



Studies search

User guide for OmnibusX web tools

Introduction

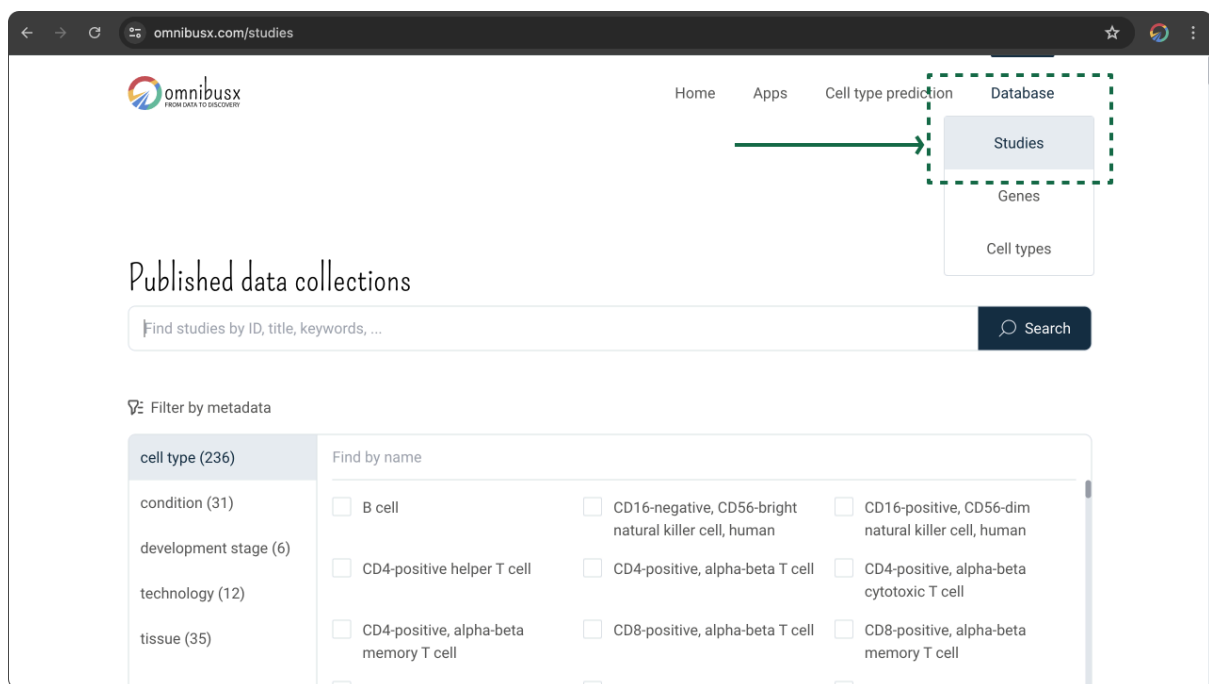
The field of single-cell biology has undergone a revolutionary transformation, driven by the rapid development and widespread adoption of single-cell RNA sequencing (scRNA-Seq) technologies. However, the exponential growth in single-cell data generation introduces new challenges in accessing needed datasets 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 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.

