11AM

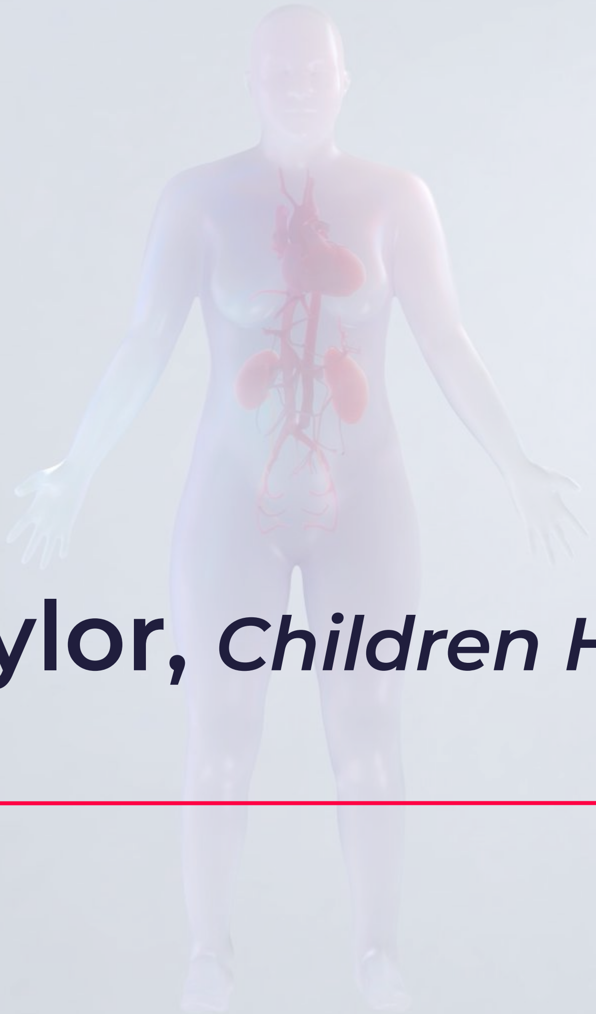
4PM in London (GMT), 1AM in Tokyo (GMT+9)

FAIR & Scalable Infrastructures

Moderator: Katy Börner, *Indiana University*

Presenters:

- Deanne Taylor, *Children's Hospital of Philadelphia*
- Ino de Bruijn, *Memorial Sloan Kettering Cancer Center*
- Bruce W. Herr II, *Indiana University*
- Jonathan Silverstein, *University of Pittsburgh*



Deanne Taylor, *Children Hospital of Philadelphia*

From Genes to Systems: Modeling Human Functional Biology with Knowledge Graphs

Deanne Taylor

15 Dec 2024

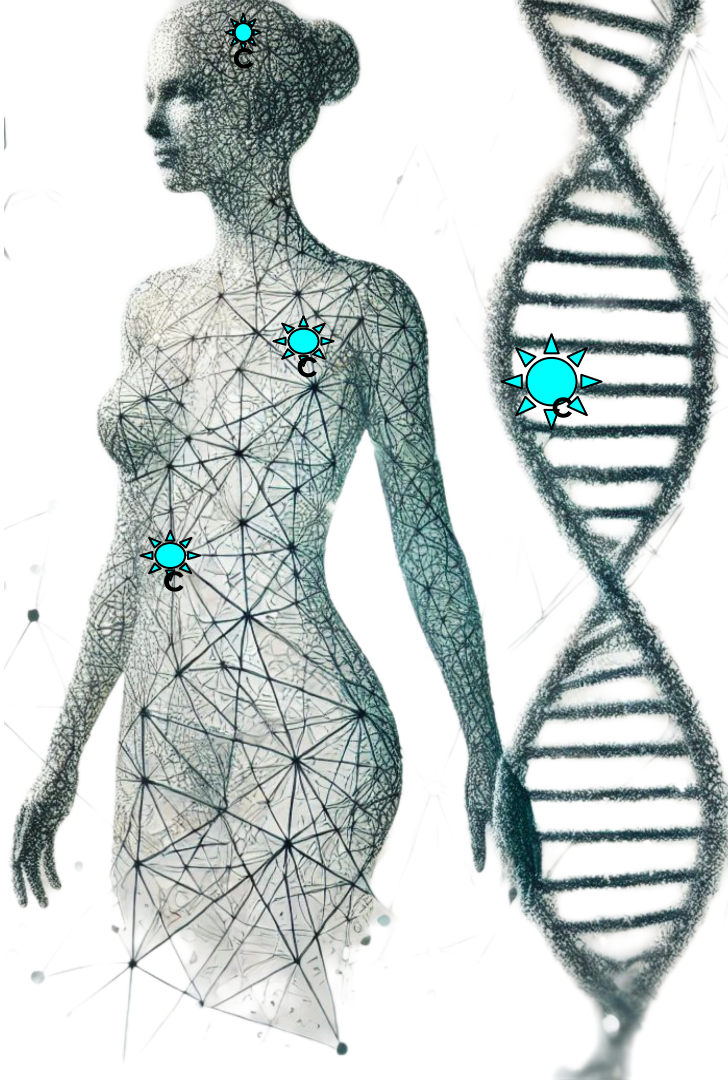
Big Questions

How are gene variations and disorders/diseases related?

How do we predict a therapy given a gene variation?

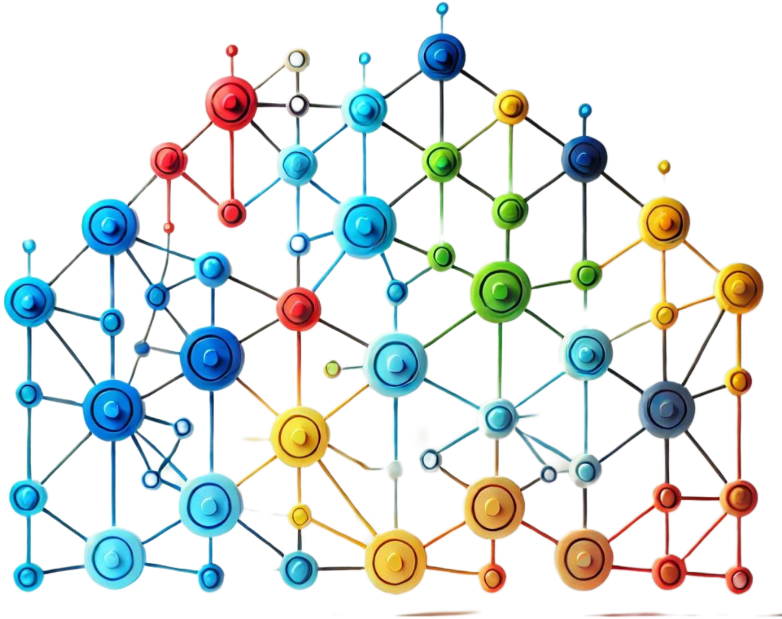
Reachable question:

Can we interconnect large biomedical datasets and use those structures to answer complex biological questions linking gene variations to diseases, and potential therapeutics?



Introduction to Knowledge Graphs (KGs)

KGs represent information as networks of nodes (entities) and edges (relationships).



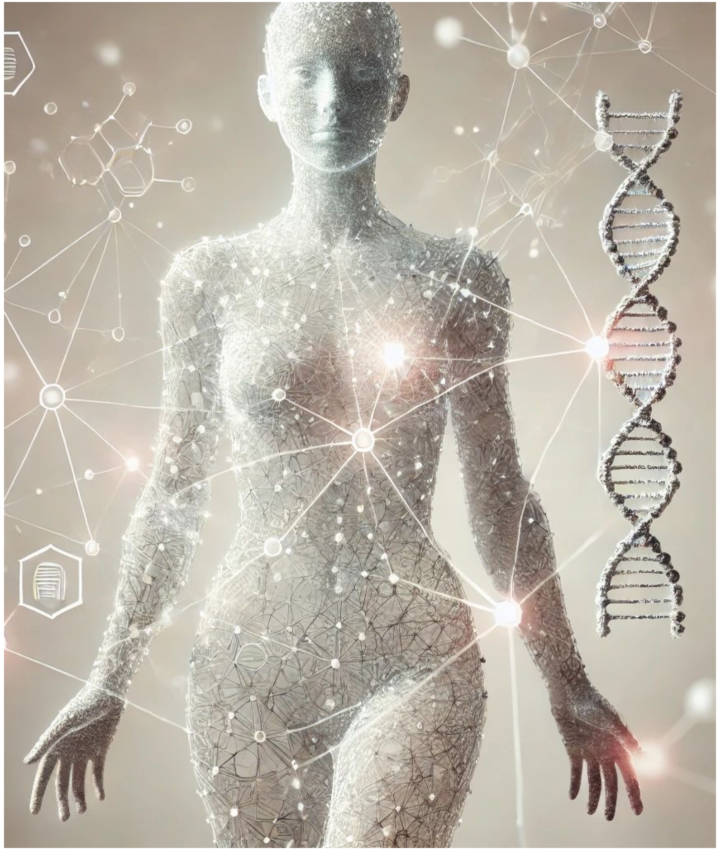
For data models of the human at all scales:

- **Node Types**: Molecules, Genes, Proteins, Diseases, Tissues, Organs, Treatments…
- **Edge Types** "Encodes," "Regulates," "Is associated with," "Treats" …

KGs are ideal for integrating diverse biomedical datasets because they preserve connections and context.

Functional Biology represented in Knowledge Graphs

- Functional biology focuses on how genes and molecular processes drive development and functioning of cells, tissues, and organs.
- KGs can provide an integrated "functional biology" layer to use in concert with anatomical maps/KGs like the Human Reference Atlas (see Bruce Herr's talk coming up!)
- This integration can also give us tools to explore how genetic variations influence human development, disorders, and disease.



Knowledge Graphs as connected data warehouses

UBKG

The **Unified Biomedical Knowledge Graph (UBKG)** is a knowledge graph infrastructure that represents a set of interrelated concepts from biomedical ontologies and vocabularies (Jonathan Silverstein, HuBMAP: https://ubkg.docs.xconsortia.org/)

Petagraph

- Built with UBKG to integrate over 20 large multi-omics human and mouse genomic datasets
- Incorporates 180+ ontologies and annotation resources like STRING, Reactome, and GENCODE.
- Focused on harmonizing omics data for rapid feature selection and hypothesis generation.
- 32 million nodes and 118 million relationships

Data Distillery Knowledge Graph (DDKG)

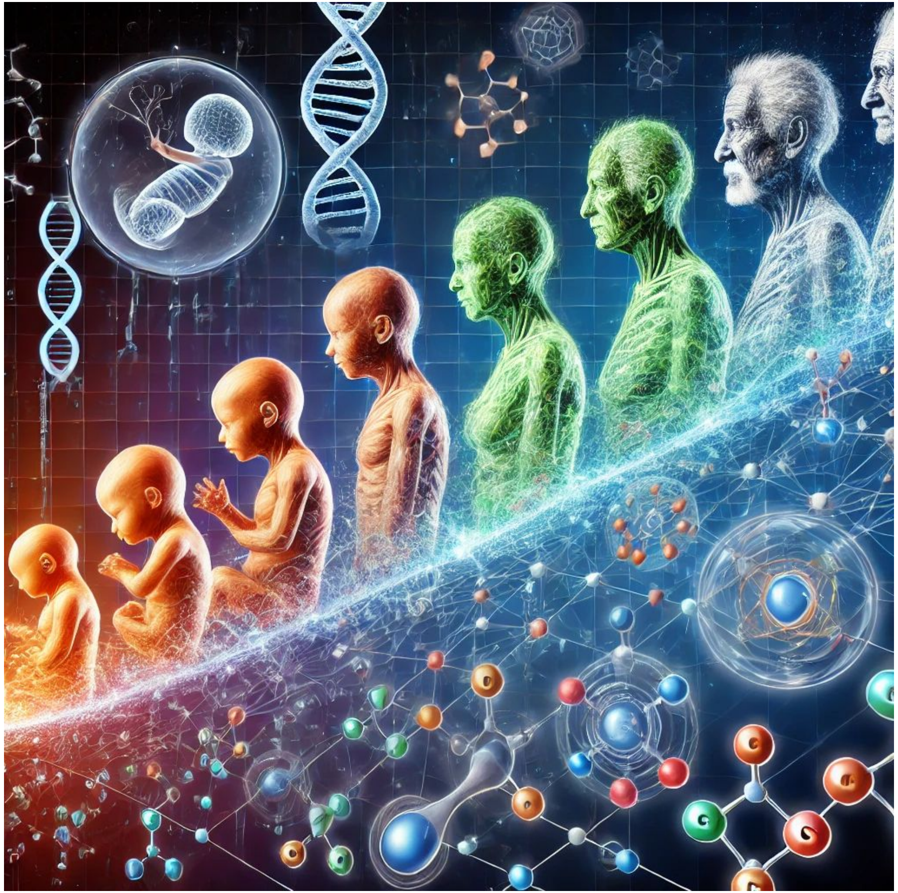
- Extends Petagraph's schema to integrate over 30 large genomics datasets in collaboration with NIH Common Fund DCCs (e.g., HuBMAP, GTEx, 4D Nucleome, LINCS…)
- Like Petagraph, is scalable for new genomics data types and cross-dataset analyses.
- Includes development of user-friendly interfaces (API, UI) for secure and efficient querying
- 40 million nodes and 300 million relationships

The future of modeling: KGs can enable a multi-dimensional human model

Precision medicine would benefit from knowledge graphs to create whole-human models from:

- Maps of human organs and tissues across human development (4D)
- Functional biology genomics data from single cells to whole body physiology
- Human genetics data
- Observational medical data
- Dynamic biomedical process models

… towards prediction and treatments of diseases and disorders.

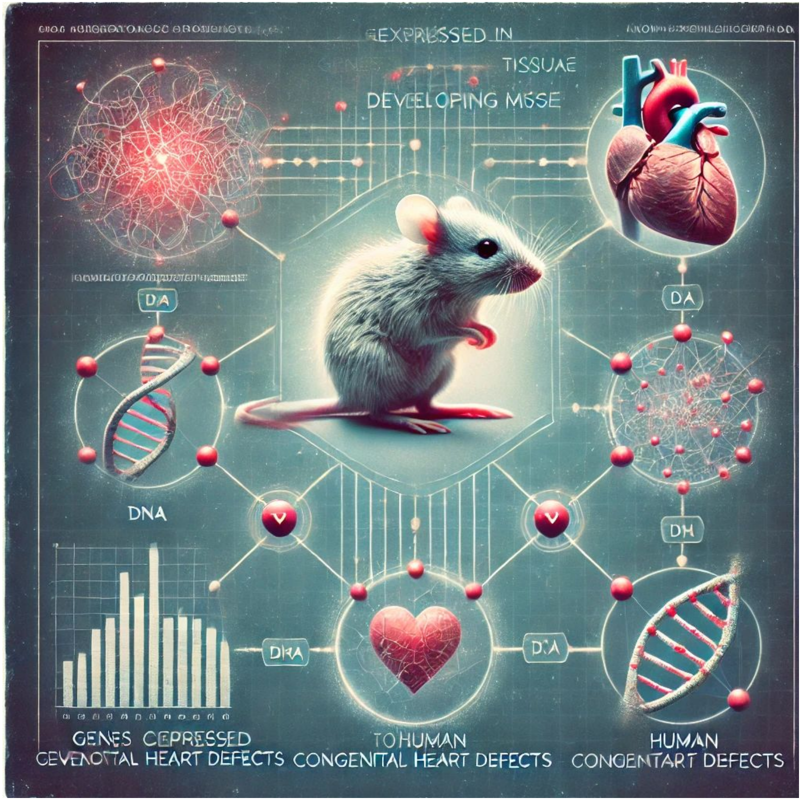


Data Distillery Use Case: Exploring Fetal Heart Development

We can use the Data Distillery KG’s corpus of integrated data to ask complex questions that would ordinarily take weeks of data integration effort.

Example: What genes linked to heart defects in mice are also actively expressed in developing human heart cells?

This information would help in predicting heart defect risks in affected families by pinpointing which genes to examine for genetic variation.

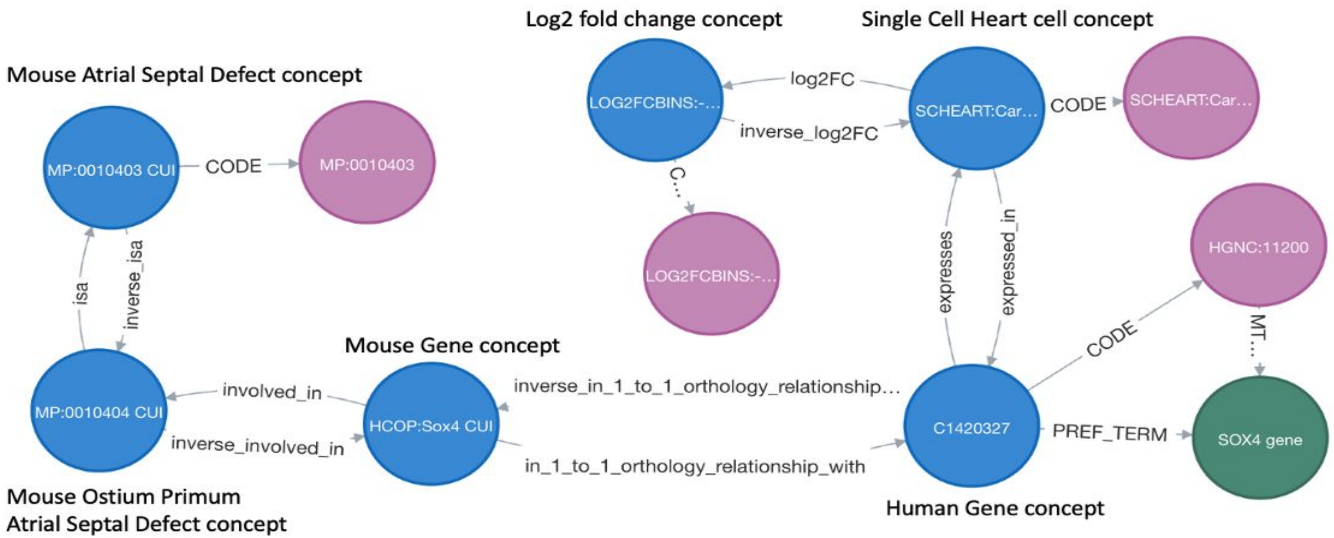


Data Distillery KG Query: What genes related to mouse heart could affect which cells in the developing human heart?

Query model in Data Distillery

Result: which developing human heart cell types express genes also linked to heart defects in mice

Query took seconds to complete.



Results

Gene symbol	Cell type	Cell Ontology	log2FC lowerbound	log2FC upperbound	pval lowerbound	pval upperbound
ATP2A2	Atrial Cardiomyocytes	CL:0002129	2.50	3.00	0	1.00E-12
ATP2A2	Ventricular Cardiomyocytes	CL:0002131	1.00	1.25	0	1.00E-12
RYR2	Atrial Cardiomyoctes	CL:0002129	1.25	1.50	0	1.00E-12
RYR2	Ventricular Cardiomyocytes	CL:0002131	1.25	1.50	0	1.00E-12
PLXND1	Endothelium/pericytes/adventitia	CL:0010008	1.25	1.50	0	1.00E-12
...	...	...	...	...	...	...

Petagraph Use Case: Drug vs Tissue Effect

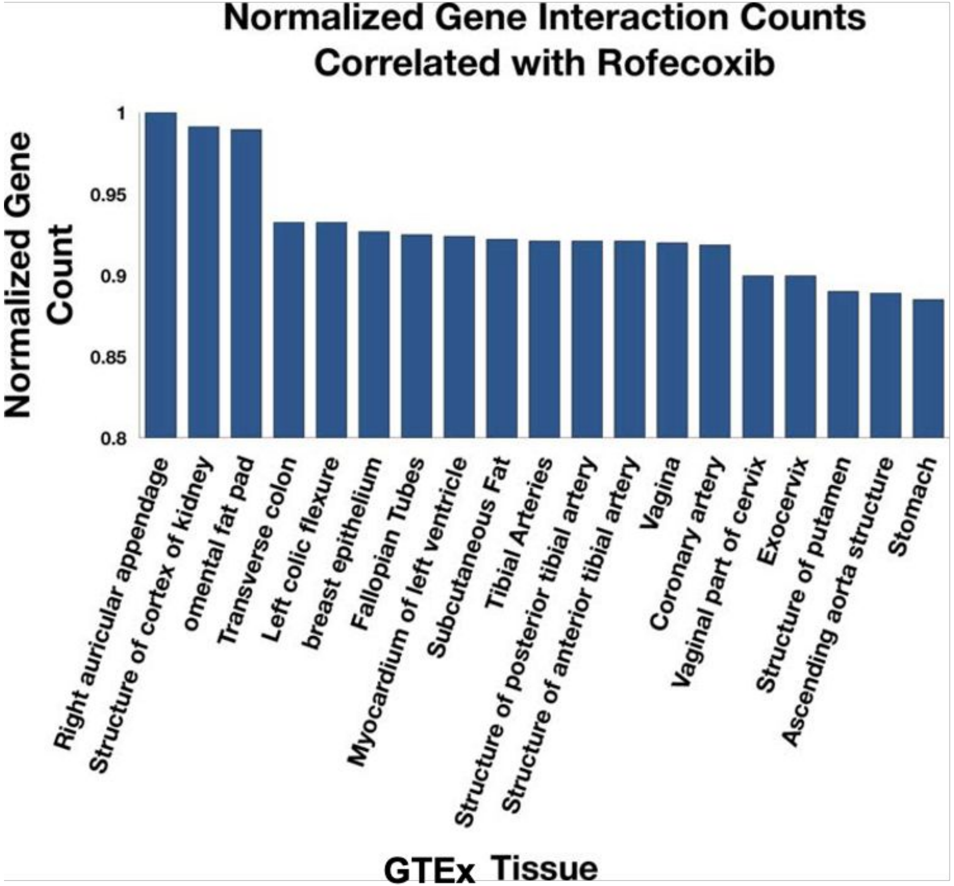
Question: How to predict what human tissues are most likely going to be affected by a drug?

Example: Rofecoxib (Vioxx) was recalled due to high cardiovascular risks.

Petagraph already has useful data integrated:

- Rofexcoxib’s gene expression signatures of dosing human cell cultures (LINCS/L1000 projects)
- Integrated with gene expression signatures across many human tissues (GTEx project).

Petagraph KG Query: What human tissues are most likely to be perturbed by rofecoxib?



Result: Heart and blood vessels, such as the right auricular appendage and myocardium of the left ventricle, were predicted as the most affected tissues based on the number of shared genes with rofecoxib's dosing profile.

Predictions align with the known cardiovascular risks of rofecoxib.

Query took seconds to complete.

KGs as FAIR and useful tools

Data Distillery and Petagraph can be freely downloaded with a UMLS license (https://www.nlm.nih.gov/databases/umls.html)

Users with a UMLS license can follow site instructions to obtain and utilize a UMLS license key at https://ubkgdownloads.xconsortia.org/

Installable with a 16G memory laptop!

