



# Studies search

User guide for OmnibusX web tools

# Introduction

Recent advances in multi-omics technologies have significantly expanded the scope of biological research by enabling detailed investigation of cellular states, molecular mechanisms, and tissue-level organization. Techniques such as bulk RNA sequencing, single-cell RNA sequencing (scRNA-seq), single-cell ATAC sequencing (scATAC-seq), and spatial transcriptomics each provide complementary views of gene expression, chromatin accessibility, and spatial context across biological systems.

However, the exponential growth in data generation introduces new challenges in accessing needed datasets and extracting human-understandable information. Traditional databases focus on indexing limited metadata like study titles, abstracts, and categorical tags. Crucially, they lack the detailed annotation efforts from authors and the comprehensive expression profiles of cells, which are key to revealing biological mechanisms. Consequently, researchers often rely on keywords to navigate to studies relevant to their research, then manually download each study for further integration to discern common patterns. This process not only demands substantial computational resources but also significant coding effort. Addressing this need, our database offers an advanced search functionality that encompasses not just traditional study information but also extends to detailed author annotations and comprehensive expression profiles. This capability sets our platform apart from conventional databases, which typically limit searches to basic metadata like titles and abstracts. With our enhanced search function, researchers can efficiently sift through extensive datasets to find studies that are directly relevant to their specific scientific queries.

Beyond dataset discovery, analyzing these data types remains computationally challenging. Researchers often rely on disparate software tools, command-line

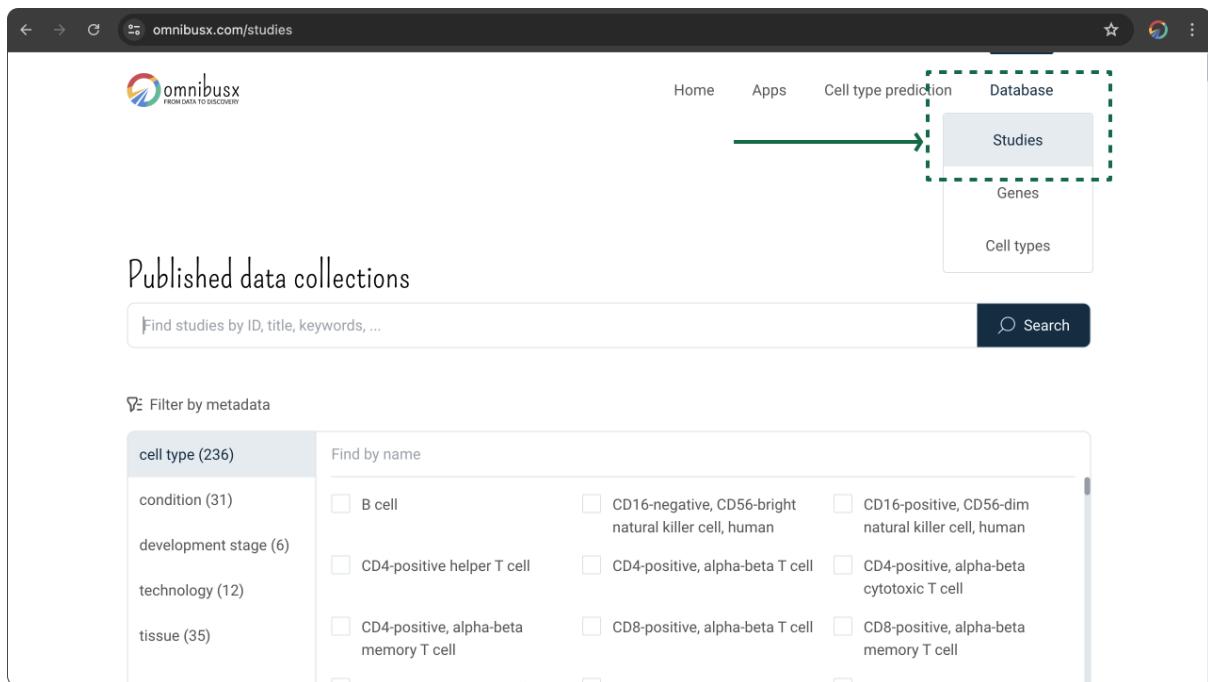
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interfaces, and complex scripting workflows, which can pose significant barriers for researchers without programming expertise. These fragmented pipelines also raise challenges for reproducibility. To overcome this, **OmnibusX** provides a unified platform for real-time data analysis. **OmnibusX** integrates widely adopted open-source packages with proprietary analytical modules into a graphical interface that does not require programming. By supporting end-to-end workflows for multiple omics technologies within a single system, **OmnibusX** eliminates common barriers in multi-omics analysis, enhances reproducibility, and empowers a broader range of researchers to conduct robust, data-driven investigations.

