

AJACS「シングルセルRNA-seqを知って・学んで・使う」  
(2024年12月23日・オンライン)

# 公共データベースから シングルセルRNA-seqデータを取得する

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# 講義内容の概要

## • 目的

- シングルセルRNA-seqのデータをまだ持っていない人や、取得前に解析の練習をしてみたい人が、公開リソースからデータを入手できるようになること
- その他、シングルセルRNA-seqに関する情報を入手できる場所を知ること

## • 内容

- シングルセルRNA-seqの主なデータ形式
- シングルセルRNA-seqが入手できるリポジトリ
- ダウンロードしたファイルを解析ソフトウェアで使う
- シングルセルRNA-seq解析に有用なウェブサイト

# シングルセルRNA-seqの主なデータ形式

# シングルセルRNA-seqの主な公開データ形式

- FASTQ形式 – 配列ならびにそのクオリティスコアが含まれるファイル

```
@SRR9291388.1 K00125:97:HLHLYBBXX:3:1101:2980:998 length=26
NGCACCTAGTCTCAACGTTCTACCAA
+SRR9291388.1 K00125:97:HLHLYBBXX:3:1101:2980:998 length=26
#AAFFJJJJFFJJJJJJJJJJJJFJJ
```

- BAM形式 – ゲノムへのマッピング結果のファイル

```
A00228:279:HFVFDVDMXX:1:1201:20754:18396 272 1 11274 0 91M * 0 0
TGGTGGCCAGCGCCCCCTGCTGGCGCCGGGGCACTGCAGGGCCCTCTTGCTTACTGTATAGTGGTGGCAGCCGCCTGCTGGCAGCTAGGG
F:FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
NH:i:5 HI:i:4 AS:i:89 nM:i:0 RE:A:I li:i:0 BC:Z:CAGCCCAC QT:Z:FFFFFFF,
CR:Z:ATTCGTTGTGTAGCAG CY:Z:FFFFF:FFFFF:FFF CB:Z:ATTCGTTGTGTAGCAG-1 UR:Z:CCGTTCCGTTGG
UY:Z:F:F:FF:FFF:F UB:Z:CCGTTCCGTTGG RG:Z:pbmc_1k_v3:0:1:HFVFDVDMXX:1
```

- H5AD形式 – 遺伝子ごとの発現量テーブル、細胞アノテーション、次元削減(クラスタリング)の結果が含まれるファイル



<https://anndata.readthedocs.io/>

# シングルセルRNA-seqが入手できるリポジトリ

INSDC (International Nucleotide Sequence Database Collaboration)  
(DDBJ / NCBI / EMBL-EBI)

## INSDC (DDBJ / NCBI / EMBL-EBI)

- 新規シーケンスを用いた論文を発表するときには、そのシーケンスデータを公開することが原則的に義務化されている(個人情報関連については例外等もあり)
- その登録先のリポジトリを DDBJ (日本)、NCBI(米国)、EBI(欧州)が運営しており、誰でもデータを入手可能である

	DDBJ	NCBI	EMBL-EBI
機能ゲノムクスデータ	<a href="#">GEA</a>	<a href="#">GEO</a>	<a href="#">ArrayExpress</a>
シーケンスデータ	<a href="#">DDBJ SRA (DRA)</a>	<a href="#">SRA</a>	<a href="#">ENA</a>
サンプル情報	<a href="#">BioSample</a>	<a href="#">BioSample</a>	<a href="#">BioSamples</a>
プロジェクト情報	<a href="#">BioProject</a>	<a href="#">BioProject</a>	BioProject

## INSDC - アクセション番号

公開データの参照に使われる「アクセション番号」

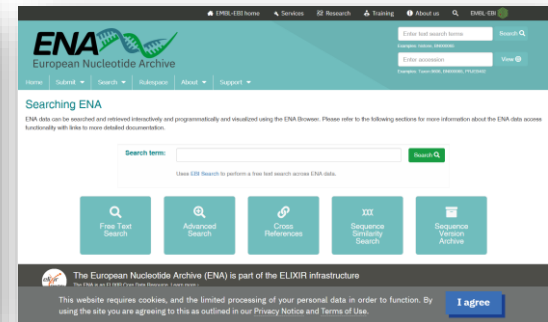
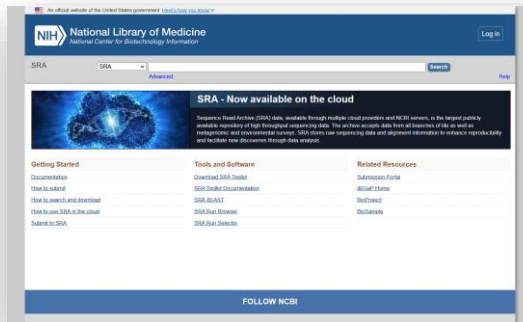
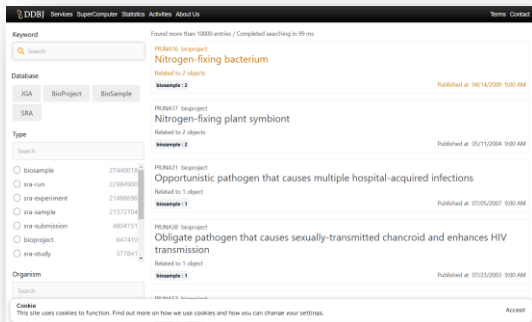
<https://ena-docs.readthedocs.io/en/latest/submit/general-guide/accessions.html>

- BioProject: “PRJ” + “E/N/D” + (アルファベット1文字) + (数字)
- SRA/DRA/ENAの “submission”: “E/D/S” + “RA” + (数字)
- SRA/DRA/ENAの “Run”: “E/D/S” + “RR” + (数字)
- NCBI GEO: “GSE” + (数字)
  - ArrayExpress上では “E-GEOD” + (数字)
- ArrayExpress: “E-MTAB-” + (数字)
- DDBJ GEA: “E-GEAD” + (数字)

# INSDC - ウェブサイトからダウンロード

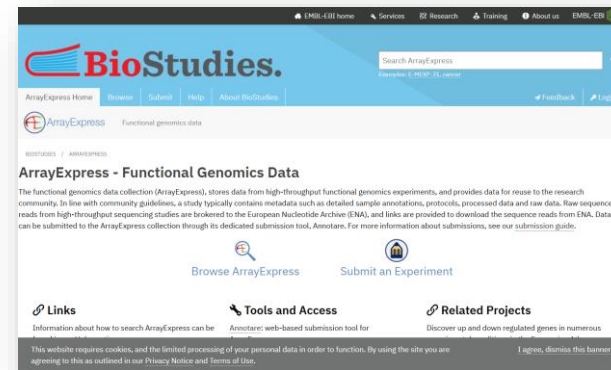
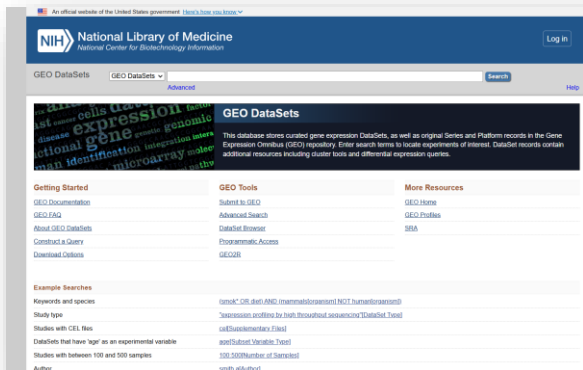
- BioProject や SRA/DRA/ENA のアクセッション番号

- DDBJ DRA: <https://ddbj.nig.ac.jp/search/>
- NCBI SRA: <https://www.ncbi.nlm.nih.gov/sra/>
- EMBL ENA: <https://www.ebi.ac.uk/ena/browser/search>



- NCBI GEOやArrayExpressionのアクセッション番号

- NCBI GEO: <https://www.ncbi.nlm.nih.gov/gds/>
- ArrayExpress: <https://www.ebi.ac.uk/biostudies/arrayexpress>





# INSDC - ダウンロードツールの利用

- SRAToolkit の `fasterq-dump` コマンドを使って、直接FASTQファイルをダウンロードすることも可能
  - 欲しいデータの SRA/DRA/ENAの“Run”アクセッション番号のリスト
  - BioProjectやSRAの他のアクセッション番号しか分からない場合は、ウェブサイト検索で取得するか、Entrez Direct がインストールされていれば、以下で取得可能

```
$ esearch -db sra -query (アクセッション番号) | efetch -format runinfo |  
cut -f 1 -d ',' ↵
```

- `fasterq-dump` コマンドの基本的な書き方は以下のとおり

```
$ fasterq-dump -S --include-technical (アクセッション番号) ↵
```

インストール方法について

[SRA Toolkit] <https://github.com/ncbi/sra-tools/wiki/02.-Installing-SRA-Toolkit>