Acknowledgements

Ben Stear	**Kids First**
Taha Mohseni Ahooyi	**Kids First**
Alan Simmons	**HuBMAP**
Jonathan C. Silverstein*	**HuBMAP**
Christopher Nemarich	KF
Christophe G. Lambert	IDG
Vincent T. Metzger	IDG
John Erol Evangelista	LINCS, DRC
Daniel J. B. Clarke	LINCS, DRC
Zhuorui Xie	LINCS, DRC
Heesu Kim	LINCS, DRC
Sherry L. Jenkins	LINCS, DRC
Avi Ma'ayan	LINCS, DRC

Mano R. Maurya	MW, DRC
Srinivasan Ramachandran	MW, DRC
Eoin Fahy	MW
Shankar Subramaniam	MW, DRC
Bernard de Bono	SPARC
Jeffrey S. Grethe	SPARC
Thomas H. Gillespie	SPARC
Fahim T. Imam	SPARC
Natallia Kokash	SPARC
Matthew, E. Roth	ERCC
Robert Fullem	ERCC
Dubravka Jevtic	ERCC
Aleks Milosavljevic	ERCC

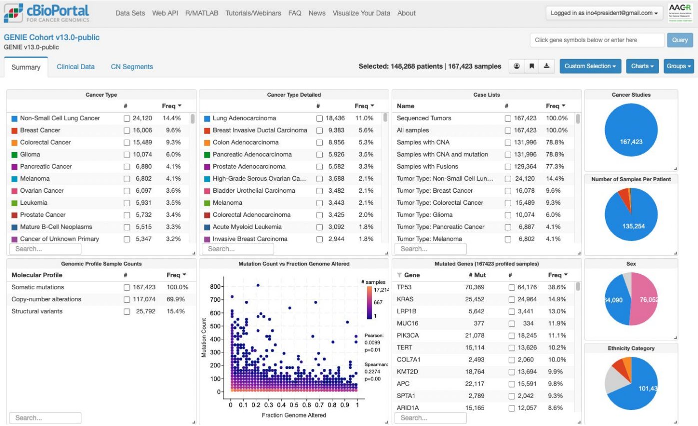
George Papanicolaou, Christy Kano NIH

Ino de Bruijn, *Memorial Sloan Kettering Cancer Center*

https://cbiportal.org & https://humantumoratlas.org

FAIR Data Portals for multimodal cancer data

cBioPortal FOR CANCER GENOMICS https://cbioportal.org



GENIE Cohort v13.0-public

GENIE v13.0-public

Selected: 148,268 patients | 167,423 samples

Cancer Type

	#	Freq
Non-Small Cell Lung Cancer	☐ 24,120	14.4%
Breast Cancer	☐ 16,006	9.6%
Colorectal Cancer	☐ 15,489	9.3%
Glioma	☐ 10,074	6.0%
Pancreatic Cancer	☐ 6,880	4.1%
Melanoma	☐ 6,802	4.1%
Ovarian Cancer	☐ 6,097	3.6%
Leukemia	☐ 5,931	3.5%
Prostate Cancer	☐ 5,732	3.4%
Mature B-Cell Neoplasms	☐ 5,515	3.3%
Cancer of Unknown Primary	☐ 5,347	3.2%

Cancer Type Detailed

	#	Freq
Lung Adenocarcinoma	☐ 18,436	11.0%
Breast Invasive Ductal Carcinoma	☐ 9,383	5.6%
Colon Adenocarcinoma	☐ 8,956	5.3%
Pancreatic Adenocarcinoma	☐ 5,926	3.5%
Prostate Adenocarcinoma	☐ 5,582	3.3%
High-Grade Serous Ovarian Ca...	☐ 3,588	2.1%
Bladder Urothelial Carcinoma	☐ 3,482	2.1%
Melanoma	☐ 3,443	2.1%
Colorectal Adenocarcinoma	☐ 3,425	2.0%
Acute Myeloid Leukemia	☐ 3,092	1.8%
Invasive Breast Carcinoma	☐ 2,944	1.8%

Case Lists

Name	#	Freq
Sequenced Tumors	☐ 167,423	100.0%
All samples	☐ 167,423	100.0%
Samples with CNA	☐ 131,996	78.8%
Samples with CNA and mutation	☐ 131,996	78.8%
Samples with Fusions	☐ 129,364	77.3%
Tumor Type: Non-Small Cell Lun...	☐ 24,120	14.4%
Tumor Type: Breast Cancer	☐ 16,078	9.6%
Tumor Type: Colorectal Cancer	☐ 15,489	9.3%
Tumor Type: Glioma	☐ 10,074	6.0%
Tumor Type: Pancreatic Cancer	☐ 6,887	4.1%
Tumor Type: Melanoma	☐ 6,802	4.1%

Genomic Profile Sample Counts

Molecular Profile	#	Freq
Somatic mutations	☐ 167,423	100.0%
Copy-number alterations	☐ 117,074	69.9%
Structural variants	☐ 25,792	15.4%

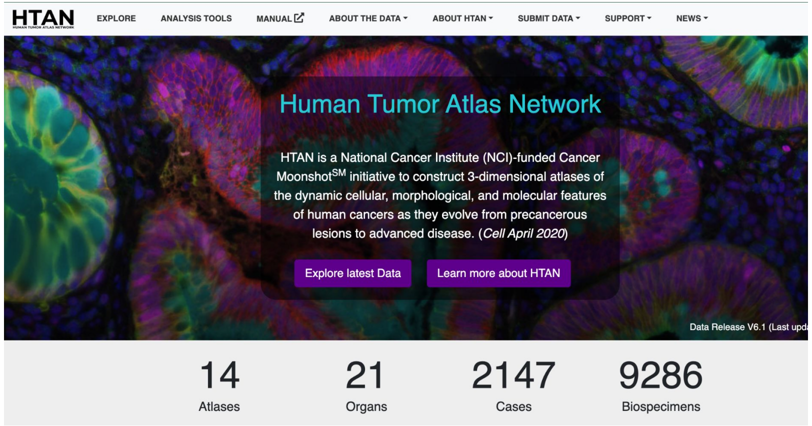
Mutated Genes (167423 profiled samples)

Gene	# Mut	#	Freq
TP53	70,369	☐ 64,176	38.6%
KRAS	25,452	☐ 24,964	14.9%
LRP1B	5,642	☐ 3,441	13.0%
MUC16	377	☐ 334	11.9%
PIK3CA	21,078	☐ 18,245	11.1%
TERT	15,114	☐ 13,626	10.2%
COL7A1	2,493	☐ 2,060	10.0%
KMT2D	18,764	☐ 13,694	9.9%
APC	22,117	☐ 15,591	9.8%
SPTA1	2,789	☐ 2,042	9.3%
ARID1A	15,165	☐ 12,057	8.6%

Memorial Sloan-Kettering Cancer Center
Dana-Farber Cancer Institute
UHN Toronto General Toronto Western Princess Margaret Toronto Rehab
The Hyve
The Children's Hospital of Philadelphia
SE4BIO

Bulk Genomics & Clinical Data Focus

HTAN HUMAN TUMOR ATLAS NETWORK https://humantumoratlas.org



Human Tumor Atlas Network

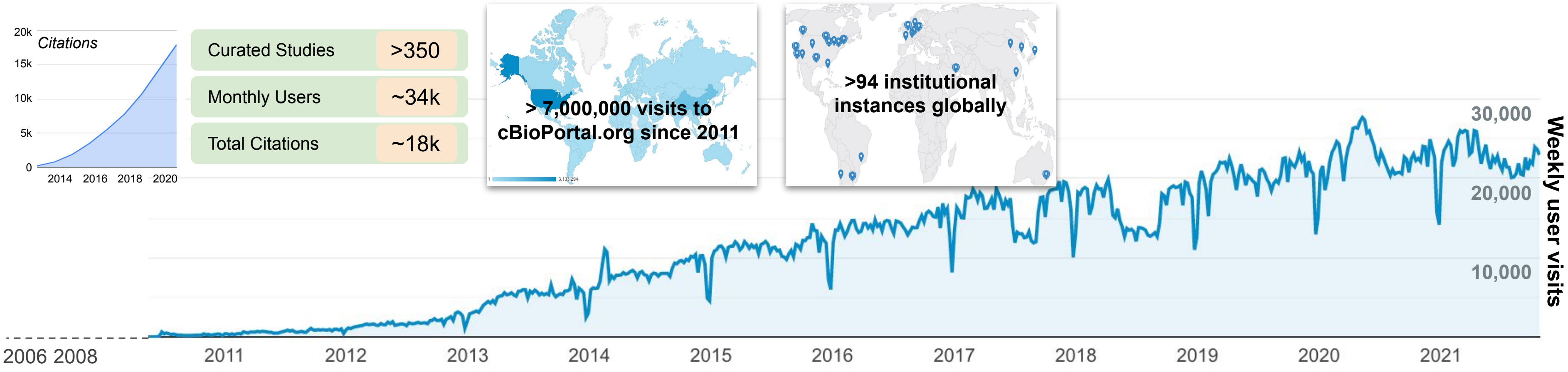
HTAN is a National Cancer Institute (NCI)-funded Cancer Moonshot^{SM} initiative to construct 3-dimensional atlases of the dynamic cellular, morphological, and molecular features of human cancers as they evolve from precancerous lesions to advanced disease. (*Cell April 2020*)

14	21	2147	9286
Atlases	Organs	Cases	Biospecimens

Memorial Sloan-Kettering Cancer Center
Dana-Farber Cancer Institute
SageBionetworks

Wide variety of assays incl single cell, multiplex imaging

cBioPortal over time https://cbioportal.org



Curated Studies	>350
Monthly Users	~34k
Total Citations	~18k

Start of cBioPortal Query/Results view

Patient View Study View

Open source transition (MSK, DFCI & Hyve)

PMCC & CHOP joined

Architecture upgraded Comparison View

Start of TCGA

First SU2C cBioPortal

Cerami et al. Cancer Discov.

cBioPortal @MSK

Gao et al. Sci Signal.

cBioPortal @PMCC

cBioPortal @DFCI

Project GENIE

cBioPortal @CHOP

ITCR funding

Start of HTAN

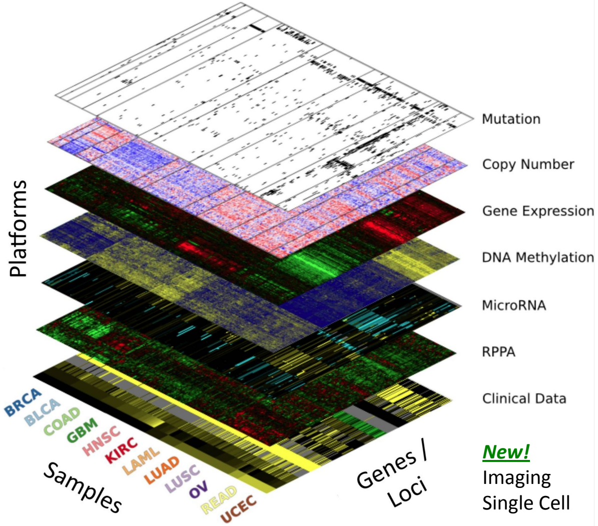
Count Me In

GENIE BPC

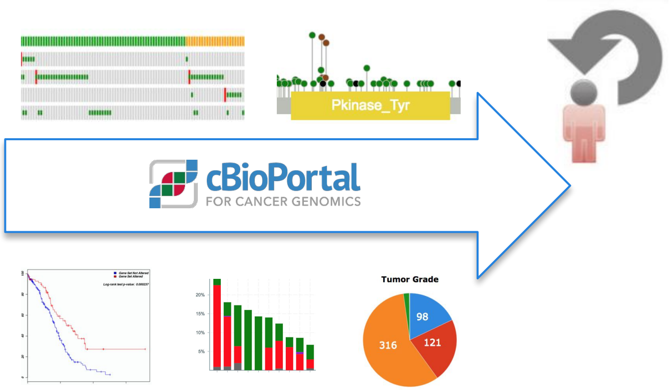
Webinars

Goal of cBioPortal

Make complex cancer genomic data **accessible** and **interpretable** for cancer biologists and clinicians



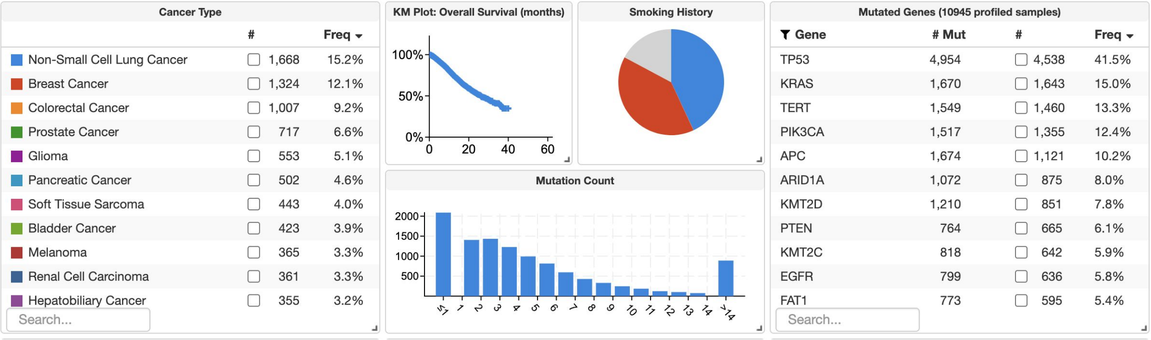
Adapted from TCGA Nat Genet 2014



Biological discovery

Clinical interpretation

Cohort exploration



Cancer Type

	#	Freq
🟦 Non-Small Cell Lung Cancer	☐ 1,668	15.2%
🟥 Breast Cancer	☐ 1,324	12.1%
🟧 Colorectal Cancer	☐ 1,007	9.2%
🟩 Prostate Cancer	☐ 717	6.6%
🟪 Glioma	☐ 553	5.1%
🟦 Pancreatic Cancer	☐ 502	4.6%
🟥 Soft Tissue Sarcoma	☐ 443	4.0%
🟩 Bladder Cancer	☐ 423	3.9%
🟥 Melanoma	☐ 365	3.3%
🟦 Renal Cell Carcinoma	☐ 361	3.3%
🟪 Hepatobiliary Cancer	☐ 355	3.2%

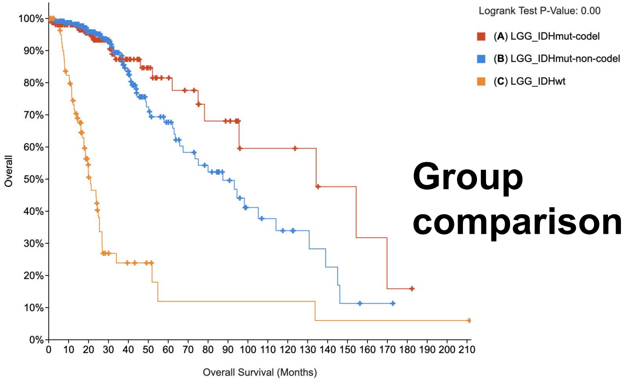
Search...

Mutated Genes (10945 profiled samples)

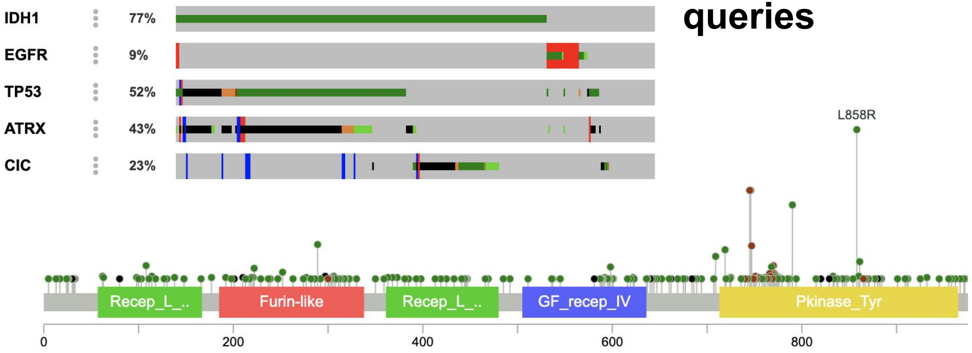
Gene	# Mut	#	Freq
TP53	4,954	☐ 4,538	41.5%
KRAS	1,670	☐ 1,643	15.0%
TERT	1,549	☐ 1,460	13.3%
PIK3CA	1,517	☐ 1,355	12.4%
APC	1,674	☐ 1,121	10.2%
ARID1A	1,072	☐ 875	8.0%
KMT2D	1,210	☐ 851	7.8%
PTEN	764	☐ 665	6.1%
KMT2C	818	☐ 642	5.9%
EGFR	799	☐ 636	5.8%
FAT1	773	☐ 595	5.4%

Search...

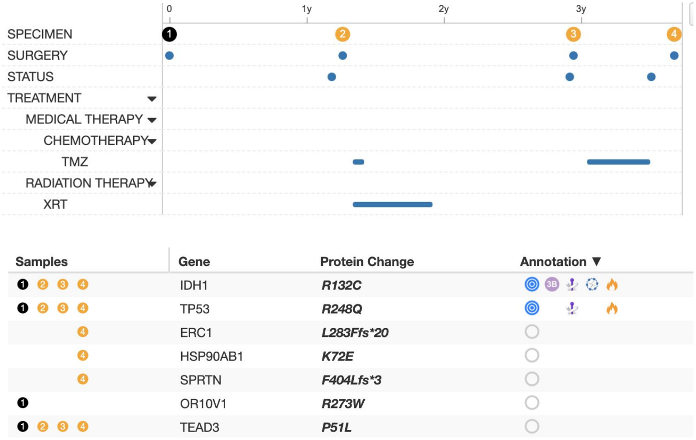
Group comparison



Gene-centric queries

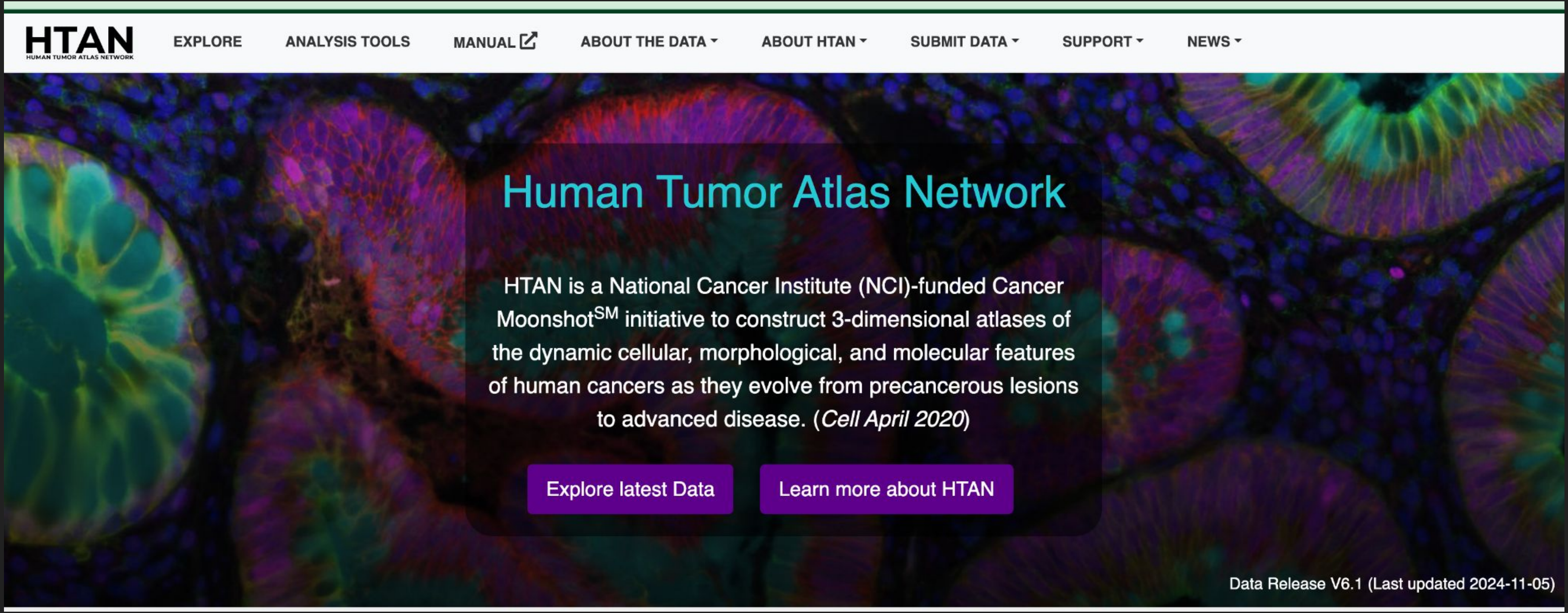


Patient visualization



Samples	Gene	Protein Change	Annotation ▼
❶ ② ③ ④	IDH1	*R132C*	
❶ ② ③ ④	TP53	*R248Q*	
④	ERC1	*L283Ffs*20*	○
④	HSP90AB1	*K72E*	○
④	SPRTN	*F404Lfs*3*	○
❶	OR10V1	*R273W*	○
❶ ② ③ ④	TEAD3	*P51L*	○

The HTAN Portal https://humantumoratlas.org/



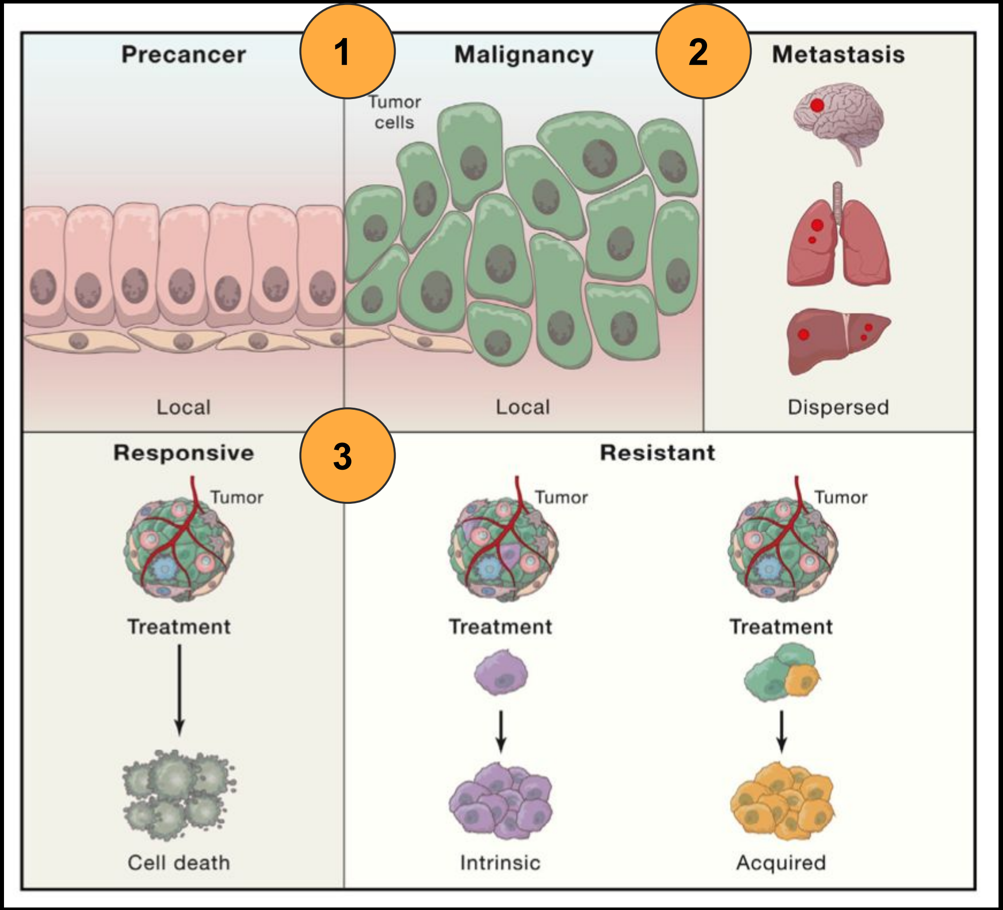
Human Tumor Atlas Network

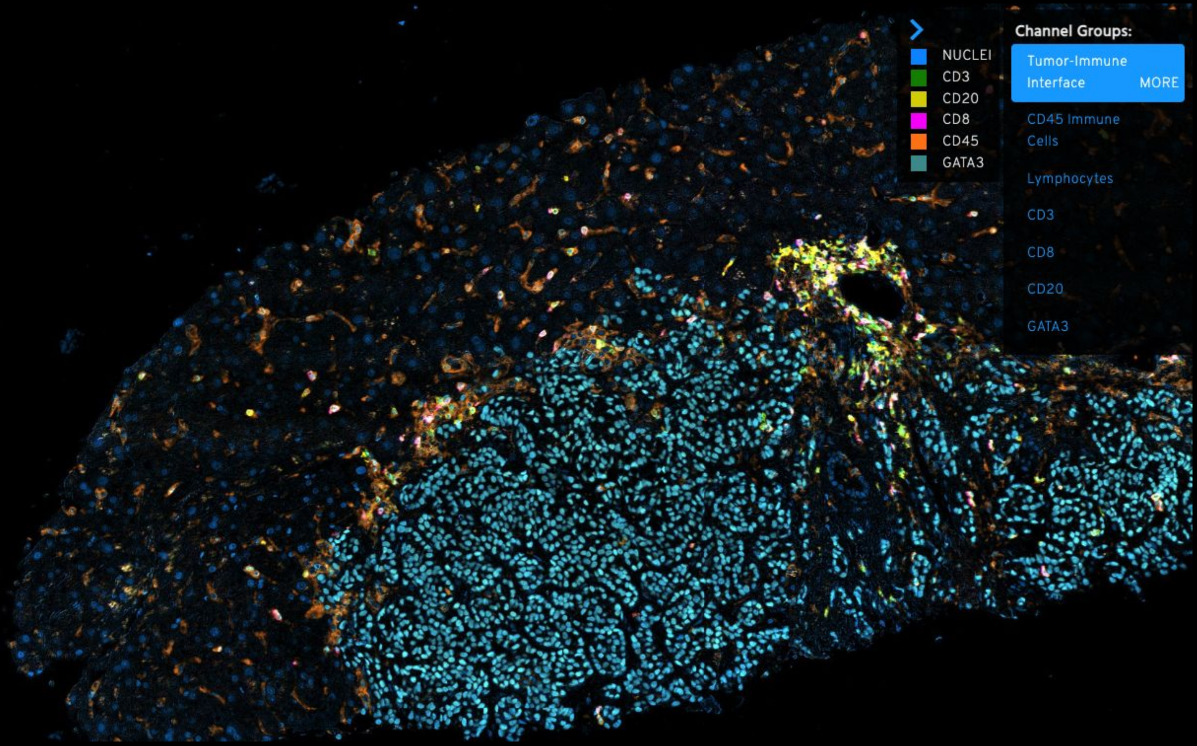
HTAN is a National Cancer Institute (NCI)-funded Cancer Moonshot^{SM} initiative to construct 3-dimensional atlases of the dynamic cellular, morphological, and molecular features of human cancers as they evolve from precancerous lesions to advanced disease. (*Cell April 2020*)

Data Release V6.1 (Last updated 2024-11-05)

Sharing data from the HTAN Consortium

HTAN is focused on **transitions** in cancer





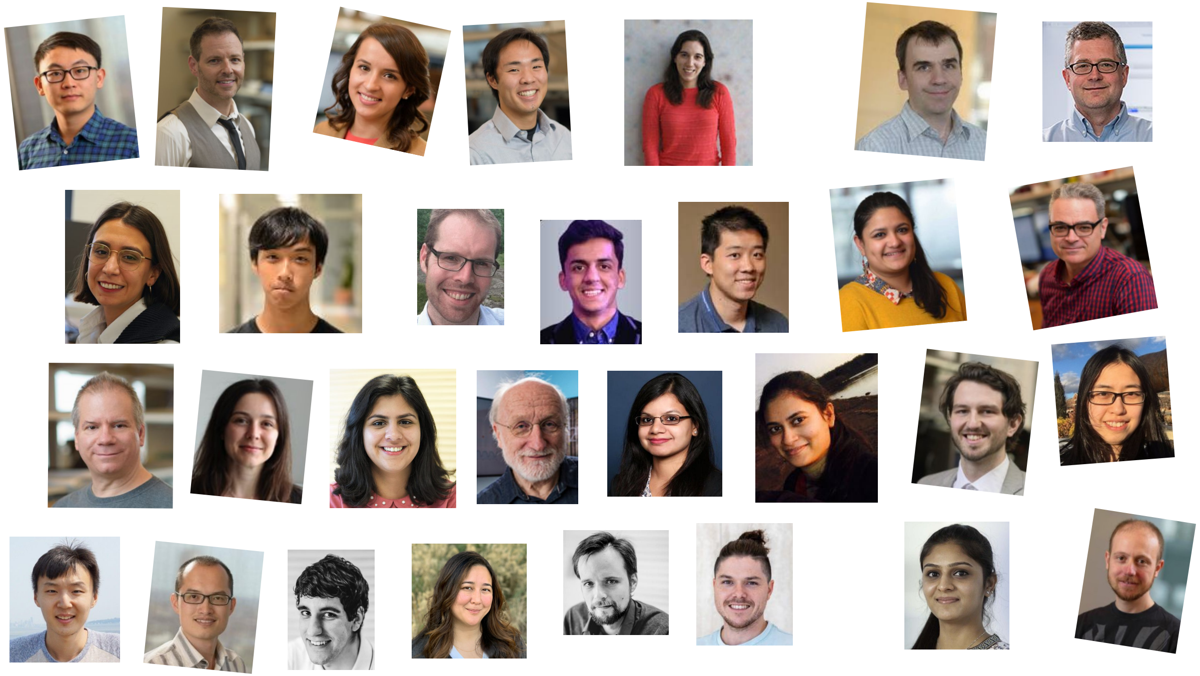
Lymphocytes in breast cancer liver metastasis biopsy (OHSU HTAN Atlas).