This guide will provide you with detailed instructions on how to utilize the Studies Search to its full potential, facilitating a smoother and more effective research process.

# Studies search

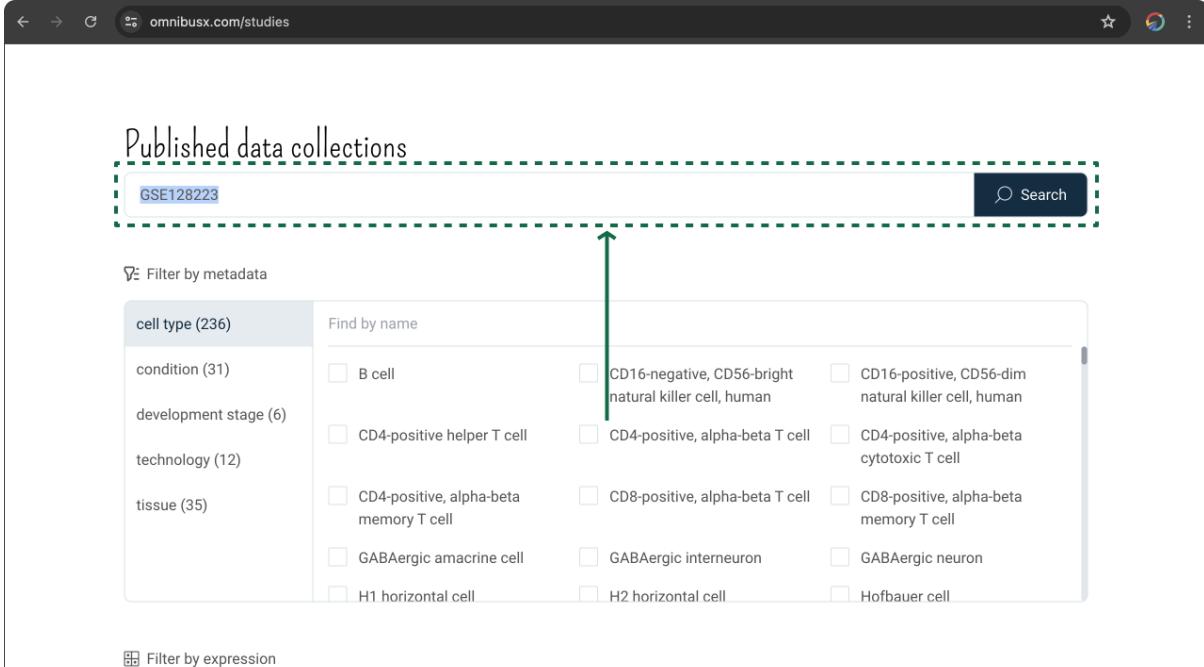
You can access the search tool directly at <https://omnibusx.com/studies>.



## 1. Queries

### 1.1. Free text search

To perform a free text search, enter your keyword in the text input and press **Enter** or click on the **Search** button. Your search will encompass all available text information related to a study, including titles, abstracts, author names, repository access IDs, and particularly, all annotations provided by the authors.



