

The Human BioMolecular Atlas Program (HuBMAP)

Rapid Technology Implementation Pre-Application Webinar

January 30th 2019, 1:00 - 2:00PM EST

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



What is the NIH Common Fund?

- Supports a set of trans-NIH scientific programs;
- "Venture capital" space for high-risk, innovative endeavors with potential for extraordinary impact;
- 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.

collaboration synergistic enable
transformative goal-driven
partnership challenges research
challenges res

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



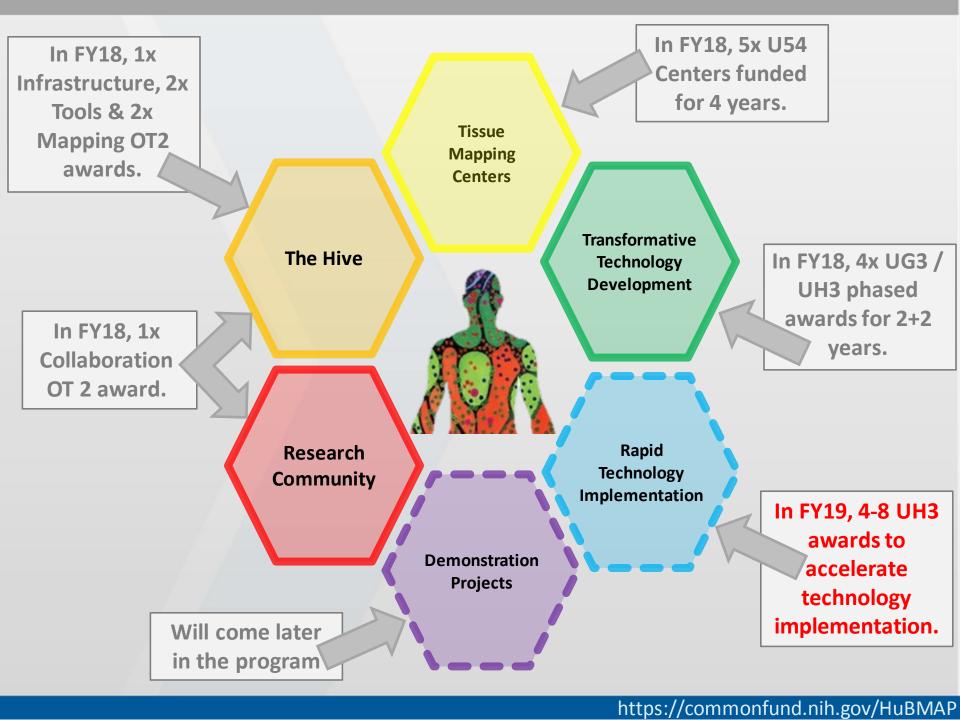
The Human BioMolecular Atlas Program (HuBMAP)

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 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



FY18 TMC & TTD Awards

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	Tissue	Imaging		Sequencing		Mass Spectromtery			Other
		RNA	Proteins	DNA	RNA	Proteins	Lipids	Metabolites	
TMCs									
Atkinson, Nick (UF) Bodenmiller (Zurich)	Spleen, Thymus	smFISH, MERFISH	IHC / IF		scRNAseq	IMC			
Cai (Caltech) Shendure, Trapnell (UW)	Vasculature	seqFISH		scATACseq	scRNAseq				
Caprioli, Spraggins (Vanderbilt)	Kidney		IHC / IF			MALDI, LC- MS/MS			Acid- shift, AF
Snyder, Nolan (Stanford)	Colon		CODEX	scATACseq	scRNAseq				
Zhang, Hagood, Sun (UCSD) Jain (WU) Kharchenko (Harvard)	Lung, Kidney	DART-FISH	DART- FISHrp	scTHSseq, SNARE-seq	snDropseq				
TTDs									
Cai (Caltech) Yuan (Harvard)	Rraact	seqFISH							
Harbury, Desai (Stanford)	Lung, Liver	LRET-ISH	LRET-IF						
Laskin (Purdue)	Lung					nano- POTS	nano-DESI	nano-POTS	
Yin (Harvard)	Tonsil	PER-DEI	SABER						

FY18 HIVE Awards

Component	Role	Award	Focus	
Collaboration	Enhance collaboration and exchange of information among Consortium members and between HuBMAP and the wider research community	Mabee (USD) Lenhardt (RENCI)	Optimizing communication channels, Team science, Consortium health	
Infrastructure	Establish, optimize and scale a reliable, accessible infrastructure for archiving and analysis of data generated initially by HuBMAP and later by the wider research community	Nystrom (CMU) Silverstein (Pitt)	Hybrid cloud storage, Data ingestion, Data management	
Tools	Develop tools for enhancing findability, accessibility, interoperability, reproducibility and	Bar-Joseph (CMU) Paten (UCSC) Teichmann (Sanger)	FAIRness, DATA QA, Containerized workflows	
	re-use of HuBMAP data	Gehlenborg (Harvard)	Visualization, APIs, Data release	
Mapping	Develop the framework for mapping	Borner (IU)	Metadata-driven mapping, Visualization, User-centered design	
	HuBMAP data in the context of the human body	Satija (NYGC) Marioni (EMBL)	Data-feature mapping, Common Coordinate Framework, Data integration	