Most HTAN groups have a focus on single cell and multi-plex imaging modalities

cBioPortal FOR CANCER GENOMICS

Many thanks to these amazing teams!

HTAN HUMAN TUMOR ATLAS NETWORK



Memorial Sloan-Kettering Cancer Center

Dana-Farber Cancer Institute

UHN Toronto General Toronto Western Princess Margaret Toronto Rehab

AACR American Association for Cancer Research

FOUNDATION gray.

The Hyve

The Children's Hospital of Philadelphia

SE4BIO

ITCR Informatics Technology for Cancer Research

Kravis Center for Molecular Oncology

BREAK THROUGH CANCER

MOVEMBER FOUNDATION

Prostate Cancer Foundation Curing Together.

cholangiocarcinoma FOUNDATION

Memorial Sloan-Kettering Cancer Center

Dana-Farber Cancer Institute

SageBionetworks

NIH NATIONAL CANCER INSTITUTE

NCI CANCER MOONSHOT Human Tumor Atlas Network A program of the National Cancer Institute of the National Institutes of Health

Bruce W. Herr II, *Indiana University (HuBMAP)*

Human Reference Atlas 5-star Linked Open Data: Construction, Publication, and Usage

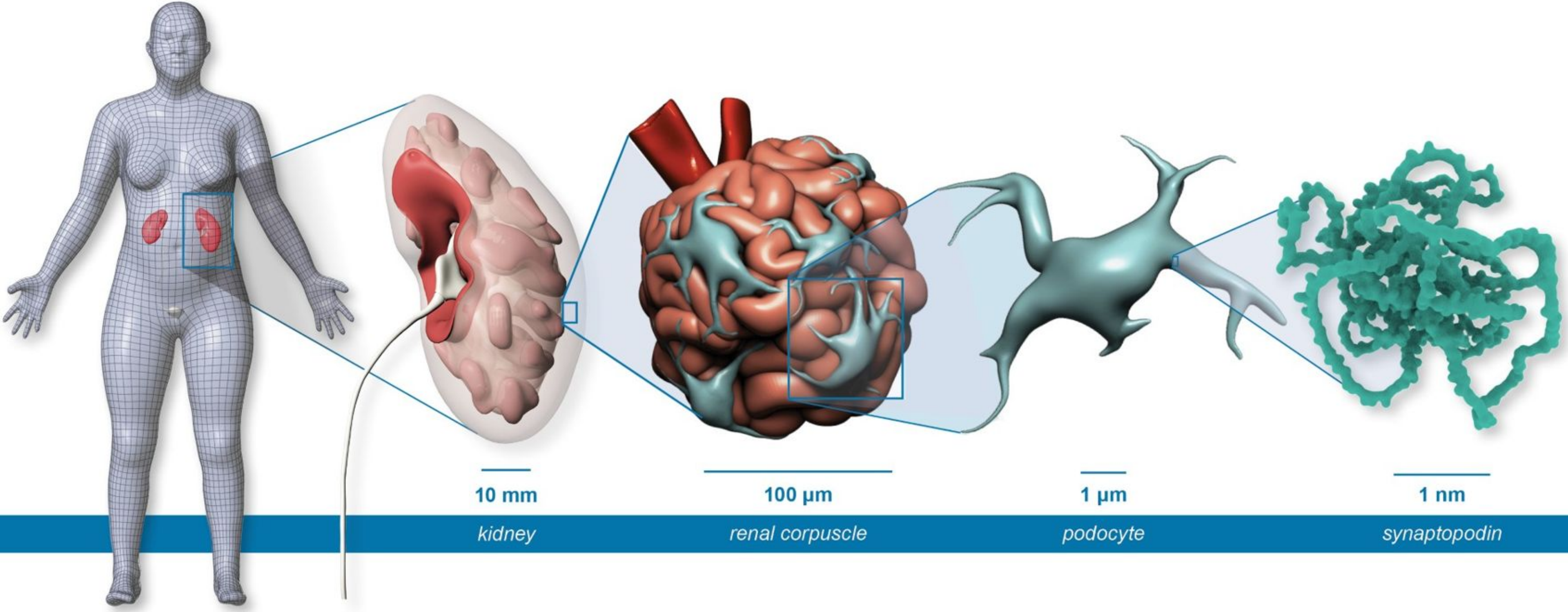
Bruce W. Herr II
Technical Director

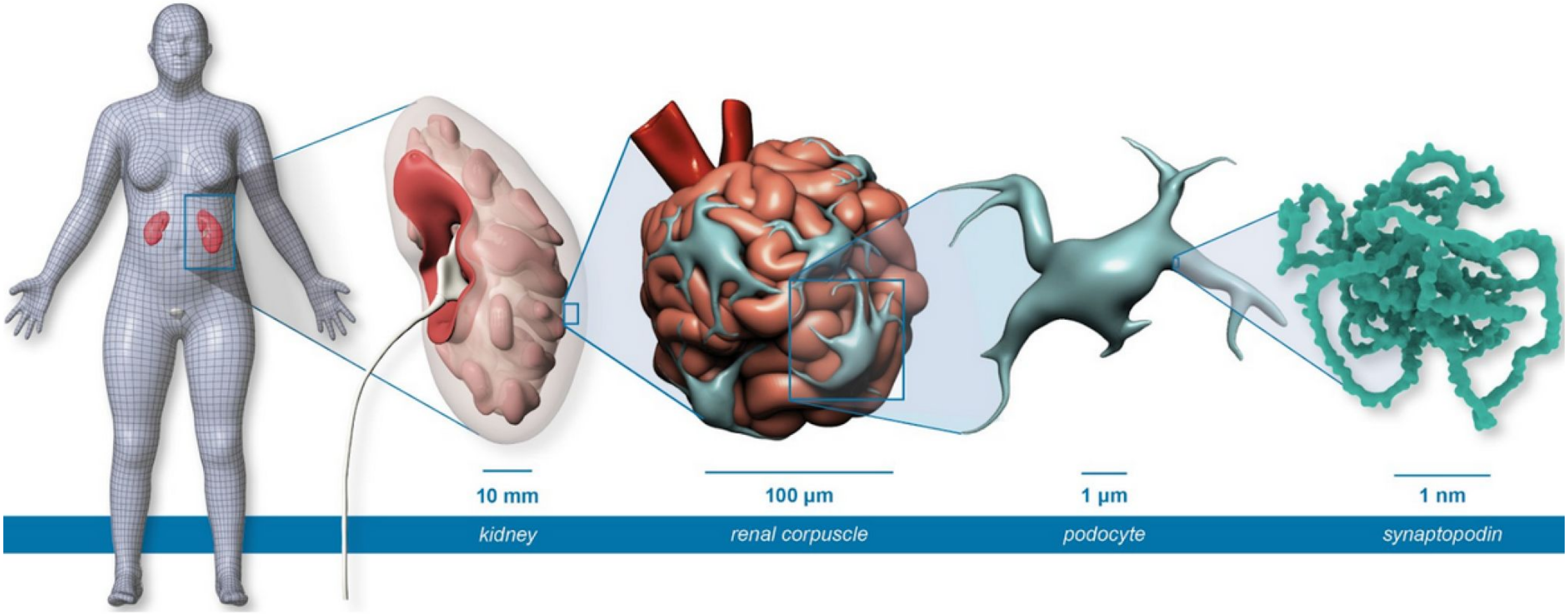
Cyberinfrastructure for Network Science Center
Department of Intelligent Systems Engineering
Luddy School of Informatics, Computing, and Engineering
Indiana University, Bloomington, IN, USA

24 Hour “Multiscale Human” Event | FAIR & Scalable Infrastructures | Virtual | December 15, 2024

Human Reference Atlas (HRA)

A comprehensive, ontologically aligned, high-resolution, three-dimensional, multiscale atlas of anatomical structures and cells in the healthy human body



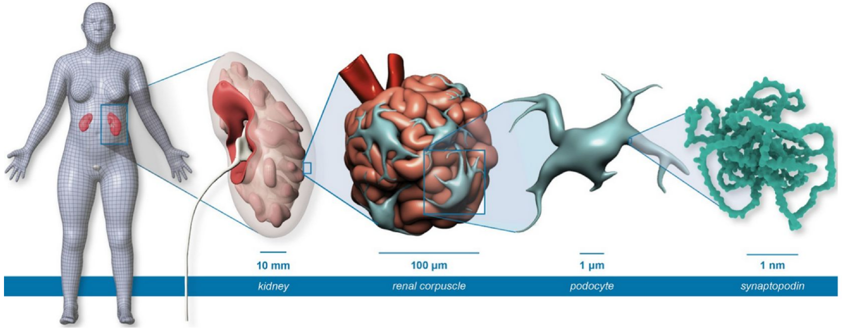


Anatomical Structures

Functional Tissue Units

Cell Types

Biomarkers Genes, Proteins, ..



Anatomical Structures | Functional Tissue Units | Cell Types | Biomarkers Genes, Proteins, .. | **Biology**

Anatomical Structures, Cell Types, and Biomarkers Tables | **Atlas**

3D Reference Organs | 2D FTU Illustrations | Organ Mapping Antibody Panels

Vascular Geometry

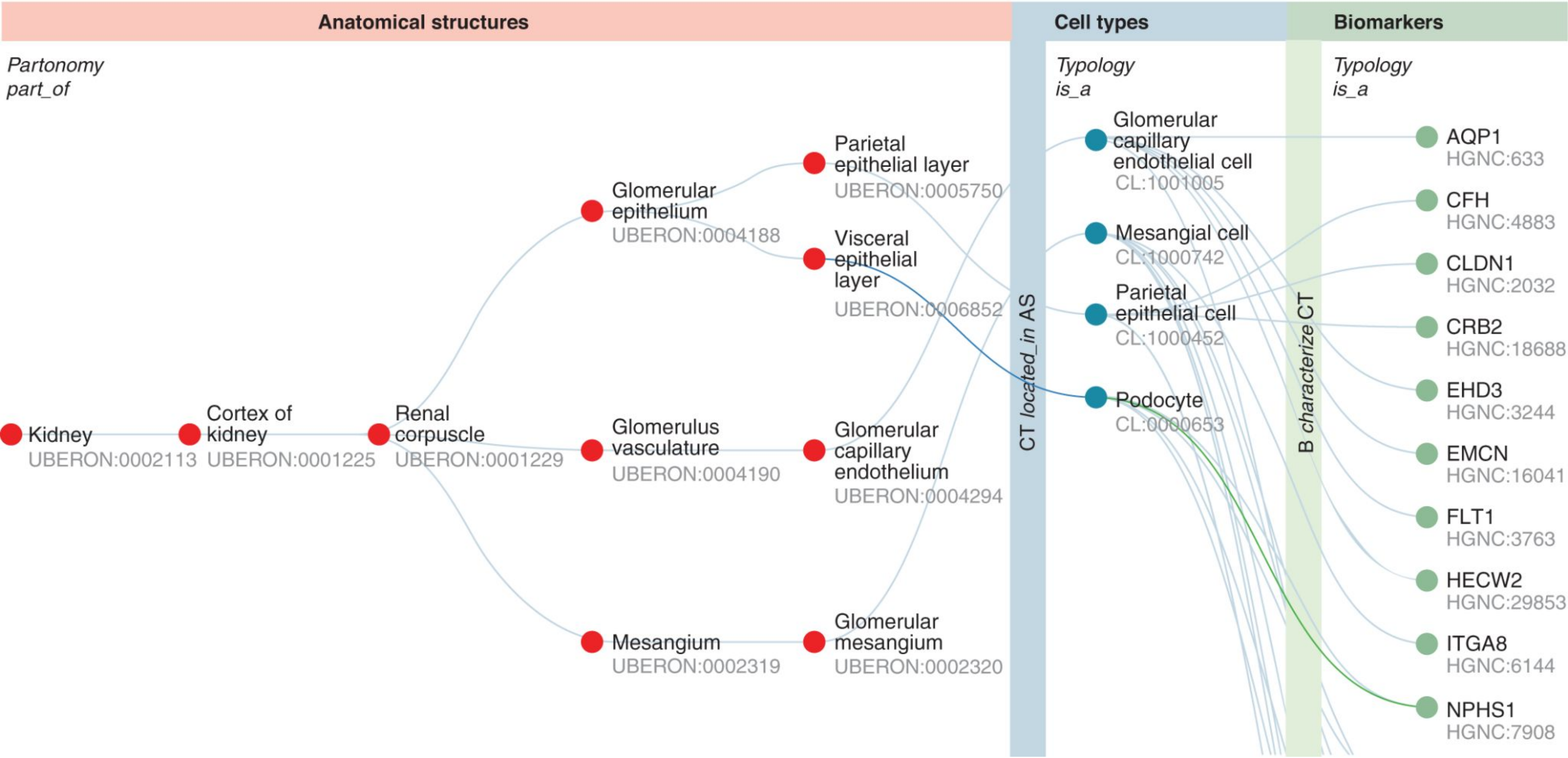
Cell Type Annotations ★

Experimental Data (Donors, Tissues, Extraction Sites, Datasets) | **Atlas++**

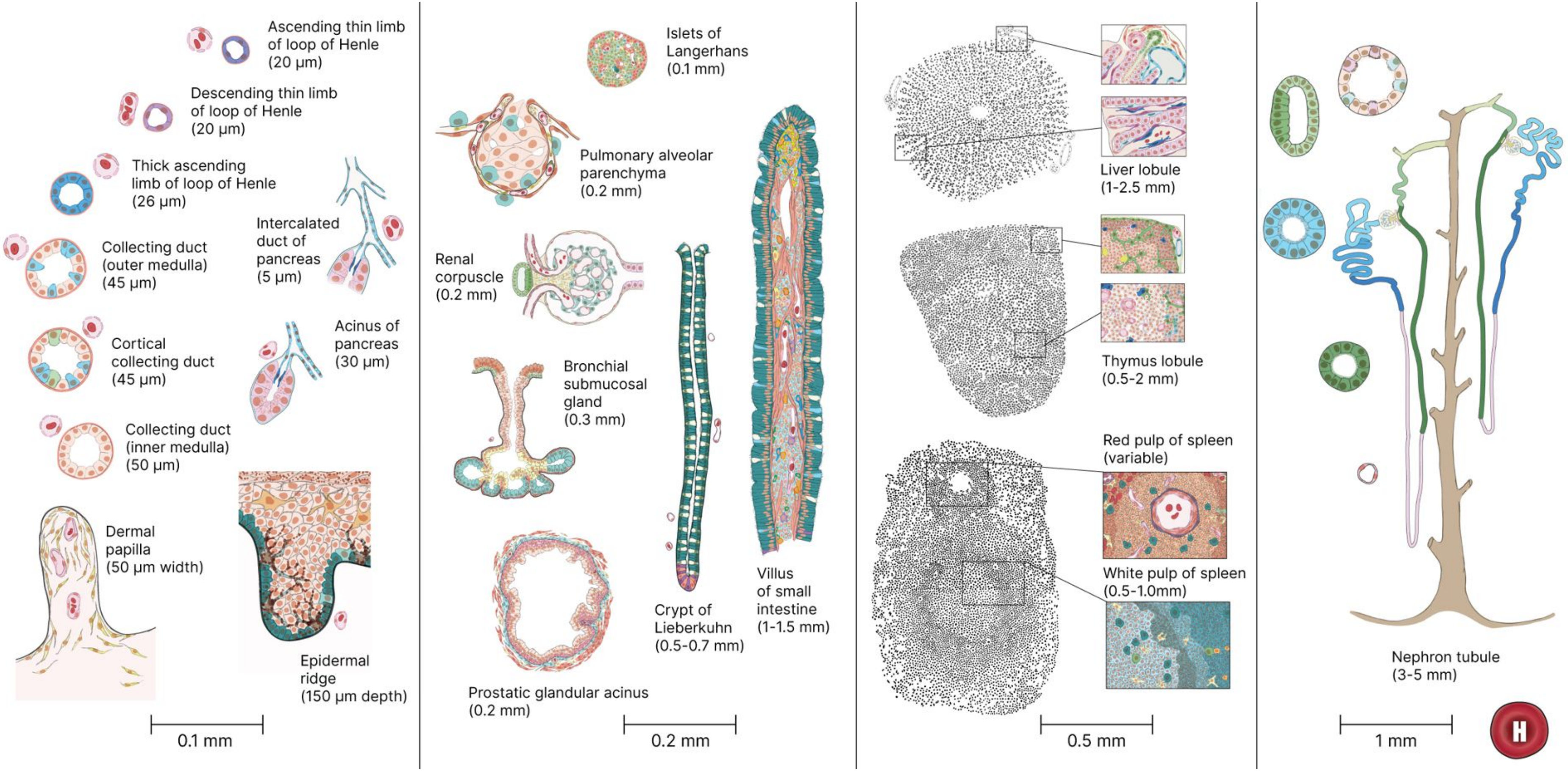
HRApop (Experimental Data + Cell Summaries)

HRAlit (HRA-relevant Literature)

HRA ASCT+B Tables

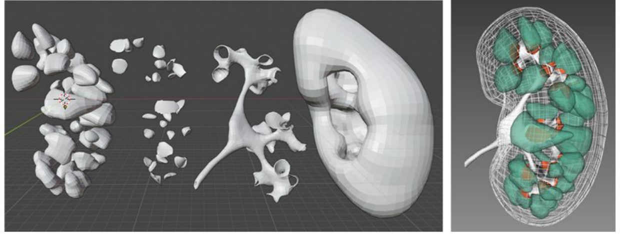


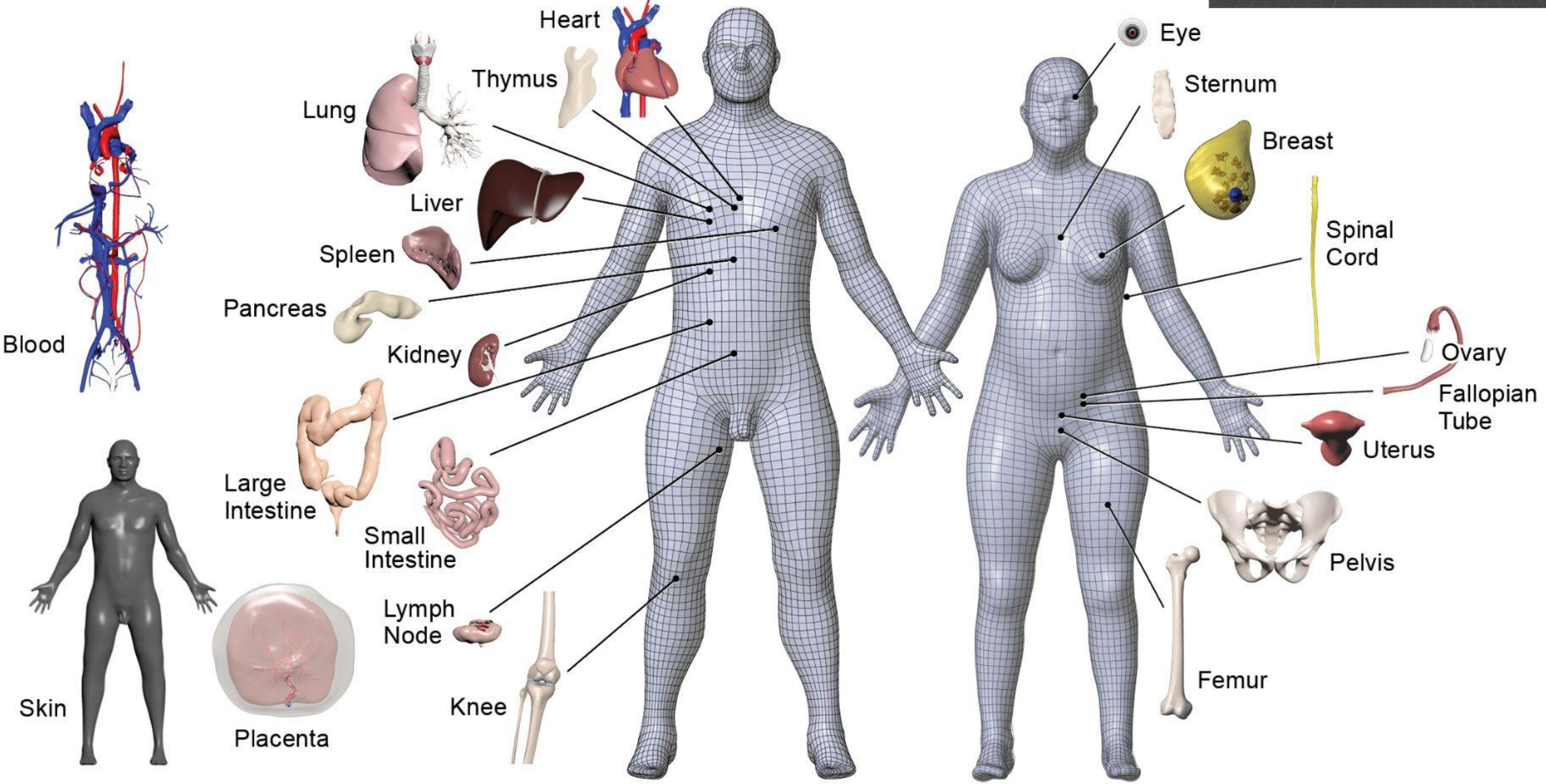
HRA Functional Tissue Unit (FTU) Illustrations



https://www.biorxiv.org/content/10.1101/2023.10.16.562593v3 | Data: https://humanatlas.io/2d-ftu-illustrations