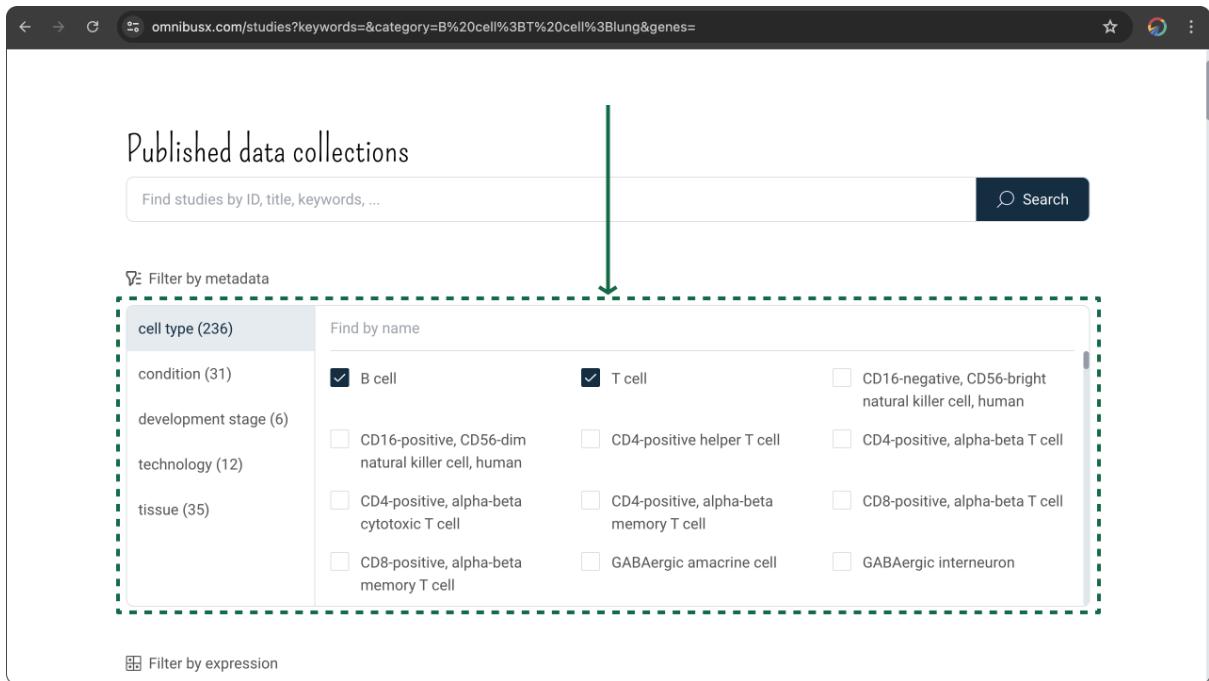
The screenshot shows the 'Published data collections' search interface. At the top, a search bar contains the text 'GSE128223'. Below the search bar is a 'Filter by metadata' section with a 'cell type (236)' dropdown. The 'Find by name' section contains a table of cell types, with a green arrow pointing from the 'Filter by metadata' section to the table. The table includes rows for B cell, CD16-negative, CD56-bright natural killer cell, human, CD16-positive, CD56-dim natural killer cell, human, CD4-positive helper T cell, CD4-positive, alpha-beta T cell, CD4-positive, alpha-beta cytotoxic T cell, CD4-positive, alpha-beta memory T cell, CD8-positive, alpha-beta T cell, CD8-positive, alpha-beta memory T cell, GABAergic amacrine cell, GABAergic interneuron, GABAergic neuron, H1 horizontal cell, H2 horizontal cell, and Hofbauer cell.

This function is especially useful for quickly locating a study by using well-known information such as the title or ID, or discovering novel annotations related to emerging cell populations that may not yet have official classifications.

## 1.2. Controlled vocabularies search

Free text search might lead to missed results due to variations in naming conventions (e.g., CD4 T cell, CD4-positive T cell, CD4+). To accommodate naming variances, OmnibusX has extensively mapped different terminologies to standardized controlled vocabularies. You can utilize this feature by clicking on the needed categories from the **Filter by metadata** panel.

Selecting multiple categories from the same group (e.g., cell types like B cell or T cell) will apply an **OR** search filter, returning studies containing any of the selected categories. Selecting categories from different groups (e.g., tissue type and cell type) will apply an **AND** search filter, returning studies that meet all selected criteria (e.g., studies from lung tissues that contain B cells or T cells).



Published data collections

Find studies by ID, title, keywords, ...

Search

Filter by metadata

cell type (236)

condition (31)

development stage (6)

technology (12)

tissue (35)

