- **Spurs subsequent biomedical advances** that otherwise would not be possible without an initial strategic investment;
- Short-term (5-10 year), **goal-driven** programs focused on developing specific deliverables (data, tools, technologies, etc.) to **catalyze research**;
- Managed by the **Office of Strategic Coordination** within the NIH Office of the Director, in partnership with the NIH Institutes and Centers.



Common Fund programs are intended to benefit the entire biomedical research community



The Human BioMolecular Atlas Program (HuBMAP)

Vision: Catalyze development of an open, global framework for comprehensively mapping the human body at a cellular resolution

HuBMAP Goals

1. Accelerate the development of the next generation of tools and techniques for constructing high resolution spatial tissue maps
2. Generate foundational 3D human tissue maps
3. Establish an open data platform
4. Coordinate and collaborate with other funding agencies, programs, and the biomedical research community
5. Support projects that demonstrate the value of the resources developed by the program

[Nature 2019: 574, 187–192](#)

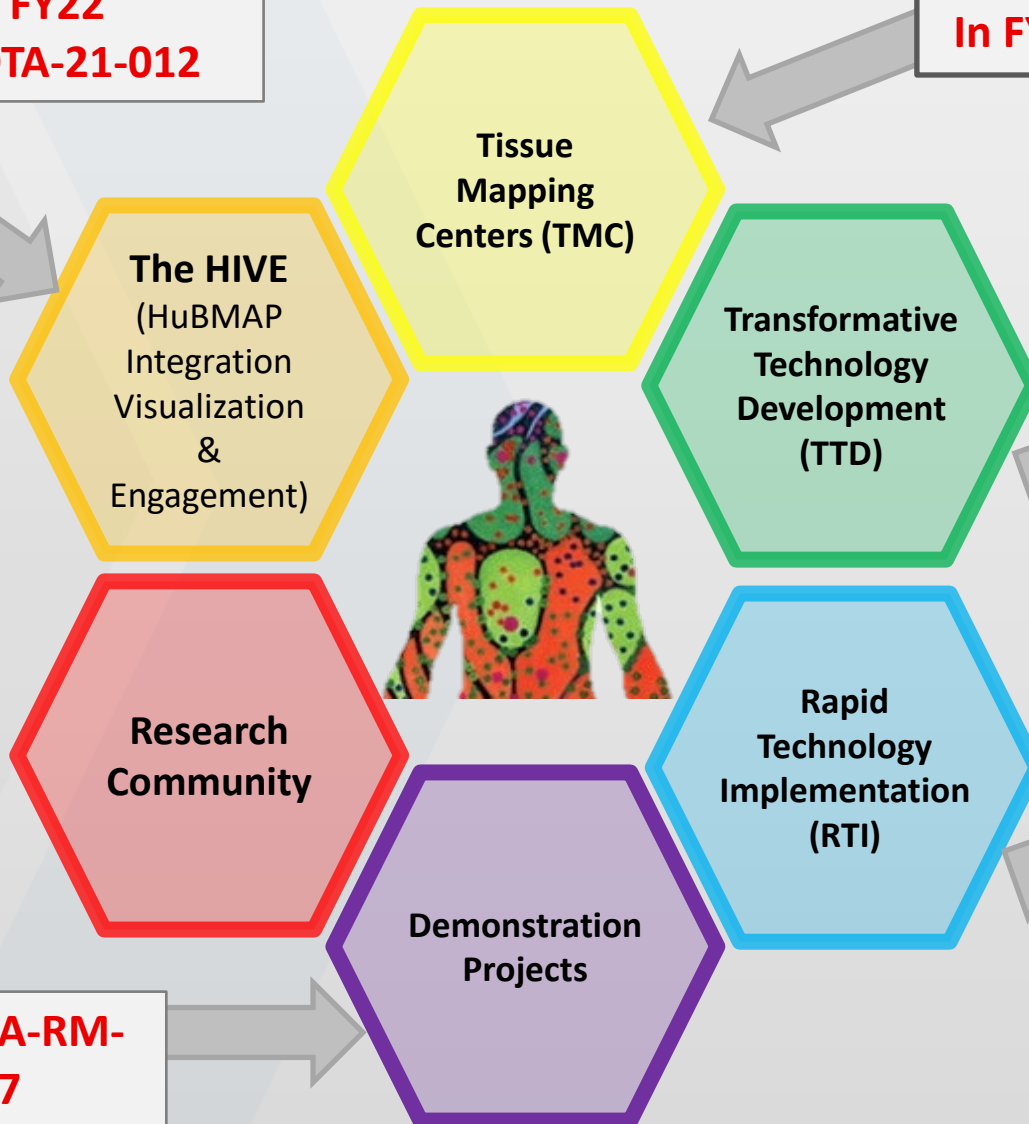
<https://www.nature.com/articles/s41586-019-1629-x>

What makes HuBMAP unique?