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

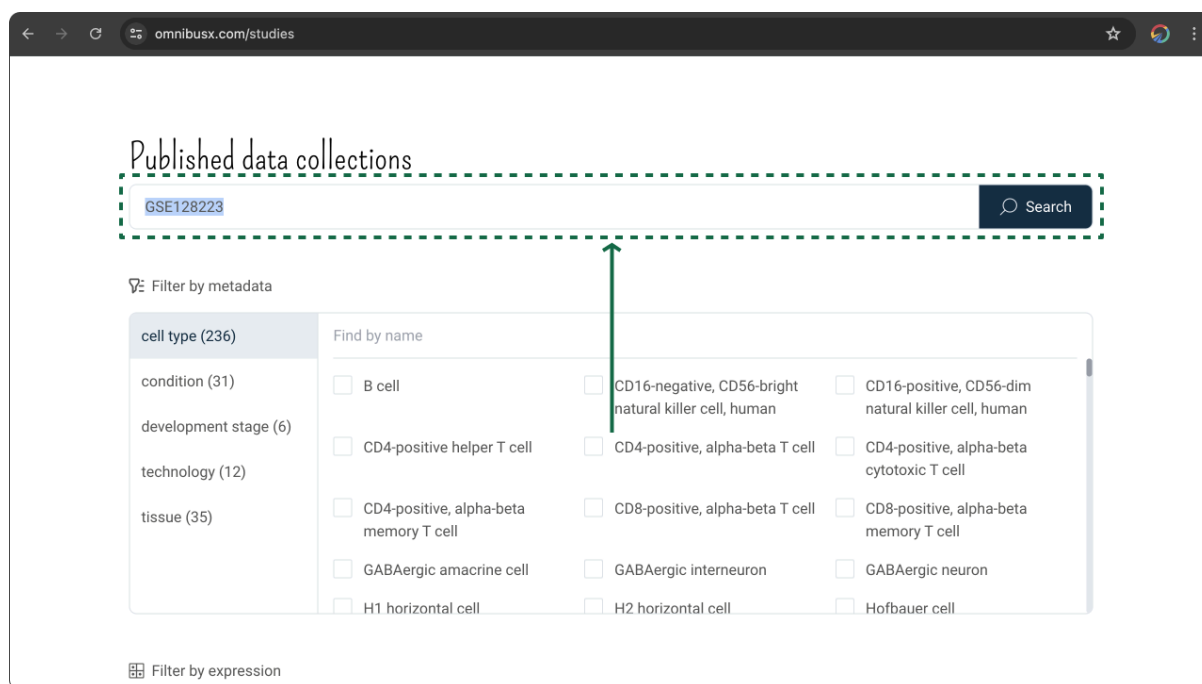
You can access the search tool directly at <https://omnibusx.com/studies>.



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.

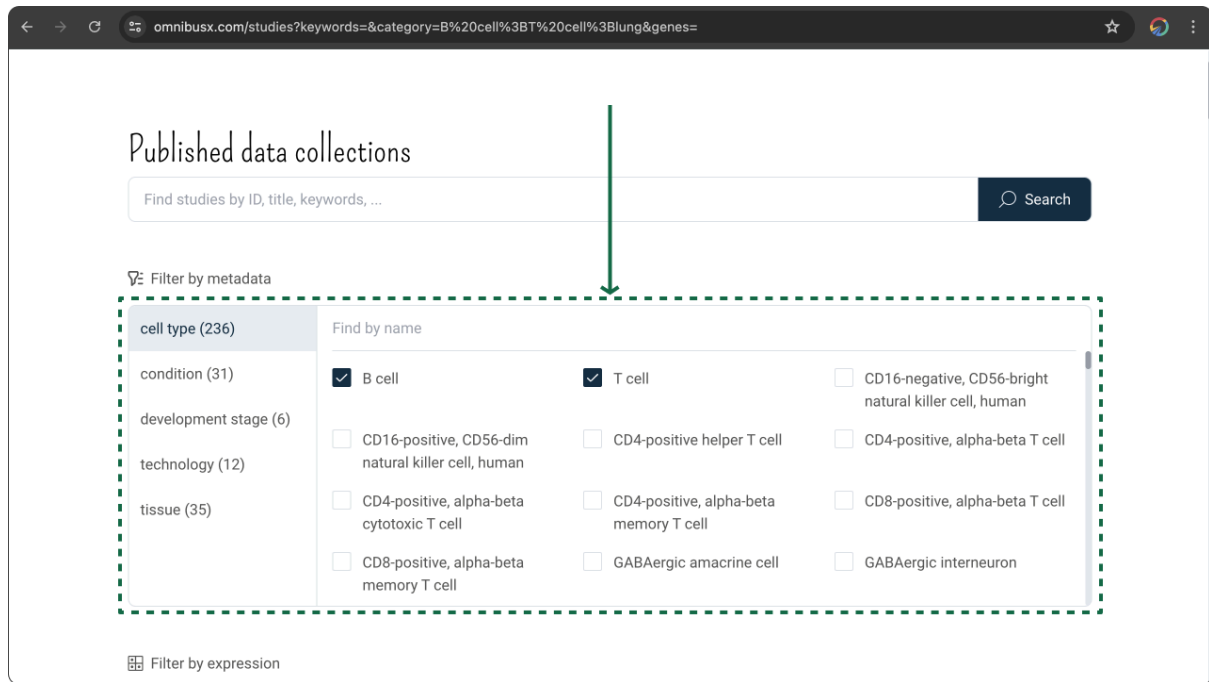


This function is especially useful for quickly locating a study by using well-known information such as the title or ID, or discovering novel annotations related to emerging cell populations that may not yet have official classifications.