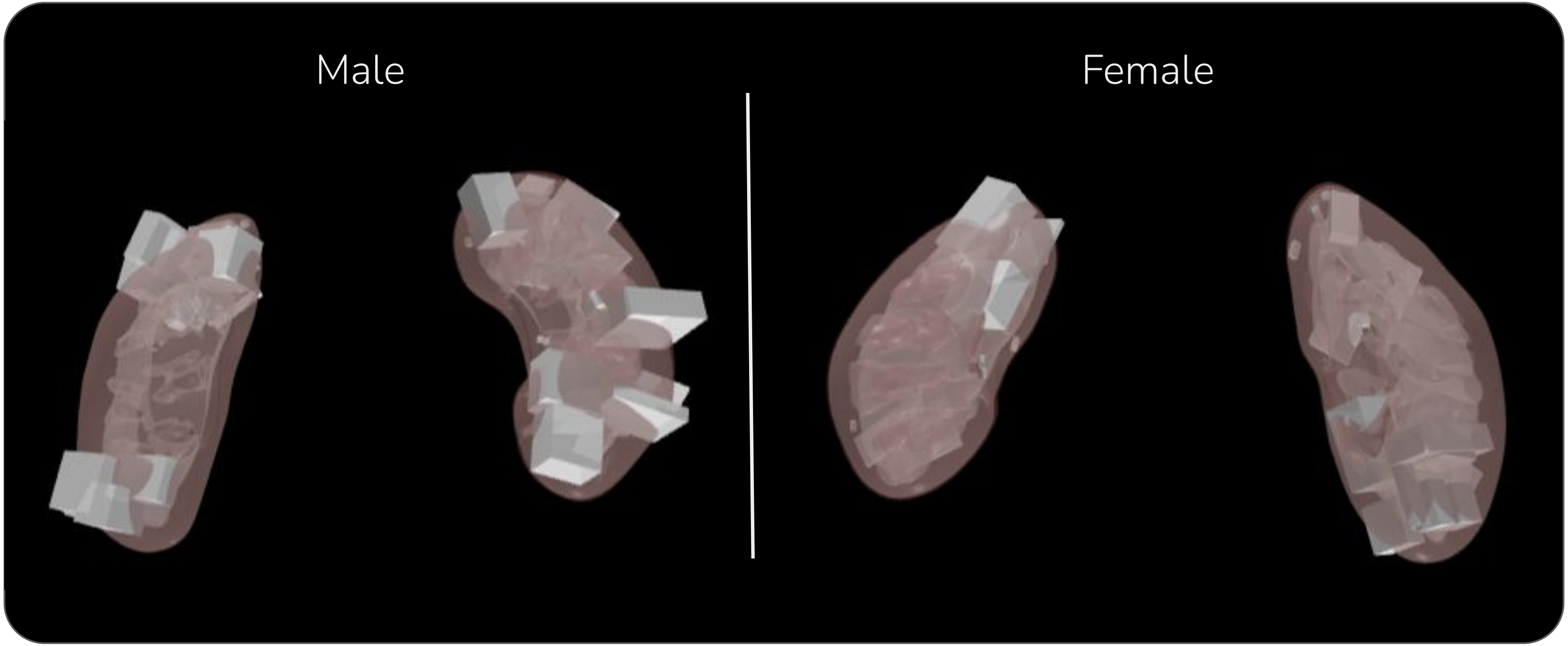
HRA 3D Reference Organs





https://www.nature.com/articles/s42003-022-03644-x | Data: https://humanatlas.io/3d-reference-library

HRA 3D Reference Organs: kidneys



126 tissue blocks with 1,198 datasets from 4 consortia

HRA Knowledge Graph Framework

Anatomical Structures, Cell Types, and Biomarkers Tables

3D Reference Organs

2D FTU Illustrations

Organ Mapping Antibody Panels

Vascular Geometry

Atlas

Experimental Data (Donors, Tissues, Extraction Sites, Datasets)

HRApop (Experimental Data + Cell Summaries)

HRAlit (HRA-relevant Literature)

Atlas++

Digital Object

HRA Digital Object Processor

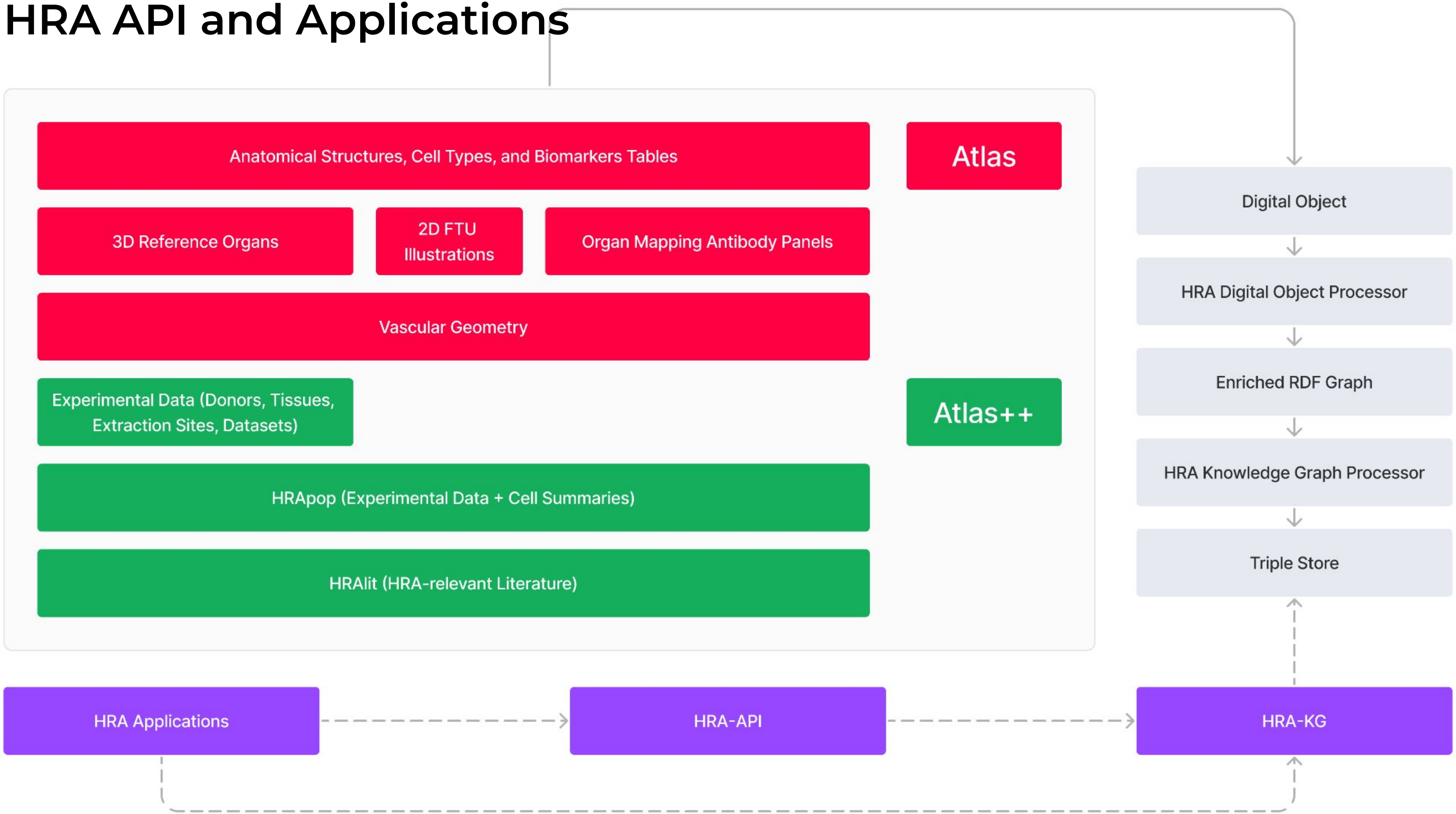
Enriched RDF Graph

HRA Knowledge Graph Processor

Triple Store

HRA-KG

HRA API and Applications



Anatomical Structures, Cell Types, and Biomarkers Tables

Atlas

3D Reference Organs

2D FTU Illustrations

Organ Mapping Antibody Panels

Vascular Geometry

Experimental Data (Donors, Tissues, Extraction Sites, Datasets)

Atlas++

HRApop (Experimental Data + Cell Summaries)

HRAlit (HRA-relevant Literature)

Digital Object

HRA Digital Object Processor

Enriched RDF Graph

HRA Knowledge Graph Processor

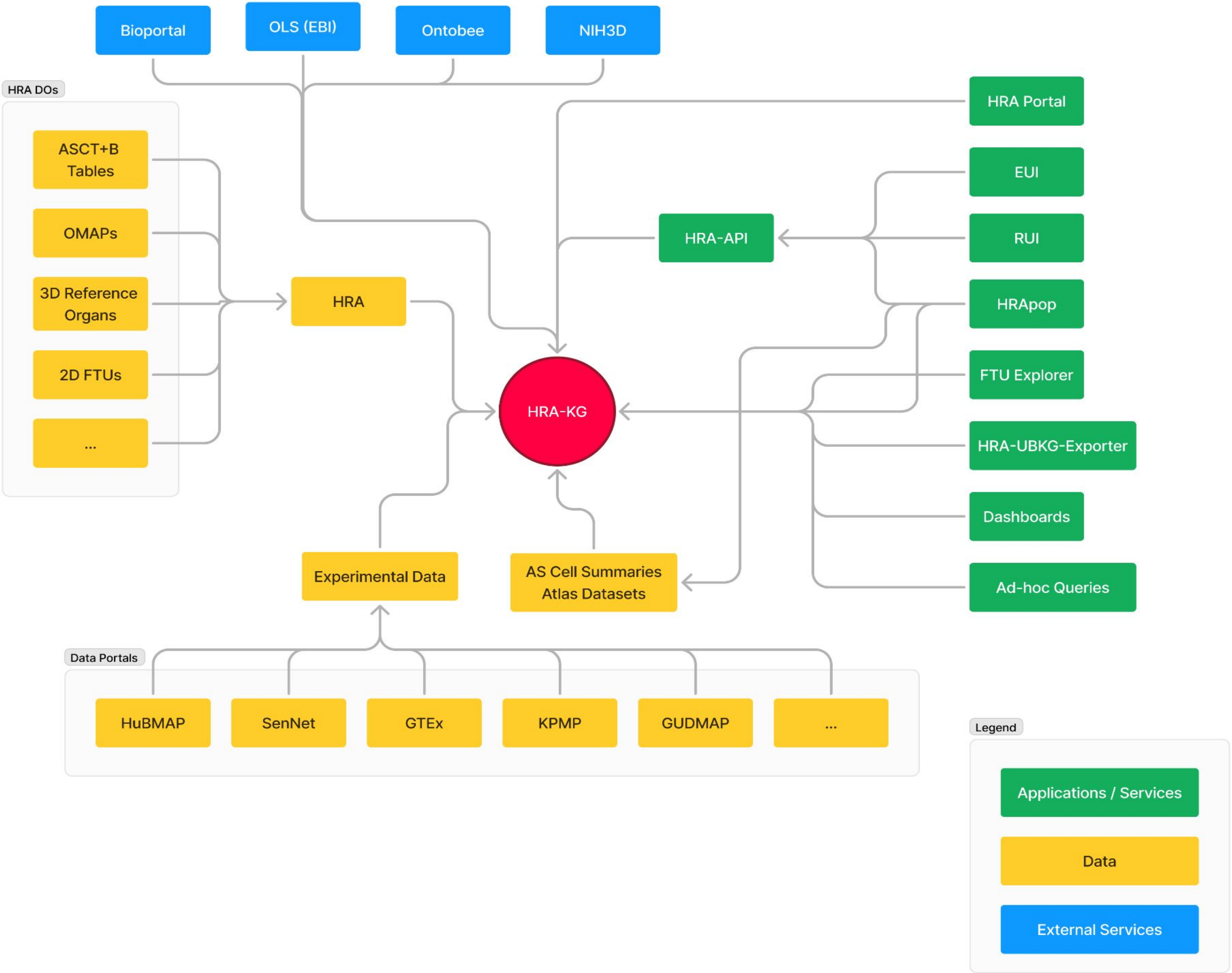
Triple Store

HRA Applications

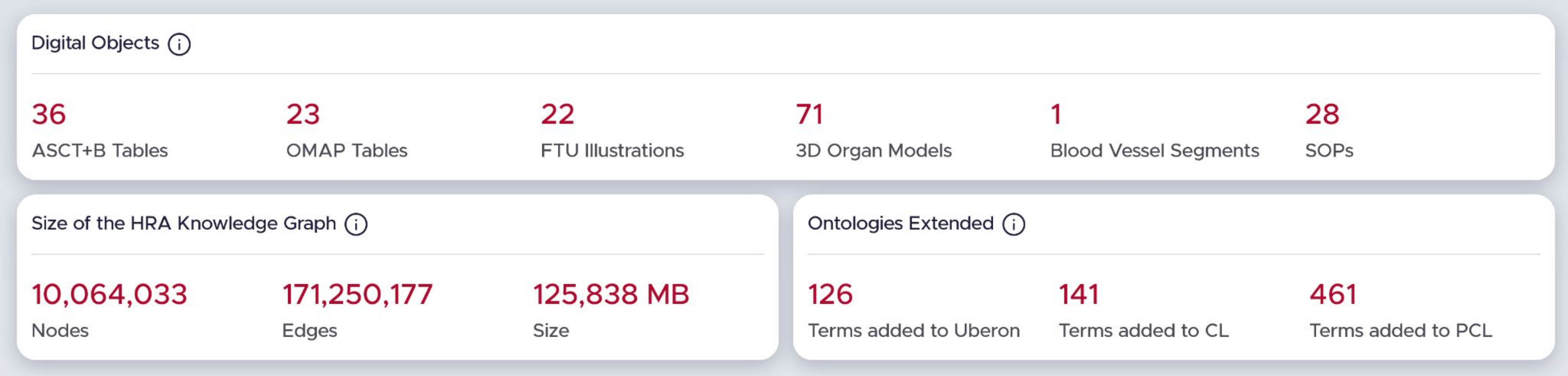
HRA-API

HRA-KG

HRA Ecosystem



HRA KG Data



Digital Objects

36	23	22	71	1	28
ASCT+B Tables	OMAP Tables	FTU Illustrations	3D Organ Models	Blood Vessel Segments	SOPs

Size of the HRA Knowledge Graph

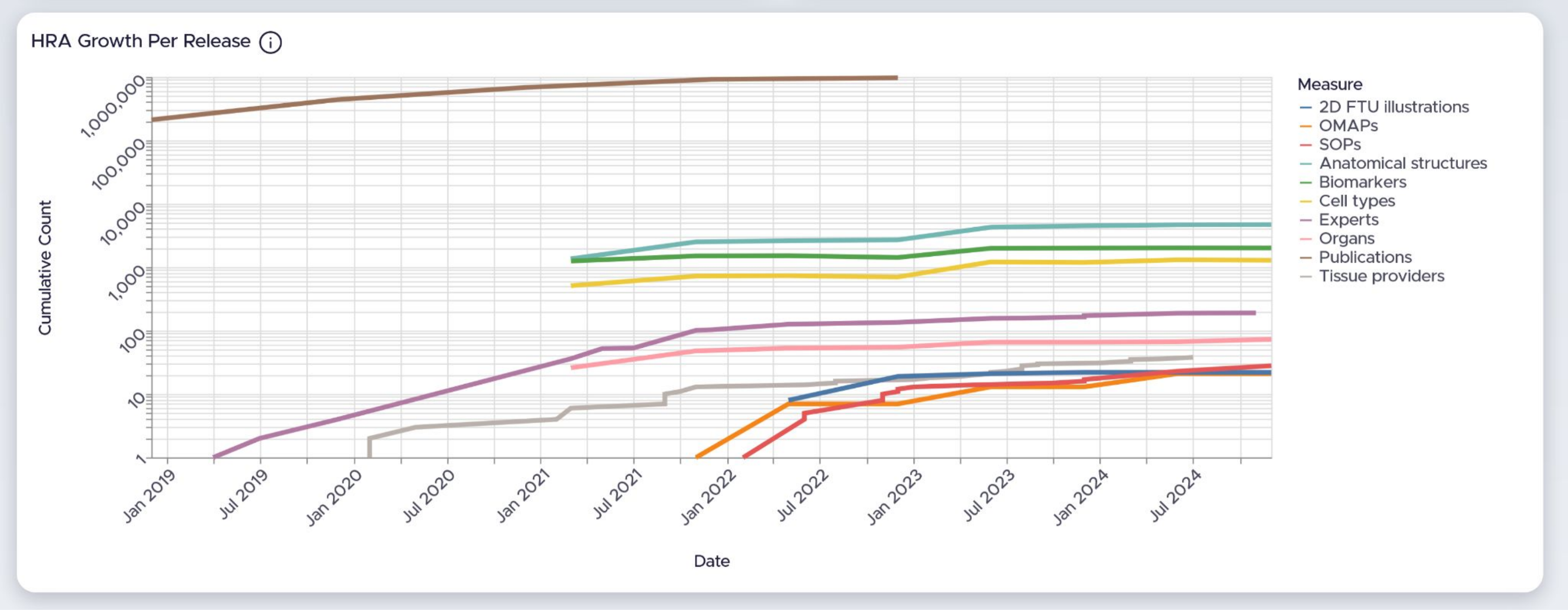
10,064,033	171,250,177	125,838 MB
Nodes	Edges	Size

Ontologies Extended

126	141	461
Terms added to Uberon	Terms added to CL	Terms added to PCL

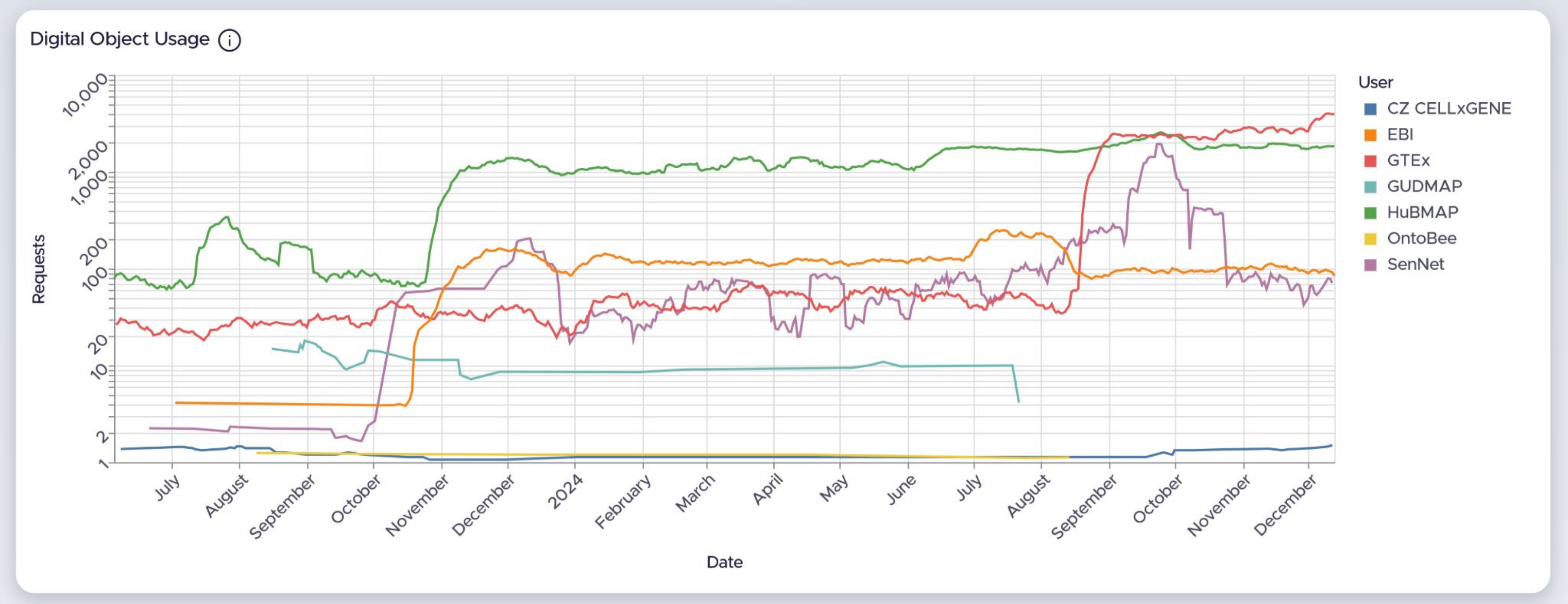
https://apps.humanatlas.io/dashboard/data

HRA KG Data

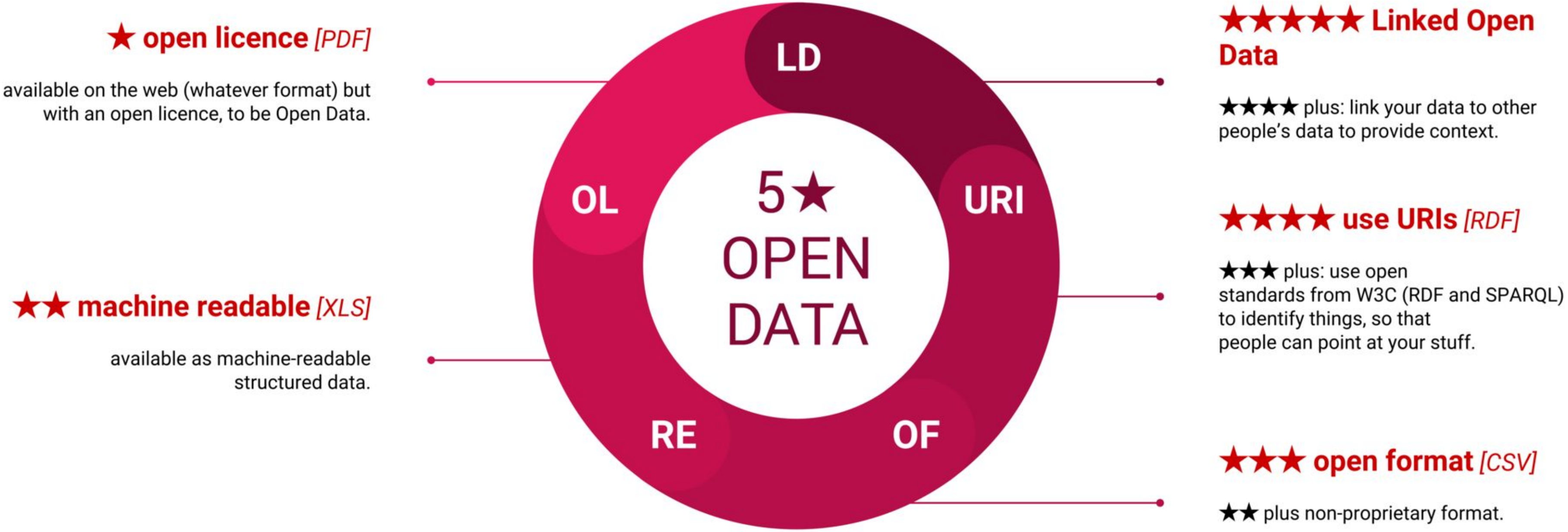


https://apps.humanatlas.io/dashboard/data

HRA KG (and other HRA products) usage



https://apps.humanatlas.io/dashboard/usage



★ open licence *[PDF]*

available on the web (whatever format) but with an open licence, to be Open Data.

★★ machine readable *[XLS]*

available as machine-readable structured data.

★★★★★ Linked Open Data

★★★★ plus: link your data to other people's data to provide context.

★★★★ use URIs *[RDF]*

★★★ plus: use open standards from W3C (RDF and SPARQL) to identify things, so that people can point at your stuff.

★★★ open format *[CSV]*

★★ plus non-proprietary format.

By Florian Thiery - Own work, CC BY 4.0, https://commons.wikimedia.org/w/index.php?curid=78100348

5 Star Linked Open Data

URLs:

- **purl**.humanatlas.io (permanent identifiers)
- **lod**.humanatlas.io (hosts digital object metadata as DCAT Datasets)
- **cdn**.humanatlas.io (hosts raw data files)

Content Negotiation:

- **purl** returns the digital object data based on accept header
  - Redirect to **lod** for humans, JSON or RDF Formats for machines
- **lod** returns the digital object metadata based on accept header
  - Return HTML for humans, JSON or RDF Formats for machines

Infrastructure

- **HRA KG** data is pre-computed and uploaded to *Amazon S3*.
- **purl/lod/cdn**.humanatlas.io is hosted using *Amazon CloudFront* which returns data hosted on *Amazon S3* and implements content negotiation via *Amazon CloudFront Functions*.
- The latest version of each digital object in RDF format is loaded into a *Blazegraph* SPARQL server hosted by *Amazon ECS* and available via *Amazon CloudFront* at https://lod.humanatlas.io/sparql. This allows ad-hoc queries of HRA KG data using SPARQL.

Scalability

- With the use of pre-computed data and hosting them as static files means the solution scales massively with low technical complexity.
- Caching from *Amazon CloudFront* and static files makes it extremely fast.
- *Blazegraph* can scale to billions of edges allowing fast ad-hoc queries.