- Focus: comprehensive 3D single cell-level maps (multimodal, multi-scale, intra- and extra-cellular) of several normal human tissues; not a survey and not all tissues
- Outcome: relationship between tissue organization and function (functional measures, functional units, network analysis)
- To understand: inter-individual variability, changes across the lifespan (CCF to integrate data into common maps)

In FY18, 1x Infrastructure, 2x Tools & 2x Mapping OT2 awards. **New FY22 announcement: OTA-21-012**

In FY18, 5x U54 Centers funded for 4 years. In FY20, 6x U54 centers; **In FY22: RFA-RM-21-026**



In FY18, 4x UG3 / awards for 2+2 years. In FY20 +5x awards.

In FY19, 4 UH3 awards to accelerate technology implementation.

In FY22: RFA-RM-21-027

Plan for Enhancing Diverse Perspectives (PEDP)

- PEDP is **required** for all applications
- Applicants are strongly encouraged to read the ROA instructions carefully and view the available PEDP guidance material: <https://commonfund.nih.gov/HuBMAP/generalfaq>
- Examples that **enhance inclusivity** include:
 - Inclusion of personnel (MPIs, PIs, Co-Is ...) from groups historically underrepresented.
 - Appropriate training at different career stages.
 - Outreach to community groups and other stakeholders.
 - Use research infrastructure for opportunities to undertake research
 - Suitable evaluation criteria for progress?

Administrative Details for All Awards

- **NIH Involvement:** There will be substantial NIH programmatic involvement in individual projects and HuBMAP Consortium activities
- **Consortium:** Abide by Consortium policies for rapid sharing, collaborative projects, regular meetings, changing goals, and milestones [<https://hubmapconsortium.org/policies/>]
- **Budgeting:** Applicants are strongly encouraged to set aside ~20% of their budget for Consortium activities, resource sharing, outreach, and meeting attendance as part of their proposed budget. NIH may modify budgets, specific aims and milestones before award.
- **RFA:** These are one-off announcements with no revisions or appeals.
- **Eligibility:** Includes traditional NIH applicants, foreign components, for-profit organizations, and NIH intramural program are eligible.
- **LOIs:** Not required, but strongly encouraged.
- **Review:** SEPs; Please pay attention to review criteria in the RFA.



RFA-RM-21-026 Tissue Mapping Centers for HuBMAP (U54)

<https://grants.nih.gov/grants/guide/rfa-files/rfa-rm-22-026.html>

Zorina Galis (NHLBI)

Tissue Mapping Centers (TMC)

- **Objective:** Generate high-resolution, multi-parameter, 3D biomolecular maps of non-diseased human organs and organ systems.
- **Period:** Up to 4 years
- **Budget:** 5-7 awards, \$12M in FY22, \$13.5M in FY23, \$15M in FY24 and \$3M in FY25.
- **Responsiveness:** NIH will prioritize supporting Centers that will build an atlas for the following organs: kidney, colon, spleen, thymus, lungs, bladder, skin, heart, female reproductive organs, eyes, bone and bone marrow, pancreas, and liver. In addition, the NIH expects to support at least one Center focused on mapping the vasculature, lymphatic, and peripheral nervous system in multiple organs.
- **Non-responsive projects:**
 - lacking plans to obtain spatial data information regarding the organization of cellular and non-cellular tissue components
 - Not proposing a minimum core set of 3 assays (multiplexed immunoassay, single cell sequencing, at least one other high spatial resolution assay)
 - Proposing to study bodily fluids, dissociated cells, diseased, non-human tissue

Tissue Mapping Centers (TMC)

Multi-component cooperative agreements:

- **Overall Vision & Coordination** describe vision, general TMC admin duties and for coordinating activities and sharing expertise and resources [6 pages]
- **Data Analysis Core (DAC)** responsible for data annotation, curation, and analysis [6 pages]
- **Organ-Specific Projects (OSPs)** responsible for generating high quality tissue maps using multiple assays for one organ or component of an organ system. A Center should focus on a single organ [12 pages]
- **Other:** Plan for Enhancing Diverse Perspectives (PEDP)

Tissue Mapping Centers (TMC)

Programmatic priorities:

- Approaches that maximize the volume of non-diseased human tissue that will be analyzed while maintaining cellular resolution and high biomolecular content
- A synergistic set of well-validated high-content, high-throughput assays for multiscale and multi-modal analysis of large volumes of tissue
- Studies that will complete building an atlas for the following organs: kidney, colon, spleen, thymus, lungs, bladder, skin, heart, female reproductive organs, eyes, bone and bone marrow, pancreas, and liver
- Centers with established informed consent from a diverse range of donors or their families with explicit consent for sharing of genomic data
- The NIH expects to support at least one Center focused on mapping the vasculature, lymphatic, and peripheral nervous system in multiple organs.

Important Dates and Information



➤ **Letter of Intent Due Date:**

✓ October 19, 2021

➤ **Application Receipt Date:**

✓ November 19, 2021

➤ **Peer Review Dates:**

✓ February 2022

➤ **Advisory Council:**

✓ May 2022

➤ **Earliest Start Date:**

✓ July 2022

- **We strongly encourage you to talk with us prior to submitting an application by emailing us at HuBMAP@mail.nih.gov**

Questions?

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RFA-RM-21-027 Demonstration Projects for the Human BioMolecular Atlas Program (U01)

<https://grants.nih.gov/grants/guide/rfa-files/RFA-RM-21-027.html>

Ajay Pillai (NHGRI)

HuBMAP Demonstration Projects

- **Objective:** Utilize HuBMAP data and resources in combination with other resources to address significant biomedical and biological questions
- **Period:** 4 years
- **Budget:** 5-9 awards, limited to \$300,000 in direct costs (excluding subcontract F&A) per year

Cooperative agreements: Awardees are expected to become key members of the HuBMAP consortium

Scope:

Software Engineering Focus

Biomedical Focus

HuBMAP Demonstration Projects

Projects are expected to

- provide feedback to strengthen HuBMAP resources,
- Increase the relevance and benefit of the outputs of the program to the larger biomedical community.

Outputs from the project will significantly enhance the overall goals of HuBMAP.

The FOA provides some examples BUT these are not exhaustive

HuBMAP Demonstration Projects

Software Engineering:

Systematic testing/enhancement of HuBMAP APIs

Enabling facile access to small labs

Methods to cross-query single cell resources

Biomedical:

Effectively utilize unique datasets (data integration) available in HuBMAP

Demonstrate utility as 'normal' human reference

Demonstrate that HuBMAP data can answer important biological questions

Focused experimental validation of HuBMAP datasets

Non-responsive projects:

- Projects where HuBMAP data/resources are incidental and not core
- Projects that do not propose well-defined outputs
- Projects whose focus is not the study of human organs, tissues, and cells
- Projects that do not include Resource Sharing Plan or PEDP

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Additional Information

Connect with us:

- General mailbox: HUBMAP@mail.nih.gov
- Website: <https://commonfund.nih.gov/HuBMAP>
- Existing Awards:
<https://commonfund.nih.gov/hubmap/fundedresearch>
- Consortium website: <https://hubmapconsortium.org/>
- Mailing list: https://list.nih.gov/cgi-bin/wa.exe?SUBED1=hubmap_news_and_information&A=1

Frequently Asked Questions:

<https://commonfund.nih.gov/HuBMAP/generalfaq>

Interested in applying:

We strongly recommend you discuss any application with us in advance and that you submit a LOI.



Questions?