[Entrez Direct] <https://www.ncbi.nlm.nih.gov/books/NBK179288/>

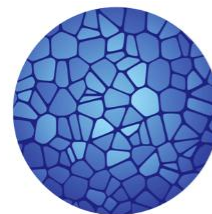
Debian/Ubuntu ではapt から、pip/biocondaでもインストール可能なものもあり

# シングルセルRNA-seqが入手できるリポジトリ

Human Cell Atlas

# Human Cell Atlas

- ヒトのすべての細胞のリファレンスマップの構築を目指す、国際共同プロジェクト
- 現在は肝臓や脂肪組織など18種類の「biological network」を対象にトランスクリプトームベースのリファレンスマップ (V1 Atlas) を構築中
  - その後、マルチオミックスのデータや、空間トランスクリプトームのデータへ拡張予定
- 2024年11月に first draft atlas に関する一連の論文が発表
  - <https://www.nature.com/collections/jccbbdahji>
- HCAのウェブサイト: <https://www.humancellatlas.org/>



**HUMAN  
CELL  
ATLAS**

# Human Cell Atlas – データプラットフォーム

- 3種類のデータプラットフォームがある(最近再構成された模様)
  - CellxGene Discover: <https://cellxgene.cziscience.com/collections>
    - 遺伝子発現プロファイル+データセットに関する最小限のメタデータ
  - HCA Data Repository:  
<https://explore.data.humancellatlas.org/projects>
    - FASTQファイル+サンプルに関する詳細なメタデータ(reference atlas構築に必要な詳細情報)
    - 今後は制限アクセス(ヒト由来サンプル等)用に使われる
  - Cell Annotation Platform: <https://celltype.info/>
    - 遺伝子発現プロファイル+細胞に関する詳細情報(細胞種等)

Platform	CellxGene Discover	HCA Data Repository	Cell Annotation Platform (CAP)
File format	Matrix - AnnData (h5ad)	FASTQ	Matrix - AnnData (h5ad)
Metadata	<b>Tier 1 metadata</b> Technical information required for integration	<b>Tier 2 metadata</b> Biological information required for downstream analysis & protected by managed access	<b>Cell annotation metadata</b> Metadata related to cell nomenclature, captured mostly on a 'per cell' basis

# Human Cell Atlas – CellxGene discover (1)

<https://cellxgene.cziscience.com/collections>

### 3. データの選択

The screenshot shows the CellxGene Collections page. On the left, there is a 'Filters' sidebar with various dropdown menus: Assay, Cell Type, Consortia, Development Stage, Disease, Organism, Publication, Publication Date, Self-Reported Ethnicity, Sex, Suspension Type, and Tissue. The main content area displays a table of collections. The table has columns for 'Collections', 'Publication', 'Tissue', 'Disease', and 'Organism'. An orange arrow points from the '3. データの選択' box to the 'An integrated transcriptomic cell atlas of human neural organoids' row in the table.

Collections	Publication	Tissue	Disease	Organism
Single cell transcriptomic analyses of the dynamic local and systemic response to cardiac injury in mice and zebrafish.	Cortada et al. (2024) Commun Biol	5 tissues	myocardial infarction normal	Mus musculus
Multimodal single-cell profiling reveals neuronal vulnerability and pathological cell states in focal cortical dysplasia	Galvão et al. (2024) iScience	4 tissues	isolated focal cortical dysplasia type II	Homo sapiens
A multi-region single nucleus transcriptomic atlas of Parkinson's disease	N. M. et al. (2024) Sci Data	5 tissues	normal Parkinson disease	Homo sapiens
A spatial human thymus cell atlas mapped to a continuous tissue axis	Yan et al. (2024) Nature	thymus	normal	Homo sapiens
An integrated transcriptomic cell atlas of human neural organoids	He et al. (2024) Nature	11 tissues	normal	Homo sapiens
Exploring the Utility of snRNA-seq in Profiling Human Bladder Tissue: A Comprehensive Comparison with scRNA-seq	No publication	urinary bladder	normal	Homo sapiens
Human and mouse dermal fibroblast atlas	No publication	15 tissues	normal 3 diseases	Homo sapiens Mus musculus
Molecular Signatures of Resilience to Alzheimer's Disease in Neocortical Layer 4 Neurons	Dharshini et al. (2024) bioRxiv	3 tissues	Alzheimer disease normal	Homo sapiens

### 1. データの選択条件の指定

### 2. 条件に合致する候補データの一覧

# Human Cell Atlas – CellxGene discover (2)

The screenshot shows the CellxGene discover interface. At the top, there is a navigation bar with 'APPLICATION' (Collections, Datasets, Gene Expression, Cell Guide, Differential Expression **NEW**) and 'CENSUS' (API, Models) sections. The main heading is 'An integrated transcriptomic cell atlas of human neural organoids'. Below this, there is a 'Human Cell Atlas (HCA)' section with a 'PLEASE NOTE' and a 'Show More' link. To the right, there are links for 'Publication' (He et al. (2024) Nature), 'Contact' (Barbara Treutlein), 'Data Source' (Zenodo), and 'Other' (devsystems-lab.github.io).

Dataset	Tissue	Disease	Assay	Organism	Cells		
The Human Neural Organoid Atlas	11 tissues	normal	8 assays	Homo sapiens	1,767,674	<a href="#">Download</a>	<a href="#">Explore</a>
HNOCA Extended: The Human Neural Organoid Atlas	11 tissues	normal	8 assays	Homo sapiens	1,920,782	<a href="#">Download</a>	<a href="#">Explore</a>

An orange arrow points from a text box at the bottom to the 'Download' button of the 'HNOCA Extended' dataset.

4. ダウンロードの選択

# Human Cell Atlas – CellxGene discover (3)

**Download Dataset**

NAME  
HNOCA Extended: The Human Neural Organoid Atlas

DATA FORMAT  
 .h5ad (AnnData v0.10)  .rds (Seurat v5)

DOWNLOAD DETAILS  
19082MB

<https://datasets.cellxgene.cziscience.com/029f6418-f2d6-4c09-8d5c-92859f95cd59.h5ad> [Copy](#)

This download link permanently references this version of the dataset. If this dataset is updated, a new download link will be created that permanently references the next version of this dataset.

Individual datasets and their versions may also be downloaded programmatically using the [Discover API](#). The [dataset schema](#) describes the required metadata embedded in all datasets submitted to CZ CELLXGENE Discover.

Cancel [Download](#)

5. ダウンロード形式の指定

6. 直接ダウンロード、もしくは指定されたURLでcurl等を用いてダウンロード

# Human Cell Atlas – HCA Data Repository (1)

<https://explore.data.humancellatlas.org/projects>

## 4. データの選択

The screenshot displays the 'HUMAN CELL ATLAS DATA EXPLORER' interface. On the left, a 'Filters' sidebar includes categories like PROJECT, DONOR, and SAMPLE with various filter options. The main area is titled 'Explore Data' and shows a table of search results. A warning message at the top states: 'Access to data explorer is limited for unauthorized users. To view all available data please contact the data manager.' The table lists project titles, access status, biological networks, and other details. An orange box highlights the 'Access' column, showing 'Required' (orange) and 'Granted' (green) statuses. A callout box explains that 'Required' items are restricted and need access procedures, while 'Granted' items are freely available.

Project Title	Access	Biological Network	Species	Organ	Library Count
<a href="#">A temporal cortex cell atlas highlights gene expression dynamics during human brain maturation</a>	Required	Inspecifie	Homo sapiens	brain	2 library
<a href="#">Single-cell connectomic analysis of adult mammalian lungs</a>	Granted	Lung	Homo sapiens	lung	10× 3' v2
<a href="#">Myofibroblast transcriptome indicates SFRP2hi fibroblast progenitors in systemic sclerosis skin</a>	Granted	Skin	Homo sapiens	skin of body	2 library
<a href="#">Evolution of neuronal cell classes and types in the vertebrate retina</a>	Granted	Eye	Homo sapiens	eye	10× 3' v3

3. アクセス方法の情報  
“Required”のものは制限アクセスデータのため入手に手続き必要  
“Granted”は自由に入手可能

1. データの選択条件の指定

2. 条件に合致する候補データの一覧



# Human Cell Atlas – HCA Data Repository (2)

The screenshot displays the Human Cell Atlas Data Explorer interface for a dataset titled "Single-cell connectomic analysis of adult mammalian lungs". The interface includes a navigation menu with "Download" selected, a "Download via curl" section with filters for Species (Homo sapiens), File Type (fastq.gz selected), and Shell (Bash), and a "Request curl Command" button. A "Current Query" sidebar shows the project name and species. A "Selected Data Summary" sidebar provides statistics on estimated cells, file size, and number of files.