FAIRness

- All data is represented in standard RDF format using standard ontologies and terminology where possible.
- Uses a well known Linked Open Data pattern.
- All data is CC BY 4 and code is MIT licensed.

Jonathan Silverstein, *University of Pittsburgh, HuBMAP and SenNet*

24hr - HuBMAP and SenNet FAIR and Scalable Infrastructures

Presented by

Jonathan Silverstein, Phil Blood, Nils Gehlenborg, Kay Metis

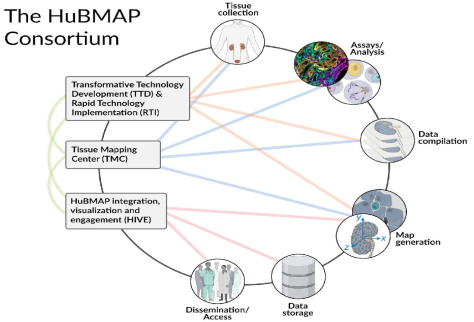
SenNet (and HuBMAP) DCC Team

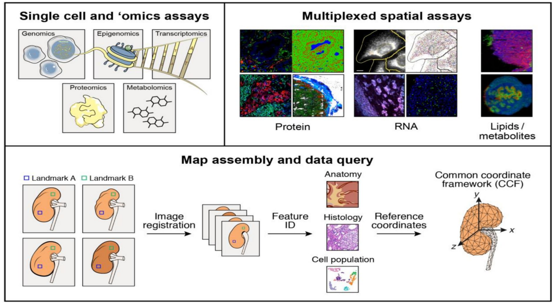
Adams, Andrew	Information Security Officer	Maier, Elizabeth	UX Designer
Adams, Etowah	Software Developer	Metis, Kay	Executive Director
Alkathan, Mariam	Project Manager	Misra, Gaurab	Project Manager
Bar-Joseph, Ziv	**PD/PI**	Moerth, Eric	Software Developer
Betancur, David	Senior Software Engineer	Morgan, Richard	Project Manager
Bidanta, Supriya	Graduate Student (research assistant)	Nguyen, Nam	Postdoctoral Scholar
Bisciotti, Joe	Project Manager	Niculcea, Emily	Staff
Blood, Philip	**PD/PI**	Puerto, Juan	Cloud Developer
Bolin, Axel	Programmer	Qaurooni, Danial	Postdoctoral Scholar, Fellow,
Borner, Katy	**Co-Investigator**	Ropelewski, Alexandar J	Senior Scientist
Bueckle, Andreas	Scientist	**Ruffalo, Matthew**	**Co-Investigator**
Burke, Christopher	Systems Engineer	Ruschman, Nancy	Project Manager
Burke, Karl	Senior Software Developer	**Satija, Rahul**	**Co-Investigator**
Cao-Berg, Ivan	Data Wrangler	Scibek, Robin	Program Management
Chiacchia, Ken	Science Writer	Shirey, Bill	Senior Software Developer
Choudhary, Saket	Postdoctoral Scholar	Sibilla, Max	Software Developer
Gehlengorg, Nils	**Co-Investigator**	**Silverstein, Jonathan C**	**PD/PI**
Ginda, Michael	Research Analyst	Simmons, Joseph Alan	Solutions Architect
Hasanaj, Euxhen	Postdoctoral Scholar	Singh, Raman Kumar	Postdoctoral Scholar
Helfer, Jesse	Project Manager	Smith, Tracey	Project Coordinator
Herr, Bruce William	Systems Architect	Soleiman, Natasha	Project Manager
Honick, Brendan	Data Curator and Metadata Librarian	Song, Qi	Graduate Student (research assistant)
Jain, Yashvardhan	Research Software Developer	Turner, Morgan	R&D Manager
Kenney, Mariah	Data Curator and Metadata Librarian	Uranic, Jackie	Data Curator and Metadata LIbrarian
Klinesmith, Holly	Communications Coordiantor	Varney, Lisa Ann	Software Developer
Lee, Young Je	Postdoctoral Scholar	Yuan, Zhou	Senior Software Developer
Madonna, Tyler	Programmer		

HuBMAP

Develop an open and global platform to map healthy cells in the human body and determine how relationships among cells affect human health

The Human Body at Cellular Resolution: The NIH Human Biomolecular Atlas Program. Snyder et al. *Nature*. 574, p. 187-192 (2019)

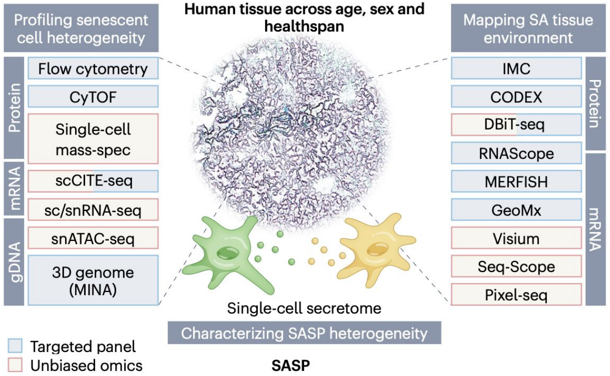




SenNet

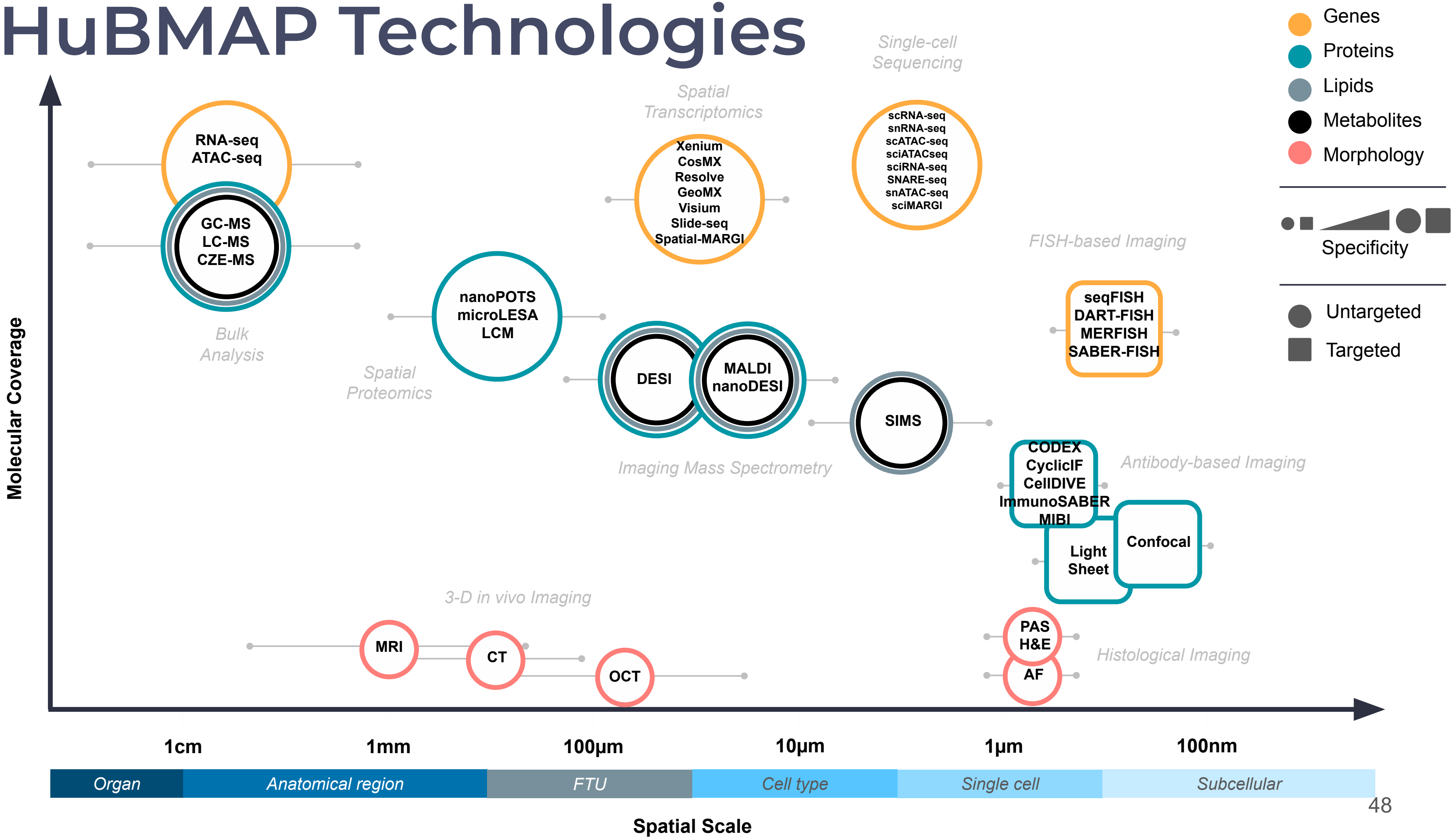
Identify and functionally characterize the heterogeneity of senescent cells across multiple tissues in human health and lifespan at single cell resolution

NIH SenNet Consortium to map senescent cells throughout the human lifespan to understand physiological health. SenNet Consortium. *Nature Aging* 2, 1090–1100 (2022)



NIH Common Fund Programs: The NIH Common Fund supports bold scientific programs that catalyze discovery across all biomedical and behavioral research. These programs enable NIH Institutes and Centers to collaborate on innovative research expected to address high priority challenges for the NIH as a whole. Each Common Fund Program typically supports dozens of centers with hundreds of millions of dollars in funding and are up to ten years in length. We lead the Infrastructure, Engagement, and Data Processing/Coordination for the two Common Fund programs HuBMAP and SenNet.

HuBMAP Technologies



PSC: A place for getting research done…

National service provider

BRIDGES-2

XSEDE Extreme Science and Engineering Discovery Environment

NSF

ACCESS

Collaborative Research

SenNet

HuBMAP

Education and training

PSC IS A JOINT COMPUTATIONAL RESEARCH CENTER BETWEEN **CARNEGIE MELLON UNIVERSITY** AND THE **UNIVERSITY OF PITTSBURGH**.

39 years of leadership

23 HPC systems
(11 of which were the first or unique)

Pioneering Artificial Intelligence and Research Computing.

CMU/Pitt Community

Networking and security

3ROX THREE RIVERS OPTICAL EXCHANGE

TRUSTED CI THE NSF CYBERSECURITY CENTER OF EXCELLENCE

ResearchSOC

Industry Partners

cerebras

Hewlett Packard Enterprise

DOROTHY AI

NVIDIA

PPG

Pitt’s high-performance computing upgrade signals accelerated translational research

By Brian Buntz | March 28, 2024

Jonathan Silverstein, professor and chief research informatics officer, and Kay Métis, Executive Director Programs and Strategic Initiatives, in the Network Operations Center (NOC) with the systems that Dell awarded to the University. (Tom Altany/University of Pittsburgh)

The University of Pittsburgh’s recent, significant expansion of its high-performance computing capabilities, courtesy of a gift from Dell Technologies, indicates a strategic commitment to using large-scale data analysis for faster translational research. The additional 9.672 gigaFLOPS of computational power – translating to nearly 9.7 trillion additional computations per second – could help Pitt’s Innovation Hub for Health Science Medical Research attract research funding in areas such as precision medicine, drug discovery, and disease modeling. Interest in high-performance computing in drug discovery has ramped up in recent years.

“These large collaborative projects, which involve hundreds of investigators, utilize a unique computational architecture we’ve installed on the Dell system,” said Jonathan C. Silverstein, MD, professor and chief research informatics officer at the University of Pittsburgh. The new system will enable secure, large-scale processing of image, genomic, and proteomic data to generate cellular and molecular maps for research.

Consortium Undergraduate Student Program

The Consortium Undergraduate Student Program is a summer research internship program for undergraduate students hosted by laboratories participating in the NIH Common Fund's Cellular Senescence (SenNet) Program.

Earlier this summer, SenNet welcomed the 2024 CUSP student cohort, all of whom interned at SenNet research sites. Get to know our 2024 CUSP students here.

If you're interested in applying to a future CUSP cohort, please view our CUSP overview video, which features interviews with our very first CUSP cohort as they detail their experiences in the program.

For more information on CUSP, either visit the CUSP homepage or contact cusp@sennetconsortium.org.

The SenNet Interview Series

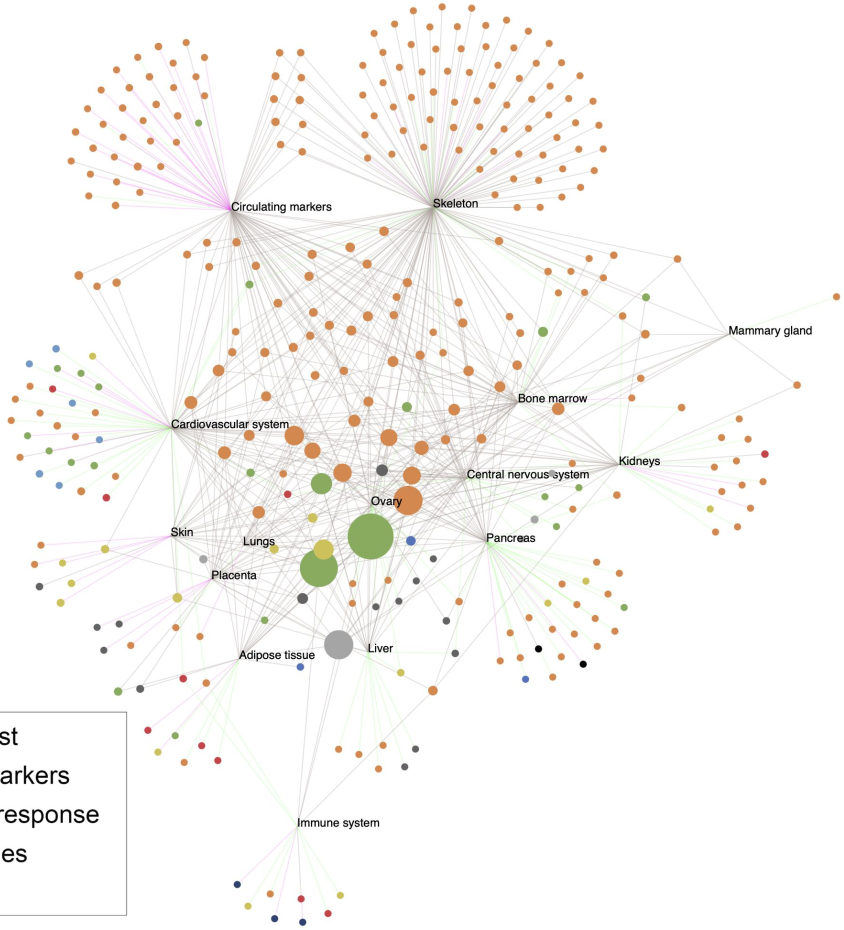
The SenNet Interview Series is an anthology of video interviews profiling the researchers contributing to the SenNet Consortium. In these interviews, scientists offer candid insights into their ongoing senescence research, initiatives within the Consortium, and the ways in which SenNet functions as both a community and a resource for senescence researchers across the U.S.

The scientists interviewed discuss their backgrounds and what initially drew them to the field of senescence research. They also share their learned experience for junior investigators and students interested in this field.

All published interviews can be watched here.

Consider subscribing to our YouTube page to be notified as soon as new interviews go live.

SenNet Biomarkers



https://docs.sennetconsortium.org/biomarkers/

Suryadevara, V., Hudgins, A.D., Rajesh, A. *et al.* SenNet recommendations for detecting senescent cells in different tissues. *Nat Rev Mol Cell Biol* (2024). https://doi.org/10.1038/s41580-024-00738-8

🟦 Resistance to apoptosis
🟧 SASP/Inflammation
⬜ Increased lysosomal content
🟥 Metabolic adaptions
🟦 Changes in morphology
🟩 Cell cycle arrest
🟦 Cell surface markers
🟨 DNA damage response
⬛ Nuclear changes

HuBMAP and SenNet Features

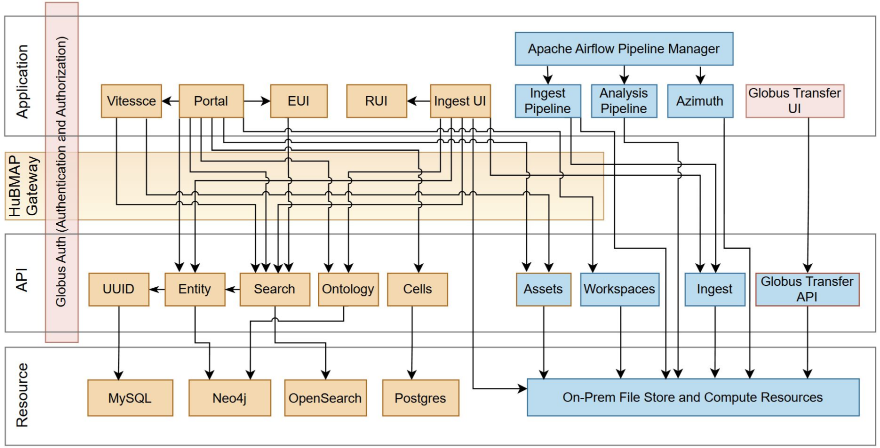
Designed for FAIRness of Data and Software

- **Flexible hybrid cloud microservices architecture** for efficient data storage, easy software integration, low barriers to computing on data (**free**, leveraging PSC national resources)
- **Portable/interoperable/reusable/reproducible pipelines** with harmonized processing
- **Robust provenance** with unique identifiers
- **Ontologies and standardized and detailed metadata** with CEDAR templates
- **Community standards** for publishing findable and accessible APIs and data
- **Open software, data, and publication policies**

Deeply collaborative: PSC and Pitt jointly designed the architecture and build and run all the backend data infrastructure and collaborate with CMU CompBio, Indiana U., Harvard, New York Genome Center and U. Florida on tools.

Software resources for atlas building: dozens of github repositories and API endpoints, reused and updated across consortia

Flexible Hybrid Cloud Microservices Architecture



HuBMAP Flexible Hybrid Cloud Microservices Architecture: AWS PSC Globus

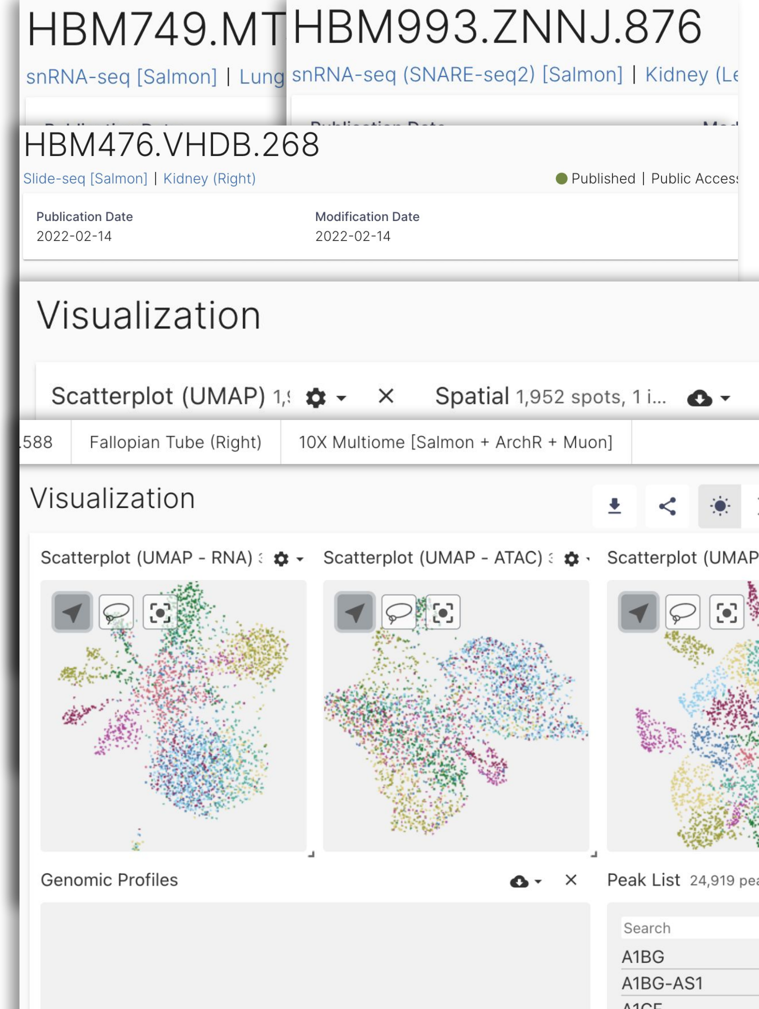
Human BioMolecular Atlas Program (HuBMAP): 3D Human Reference Atlas Construction and Usage.
Borner, et al. bioRxiv 2024.03.27.587041; doi: https://doi.org/10.1101/2024.03.27.587041

Efficient data access and processing at scale: thousands of datasets on-premises, leveraging investments by NSF and others to provide **free access** national scientific community

Easy software integration: Tools wrapped and integrated as-is using CWL and Docker, e.g. Azimuth

HuBMAP Analysis Pipelines

- sc/snRNA-seq: Salmon quantification, Scanpy + scVelo downstream analysis
- sc/snATAC-seq: HISAT2 + ArchR
- Sequencing spatial transcriptomics: Salmon quantification, Scanpy + scVelo downstream analysis
  - Visium (without probes), Slide-seq
  - Harmonized with sc/snRNA-seq outputs, including output file format (addition of spatial coordinates for each capture bead)
- Multiome RNA-seq & ATAC-seq: subsets of RNA-seq and ATAC-seq pipelines used directly, embedded in multiome pipeline
- Imaging (not currently represented in ATLAS-D2K):
  - Multichannel imaging with segmentation masks: SPRM
  - CODEX (v1): Cytokit (+ SPRM)
  - PhenoCycler (CODEX v2), CellDIVE, MIBI: DeepCell (+ SPRM)
  - FISH (merFISH, DARTFISH): PIPEFISH pipeline
  - 3D segmentation and analysis: IMC complete, CODEX under development



HBM749.MT

snRNA-seq [Salmon] | Lung

HBM993.ZNNJ.876

snRNA-seq (SNARE-seq2) [Salmon] | Kidney (Le

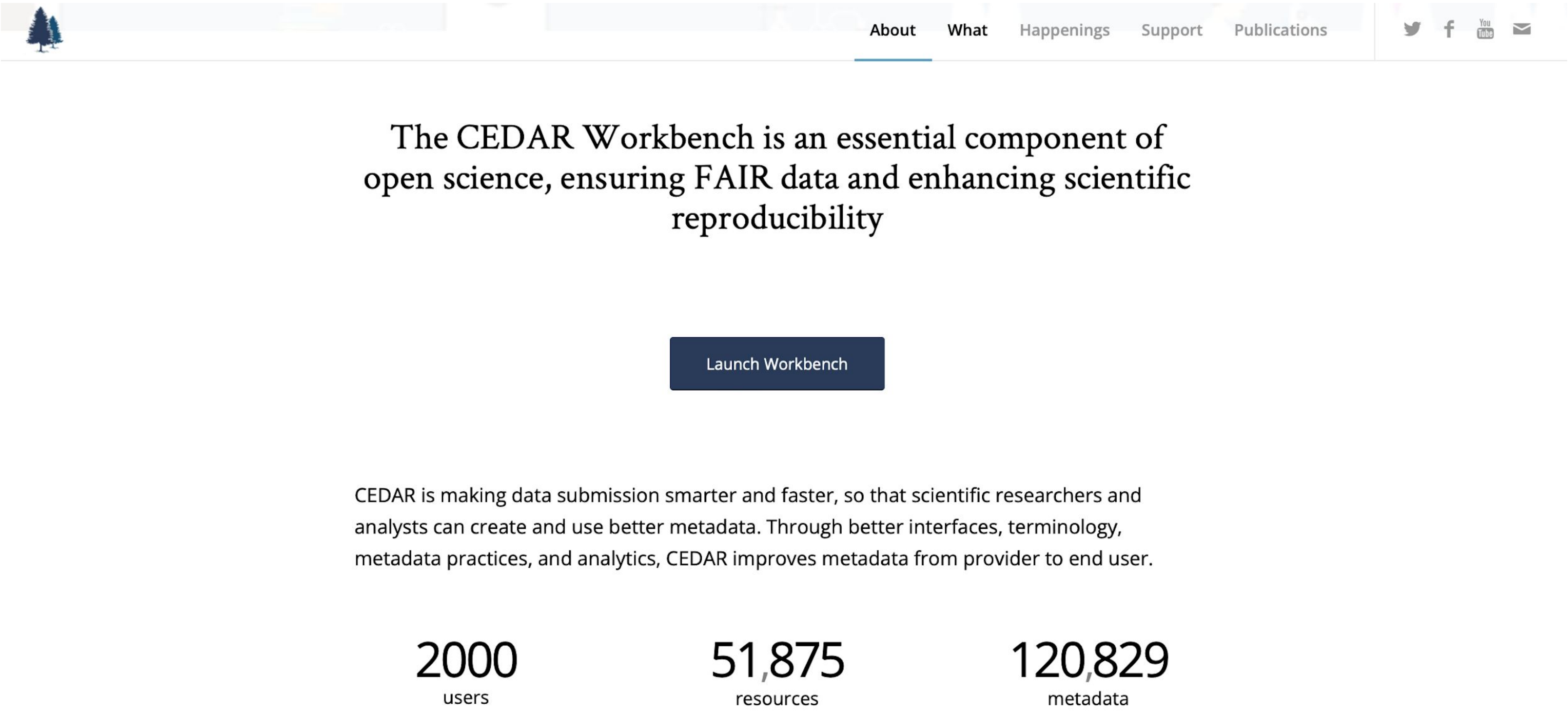
HBM476.VHDB.268

Slide-seq [Salmon] | Kidney (Right)

● Published | Public Acces

Publication Date 2022-02-14

Modification Date 2022-02-14



The CEDAR Workbench is an essential component of open science, ensuring FAIR data and enhancing scientific reproducibility

CEDAR is making data submission smarter and faster, so that scientific researchers and analysts can create and use better metadata. Through better interfaces, terminology, metadata practices, and analytics, CEDAR improves metadata from provider to end user.