Find by name

B cell

T cell

CD16-positive, CD56-dim natural killer cell, human

CD4-positive helper T cell

CD4-positive, alpha-beta T cell

CD8-positive, alpha-beta memory T cell

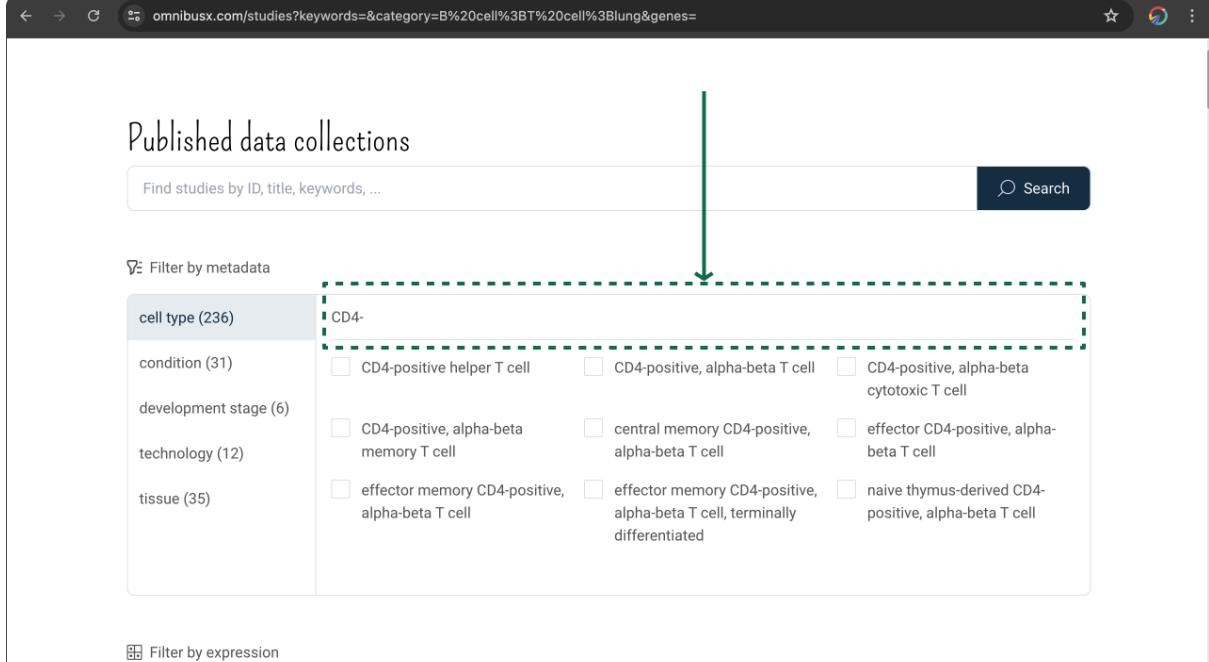
CD4-positive, alpha-beta memory T cell

GABAergic amacrine cell

GABAergic interneuron

Filter by expression

You can quickly find and select your target categories by typing the name into the filter input box above the metadata panel.



Published data collections

Find studies by ID, title, keywords, ...

Search

Filter by metadata

cell type (236)

CD4-

condition (31)

development stage (6)

technology (12)

tissue (35)

Find by name

CD4-positive helper T cell

CD4-positive, alpha-beta T cell

CD4-positive, alpha-beta cytotoxic T cell

central memory CD4-positive, alpha-beta T cell

effector CD4-positive, alpha-beta T cell

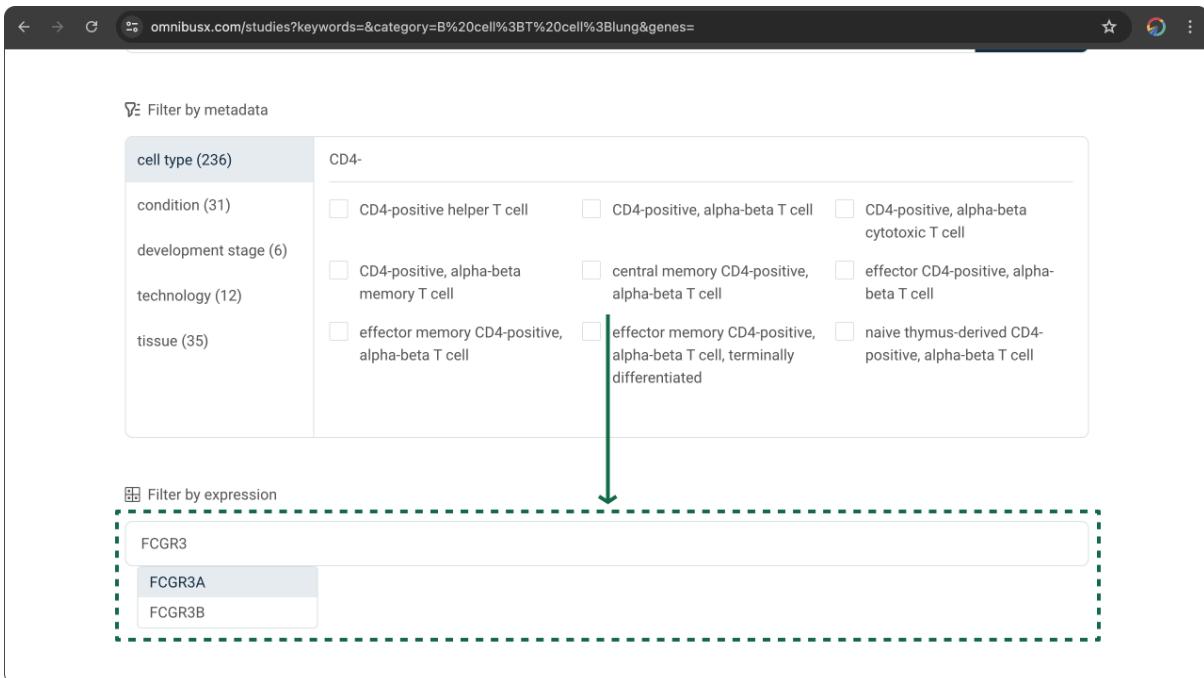
effector memory CD4-positive, alpha-beta T cell, terminally differentiated