**5. Downloadタブを選択**

**6. 必要なファイルを選択**

**7. ダウンロード用のコマンドを発行**

File Type	Count	File Size
<input checked="" type="checkbox"/> fastq.gz	6	33.98 GB
<input type="checkbox"/> mtz.gz	14	113.80 MB
<input type="checkbox"/> tsv.gz	28	4.10 MB

Category	Value
Estimated Cells	17.9k
File Size	33.98 GB
Files	6
Projects	1
Species	Homo sapiens
Donors	2

# Human Cell Atlas – HCA Data Repository (3)

The screenshot displays the Human Cell Atlas Data Explorer interface. The main heading is "Single-cell connectomic analysis of adult mammalian lungs". Below the heading, there are tabs for "Overview", "Metadata", "Matrices", "Download", and "Export". The "Download" tab is active. A section titled "Your curl Command is Ready" provides instructions on how to download the data using a curl command. The command is highlighted with an orange box and an arrow pointing to a callout box at the bottom of the page. To the right, there is a "Current Query" section with details about the project and data format, and a "Selected Data Summary" section with statistics on cells, file size, and files.

HUMAN CELL ATLAS  
DATA EXPLORER

Help & Documentation Sign In

Explore > Single-cell connectomic an...

## Single-cell connectomic analysis of adult mammalian lungs

Access Granted Updated September 27, 2024

Overview Metadata Matrices **Download** Export

**Your curl Command is Ready**

Execute the curl command below in your terminal to download the selected data.

**Please note** Data normalization and batch correction may differ between projects and processing methods. For details see [Matrix Normalization and Batch Correction](#).

```
curl --location --fail
https://service.azul.data.humancellatlas.org/manifest/files/ksQw1KVkY3A0M6RjdX.JsxBAyo8LHXyVdMr0X6jT-
rnFxxBA-zvMrA5JWILycxVob0Zx1xCakxQ9Y5sitC6a0waJf-MuVKncGs-nZUuDwKkHFjnZ9nQ | curl --fail-early --
continue-at - --retry 15 --retry-delay 10 --config -
```

**Current Query**

Project  
MammalLungConnectomeRareDon

Genus Species  
Homo sapiens

File Format  
fastq.gz

**Selected Data Summary**

Estimated Cells  
17.9k

File Size  
33.98 GB

Files  
6

Projects

8. ダウンロード用の(curlの)コマンド

# シングルセルRNA-seqが入手できるリポジトリ

10x Genomics社の Dataset サイト

# 10x Genomics社の Dataset サイト

- 10x Genomics 社のウェブサイトで、10x Genomics社で取得したデータが公開されている
  - <https://www.10xgenomics.com/datasets>
  - Creative Commons Attribution licenseで公開
- 何種類かのサンプルに対して、10x Genomics 社の様々なプロトコルで生産したデータが入手

The screenshot shows the 10x Genomics Datasets website. The header includes the 10x Genomics logo, navigation links for Products, Resources, Support Hub, and Company, and buttons for Store and Search. The main heading is "Datasets" with the subtitle "Explore and download datasets created by 10x Genomics." Below this, three featured datasets are displayed: Chromium Single Cell (10k Human DTC Melanoma, Chromium GEM-X Single Cell 3'), Visium Spatial (Visium HD Spatial Gene Expression Library, Human Breast Cancer (Fresh Frozen)), and Xenium In Situ (FFPE Human Ovarian Cancer with 5K Human Pan Tissue and Pathways Panel plus 100 Custom Genes). A search bar is present, and below it are top search categories like PBMC, Xenium, HD, GEM-X, Flex, Cell Segmentation, Breast Cancer, Mouse Brain, Brain, Lung, and FFPE. A filter sidebar on the left allows filtering by software, pipeline version, 10x instrument, and sample type. The main content area shows a table of datasets with columns for Datasets, Product, Species, Sample type, and Preservation.

Filter datasets	Clear all	←	Datasets (Showing 219 datasets)	Product	Species	Sample type	Preservation
Software	+	▲	Human Kidney Nuclei GEM-X Flex Gene Expression with Automated Cell Annotation	Single Cell Gene Expression v4	Human	Kidney	Fixed
Pipeline version	+	▲	60k Human PBMCs Stained with 8 TotalSeq™-B Human Hashtags (Donor 1-4, 4 samples)	Single Cell Gene Expression v4	Human	Blood	Cryopreserved
10x instrument	+	▲					
Sample type		▼					

# 10x Genomics社の Dataset サイト (1)

<https://www.10xgenomics.com/datasets>

## 3. データの選択

The screenshot shows the 10x Genomics datasets website interface. At the top, there is a search bar labeled "Search datasets". Below it, there are "Top searches" for various categories like PBMC, Xenium, HD, GEM-X, Flex, Cell Segmentation, Breast Cancer, Mouse Brain, Brain, Lung, and FFPE. On the left, a "Filter datasets" sidebar is visible with a "Clear all" button and various filter categories such as "10x Genomics product", "Platform", "Product", "Chemistry version", "Additional application", "Software", "Pipeline version", "10x instrument", "Sample type", "Species", "Sample/tissue type", "Preservation method", "Disease state", and "Cells or nuclei". The main content area displays a table of datasets with columns for "Product", "Species", "Sample type", and "Preservation". An orange arrow points from the "3. データの選択" label to the "5k Human PBMCs (Donor 4)" row in the table.

Product	Species	Sample type	Preservation
Human Kidney Nuclei GEM-X Flex Gene Expression with Automated Cell Annotation	Human	Kidney	Fixed
60k Human PBMCs Stained with 8 TotalSeq™-B Human Hashtags (Donors 1-4, 4 samples)	Human	Blood	Cryopreserved
5k Human PBMCs (Donor 4)	Human	Blood	Cryopreserved
5k Human PBMCs (Donor 3)	Human	Blood	Cryopreserved
5k Human PBMCs (Donor 2)	Human	Blood	Cryopreserved
5k Human PBMCs (Donor 1) with Automated Cell Annotation	Human	Blood	Cryopreserved
20k Human PBMCs Multiplex Sample (Donors 1-4)	Human	Blood	Cryopreserved
10k Human Diseased PBMCs (Myelofibrosis) Freshly Processed	Human	Blood	Fresh

1. データの選択条件・キーワードの指定

2. 条件に合致する候補データの一覧

# 10x Genomics社の Dataset サイト (2)

## 4. 該当のタブを選択

“Input files”: FASTQファイルやサンプル情報のファイル

“Output and Supplemental files”: CellRanger等のプログラムの出力ファイル

10x GENOMICS Products Res

< All datasets

### 5k Human PBMCs (Donor 4)

Single Cell Gene Expression dataset analyzed using Cell Ranger 9.0.0

Mapped **95.7%**

#### Assess data quality

View summary metrics to assess data quality and more.

Visualize and explore data

Discover differentially expressed genes, visualize your favorite genes, and explore your data with our visualization software.

View summary

Explore data

Dataset overview

Output and supplemental files

Input files

Learn about Chromium analysis

Batch download

File type	Size	md5sum
TAR	17.3 GB	97f56ba33471572d4d7dc98830180a24
CSV	243 B	c56cfc73b177221de7d70df6e34f5a6b

FASTQs

Multi Config CSV

## 5. 該当ファイルの選択

# ダウンロードしたファイルを解析ソフトウェアで使う

ダウンロードしたFASTQデータを CellRangerで使う

# ダウンロードしたFASTQデータを CellRangerで使う

- 必要となるFASTQファイル

- シングルセルRNA-seqの場合は、基本的に R1 (read1) と R2 (read2)のファイルがあればよい(ただし、3' v1 chemistry を使っている場合は I1 (index1) ファイルが必要)

10x Genomics Library: Chemistry version	Recommended	Alternative
Gene Expression*: 3' v3.1, 3' LT v3.1, 3' v3, 3' v2, 5' v2, 5' v1.1, 5' v1	R1 and R2 FASTQs	10x BAM
Visium FF & FFPE	1. R1 and R2 FASTQs; 2. Image (submitted as processed data file)	1. 10x BAM; 2. Image (submitted as processed data file)
Feature Barcode: Cell Surface Protein, CRISPR Screening	R1 and R2 FASTQs	10x BAM
3' CellPlex**	10x per-sample BAM (see here)	N/A
5' TCR/BCR***: v2, v1.1, v1	R1 and R2 FASTQs	N/A
Multiome Gene Expression	R1 and R2 FASTQs	10x BAM
Multiome ATAC****	10x BAM	N/A
ATAC****: v1.1, v1	10x BAM	N/A
Chromium Genome, Single Cell DNA	R1 and R2 FASTQs	10x BAM

\*Note that for 3' v1 chemistry, uploading only R1 and R2 FASTQ files is NOT sufficient for others to reproduce the analysis. In this version, 10x Genomics BAM file is the recommended file.