2000 users

51,875 resources

120,829 metadata

FAIR principles: Acronym for Findable, Accessible, Interoperable, and Reusable, which is a way of sharing data to maximize its utility

Sequence Assays

10x Multiome

Prepare your metadata based on the latest metadata schema using one of the template files below. See the instructions in the Metadata Validation Workflow document for more information on preparing and validating your metadata.tsv file prior to submission.

Related files:

- Excel template: For metadata entry.
- TSV template: Alternative for metadata entry.

REQUIRED - For this assay, you must also prepare and submit two additional metadata.tsv files following the metadata schemas linked here for RNAseq and ATACseq. For additional documentation on this dataset type, please visit here.

Metadata schema

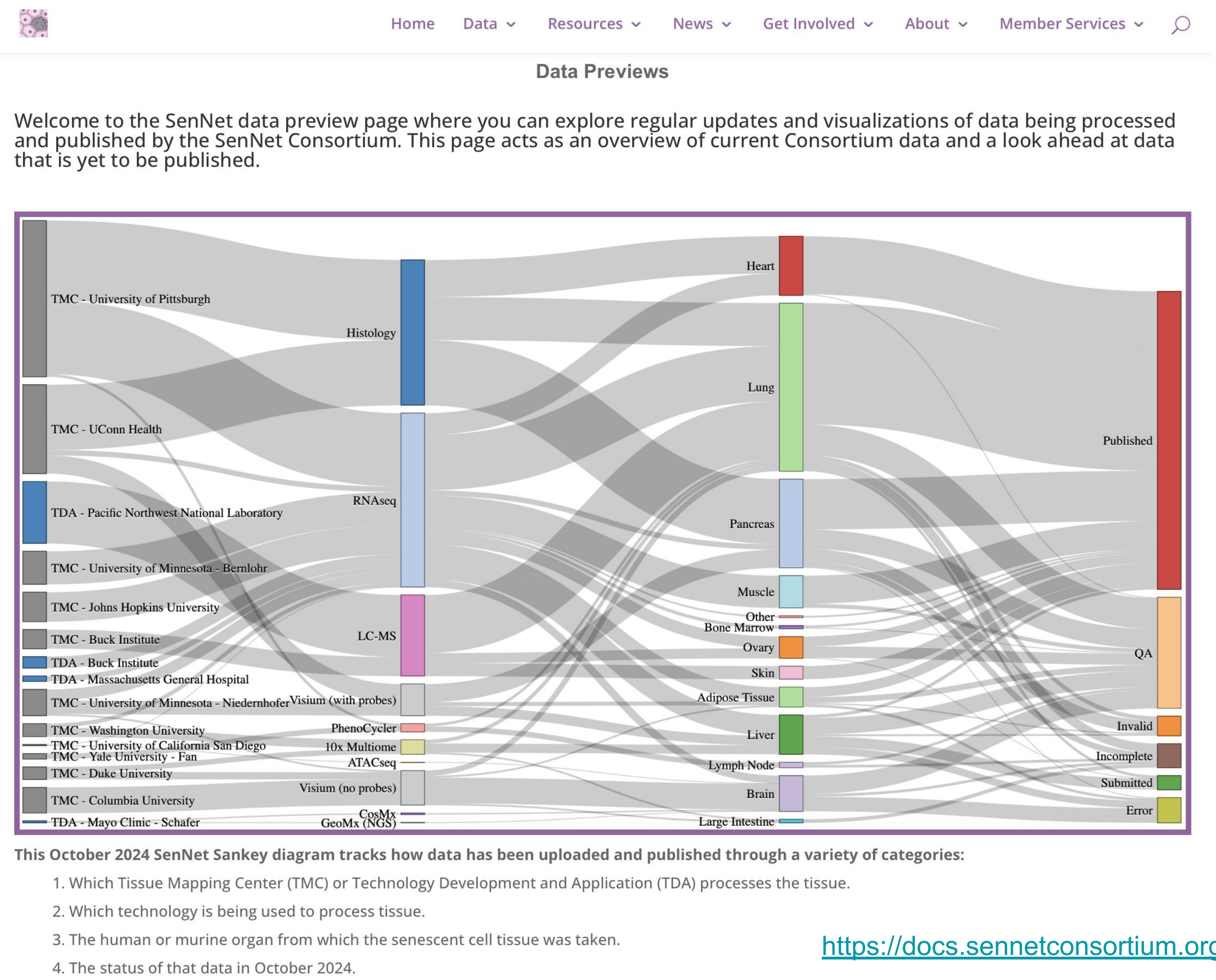
Version 2 (use this one)

Directory schemas

Version 2.0 (use this one)

pattern	required?	description
`extras\/.*`	✓	Folder for general lab-specific files related to the dataset.
`extras\/expected_cell_count\.txt`		The expected cell count for the RNA sequencing dataset. This is an optional file that, if present, will be used by the HIVE's RNA sequencing analysis pipeline. With some datasets, knowing the expected cell count has improved the output of the HIVE analysis pipeline.
`raw\/.*`	✓	All raw data files for the experiment.


START
START
Excel metadata file
(created by CEDAR and populated by TMC)
TSV metadata file
(created by TMC or CEDAR and populated by TMC)
CEDAR Validator
(web interface)
Failed validation
CEDAR Validator
(web interface or API)
Failed validation
Validated
TSV metadata file
(created and populated by CEDAR Validator)
Validated
Ingest
END



Data Previews

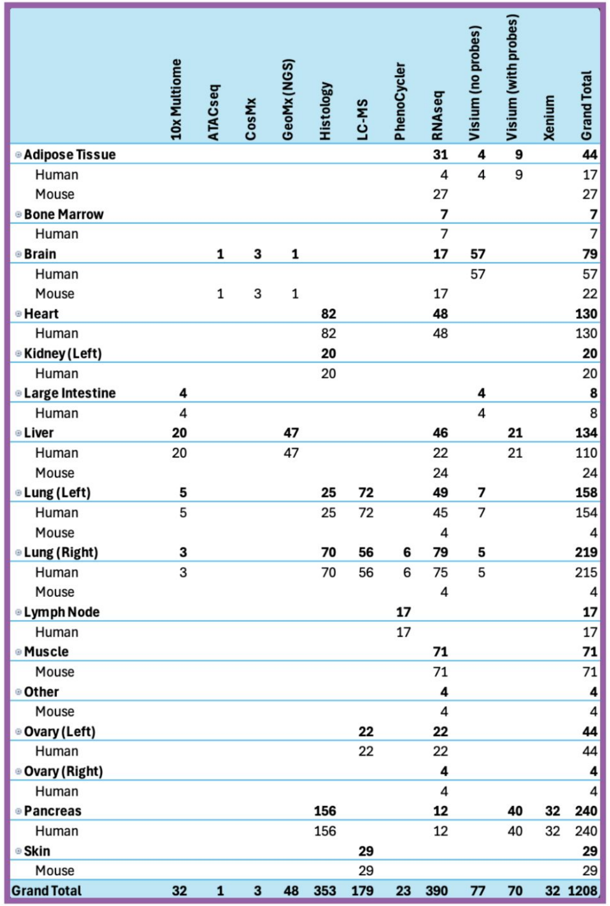
Welcome to the SenNet data preview page where you can explore regular updates and visualizations of data being processed and published by the SenNet Consortium. This page acts as an overview of current Consortium data and a look ahead at data that is yet to be published.

This October 2024 SenNet Sankey diagram tracks how data has been uploaded and published through a variety of categories:

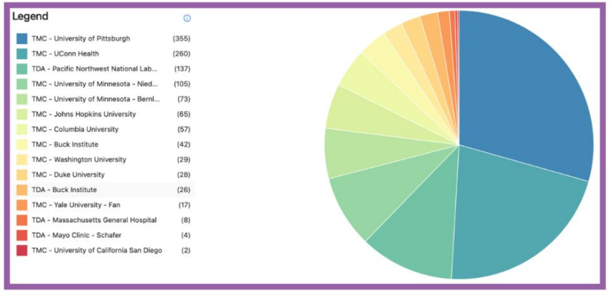
1. Which Tissue Mapping Center (TMC) or Technology Development and Application (TDA) processes the tissue.
2. Which technology is being used to process tissue.
3. The human or murine organ from which the senescent cell tissue was taken.
4. The status of that data in October 2024.

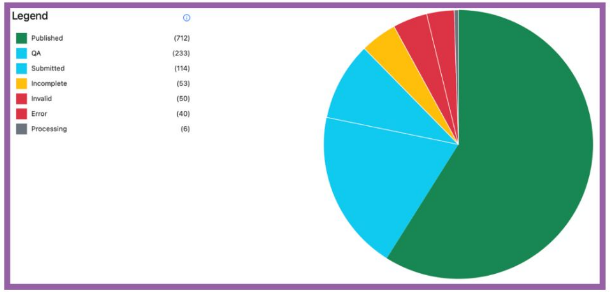
https://docs.sennetconsortium.org/data-sankey/

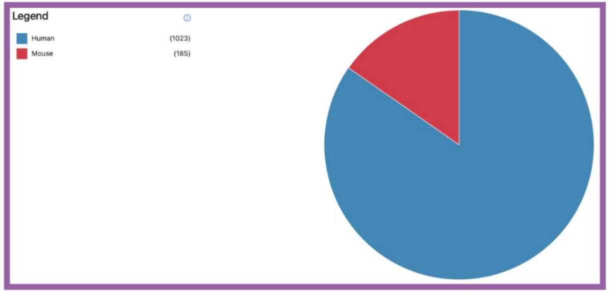
The Sankey visualization above and the graph and table below are created directly from the data dashboard, which is only accessible to Consortium members, and which details operational information about primary datasets at all statuses, enabling a preview of upcoming data and detailed tracking by Consortium members. The public sees only published datasets in the data portal whereas all data submitted is shared in the portal by Consortium members.

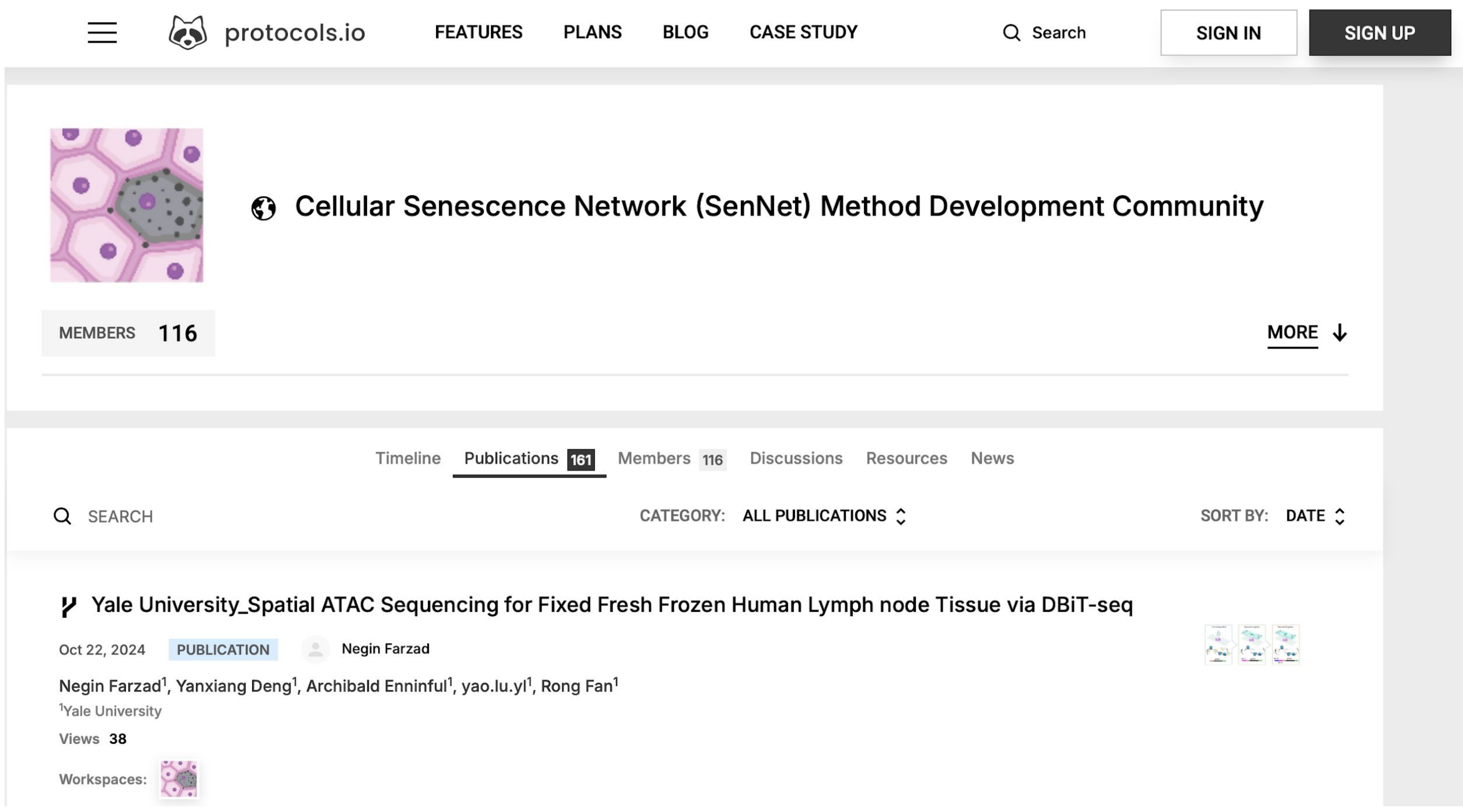


	10x Multiome	ATACseq	CosMx	GeoMx (NGS)	Histology	LC-MS	PhenoCycler	RNAseq	Visium (no probes)	Visium (with probes)	Xenium	Grand Total
⊖ Adipose Tissue								**31**	**4**	**9**		**44**
Human								4	4	9		17
Mouse								27				27
⊖ Bone Marrow								**7**				**7**
Human								7				7
⊖ Brain		**1**	**3**	**1**				**17**	**57**			**79**
Human									57			57
Mouse		1	3	1				17				22
⊖ Heart					**82**			**48**				**130**
Human					82			48				130
⊖ Kidney (Left)					**20**							**20**
Human					20							20
⊖ Large Intestine	**4**								**4**			**8**
Human	4								4			8
⊖ Liver	**20**			**47**				**46**		**21**		**134**
Human	20			47				22		21		110
Mouse								24				24
⊖ Lung (Left)	**5**				**25**	**72**		**49**	**7**			**158**
Human	5				25	72		45	7			154
Mouse								4				4
⊖ Lung (Right)	**3**				**70**	**56**	**6**	**79**	**5**			**219**
Human	3				70	56	6	75	5			215
Mouse								4				4
⊖ Lymph Node							**17**					**17**
Human							17					17
⊖ Muscle								**71**				**71**
Mouse								71				71
⊖ Other								**4**				**4**
Mouse								4				4
⊖ Ovary (Left)						**22**		**22**				**44**
Human						22		22				44
⊖ Ovary (Right)								**4**				**4**
Human								4				4
⊖ Pancreas					**156**			**12**		**40**	**32**	**240**
Human					156			12		40	32	240
⊖ Skin						**29**						**29**
Mouse						29						29
Grand Total	**32**	**1**	**3**	**48**	**353**	**179**	**23**	**390**	**77**	**70**	**32**	**1208**









Cellular Senescence Network (SenNet) Method Development Community

MEMBERS 116

Yale University_Spatial ATAC Sequencing for Fixed Fresh Frozen Human Lymph node Tissue via DBiT-seq

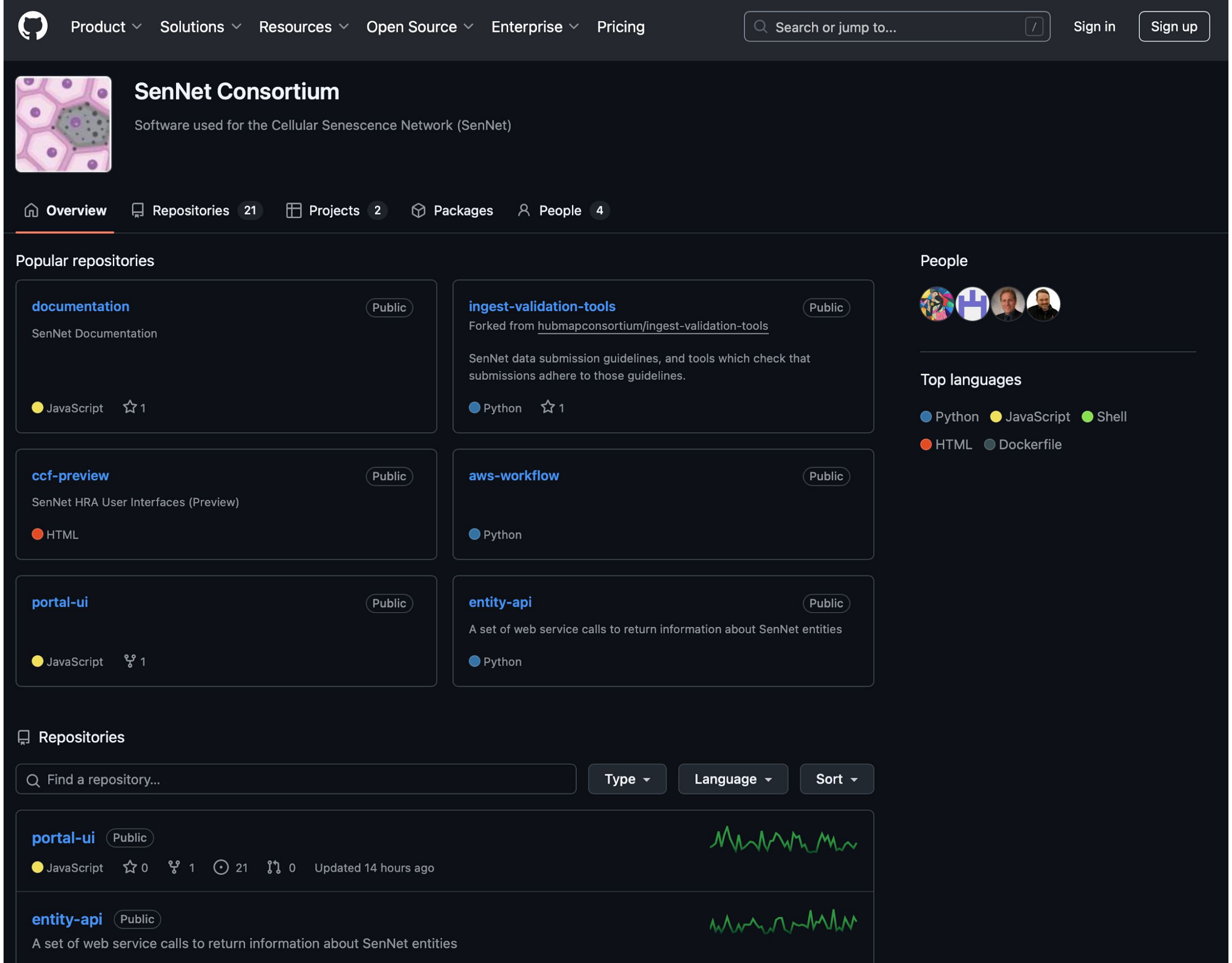
Oct 22, 2024 PUBLICATION Negin Farzad

Negin Farzad[1], Yanxiang Deng[1], Archibald Enninful[1], yao.lu.yl[1], Rong Fan[1]

[1]Yale University

Views 38

Workspaces:



SenNet Consortium

Software used for the Cellular Senescence Network (SenNet)

Popular repositories

documentation Public
SenNet Documentation
● JavaScript ☆ 1

ingest-validation-tools Public
Forked from hubmapconsortium/ingest-validation-tools
SenNet data submission guidelines, and tools which check that submissions adhere to those guidelines.
● Python ☆ 1

ccf-preview Public
SenNet HRA User Interfaces (Preview)
● HTML

aws-workflow Public
● Python

portal-ui Public
● JavaScript 1

entity-api Public
A set of web service calls to return information about SenNet entities
● Python

People

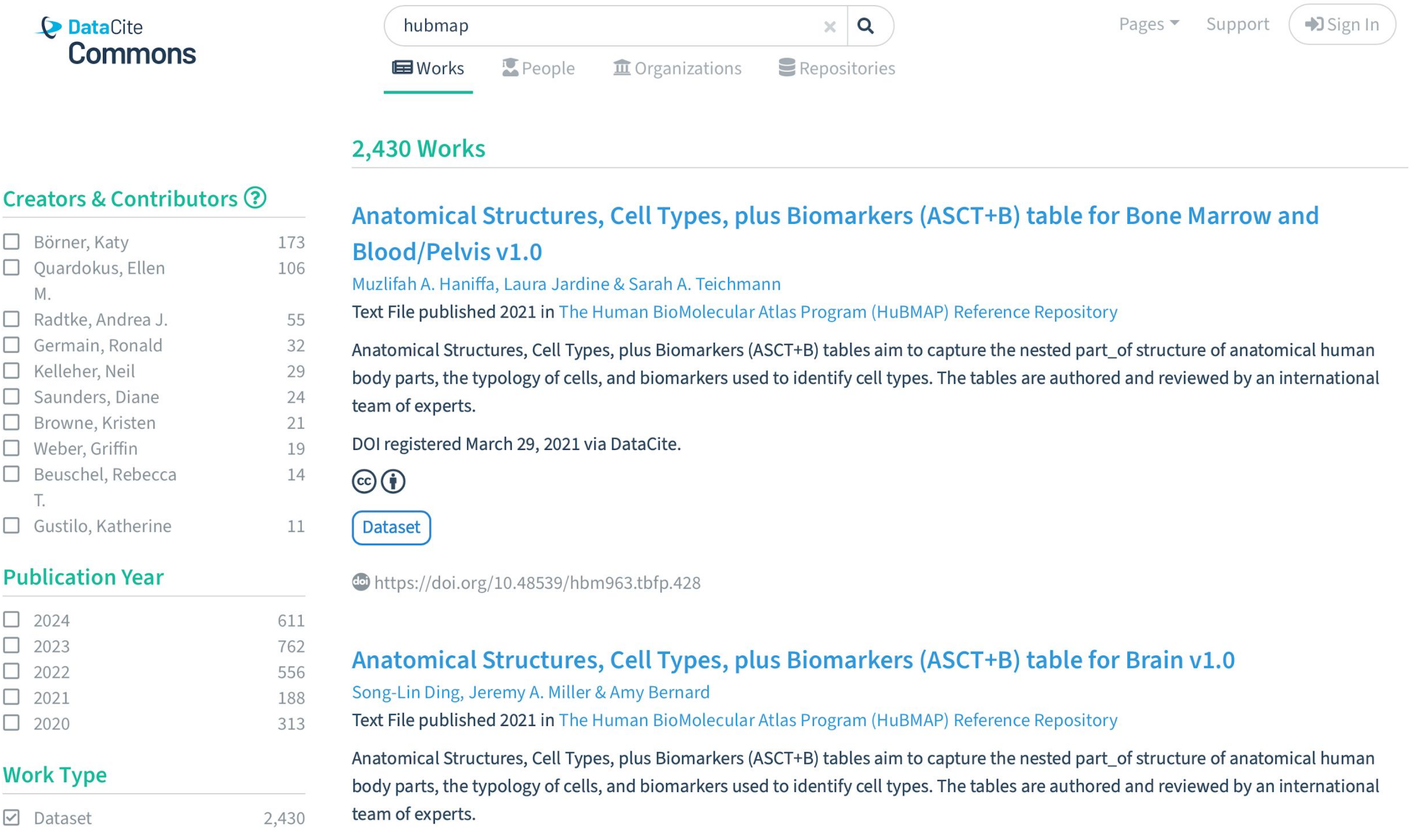
Top languages

● Python ● JavaScript ● Shell
● HTML ● Dockerfile

Repositories

portal-ui Public
● JavaScript ☆ 0 1 21 0 Updated 14 hours ago

entity-api Public
A set of web service calls to return information about SenNet entities



2,430 Works

Creators & Contributors ?