naive thymus-derived CD4-positive, alpha-beta T cell

Filter by expression

## 1.3. Expression search

This advanced feature of OmnibusX allows you to efficiently locate studies that report the expression of specific genes, saving significant time that would otherwise be spent downloading and processing datasets to verify gene expression. To use this feature, input the gene name into the search box in the **Filter by expression** section. As you type, OmnibusX will suggest related genes which you can select directly.



The screenshot shows the OmnibusX search interface. At the top, there is a navigation bar with a back arrow, forward arrow, and a search bar containing the URL 'omnibusx.com/studies?keywords=&category=B%20cell%3BT%20cell%3Blung&genes='.

Below the navigation bar, there are two main sections: 'Filter by metadata' and 'Filter by expression'.

**Filter by metadata:** This section is currently active, indicated by a grey background. It includes a sidebar with categories: 'cell type (236)', 'condition (31)', 'development stage (6)', 'technology (12)', and 'tissue (35)'. The main content area shows a list of cell types under the 'CD4-' category, such as 'CD4-positive helper T cell', 'CD4-positive, alpha-beta T cell', 'CD4-positive, alpha-beta cytotoxic T cell', 'CD4-positive, alpha-beta memory T cell', 'central memory CD4-positive, alpha-beta T cell', 'effector CD4-positive, alpha-beta T cell', 'effector memory CD4-positive, alpha-beta T cell', 'effector memory CD4-positive, alpha-beta T cell, terminally differentiated', and 'naive thymus-derived CD4-positive, alpha-beta T cell'. Each item is preceded by a checkbox.

**Filter by expression:** This section is shown below the metadata section, separated by a dashed green line. It includes a search bar with the text 'FCGR3' and a list of suggestions: 'FCGR3A' and 'FCGR3B'. A green arrow points from the 'Filter by expression' section down to the suggestions.

## 2. Results

Once your search is executed, all matching studies will be displayed in a tabular format. The number above the table provides a summary of the total search results. The table enables quick access to basic information for each study, including the title, reference URL, data deposited URL, and the number of cells. For each dataset associated with a study, all queries matching your search criteria will be listed for easy review. Original author annotations are displayed rather than controlled vocabularies to highlight potentially novel annotations that may be of

interest. You can click the **Explore** button associated with each study to delve deeper into detailed data and further investigate the study's specifics.

14 studies 21 datasets 3,013,122 cells

Matched results

Sort results

Basic information

Matched queries

Explore

View detail

### 3. Explore

On selecting the **Explore** option for a specific study, you will be presented with comprehensive information about that study. This includes:

- **Title, Authors, and Abstract:** Fundamental details providing a quick overview of the study's scope and purpose.

omnibusx.com/studies/348da6dc-5bf6-435d-adc5-37747b9ae38a

# Immunophenotyping of COVID-19 and influenza highlights the role of type I interferons in development of severe COVID-19

Jeong Seok Lee, Seongwan Park, Hye Won Jeong, Jin Young Ahn, Seong Jin Choi, Hoyoung Lee, Baekgyu Choi, Su Kyung Nam, Moa Sa, Ji-Soo Kwon, Su Jin Jeong, Heung Kyu Lee, Sung Ho Park, Su-Hyung Park, Jun Yong Choi, Sung-Han Kim, Inkyung Jung, Eui-Cheol Shin