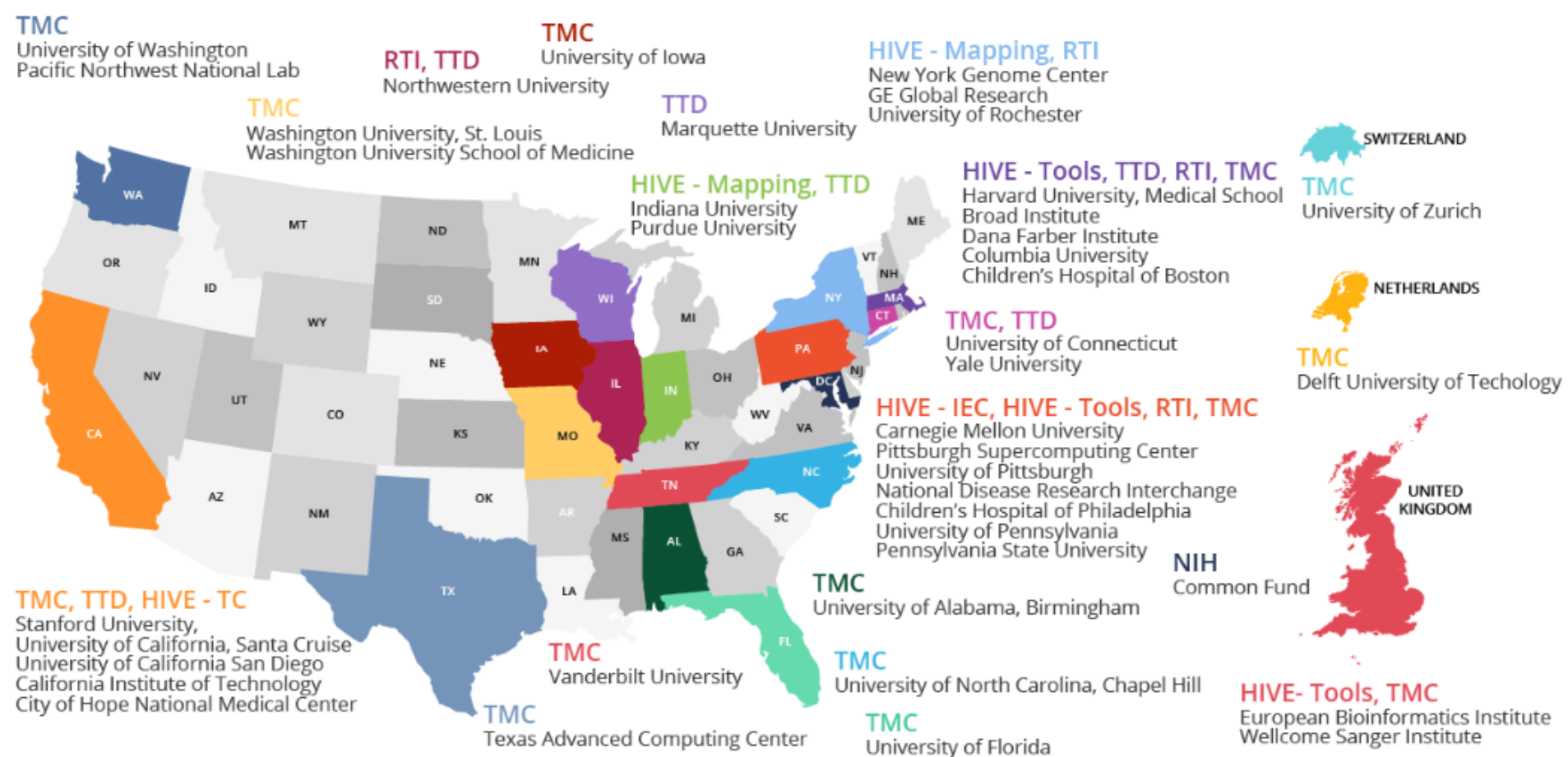
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HuBMAP Consortium



The Common Fund

HuBMAP Contributing Sites



HuBMAP Assays

IMAGING

DNA/RNA

DART-FISH
seqFISH
smFISH
MERFISH
Slide-seq
SABER-FISH
GeoMx

Lipids/Metabolites

MALDI Imaging MS
SIMS Imaging
DESI Imaging MS
NanoDESI Imaging MS

Proteins

Multiplexed IF
IHC
Lightsheet
CODEX
Cell DIVE
DART-FISH
CyTOF Imaging
MALDI Imaging MS
nanoPOTS
MIBI
Immuno-SABER

Other

MR Imaging
CT Imaging
Autofluorescence
Stained Microscopy

SEQUENCING

snDropseq
scRNAseq
snRNA-seq
snATAC-seq
sciRNAseq
sciATACseq
scTHSseq
SNAREseq
scATACseq