☐	Börner, Katy	173
☐	Quardokus, Ellen M.	106
☐	Radtke, Andrea J.	55
☐	Germain, Ronald	32
☐	Kelleher, Neil	29
☐	Saunders, Diane	24
☐	Browne, Kristen	21
☐	Weber, Griffin	19
☐	Beuschel, Rebecca T.	14
☐	Gustilo, Katherine	11

Publication Year

☐	2024	611
☐	2023	762
☐	2022	556
☐	2021	188
☐	2020	313

Work Type

☑	Dataset	2,430

Anatomical Structures, Cell Types, plus Biomarkers (ASCT+B) table for Bone Marrow and Blood/Pelvis v1.0

Muzlifah A. Haniffa, Laura Jardine & Sarah A. Teichmann

Text File published 2021 in The Human BioMolecular Atlas Program (HuBMAP) Reference Repository

Anatomical Structures, Cell Types, plus Biomarkers (ASCT+B) tables aim to capture the nested part_of structure of anatomical human body parts, the typology of cells, and biomarkers used to identify cell types. The tables are authored and reviewed by an international team of experts.

DOI registered March 29, 2021 via DataCite.

Dataset

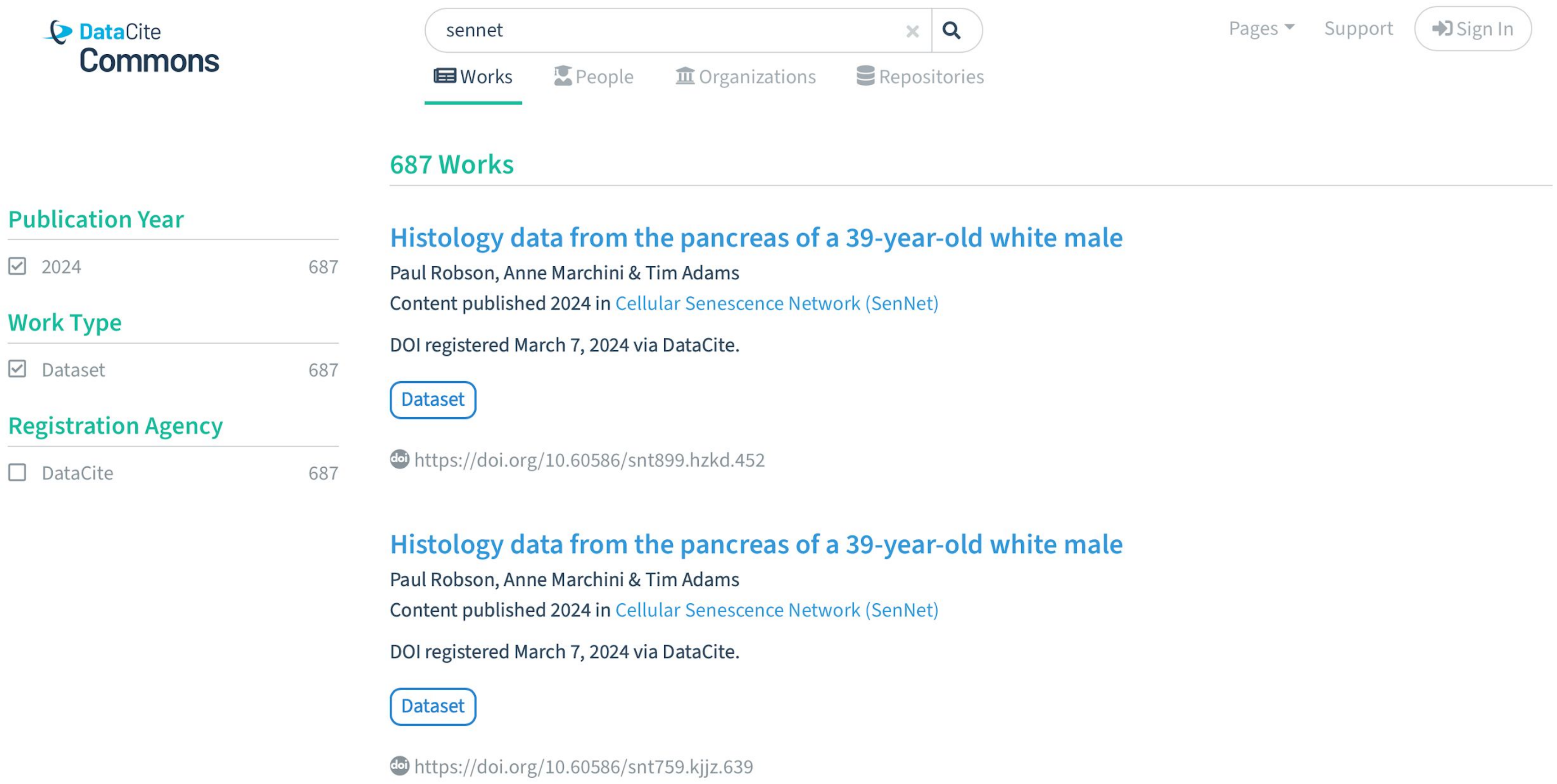
https://doi.org/10.48539/hbm963.tbfp.428

Anatomical Structures, Cell Types, plus Biomarkers (ASCT+B) table for Brain v1.0

Song-Lin Ding, Jeremy A. Miller & Amy Bernard

Text File published 2021 in The Human BioMolecular Atlas Program (HuBMAP) Reference Repository

Anatomical Structures, Cell Types, plus Biomarkers (ASCT+B) tables aim to capture the nested part_of structure of anatomical human body parts, the typology of cells, and biomarkers used to identify cell types. The tables are authored and reviewed by an international team of experts.



sennet

687 Works

Publication Year

☑ 2024 687

Work Type

☑ Dataset 687

Registration Agency

☐ DataCite 687

Histology data from the pancreas of a 39-year-old white male

Paul Robson, Anne Marchini & Tim Adams

Content published 2024 in Cellular Senescence Network (SenNet)

DOI registered March 7, 2024 via DataCite.

Dataset

https://doi.org/10.60586/snt899.hzkd.452

Histology data from the pancreas of a 39-year-old white male

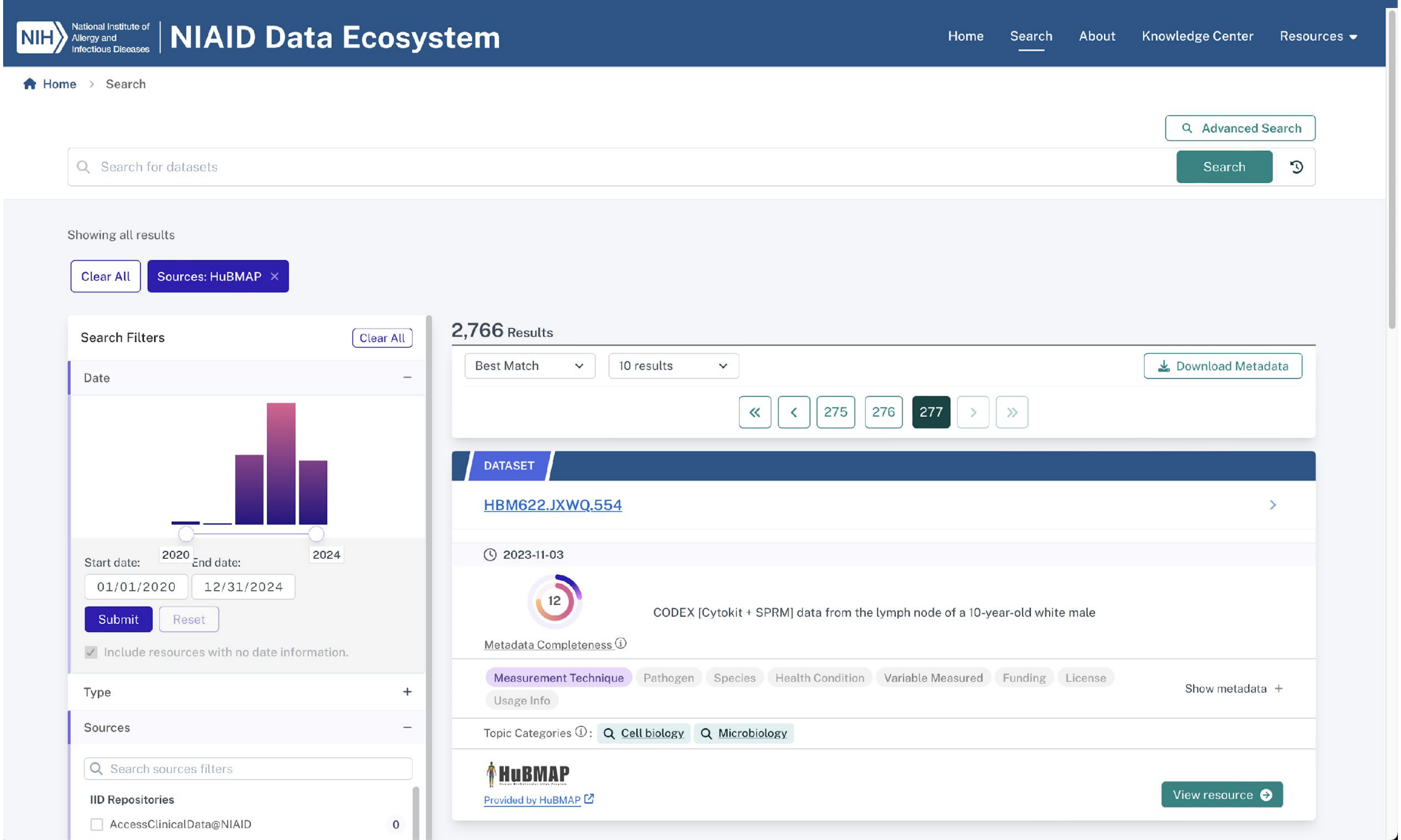
Paul Robson, Anne Marchini & Tim Adams

Content published 2024 in Cellular Senescence Network (SenNet)

DOI registered March 7, 2024 via DataCite.

Dataset

https://doi.org/10.60586/snt759.kjjz.639



Showing all results

Start date: 01/01/2020
End date: 12/31/2024

☑ Include resources with no date information.

☐ AccessClinicalData@NIAID 0

2,766 Results

Best Match
10 results

HBM622.JXWQ.554

2023-11-03

12
Metadata Completeness

CODEX [Cytokit + SPRM] data from the lymph node of a 10-year-old white male

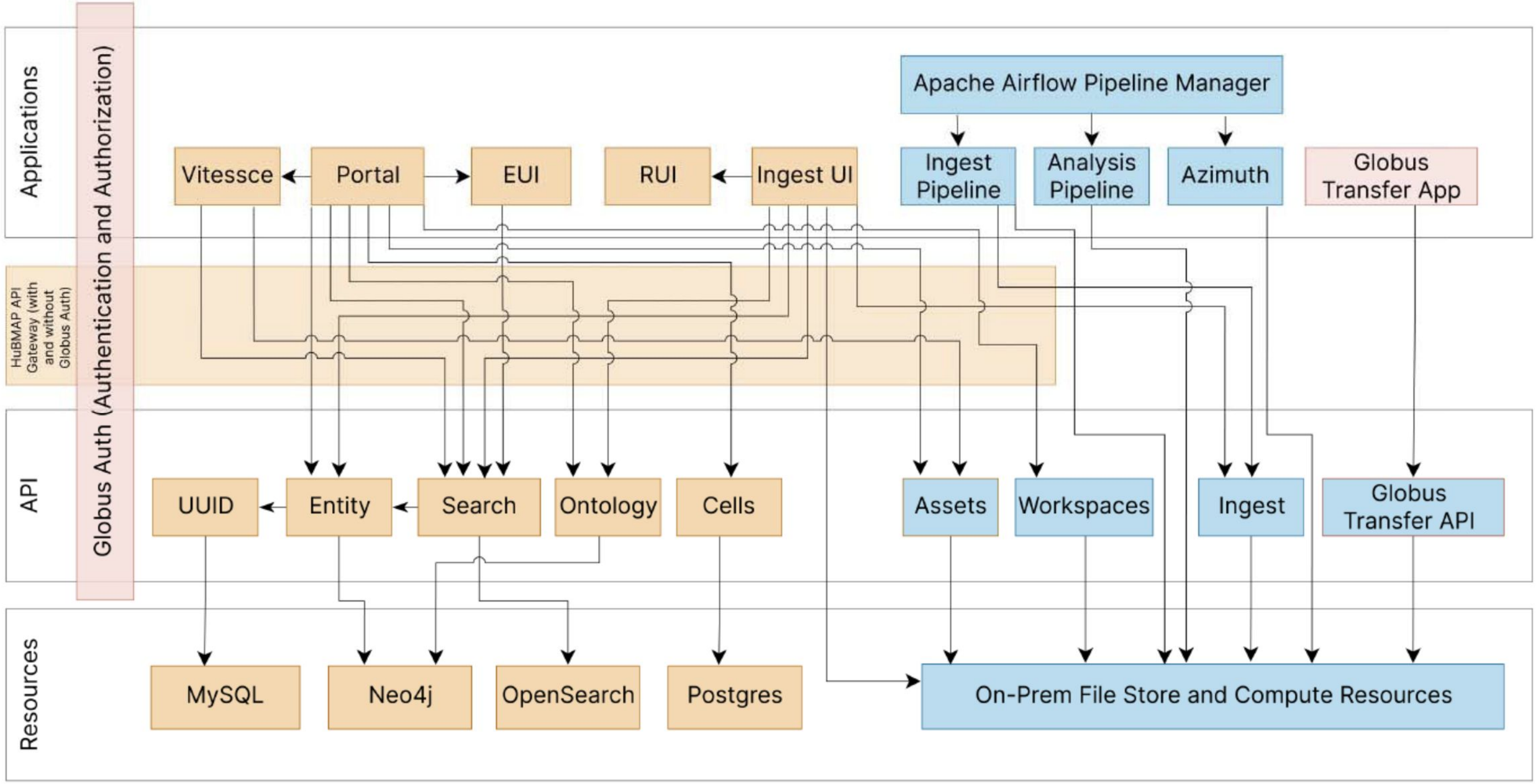
Topic Categories: Cell biology, Microbiology

Provided by HuBMAP

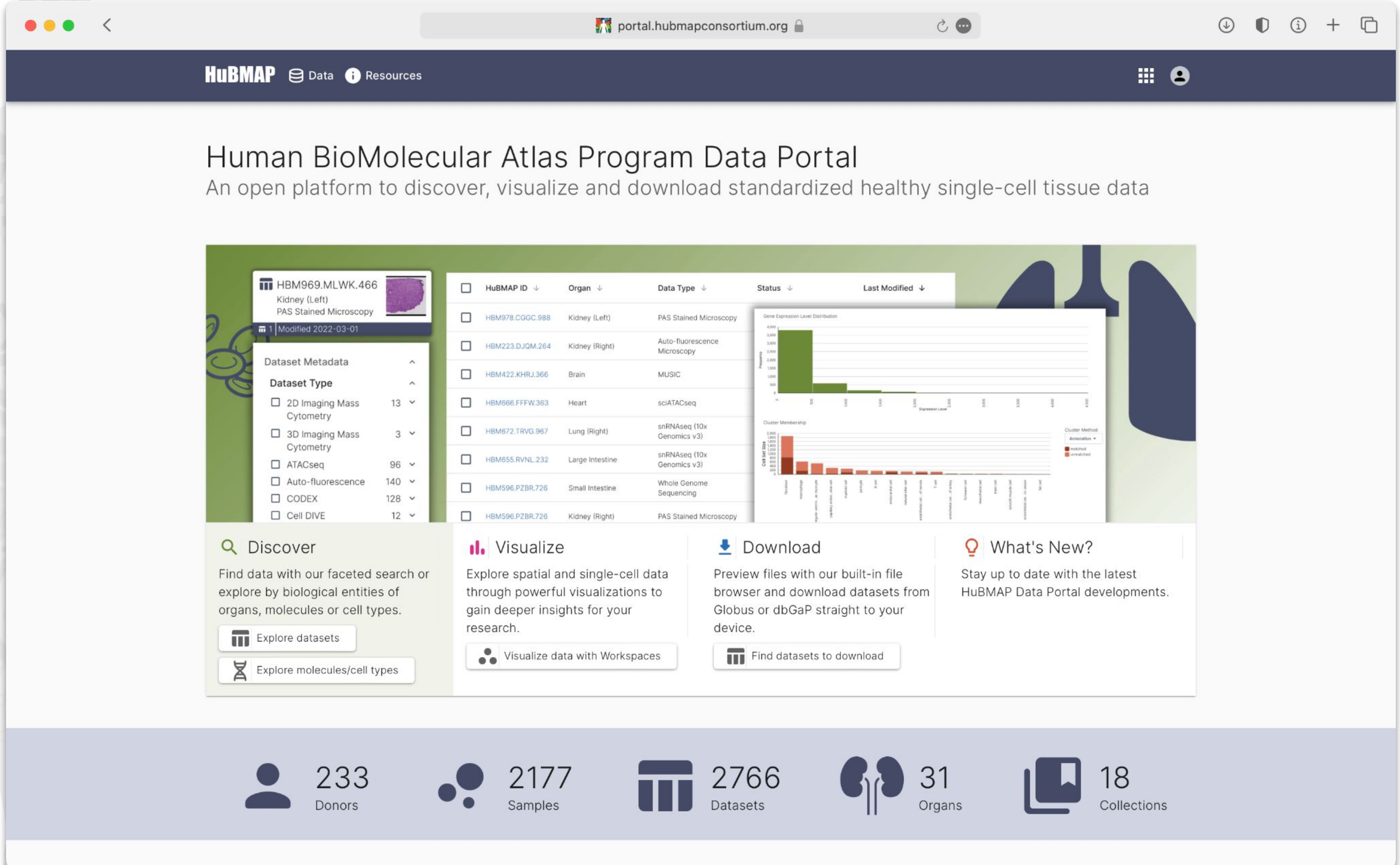
Flexible hybrid cloud infrastructure -> atlas

1) **Curation and Ingestion:** Semi-automated data ingestion currently from data providers, and in the future from community partners, and the general research community, to maximize efficiency and usefulness for building the HRA
2) **Integration:** Automated analysis and annotation of ingested data and alignment of these annotations to the HRA via the UBKG
3) **Findability and Accessibility:** Manifestation of backend resources in the modular architecture of APIs and containers, services, and documentation that currently minimizes user friction in integrated searching, querying, analyzing, and viewing of data, and in the future of tissue maps at multiple spatial scales and among multiple layers of information
4) **Interoperability:** Use of the deployment of the UBKG to translate data, HRA assets, and community data among one another via ontologies
5) **Analysis:** Infrastructure support to currently enable users with interactive analyses of HuBMAP data via Jupyter notebooks, and in the future, batch workflows among both HuBMAP and user-contributed data and tools, including integration and mapping against the HRA
6) **Sustainability:** HuBMAP’s flexible hybrid cloud infrastructure—efficiently leveraging on-premises resources at PSC for services that would incur significant public cloud charges, such as data storage, processing, analysis, and download facilitates sustainment of open tools, data, and infrastructure beyond the end of the HuBMAP program.

Flexible hybrid cloud infrastructure -> atlas



HuBMAP Flexible Hybrid Cloud Microservices Architecture: AWS PSC Globus



Human BioMolecular Atlas Program Data Portal

An open platform to discover, visualize and download standardized healthy single-cell tissue data

HBM969.MLWK.466
Kidney (Left)
PAS Stained Microscopy
1 Modified 2022-03-01

Dataset Metadata

Dataset Type

☐ 2D Imaging Mass Cytometry 13
☐ 3D Imaging Mass Cytometry 3
☐ ATACseq 96
☐ Auto-fluorescence 140
☐ CODEX 128
☐ Cell DIVE 12

☐	HuBMAP ID	Organ	Data Type	Status	Last Modified
☐	HBM978.CGGC.988	Kidney (Left)	PAS Stained Microscopy		
☐	HBM223.DJQM.264	Kidney (Right)	Auto-fluorescence Microscopy		
☐	HBM422.KHRJ.366	Brain	MUSIC		
☐	HBM666.FFFW.363	Heart	sciATACseq		
☐	HBM672.TRVG.967	Lung (Right)	snRNAseq (10x Genomics v3)		
☐	HBM655.RVNL.232	Large Intestine	snRNAseq (10x Genomics v3)		
☐	HBM596.PZBR.726	Small Intestine	Whole Genome Sequencing		
☐	HBM596.PZBR.726	Kidney (Right)	PAS Stained Microscopy		

Discover

Find data with our faceted search or explore by biological entities of organs, molecules or cell types.

Visualize

Explore spatial and single-cell data through powerful visualizations to gain deeper insights for your research.

Download

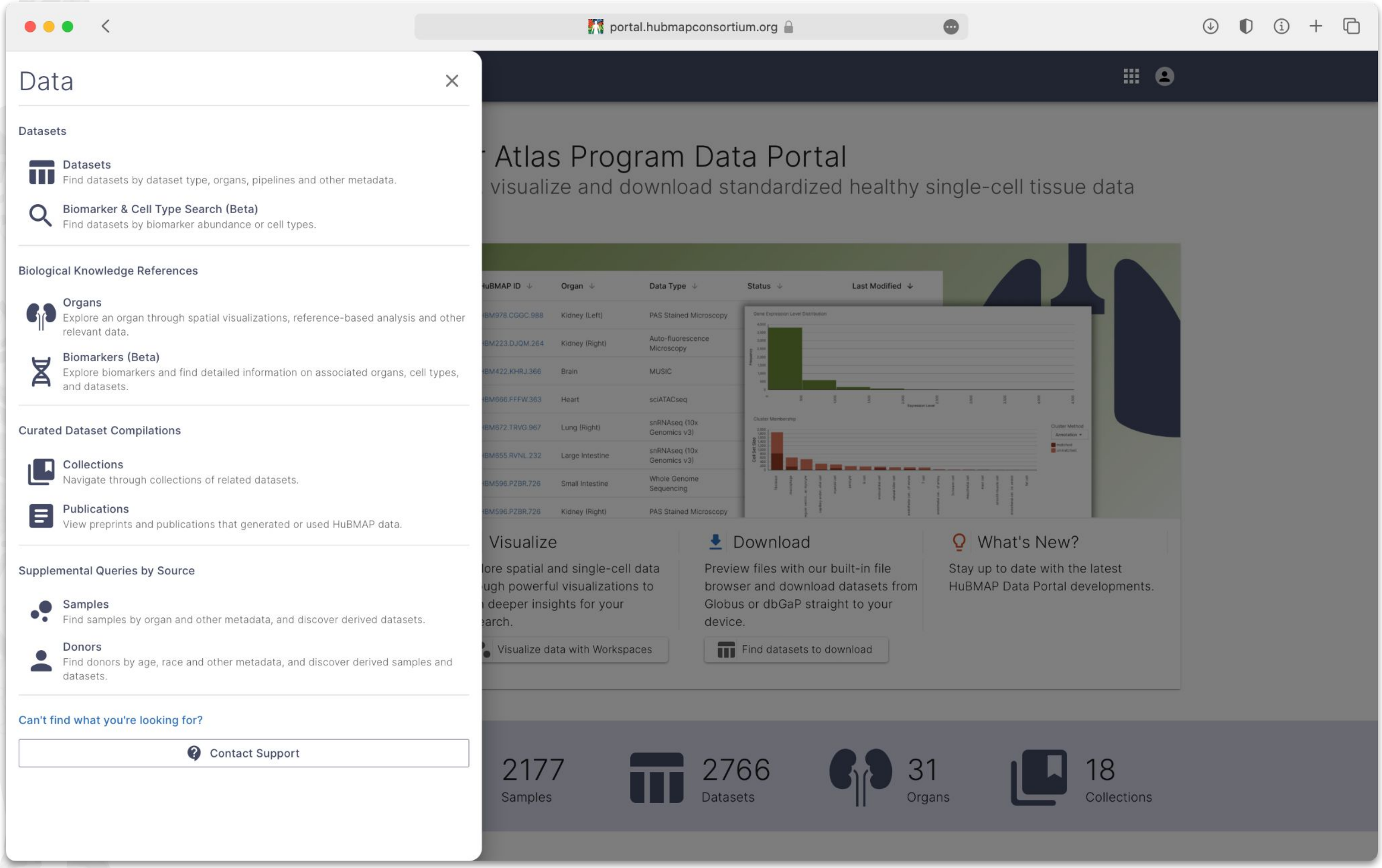
Preview files with our built-in file browser and download datasets from Globus or dbGaP straight to your device.

What's New?

Stay up to date with the latest HuBMAP Data Portal developments.