<https://kb.10xgenomics.com/hc/en-us/articles/360024716391-What-format-of-10x-Genomics-data-should-I-submit-to-NCBI-GEO-SRA>



# ダウンロードしたFASTQデータを CellRangerで使う

- 実験chemistryごとのread長の構成

	Read1 (R1)	i7 index (I1)	i5 index (I2)	Read2 (R2)
3' v4	<u>28</u>	10	10	<u>Insert &gt;=90</u>
3' v3 DL	<u>28</u>	10	10	<u>Insert &gt;=90</u>
3' v3/v3.1	<u>28</u>	8	-	<u>Insert &gt;=91</u>
3' v2	<u>26</u>	8	-	<u>Insert &gt;=98</u>
3' v1	<u>Insert &gt;=98</u>	<u>14 (R3)</u>	8 (I1)	<u>10</u>
5' v3	<u>28(+TSO+Insert)</u>	10	10	<u>Insert &gt;=90</u>
5' v2 DL	<u>28(+TSO+Insert)</u>	10	10	<u>Insert &gt;=90</u>
5' v1/v1.1	<u>26(+TSO+Insert)</u>	8	-	<u>Insert &gt;=91</u>

ダウンロードして得られた複数のFASTQファイルのうち、  
どれが Read1 (R1)、Read2 (R2)、i7 index (I1) をread長で推定する

# ダウンロードしたFASTQデータを CellRangerで使う

## • 処理の流れ(例: SRR9291388)

### 1. FASTQファイルをダウンロード

```
$ fasterq-dump -S --include-technical SRR9291388
```

以下の3つのファイルが生成される

- SRR9291388\_1.fastq
- SRR9291388\_2.fastq
- SRR9291388\_3.fastq

### 2. read長の確認をする

```
$ head -1 SRR9291388_*.fastq
```

```
==> SRR9291388_1.fastq <==  
@SRR9291388.1 K00125:97:HLHLYBBXX:3:1101:2980:998 length=26  
  
==> SRR9291388_2.fastq <==  
@SRR9291388.1 K00125:97:HLHLYBBXX:3:1101:2980:998 length=98  
  
==> SRR9291388_3.fastq <==  
@SRR9291388.1 K00125:97:HLHLYBBXX:3:1101:2980:998 length=8
```

# ダウンロードしたFASTQデータを CellRangerで使う

- 処理の流れ(例: SRR9291388)

### 3. ファイルとReadの種類に対応づけと、ファイル名の変更

ダウンロードファイル名	Readの種類	CellRanger用ファイル名
SRR9291388_1.fastq	R1	SRR9291388_S1_L001_R1_001.fastq
SRR9291388_2.fastq	R2	SRR9291388_S1_L001_R2_001.fastq
SRR9291388_3.fastq	I1	SRR9291388_S1_L001_I1_001.fastq (なくてもよい)

CellRanger用のFASTQファイル名に変更する必要がある

“[Sample Name]\_S1\_L00[Lane Number]\_[Read Type]\_001.fastq.gz”

(CellRanger 4.0以降は L00[Lane Number] は省略可能)

# ダウンロードしたFASTQデータを CellRangerで使う

- 処理の流れ(例: SRR9291388)

## 4. CellRanger の実行

```
$ cellranger count --id=(任意のID) --create-bam=true  
--transcriptome=(reference transcriptomeファイルのあるディレクトリ)  
--fastqs=(3.用意したFASTQファイルのあるディレクトリ) ↵
```

実行例:

```
$ cellranger count --id=SRR9291388 --create-bam=true  
--transcriptome=/data/refdata-gex-GRCh38-2024-A/  
--fastqs=$HOME/work/fastqs/ ↵
```

Chemistry は自動判定されるが、判定に問題がある場合は “--chemistry” オプションで明示的に指定する

CellRangerプログラムと、reference transcriptome の設定は完了しているものとする

# ダウンロードしたファイルを解析ソフトウェアで使う

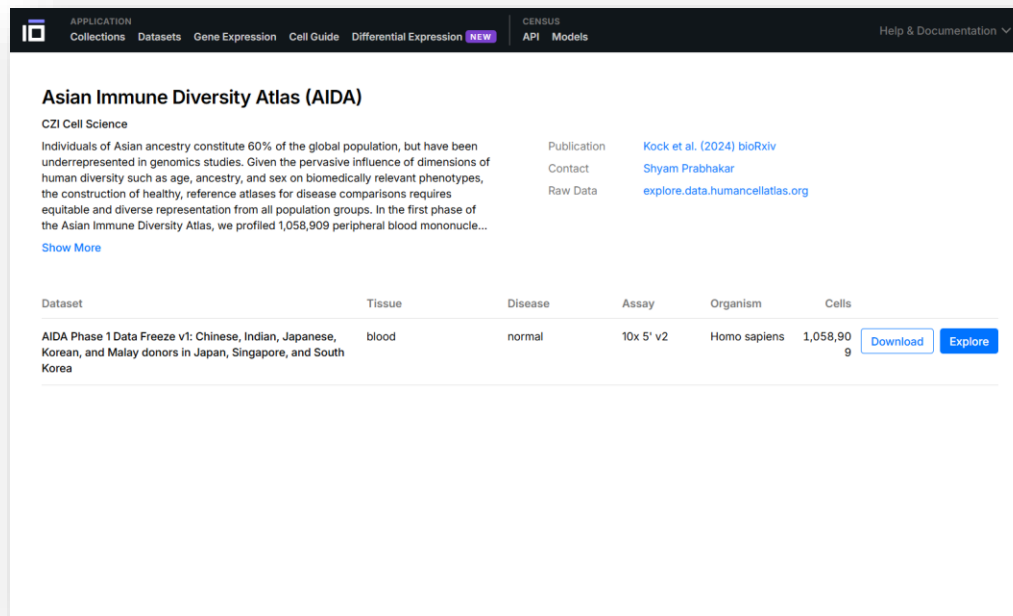
ダウンロードしたH5ADファイルを Scanpy で使う

# ダウンロードしたH5ADファイルを Scanpy で使う

## • 処理の流れ (Asian Immune Diversity Atlasのデータ)

### 1. H5AD形式のファイルのダウンロード

<https://cellxgene.cziscience.com/collections/ced320a1-29f3-47c1-a735-513c7084d508>



The screenshot shows the Cellxgene website interface for the Asian Immune Diversity Atlas (AIDA) dataset. The page includes a navigation bar with options like 'APPLICATION', 'Collections', 'Datasets', 'Gene Expression', 'Cell Guide', 'Differential Expression', 'CENBUS', 'API', and 'Models'. The main content area features the title 'Asian Immune Diversity Atlas (AIDA)' and a brief description of the dataset. Below the description is a table with columns for 'Dataset', 'Tissue', 'Disease', 'Assay', 'Organism', and 'Cells'. The table contains one entry: 'AIDA Phase 1 Data Freeze v1: Chinese, Indian, Japanese, Korean, and Malay donors in Japan, Singapore, and South Korea', with 'blood' as the tissue, 'normal' as the disease, '10x 5' v2' as the assay, 'Homo sapiens' as the organism, and '1,058,909' as the number of cells. There are 'Download' and 'Explore' buttons next to the cell count.

Dataset	Tissue	Disease	Assay	Organism	Cells
AIDA Phase 1 Data Freeze v1: Chinese, Indian, Japanese, Korean, and Malay donors in Japan, Singapore, and South Korea	blood	normal	10x 5' v2	Homo sapiens	1,058,909

最終的に “2a99fd19-9a29-48c3-9d65-47467fd7cefe.h5ad” というファイルがダウンロードされる

ファイル名が長いので、以下“AIDA.h5ad” に変更して説明する

# ダウンロードしたH5ADファイルを Scanpy で使う

- 処理の流れ (Asian Immune Diversity Atlasのデータ)

## 2. Python の scanpy パッケージをロードしデータの読み込み

```
import scanpy↵  
aida = scanpy.read_h5ad('AIDA.h5ad',backed='r')↵
```

# ダウンロードしたH5ADファイルを Scanpy で使う

- 処理の流れ (Asian Immune Diversity Atlasのデータ)

## 3. 読み込んだデータの確認

```
aida
```

```
AnnData object with n_obs × n_vars = 1058909 × 36161 backed at 'AIDA.h5ad'  
  obs: 'mapped_reference_assembly', 'alignment_software', 'library_uuid',  
'assay_ontology_term_id', 'library_starting_quantity', 'is_primary_data',  
'cell_type_ontology_term_id', 'author_cell_type', 'sample_uuid',  
'tissue_ontology_term_id', 'development_stage_ontology_term_id',  
'sample_derivation_process', 'donor_BMI_at_collection',  
'suspension_derivation_process', 'suspension_enriched_cell_types',  
'suspension_percent_cell_viability', 'suspension_uuid', 'suspension_type',  
'donor_id', 'self_reported_ethnicity_ontology_term_id',  
'donor_living_at_sample_collection', 'organism_ontology_term_id',  
'disease_ontology_term_id', 'sex_ontology_term_id', 'Country', 'nCount_RNA',  
'nFeature_RNA', 'Ethnicity_Selfreported', 'TCR_VDJdb', 'TCRa_V_gene',  
'TCRa_D_gene', 'TCRa_J_gene', 'TCRa_C_gene', 'TCRb_V_gene', 'TCRb_D_gene',  
'TCRb_J_gene', 'TCRb_C_gene', 'TCR_Clonality', 'TCR_Clone_ID', 'BCR_VDJ_V_call',  
'BCR_VDJ_D_call', 'BCR_VDJ_J_call', 'BCR_VDJ_C_call', 'BCR_VJ_V_call',  
'BCR_VJ_J_call', 'BCR_VJ_C_call', 'BCR_Clonality', 'BCR_Clone_size',  
'BCR_mu_freq', 'tissue_type', 'cell_type', 'assay', 'disease', 'organism', 'sex',  
'tissue', 'self_reported_ethnicity', 'development_stage', 'observation_joinid'  
  var: 'feature_is_filtered', 'feature_name', 'feature_reference',  
'feature_biotype', 'feature_length', 'feature_type'  
  uns: 'citation', 'default_embedding', 'schema_reference', 'schema_version',  
'title'  
  obsm: 'X_umap'
```