## Abstract

Although most severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)-infected individuals experience mild coronavirus disease 2019 (COVID-19), some patients suffer from severe COVID-19, which is accompanied by acute respiratory distress syndrome and systemic inflammation. To identify factors driving severe progression of COVID-19, we performed single-cell RNA sequencing using peripheral blood mononuclear cells (PBMCs) obtained from healthy donors, patients with mild or severe COVID-19, and patients with severe influenza. Patients with COVID-19 exhibited hyperinflammatory signatures across all types of cells among PBMCs, particularly up-regulation of the tumor necrosis factor/interleukin-1 $\beta$  (TNF/IL-1 $\beta$ )-driven inflammatory response as compared with severe influenza. In classical monocytes from patients with severe COVID-19, type I interferon (IFN) response coexisted with the TNF/IL-1 $\beta$ -driven inflammation, and this was not seen in patients with milder COVID-19. We documented type I IFN-driven inflammatory features in patients with severe influenza as well. On the basis of this, we propose that the type I IFN response plays a pivotal role in exacerbating inflammation in severe COVID-19.

## Datasets

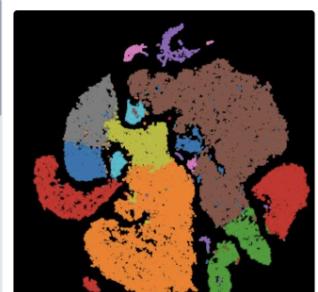
1. Immunophenotyping of COVID-19 and influenza highlights the role of type I interferons in development of severe COVID-19

- **Annotations:** All available annotations from the authors are accessible. This section allows you to toggle between different fields from the summary table to explore various aspects of the study in greater depth.

omnibusx.com/studies/348da6dc-5bf6-435d-adc5-37747b9ae38a

## Datasets

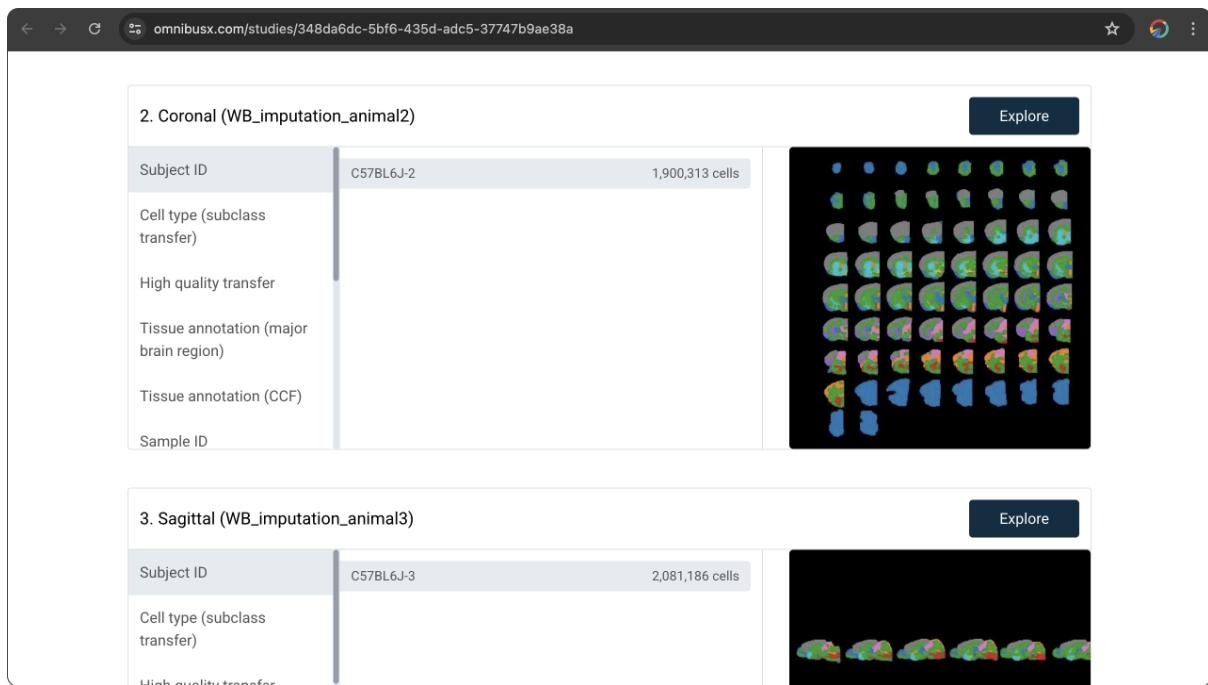
1. Immunophenotyping of COVID-19 and influenza highlights the role of type I interferons in development of severe COVID-19