233 Donors
2177 Samples
2766 Datasets
31 Organs
18 Collections

https://portal.hubmapconsortium.org/



Data

Datasets

Datasets
Find datasets by dataset type, organs, pipelines and other metadata.

Biomarker & Cell Type Search (Beta)
Find datasets by biomarker abundance or cell types.

Biological Knowledge References

Organs
Explore an organ through spatial visualizations, reference-based analysis and other relevant data.

Biomarkers (Beta)
Explore biomarkers and find detailed information on associated organs, cell types, and datasets.

Curated Dataset Compilations

Collections
Navigate through collections of related datasets.

Publications
View preprints and publications that generated or used HuBMAP data.

Supplemental Queries by Source

Samples
Find samples by organ and other metadata, and discover derived datasets.

Donors
Find donors by age, race and other metadata, and discover derived samples and datasets.

Can't find what you're looking for?

Contact Support

Atlas Program Data Portal

visualize and download standardized healthy single-cell tissue data

uBMAP ID	Organ	Data Type	Status	Last Modified
BM978.CGGC.988	Kidney (Left)	PAS Stained Microscopy		
BM223.DJQM.264	Kidney (Right)	Auto-fluorescence Microscopy		
BM422.KHRJ.366	Brain	MUSIC		
BM666.FFFW.363	Heart	sciATACseq		
BM872.TRVG.967	Lung (Right)	snRNAseq (10x Genomics v3)		
BM655.RVNL.232	Large Intestine	snRNAseq (10x Genomics v3)		
BM596.PZBR.726	Small Intestine	Whole Genome Sequencing		
BM596.PZBR.726	Kidney (Right)	PAS Stained Microscopy		

Visualize
lore spatial and single-cell data ugh powerful visualizations to deeper insights for your earch.

Visualize data with Workspaces

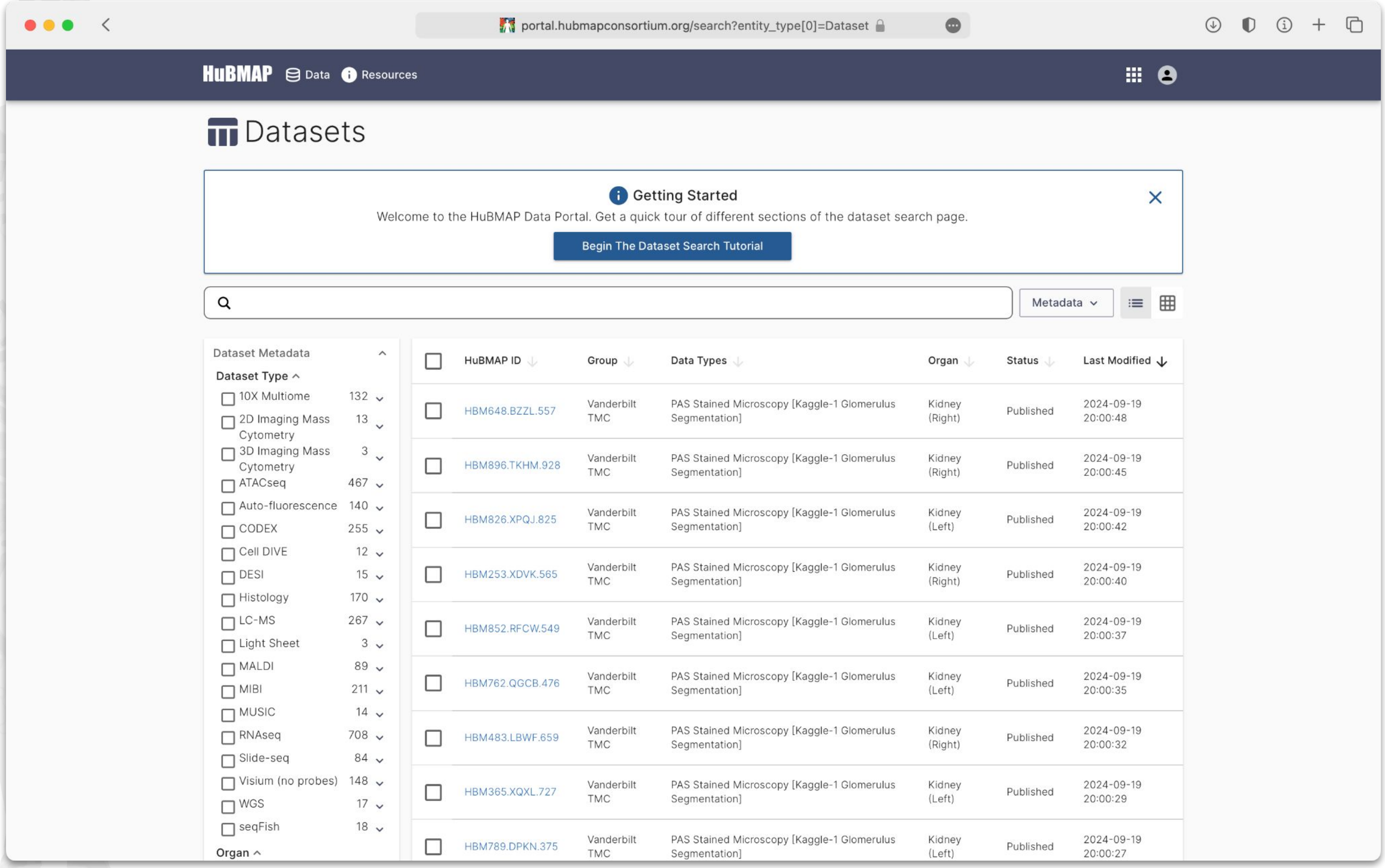
Download
Preview files with our built-in file browser and download datasets from Globus or dbGaP straight to your device.

Find datasets to download

What's New?
Stay up to date with the latest HuBMAP Data Portal developments.

2177	2766	31	18
Samples	Datasets	Organs	Collections

https://portal.hubmapconsortium.org/



portal.hubmapconsortium.org/search?entity_type[0]=Dataset

Datasets

Getting Started

Welcome to the HuBMAP Data Portal. Get a quick tour of different sections of the dataset search page.

Dataset Metadata

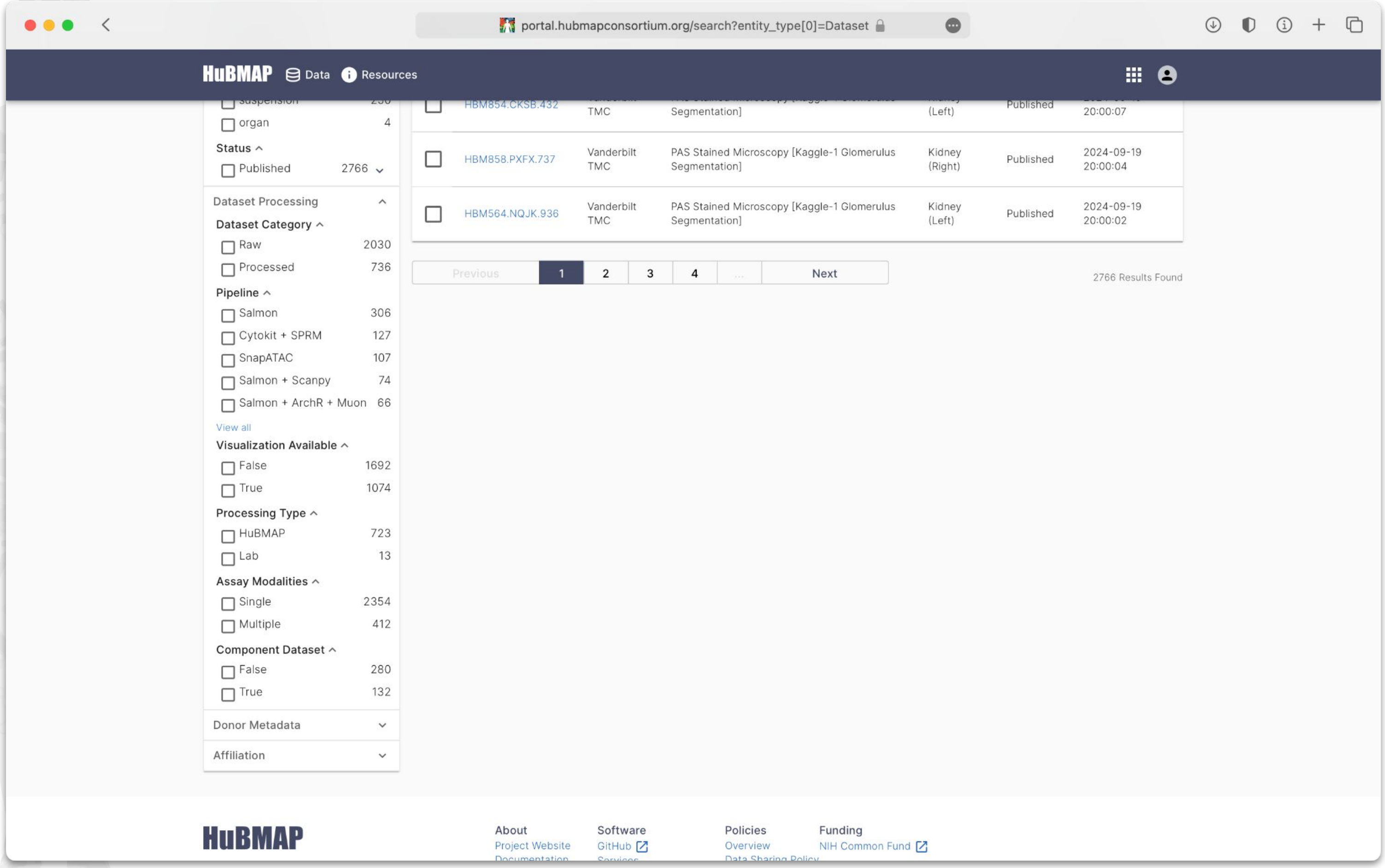
Dataset Type

☐	10X Multiome	132
☐	2D Imaging Mass Cytometry	13
☐	3D Imaging Mass Cytometry	3
☐	ATACseq	467
☐	Auto-fluorescence	140
☐	CODEX	255
☐	Cell DIVE	12
☐	DESI	15
☐	Histology	170
☐	LC-MS	267
☐	Light Sheet	3
☐	MALDI	89
☐	MIBI	211
☐	MUSIC	14
☐	RNAseq	708
☐	Slide-seq	84
☐	Visium (no probes)	148
☐	WGS	17
☐	seqFish	18

Organ

☐	HuBMAP ID	Group	Data Types	Organ	Status	Last Modified
☐	HBM648.BZZL.557	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Right)	Published	2024-09-19 20:00:48
☐	HBM896.TKHM.928	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Right)	Published	2024-09-19 20:00:45
☐	HBM826.XPQJ.825	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Left)	Published	2024-09-19 20:00:42
☐	HBM253.XDVK.565	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Right)	Published	2024-09-19 20:00:40
☐	HBM852.RFCW.549	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Left)	Published	2024-09-19 20:00:37
☐	HBM762.QGCB.476	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Left)	Published	2024-09-19 20:00:35
☐	HBM483.LBWF.659	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Right)	Published	2024-09-19 20:00:32
☐	HBM365.XQXL.727	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Left)	Published	2024-09-19 20:00:29
☐	HBM789.DPKN.375	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Left)	Published	2024-09-19 20:00:27

https://portal.hubmapconsortium.org/search?entity_type%5B0%5D=Dataset


portal.hubmapconsortium.org/search?entity_type[0]=Dataset

☐ suspension
☐ organ 4

Status
☐ Published 2766

Dataset Processing

Dataset Category
☐ Raw 2030
☐ Processed 736

Pipeline
☐ Salmon 306
☐ Cytokit + SPRM 127
☐ SnapATAC 107
☐ Salmon + Scanpy 74
☐ Salmon + ArchR + Muon 66

View all

Visualization Available
☐ False 1692
☐ True 1074

Processing Type
☐ HuBMAP 723
☐ Lab 13

Assay Modalities
☐ Single 2354
☐ Multiple 412

Component Dataset
☐ False 280
☐ True 132

Donor Metadata

Affiliation

☐	HBM854.CKSB.432	TMC	Segmentation]	(Left)	Published	20:00:07
☐	HBM858.PXFX.737	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Right)	Published	2024-09-19 20:00:04
☐	HBM564.NQJK.936	Vanderbilt TMC	PAS Stained Microscopy [Kaggle-1 Glomerulus Segmentation]	Kidney (Left)	Published	2024-09-19 20:00:02

2766 Results Found

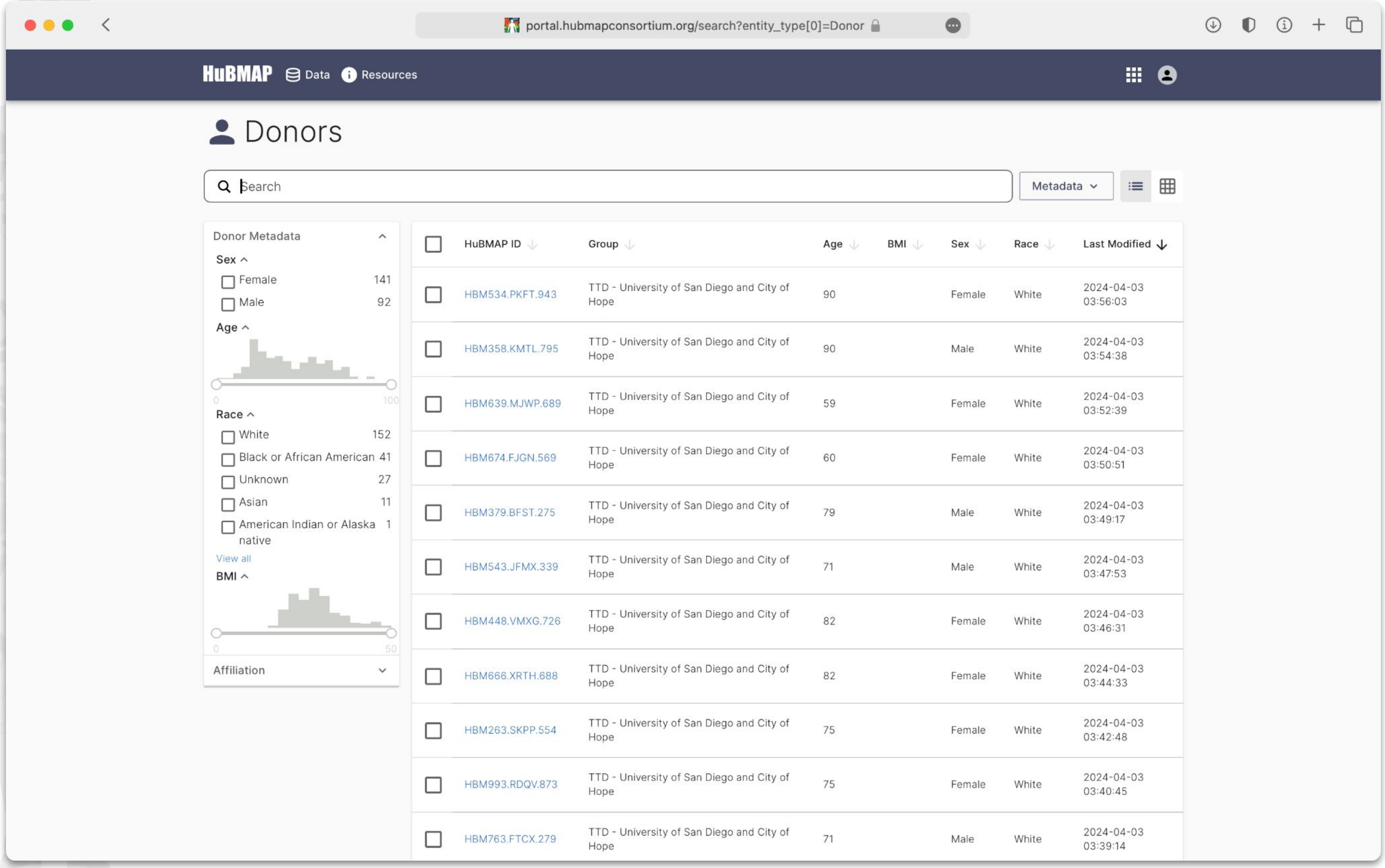
About
Project Website

Software
GitHub

Policies
Overview

Funding
NIH Common Fund

https://portal.hubmapconsortium.org/search?entity_type%5B0%5D=Dataset



Donors

Search

Donor Metadata

Sex
- ☐ Female 141
- ☐ Male 92

Age

Race
- ☐ White 152
- ☐ Black or African American 41
- ☐ Unknown 27
- ☐ Asian 11
- ☐ American Indian or Alaska native 1

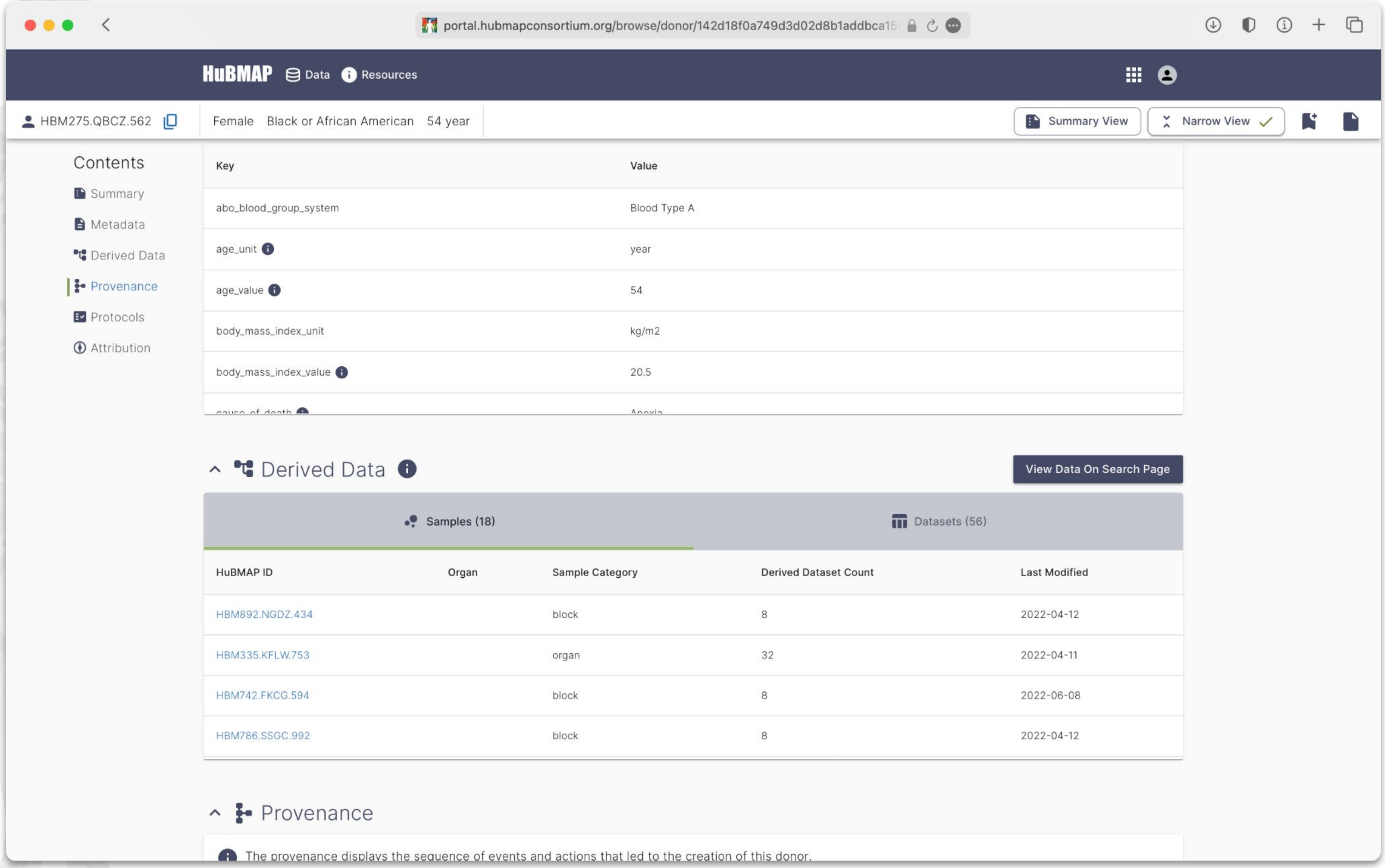
View all

BMI

Affiliation

☐	HuBMAP ID	Group	Age	BMI	Sex	Race	Last Modified
☐	HBM534.PKFT.943	TTD - University of San Diego and City of Hope	90		Female	White	2024-04-03 03:56:03
☐	HBM358.KMTL.795	TTD - University of San Diego and City of Hope	90		Male	White	2024-04-03 03:54:38
☐	HBM639.MJWP.689	TTD - University of San Diego and City of Hope	59		Female	White	2024-04-03 03:52:39
☐	HBM674.FJGN.569	TTD - University of San Diego and City of Hope	60		Female	White	2024-04-03 03:50:51
☐	HBM379.BFST.275	TTD - University of San Diego and City of Hope	79		Male	White	2024-04-03 03:49:17
☐	HBM543.JFMX.339	TTD - University of San Diego and City of Hope	71		Male	White	2024-04-03 03:47:53
☐	HBM448.VMXG.726	TTD - University of San Diego and City of Hope	82		Female	White	2024-04-03 03:46:31
☐	HBM666.XRTH.688	TTD - University of San Diego and City of Hope	82		Female	White	2024-04-03 03:44:33
☐	HBM263.SKPP.554	TTD - University of San Diego and City of Hope	75		Female	White	2024-04-03 03:42:48
☐	HBM993.RDQV.873	TTD - University of San Diego and City of Hope	75		Female	White	2024-04-03 03:40:45
☐	HBM763.FTCX.279	TTD - University of San Diego and City of Hope	71		Male	White	2024-04-03 03:39:14

https://portal.hubmapconsortium.org/search?entity_type%5B0%5D=Donor



Key	Value
abo_blood_group_system	Blood Type A
age_unit	year
age_value	54
body_mass_index_unit	kg/m2
body_mass_index_value	20.5
cause_of_death	Anoxia

Derived Data

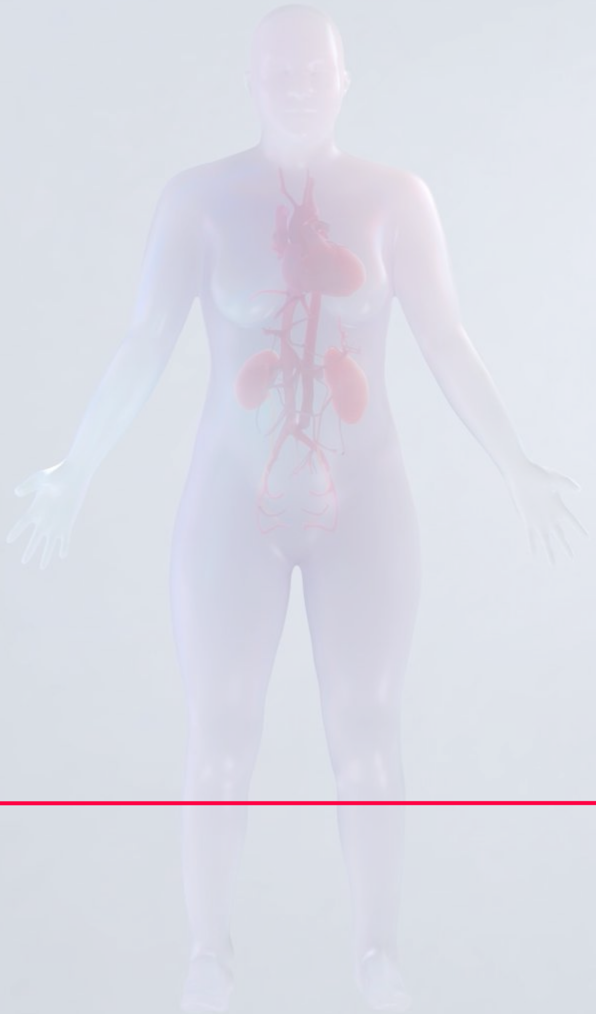
HuBMAP ID	Organ	Sample Category	Derived Dataset Count	Last Modified
HBM892.NGDZ.434		block	8	2022-04-12
HBM335.KFLW.753		organ	32	2022-04-11
HBM742.FKCG.594		block	8	2022-06-08
HBM786.SSGC.992		block	8	2022-04-12

Provenance

The provenance displays the sequence of events and actions that led to the creation of this donor.

https://portal.hubmapconsortium.org/browse/donor/142d18f0a749d3d02d8b1addbca15589

Q&A



https://humanatlas.io/events/2024-24h

Questions

How do we best capture data for a Multiscale Human?

How do we map a Multiscale Human?

How do we model a Multiscale Human?

How can LLMs or RAGs be used to advance science and clinical practice?

How to safeguard privacy?

Thank you