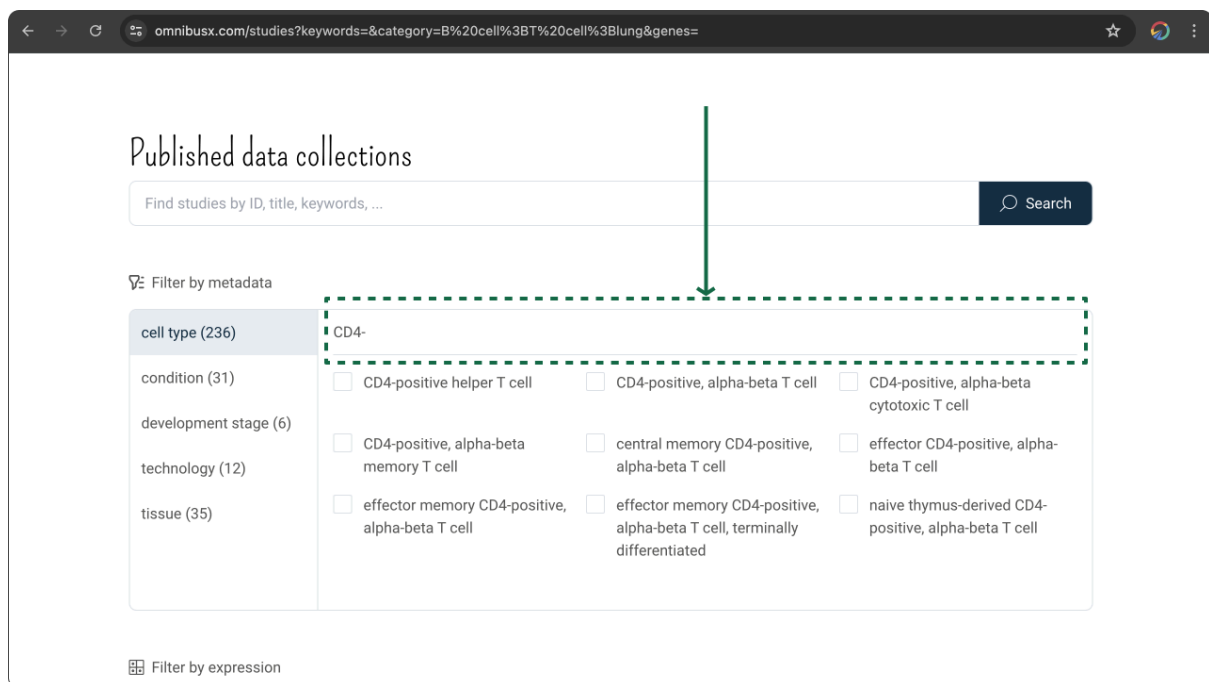
1.2. Controlled vocabularies search

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).