Metadata			Preview
Sample ID	nCoV 2	4999 cells	
Disease group	Flu 1	4895 cells	
Comorbidity	Normal 2	4646 cells	
Hospital day	nCoV 6	4526 cells	
WBC per microL	Normal 3	4490 cells	
Neutrophil per microL (%)	nCoV 1	4464 cells	
Lymphocyte per microL (%)	nCoV 11	4425 cells	
	Normal 1	4331 cells	

Analyze this study

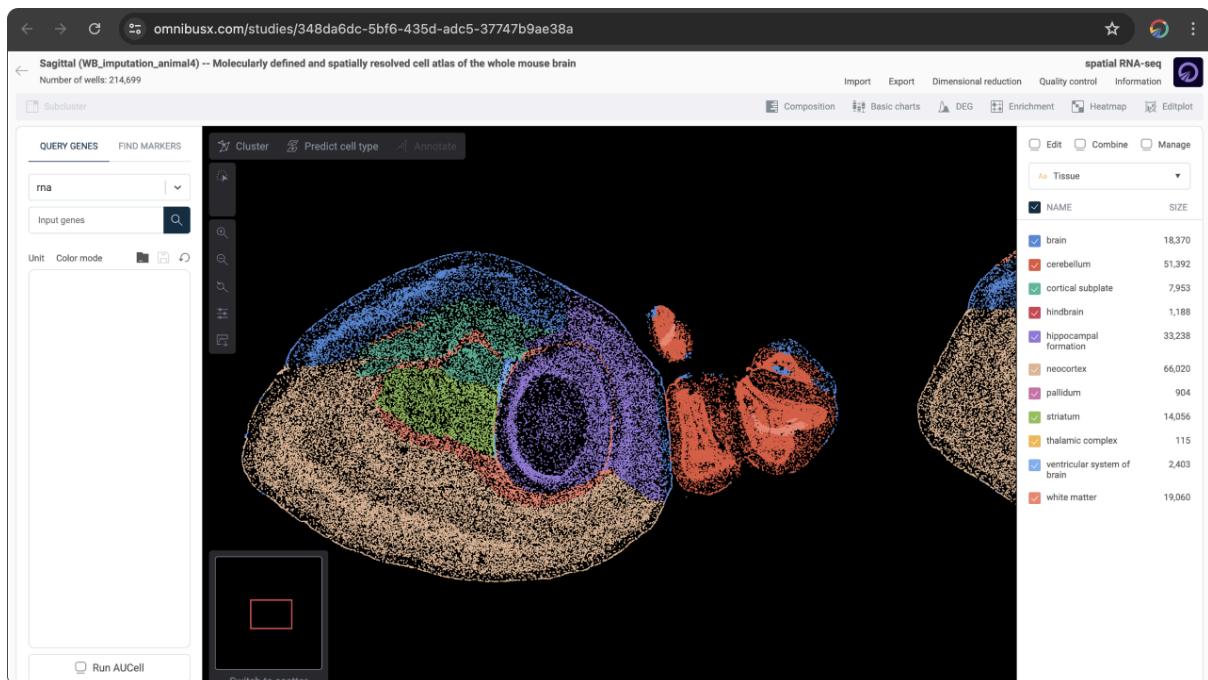


- **Real-time analysis:** Click the **Explore** button corresponding to any dataset to begin analyzing it immediately.



For a detailed walkthrough of the analysis, please refer to our user guides:

- [Single-cell RNA-seq, scATAC-seq, and bulk RNA-seq analysis](#)
- [Spatial analysis](#)



# Thank you!

We extend our heartfelt gratitude to all users of the OmnibusX Multi-Omics Database. Your engagement and feedback are invaluable to us and are what drive continuous improvement and innovation within our database. We are committed to supporting the scientific community by providing robust tools that facilitate groundbreaking research and discovery.

If you have suggestions, feedback, or would like to share how OmnibusX has assisted in your research endeavors, please do not hesitate to reach out to us at [support@omnibusx.com](mailto:support@omnibusx.com). Your stories inspire us, and your feedback helps us refine our tools to better serve your needs.