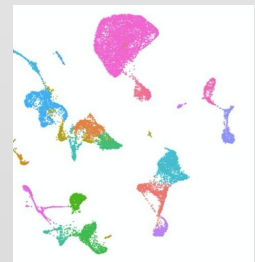
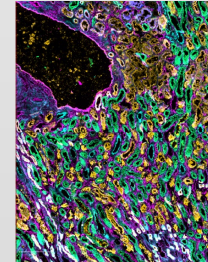
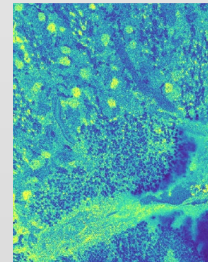
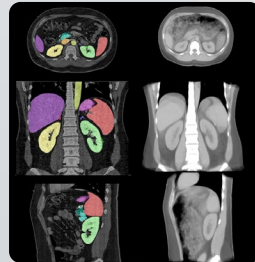
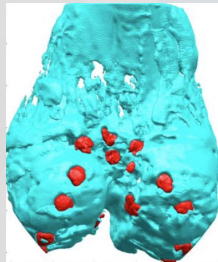
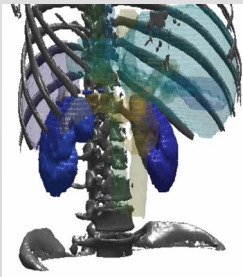
BULK OMICS

Lipids/Metabolites

LC-MS/MS

Proteins

Bottom-up LC-MS/MS
Top-down LC-MS/MS
TMT LC-MS/MS



Data on HuBMAP Portal



The Common Fund

Heart	Lung	Liver	Pancreas	Kidney	Spleen	Thymus	Lymph node	Large intestine	Small intestine
sciATAC-seq	sciATAC-seq	sciATAC-seq	sciATAC-seq	Autofluorescence Microscopy	CODEX	CODEX	CODEX	Bulk ATAC-seq	Bulk ATAC-seq
sciATAC-seq [SnapATAC]	sciATAC-seq [SnapATAC]	sciATAC-seq [SnapATAC]	sciATAC-seq [SnapATAC]	MALDI IMS negative	CODEX [Cytokit + SPRM]	CODEX [Cytokit + SPRM]	CODEX [Cytokit + SPRM]	Bulk ATAC-seq [BWA + MACS2]	Bulk ATAC-seq [BWA + MACS2]
seqFISH	snRNA-seq			MALDI IMS positive	Imaging Mass Cytometry	Imaging Mass Cytometry	Imaging Mass Cytometry	Bulk RNA-seq	Bulk RNA-seq
seqFISH [Lab Processed]	snRNA-seq [Salmon]			PAS Stained Microscopy	Lightsheet Microscopy	Lightsheet Microscopy	Lightsheet Microscopy	Bulk RNA-seq [Salmon]	Bulk RNA-seq [Salmon]
				scATAC-seq (SNARE-seq) [Lab Processed]	scRNA-seq (10x Genomics)	scRNA-seq (10x Genomics)	scRNA-seq (10x Genomics)	CODEX	CODEX
				SNARE-seq	scRNA-seq (10x Genomics) [Salmon]	scRNA-seq (10x Genomics) [Salmon]	scRNA-seq (10x Genomics) [Salmon]	CODEX [Cytokit + SPRM]	CODEX [Cytokit + SPRM]
				snRNA-seq				snATAC-seq	sciATAC-seq
				snRNA-seq (SNARE-seq) [Lab Processed]				snATAC-seq [Snap-ATAC]	sciATAC-seq [SnapATAC]
				snRNA-seq [Salmon]				snRNA-seq	seqFISH
				Untargeted LC-MS				snRNA-seq [Salmon]	seqFISH
								Targeted Shotgun / Flow-injection LC-MS	seqFISH [Lab Processed]
								TMT LC-MS	seqFISH [Lab Processed]
								Untargeted LC-MS	Targeted Shotgun / Flow-injection LC-MS
								Whole Genome Sequencing	TMT LC-MS
									Untargeted LC-MS
									Whole Genome Sequencing

- Pending**
- Vasculature
 - Bone & Bone Marrow
 - Tonsil
 - Skin
 - Uterus
 - Fallopian Tubes
 - Ovary
 - Placenta
 - Breast

<https://portal.hubmapconsortium.org/>