Key Points for All HuBMAP Awards

- ➤ HuBMAP projects will generate <u>high resolution</u>, <u>high content</u>, <u>high-throughput</u> biomolecular data to generate 3D tissue maps of <u>non-diseased</u>, <u>human tissue</u>
- > NIH intends that the <u>products of HuBMAP will be broadly and rapidly</u> available
 - Comprehensive Sharing Plan required expectation that data are shared with Consortium quarterly and pre-publication
- ➤ All applicants should define a clear set of <u>annual milestones and a timeline</u>, including goals for data generation and sharing
- Awardees must be prepared to adjust, add, or delete items from their proposed plan to align with evolving program progress and goals
- > Successful applicants are expected to propose and set aside funds for collaborative work with other members of the Consortium



Rapid Technology Implementation for HuBMAP (UH3) (RFA-RM-19-002)

Jerry Li (NCI)



Rapid Technology Implementation RFA Overview

- Objective: Rapidly and systematically implement promising technologies into the HuBMAP Consortium to broaden and deepen the Consortium's range of technologies and expertise.
- Period: Up to 3 years
- Budget: As needed (estimate of 4-8 awards, total of \$3M total costs)

Projects are expected to:

- (1) significantly extend existing capabilities of the Consortium,
- (2) use a <u>milestone-driven</u> engineering approach that considers iterative design, testing and evaluation,
- (3) complement and integrate with existing technologies and pipelines used by the HuBMAP Consortium

Rapid Technology Implementation RFA Key Points

- Types of Technology: Broad (see areas of particular interest)
- Stage of Development: Demonstration of use of technology for analyzing mammalian tissue should have already been published (by time of review)
- **Tissues**: Projects should propose tissue / data types they will study inhouse, identify tissues / data they will work with existing Consortium; avoid duplication of tissue types with existing efforts
- Implementation Plan: clear timeline, quantitative milestones; description of benchmarking and integration with consortium pipelines; usability plan; interactions with the consortium
- **Synergy**: Important to highlight synergy with existing efforts (both HuBMAP as well as similar programs)

Rapid Technology Implementation RFA

Technologies of particular interest include, but are not limited to:

- High-sensitivity, high-resolution imaging techniques that can rapidly provide spectral data over large areas of tissue
- Quantitative image analysis and mass spectrometry analysis tools
- Large, well-curated, well-annotated datasets of human anatomy and associated tools to assist with building a robust common coordinate framework system
- Tools for rapid, high-resolution, in situ sequencing and analysis of a wide panel of nucleic acids derived from multiple tissues
- Technologies for quantitative, comprehensive assessment of the extracellular environment
- Sensitive and high-specificity assays for identification of different functional states of biomolecules
- Multi-scale data collection and integration methods from the molecular level to cellular and tissue levels.
- Data visualization methods for intuitive atlas comparison and analysis.

Rapid Technology Implementation RFA

Applications addressing the following topics will be deemed non-responsive and will not be reviewed:

- Projects primarily <u>focused on the pursuit of a biochemical mechanism</u> that does not result in a technology that will significantly improve the Consortium's capabilities to spatially map human tissues;
- Projects proposing <u>technologies that significantly overlap</u> with those currently used by the Consortium or that are not compatible with existing assays or analysis techniques used by the Consortium;
- Projects proposing <u>technologies primarily for studying bio-fluids or dissociated</u> cells;
- <u>Projects without published results</u> reliably demonstrating proof-of-principle for the proposed technology using mammalian tissue;
- Projects that do not propose a detailed implementation plan

Administrative Details

- > NIH Involvement: There will be substantial NIH programmatic involvement in individual projects and Consortium activities
- ➤ Consortium: Abide by policies for rapid sharing, collaborative projects, regular meetings, changing goals and milestones
- ➤ **Budgeting**: Applicants are encouraged to budget for Consortium activities, resource sharing, outreach, and meeting attendance as part of their proposed budget. NIH may modify budgets on award.
- > RFA: These are one-off announcements with no revisions or appeals.
- > For RTI RFA:
 - ➤ Eligibility: Foreign institutions / for-profit organizations / NIH intramural program are eligible to apply
 - > LOIs: Not required, but strongly encouraged.
 - > Review: Review will be in a SEP. Please pay attention to review criteria are given in the RFA.

Important Dates



√ February 14, 2019



- ✓ March 14, 2019
- Review Dates:
 - ✓ May/June 2019
- > Advisory Council:
 - ✓ August 2019
- > Earliest Start Date:
 - ✓ September 2019
- > Kickoff Meeting:
 - ✓ September 23-25, 2019 (subject to change)



Questions?

To submit questions please use the Q&A box. Following the webinar, questions can be sent to HuBMAP@mail.nih.gov

Additional Information



Connect with us:

- General mailbox: <u>HUBMAP@mail.nih.gov</u>
- Website: https://commonfund.nih.gov/HuBMAP
- 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/faqs

Interested in applying:

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

HuBMAP Technology RFAs

Funding Opportunity	Technology Readiness Level (TRL)	Description	
Transformative	1	Basic principles observed	
Technology Development	2	Technology concept formulated	
UG3 phase	3	Experimental proof of concept	
Transformative Technology Development		Technology validated in lab	
– UH3 phase	5	Technology validated in relevant environment	
	6	Technology demonstrated in relevant environment	
Rapid Technology Implementation – UH3	7	System prototype demonstration in operational environment	
	8	System complete and qualified	
Tissue Mapping Centers	9	Actual system proven in operational environment	