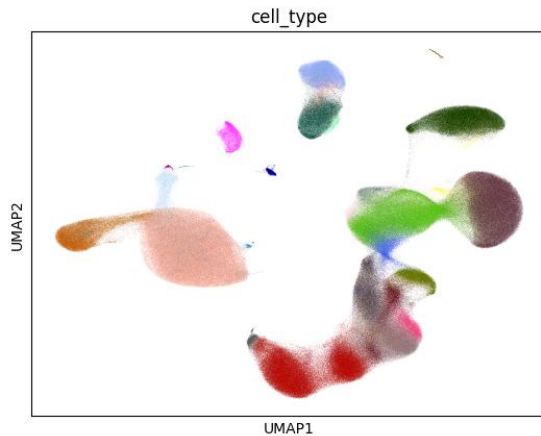


# ダウンロードしたH5ADファイルを Scanpy で使う

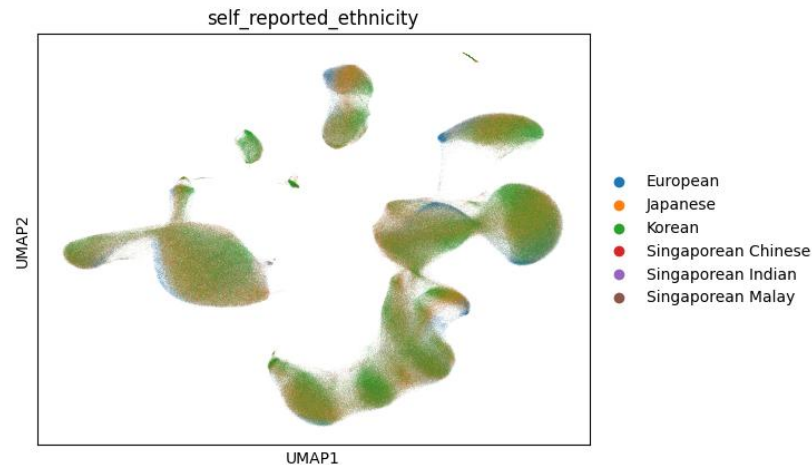
- 処理の流れ (Asian Immune Diversity Atlasのデータ)

## 4. scanpy上での解析(以下はデータに含まれている UMAPプロットの作成)

```
scanpy.pl.umap(aida, color='cell_type') ↵  
scanpy.pl.umap(aida, color='self_reported_ethnicity') ↵
```



- T cell
- erythrocyte
- platelet
- B cell
- dendritic cell
- monocyte
- natural killer cell
- CD4-positive, alpha-beta T cell
- CD8-positive, alpha-beta T cell
- plasmacytoid dendritic cell
- mature B cell
- plasma cell
- memory B cell
- naive B cell
- CD8-positive, alpha-beta cytotoxic T cell
- gamma-delta T cell
- regulatory T cell
- naive thymus-derived CD4-positive, alpha-beta T cell
- naive thymus-derived CD8-positive, alpha-beta T cell
- central memory CD4-positive, alpha-beta T cell
- effector memory CD4-positive, alpha-beta T cell
- CD8-positive, alpha-beta memory T cell
- CD4-positive, alpha-beta cytotoxic T cell
- CD16-negative, CD56-bright natural killer cell, human
- CD16-positive, CD56-dim natural killer cell, human
- mucosal invariant T cell
- conventional dendritic cell
- CD14-positive monocyte
- innate lymphoid cell
- CD141-positive myeloid dendritic cell
- CD14-low, CD16-positive monocyte
- CD1c-positive myeloid dendritic cell
- double negative T regulatory cell



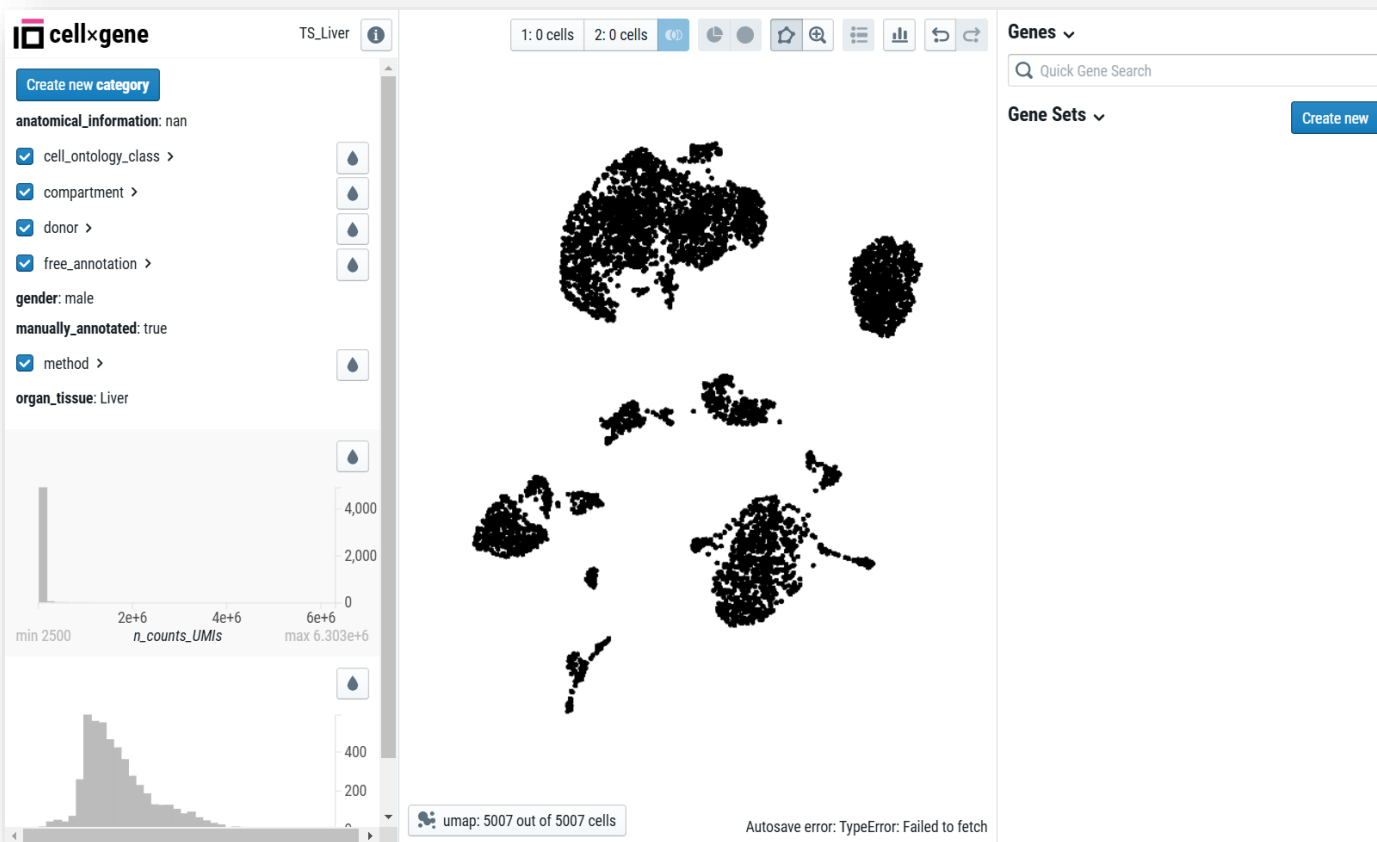
- European
- Japanese
- Korean
- Singaporean Chinese
- Singaporean Indian
- Singaporean Malay