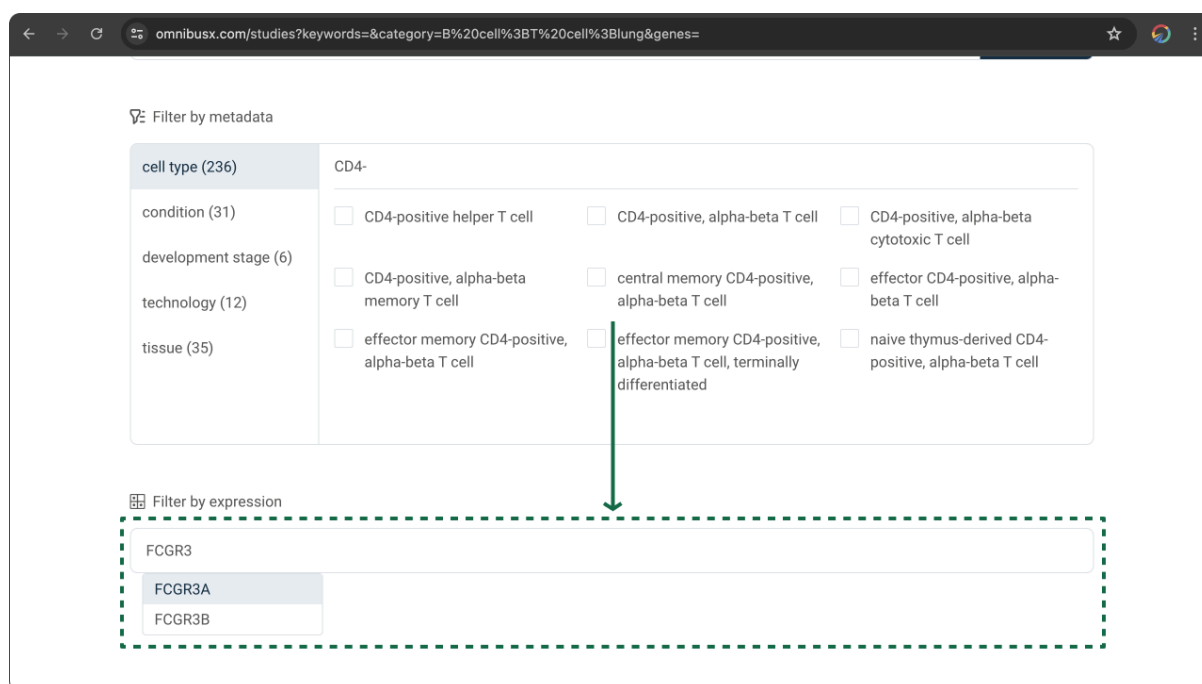


You can quickly find and select your target categories by typing the name into the filter input box above the metadata panel.



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.



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.

The screenshot displays the search results interface on omnibusx.com. At the top, a search bar shows 14 studies, 21 datasets, and 3,013,122 cells. Below this, a table lists search results. The first result is titled 'A molecular cell atlas of the human lung from single cell RNA sequencing' with 75,071 cells. It includes a DOI link and a 'Deposited data' icon. Below the title, it shows 'Dataset 1: Krasnow Lab Human Lung Cell Atlas, 10X' with tags for tissue (blood), cell type (CD8+ Memory/Effector T), and expressed genes (LAG3). The second result is 'Immunophenotyping of COVID-19 and influenza highlights the role of type I interferons in development of severe COVID-19' with 59,572 cells, also showing a DOI, dataset information, and tags for tissue (blood), cell type (CD8, non-EM-like), and expressed genes (LAG3). An 'Explore' button is visible next to each study entry. Annotations with arrows point to specific elements: 'Matched results' points to the search bar; 'Sort results' points to the 'Total cells' column header; 'Basic information' points to the study title and DOI; 'Matched queries' points to the 'blood' and 'CD8+ Memory/Effector T' tags; and 'View detail' points to the 'Explore' button for the second study.

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 β (TNF/IL-1 β)-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 β -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

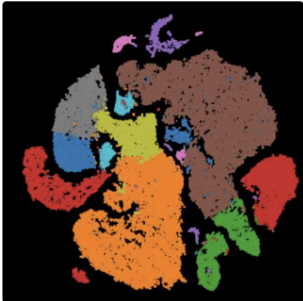
1. Immunophenotyping of COVID-19 and influenza highlights the role of type I interferons in development of severe COVID-19

- **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	
	nCoV 6 4526 cells	
Hospital day	Normal 3 4490 cells	
	nCoV 1 4464 cells	
WBC per microL	nCoV 11 4425 cells	
Neutrophil per microL (%)	Normal 1 4331 cells	
Lymphocyte per microL		

Analyze this study

 [Dataset 1](#)

- **Data source** and **Accession IDs:** Direct links to the original data sources and relevant accession IDs, facilitate easy access to raw data.



The screenshot shows a web browser window with the URL `omnibusx.com/studies/348da6dc-5bf6-435d-adc5-37747b9ae38a`. The page features a header with a navigation bar and a main content area. The navigation bar includes a "Run as Cell" button, a "Visualize & analyze" button, and a "Download OmnibusX" button. The main content area is divided into three sections: "Source data", "Alias names", and "Cite this study".

Source data
<https://cellxgene.cziscience.com/collections/4f889ffc-d4bc-4748-905b-8eb9db47a2ed>

Alias names
GSE149689, E-GEOD-149689, PMID32651212, PMC7402635

Cite this study
Lee, J.S., Park, S., Jeong, H.W., Ahn, J.Y., Choi, S.J., Lee, H., Choi, B., Nam, S.K., Sa, M., Kwon, J.S. and Jeong, S.J., 2020. Immunophenotyping of COVID-19 and influenza highlights the role of type I interferons in development of severe COVID-19. *Science immunology*, 5(49), p.eabd1554.
<https://doi.org/10.1126/sciimmunol.abd1554>

Thank you!

We extend our heartfelt gratitude to all users of the OmnibusX Studies Search platform. 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@omnibux.com. Your stories inspire us, and your feedback helps us refine our tools to better serve your needs.