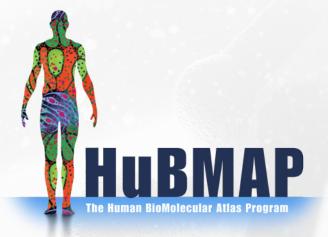


The Human BioMolecular Atlas Program (HuBMAP)

A Framework for Mapping the Human Body

Multicellular organisms have specialized cells with distinct functions. The organization and variability of these cells have a profound impact on the function of different tissues, process of aging, and emergence of diseases and conditions. Recently developed technologies are allowing researchers to explore cells on the individual (single cell) level and provide an opportunity to better understand how tissue organization influences cellular function. The Human BioMolecular Atlas Program (HuBMAP) will catalyze development of an open, global framework for comprehensively mapping the human body at a cellular resolution leading to a deeper multidimensional description of individual cells within their functional and 3D tissue context.



https://commonfund.nih.gov/hubmap

The overall goals of the NIH Common Fund Human Biomolecular Atlas Program (HuBMAP) are to (1) accelerate development of the next generation of tools and techniques for constructing high-resolution spatial tissue maps that quantify multiple types of biomolecules; (2) generate foundational 3D tissue maps using validated high-content, high-throughput imaging and omics assays; (3) establish an open data platform that will develop novel approaches to integrating, visualizing, and modeling imaging and omics data to build multidimensional maps, and making data rapidly findable, accessible, interoperable, and reusable by the global research community; (4) coordinate and collaborate with other funding agencies, programs, and the biomedical research community to build the architecture and tools for mapping the human body with cellular resolution; and (5) support projects that demonstrate the value of the resources developed by the program to study individual variation and tissue changes across the lifespan and the health-disease continuum.

HuBMAP will scale-up the scope of tissues, technologies, data management, and community engagement over the course of the program. The program will have four stages: a setup phase in Fiscal Year (FY) 2018, a scale-up phase for FY19–FY21, a production phase for FY22–FY24, and a transition phase in FY25. All activities are pending the availability of funds.





Program Initiatives

I. Technology Development

Transformative Technology Development—This set of initiatives, the first of which will be issued in FY18, will accelerate the development of *in situ* imaging and sequencing approaches, single cell proteomics, methylomics and metabolomics, as well as analysis of the extracellular environment that have the potential to transform 3D human tissue mapping.

Rapid Technology Development—This set of initiatives, which is planned to start in FY19, will focus on nimble development and integration of existing imaging and dissociative technologies that will enhance data collection and validation during the program, and expanding throughput, multiplexing or discrimination of different classes of biomolecules.

II. Tissue Mapping Centers

These Centers, which will be initially funded in FY18, will build, benchmark, standardize, validate, and generate extensive data from high-content, high-throughput imaging and omics technologies to produce comprehensive 3D tissues maps with cellular spatial resolution. These Centers will integrate and optimize all parts of the data generation pipeline, from tissue collection and preservation through to map reconstruction, integrating both imaging and omics data and analysis.

III. HuBMAP Integration, Visualization, and Engagement (HIVE) Center

This Center, which will be funded in FY18, will have responsibility for (1) managing the data generated by the Consortium;

- (2) coordinating internal and external Consortium activities;
- (3) developing novel tools for visualizing, searching, and modeling data; and (4) building an atlas of tissue maps.

IV. Demonstration Projects

The goal of this initiative, which will start halfway through the program, is to demonstrate how HuBMAP resources, in combination with new or other data sets or biospecimens as needed, can be used to build better statistical and analytical tools and models of cellular organization and communication in tissues.

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