# ダウンロードしたファイルを解析ソフトウェアで使う

ダウンロードしたH5ADファイルを cellxgene で使う

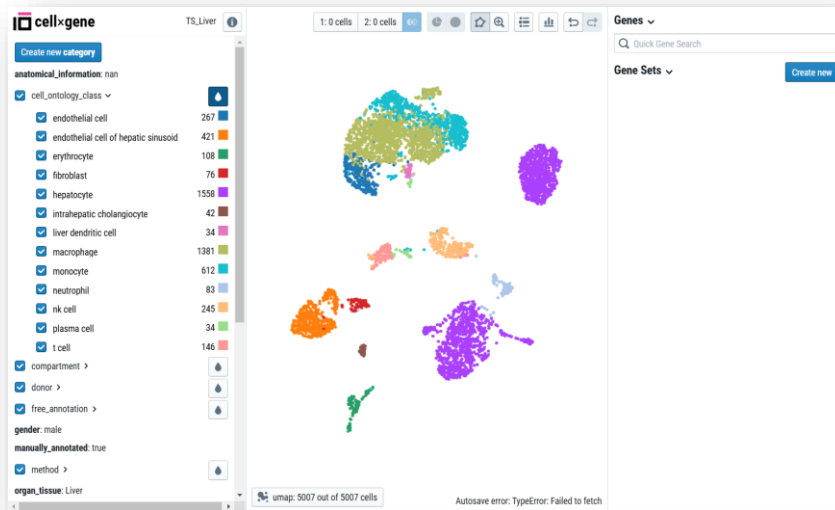
# ダウンロードしたH5ADファイルを cellxgene で使う

- cellxgene (<https://github.com/chanzuckerberg/cellxgene>)
  - シングルセルRNA-seqの結果(クラスタリングや細胞アノテーション情報)を参照したり、自分で細胞へのアノテーションを付与したりできるウェブベースのツール



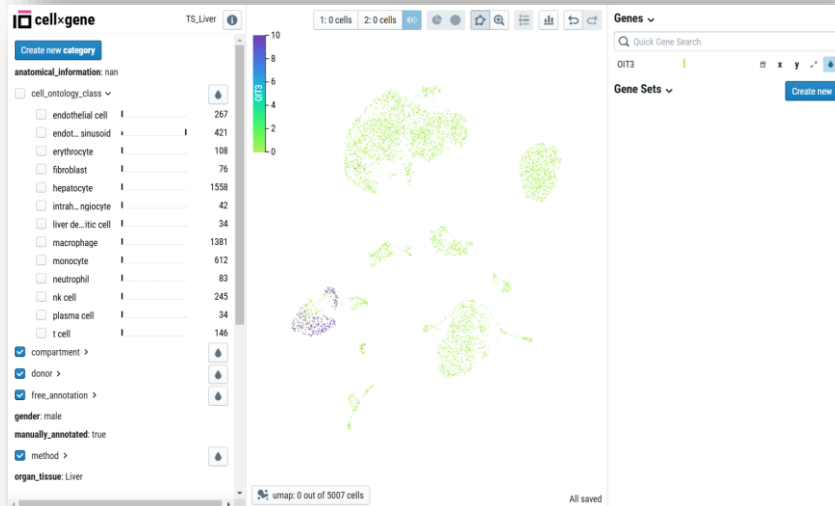
# ダウンロードしたH5ADファイルを cellxgene で使う

- cellxgene (<https://github.com/chanzuckerberg/cellxgene>)



提供されている細胞アノテーションによる色付け表示

(自分で細胞アノテーション/カテゴリ分けを行うこともできる)



指定した遺伝子の発現量による色付け表示

# ダウンロードしたH5ADファイルを cellxgene で使う

- cellxgeneで必要となるH5ADファイルの要件

- Matrix data (usually raw or normalized expression values) in `anndata.X`
- At least one embedding (e.g., tSNE, UMAP) in `anndata.obsm`, specified with the prefix `X_` (e.g., by default scanpy stores UMAP coordinates in `anndata.obsm['X_umap']`)
- A unique identifier is required for each cell, which by default will be pulled from the `obs` DataFrame index. If the index is not unique or does not contain the cell ID, an alternative column can be specified with `--obs-names`
- A unique identifier is required for each gene, which by default will be pulled from the `var` DataFrame index. If the index is not unique or does not contain the gene ID, an alternative column can be specified with `--var-names`

[https://cellxgene.cziscience.com/docs/05\\_\\_Annotate%20and%20Analyze%20Your%20Data/5\\_3\\_\\_Preparing%20Data](https://cellxgene.cziscience.com/docs/05__Annotate%20and%20Analyze%20Your%20Data/5_3__Preparing%20Data)

# ダウンロードしたH5ADファイルを cellxgene で使う

- cellxgene のインストール (pipが利用可能とする)

```
$ pip install cellxgene ↵
```

他の方法でのインストール方法については(Docker利用等)、以下を参照

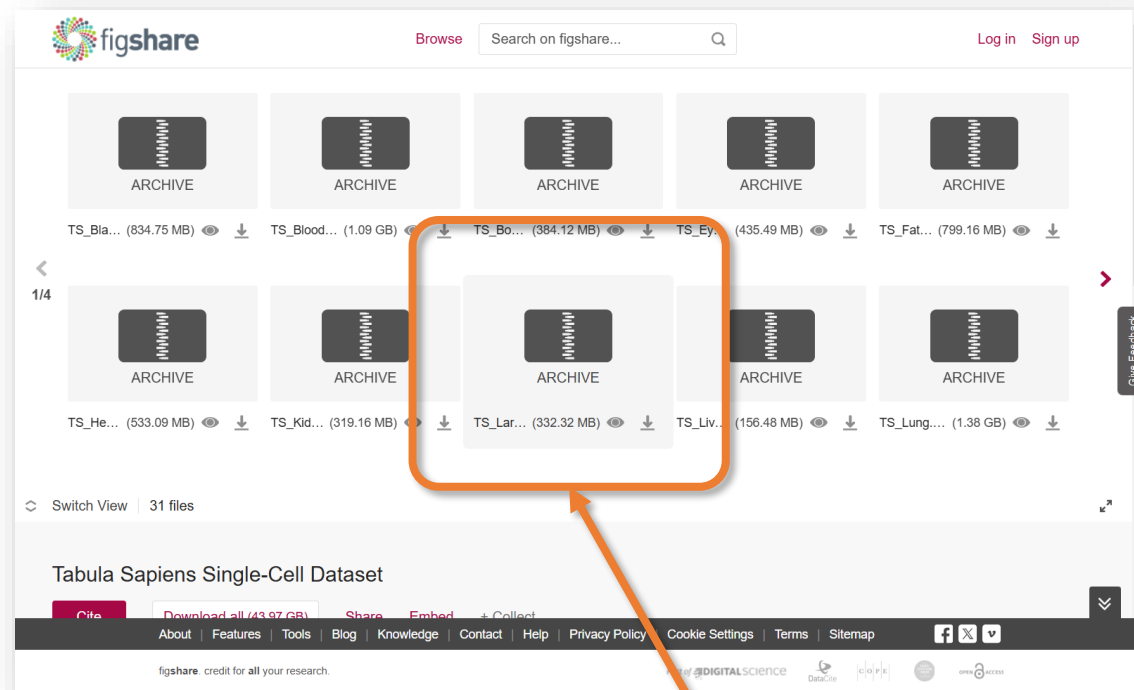
[https://cellxgene.cziscience.com/docs/05\\_\\_Annotate%20and%20Analyze%20Your%20Data/5\\_1\\_\\_Getting%20Started:%20Install,%20Launch,%20Quick%20Start](https://cellxgene.cziscience.com/docs/05__Annotate%20and%20Analyze%20Your%20Data/5_1__Getting%20Started:%20Install,%20Launch,%20Quick%20Start)

# ダウンロードしたH5ADファイルを cellxgene で使う

## • 処理の流れ (Tabula sapiensのLiverデータ)

### 1. H5AD形式のファイルのダウンロード (figshareより)

[https://figshare.com/articles/dataset/Tabula\\_Sapiens\\_release\\_1\\_0/14267219](https://figshare.com/articles/dataset/Tabula_Sapiens_release_1_0/14267219)



下向き矢印のアイコンをクリックするとZIPファイルがダウンロードされるので unzipコマンドや、7-zip等のツールで展開すると“TS\_Liver.h5ad”というファイルが作成される

# ダウンロードしたH5ADファイルを cellxgene で使う

- 処理の流れ (Tabula sapiensのLiverデータ)

## 2. cellxgene の起動

```
$ cellxgene launch TS_Liver.h5ad
```

```
[cellxgene] Starting the CLI...  
[cellxgene] Loading data from TS_Liver.h5ad, this may take a while...  
[cellxgene] Warning: Anndata data matrix is sparse, but not a CSC (columnar) matrix.  
Performance may be improved by using CSC.  
[cellxgene] Warning: Var annotation 'gene_symbol' has 57316 categories, this may be  
cumbersome or slow to display. We recommend setting the --max-category-items option to  
500, this will hide categorical annotations with more than 500 categories in the UI  
WARNING:root:Type float64 will be converted to 32 bit float and may lose precision.  
WARNING:root:Type float64 will be converted to 32 bit float and may lose precision.  
WARNING:root:Type float64 will be converted to 32 bit float and may lose precision.  
WARNING:root:Type float64 will be converted to 32 bit float and may lose precision.  
[cellxgene] Launching! Please go to http://localhost:5005 in your browser.  
[cellxgene] Type CTRL-C at any time to exit.
```

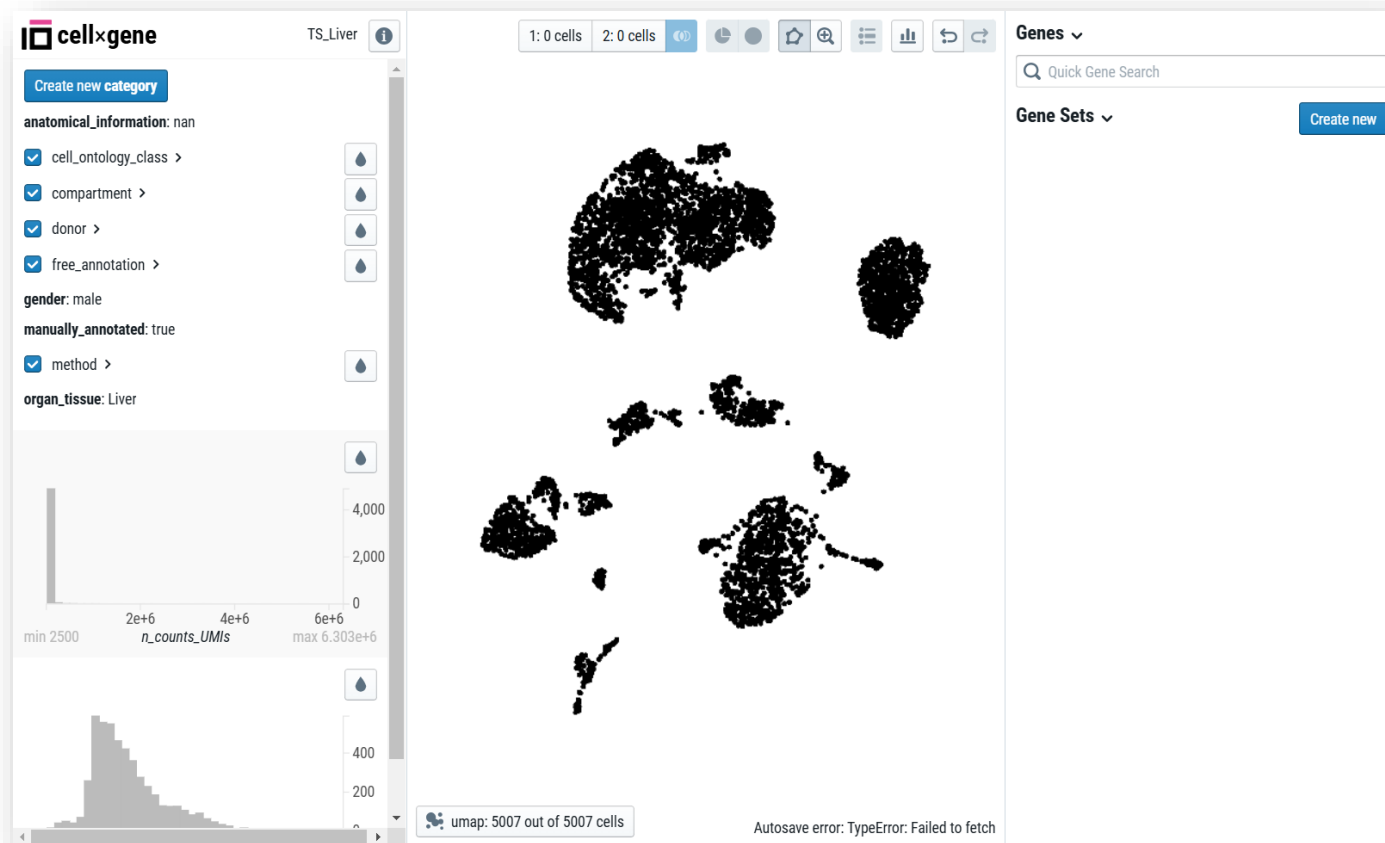
このアドレスをGoogle Chrome等のウェブブラウザで開く



# ダウンロードしたH5ADファイルを cellxgene で使う

## • 処理の流れ (Tabula sapiensのLiverデータ)

### 3. ウェブブラウザでの表示



# シングルセルRNA-seq解析に有用なウェブサイト

# EBI – Single-cell Expression Atlas

- <https://www.ebi.ac.uk/gxa/sc/>
- 様々な生物種の公開シングルセルRNA-seqデータを収集して再解析し、例えば、遺伝子名等でデータセット横断的に検索して、マーカー遺伝子や細胞クラスターの情報などが見られるようにしたウェブサイト

The screenshot displays the EBI Single Cell Expression Atlas interface. At the top, there is a navigation bar with links for Home, Browse experiments, Download, Release notes, Help, and Support. The main header features the site logo, the title "Single Cell Expression Atlas", and the subtitle "Single cell gene expression across species". A search bar is present with the gene ID "657" entered and a "Search" button. To the right, there is a "Query bulk expression" button and a "Back to Expression Atlas" button. Below the search bar, the results for "657 (ENSG00000107779)" are shown, indicating it is expressed in "Homo sapiens". The results table includes columns for Species, Marker genes, Title, Experimental variables, and Number of assays. The "Marker genes" column lists several clusters (1, 10, 11, 12, 13, 16, 2, 3, 4, 5, 7, 9 for k = 19, and 11 for k = 45). The "Title" column shows "GTEx: snRNAseq atlas". The "Experimental variables" column lists "organism part", "sampling site", "inferred cell type - authors labels", and "inferred cell type - ontology labels". The "Number of assays" column shows "209,126". A footer banner at the bottom states: "This website requires cookies, and the limited processing of your personal data in order to function. By using the site you are agreeing to this as outlined in our Privacy Notice and Terms of Use. I agree, dismiss this banner".

EMBL-EBI Services Research Training About us

## Single Cell Expression Atlas

Single cell gene expression across species

Query bulk expression  
Back to Expression Atlas

Home Browse experiments Download Release notes Help Support

Gene ID or gene symbol: 657 Species: Any

Search

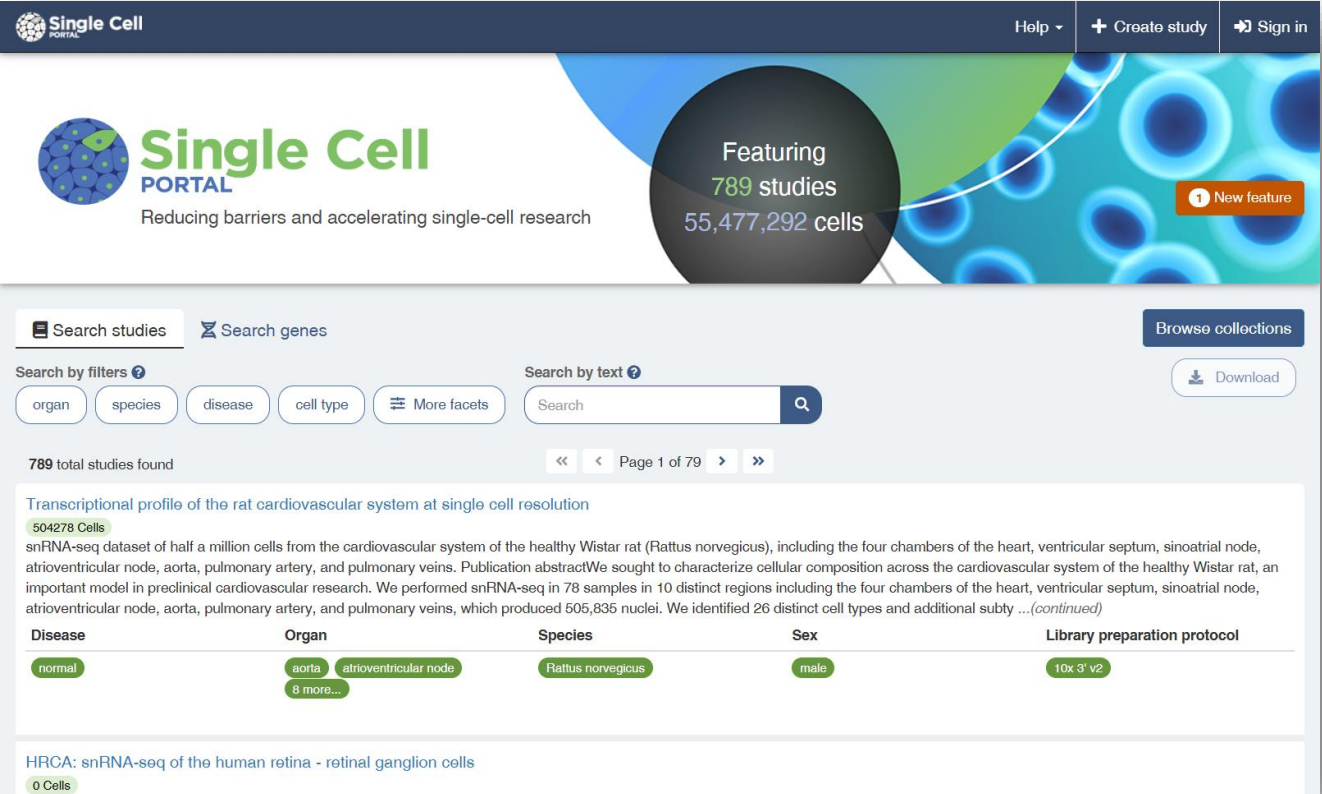
Organism part: Select... 657 (ENSG00000107779) is expressed in:

Species	Marker genes	Title	Experimental variables	Number of assays
Homo sapiens	<ul style="list-style-type: none"><li>See cluster 1, 10, 11, 12, 13, 16, 2, 3, 4, 5, 7, 9 for k = 19</li><li>See cluster 11 for k = 45</li></ul>	GTEx: snRNAseq atlas	<ul style="list-style-type: none"><li>organism part</li><li>sampling site</li><li>inferred cell type - authors labels</li><li>inferred cell type - ontology labels</li></ul>	209,126

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# Broad Institute – single-cell portal

- <https://singlecell.broadinstitute.org/>
- 公開シングルセルRNA-seqデータの再解析を行い、各データセットごとのクラスタリング結果の図を参照したり、興味のある遺伝子について細胞ごとの発現プロファイルを参照したりできるウェブサイト



The screenshot displays the Single Cell Portal interface. At the top, there is a navigation bar with the logo, a 'Help' dropdown, and buttons for 'Create study' and 'Sign in'. Below the navigation bar is a large banner with the 'Single Cell PORTAL' logo and the tagline 'Reducing barriers and accelerating single-cell research'. A circular graphic on the right of the banner states 'Featuring 789 studies' and '55,477,292 cells', with a 'New feature' badge. The main content area includes search filters for 'organ', 'species', 'disease', and 'cell type', along with a 'Search by text' input field. Below the search filters, it indicates '789 total studies found' and shows 'Page 1 of 79'. The first study result is titled 'Transcriptional profile of the rat cardiovascular system at single cell resolution' with 504,278 cells. The abstract describes an snRNA-seq dataset from a healthy Wistar rat. A table below the abstract lists study details:

Disease	Organ	Species	Sex	Library preparation protocol
normal	aorta, atrioventricular node, 8 more...	Rattus norvegicus	male	10x 3' v2

The second study result is 'HRCA: snRNA-seq of the human retina - retinal ganglion cells' with 0 cells.

# RIKEN – scPortalen 2

- <https://single-cell.riken.jp/>
- 公開シングルセルRNA-seqのメタデータの修正や再計算を行い、再利用を促進することを目的としたデータベース
- 解析結果のダウンロードやCellxGeneでの参照などが可能となっている

**SCPortalen2**

Toggle Sidebar

**SCPortalen2**  
— A truly cell-centric database, from RIKEN IMS.

**\*NEW\*** - We have added a new Database Discovery Environment, accessible from the side-bar. Here, using common metadata metrics, you can explore publicly available scRNAseq datasets, indexed from NCBI Sequence Read Archive (SRA).

The SCPortalen Database can be cited with the main publication:

Abugessaisa, I., Noguchi, S., Böttcher, M., Hasegawa, A., Kouno, T., Kato, S., Tada, Y., Ura, H., Abe, K., Shin, J. W., Plessey, C., Corinici, P., & Kasukawa, T. (2018). **SCPortalen: Human and mouse single-cell centric database**. *Nucleic Acids Research*, 46(D1), D781–D787. <https://doi.org/10.1093/nar/gkx949>

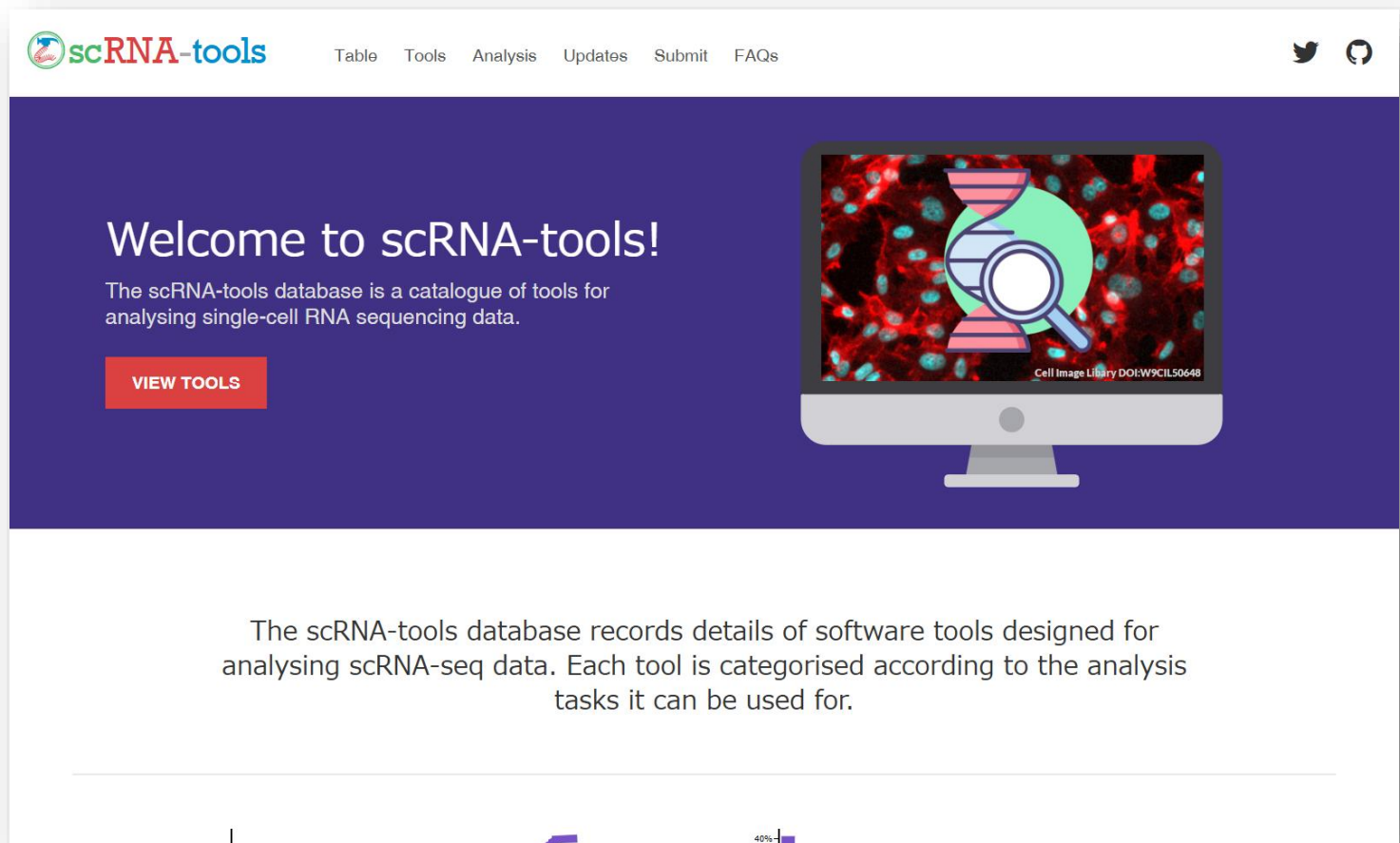
RIKEN Center for Integrative Medical Sciences  
理化学研究所 生命医学研究センター

SCPortalen2: 5' end data, new data visualization and limitless exploration.

We now present SCPortalen2! But what's changed? In this new version we've made some changes to improve the quantity and quality of data as well as a new service to explore thousands of scRNA-seq

# scRNA-tools

- <https://www.scrna-tools.org/>
- シングルセルRNA-seqの解析に用いられる様々なソフトウェアに関するデータベース



The screenshot shows the homepage of the scRNA-tools website. The header features the logo "scRNA-tools" on the left, navigation links "Table", "Tools", "Analysis", "Updates", "Submit", and "FAQs" in the center, and social media icons for Twitter and GitHub on the right. The main content area has a dark blue background with the text "Welcome to scRNA-tools!" and a sub-header "The scRNA-tools database is a catalogue of tools for analysing single-cell RNA sequencing data." Below this is a red button labeled "VIEW TOOLS". To the right is an illustration of a computer monitor displaying a DNA double helix and a magnifying glass over a cell image. The footer contains the text: "The scRNA-tools database records details of software tools designed for analysing scRNA-seq data. Each tool is categorised according to the analysis tasks it can be used for."

## まとめ – Take-home messages

- すでに多くのシングルセルRNA-seqのデータが公共リポジトリ等から入手可能である
  - INSDC (DDBJ / NCBI / EMBL-EBI)
  - Human Cell Atlas 関連サイト
  - 10x Genomics 社の提供するデータセット など
- これらを利用することで今からでもシングルセルRNA-seqのデータ解析がスタートできる
  - データ解析手法の勉強
  - 自分の研究対象に近いデータセットを解析することで、研究の見通しを立てられる
- シングルセルRNA-seqは関連情報も多く存在する
  - シングルセルRNA-seqデータや解析方法も用意に入手可能
  - ただし、シングルセルRNA-seqの解析手法の取得も重要であるが、常にアップデートし続けていくことも重要