

Genes search

User guide for OmnibusX web tools

omnibusx.com

Introduction

Single-cell RNA sequencing (scRNA-Seq) technologies have revolutionized the field of single-cell biology, providing unprecedented insights into the complexities of biological systems. However, the rapid growth of data generation has presented significant challenges in data management and utilization. Researchers often face difficulties in accessing and integrating vast datasets, requiring extensive computational resources and coding effort.

To address these challenges, we have developed a comprehensive database with advanced computational tools that efficiently index massive datasets, enabling swift access to author annotations and detailed cell expression profiles. Our user-friendly interface allows researchers to quickly retrieve the expression patterns of target genes across various cell types and tissues, significantly reducing the time required for data processing.

The Gene Search tool, powered by our extensive database, helps identify common gene expression patterns across cell types and tissues. This guide will help you fully leverage the capabilities of the Gene Search tool to enhance your research outcomes.

Genes search

You can access the search tool directly at https://omnibusx.com/genes.

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	Somnibusx		Home	Apps	Cell type prediction	Database		
						Studies		
						Genes		
					·	Cell types		
	Query gene across published	studies						
	Input a gene					🔎 Query		
	Summary of the data curation process							
	1. Retrieval	2. Noise reduction		3. S	tandardization			
	Published data is downloaded from its respective repository.	Background noise is eliminated data accuracy.	to ensure	Aut tiss voc	hor annotations, such as ue, are mapped to a cons abulary.	cell type and sistent, controlled		

1. Queries

You can begin by entering the target gene name into the input box on the **Gene search** page. As you type, OmnibusX will dynamically suggest related gene names, allowing you to select the correct one directly from the dropdown menu.

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			Home	Apps	Cell type prediction	Database			
	Query gene across published	l studies							
	FGFBP					🔎 Query			
	FGFBP1						1		
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	Summary of the data curation process								
	1. Retrieval	2. Noise reduction		3. 9	Standardization				
	Published data is downloaded from its respective repository.	Background noise is eliminate data accuracy.	d to ensure	Aut tiss voo	thor annotations, such as sue, are mapped to a con cabulary.	s cell type and sistent, controllec	ł		

2. Explore

After triggering the search, all results related to the queried gene will be retrieved and presented in two formats: table and visualization plot. In each plot, each cell population is represented by a dot, with the dot color indicating the number of supporting studies and the dot size reflecting the average expression coverage of the gene from those studies. Gene expression interpretations can be summarized as follows:

- **Specificity**: The fewer cell types or tissues a gene is expressed in, the more specific it is considered.
- **Reliability**: The greater the number of supporting studies, the more reliable the expression data.
- Capture rate: Higher expression coverage suggests that a gene is characteristic of certain cell types or tissues; conversely, low coverage may suggest the presence of a sub-population or limitations in detection technologies.

2.1. Gene expression across cell types

All cell types and subtypes that express the queried gene are visualized using the ontology from Cell Ontology. A complex ontology structure indicates widespread gene expression across cell types, while a simple structure suggests greater specificity.



From the result table, you can access all supported studies for the expression of the queried gene in a cell type by clicking on the **Explore** button. You can also click on the cell type name to directly jump to the **Cell types search** function of OmnibusX to further study the characteristics of the cell type.

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	I. Expression across cell types														
	Cell ontology Data table														
	Name	Number of supported studies \uparrow	Average coverage												
	natural killer cell	32 studies	61% ± 21%	🗊 Explore											
	CD16-positive, CD56-dim natural killer cell, human	15 studies	75% ± 13%	戻 Explore											
	mature NK T cell	13 studies	59% ± 22%	🗊 Explore											
	CD8-positive, alpha-beta T cell	10 studies	46% ± 19%	戻 Explore											
	gamma-delta T cell	10 studies	41% ± 11%	厊 Explore											
	CD16-negative, CD56-bright natural killer cell, human	6 studies	33% ± 21%	戻 Explore											
	CD8-positive, alpha-beta memory T cell	6 studies	36% ± 11%	🗊 Explore											

2.2. Gene expression across tissues

Tissues are sorted by the number of supporting studies for the expression of the queried gene. Tissues expressing the queried gene are visualized along with all other tissues to depict the tissue specificity of the gene.

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	II. Expre	ession a	cross tis	ssue																	
	sc-RNAseq data Data table																				
	Number of	supported	d studies 20	5											Av	verage cov	erage 				
	•	•	0	0																	
	peripheral blood	lung	lymph node	thymus	abdomen	adipose	adrenal gland	bladder	Diood vessel	hlood vessel	bone marrow	brain	breast	diaphragm	esophagus	eye	gingiva	heart			
	intestine	kidney	liver	muscle	nasal cavity	nasopharynx	nose	ovary	pancreas	placenta	prostate	skin	spinal column	spleen	stomach	tonsil	ureter	uterus			

From the result table, you can access all supported studies for the expression of the queried gene in a tissue by clicking on the **Explore** button.

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	II. Expression across tis	sue					
	sc-RNAseq data	Data table	-				
	Name		Number of supported studies $\ $	Average coverage			
	peripheral blood		20 studies	37% ± 10%	🗊 Explore		
	lung		5 studies	34% ± 17%	戻 Explore		
	lymph node		4 studies	44% ± 13%	厊 Explore		
	thymus		3 studies	58% ± 29%	戻 Explore		
	Bulk RNAseq data	Data table					_

2.3. Gene expression from bulk RNA-seq data

In addition to expression data from single-cell databases, we also retrieve gene expression from bulk RNA-seq datasets, including GTEx for normal tissue and TCGA for cancer tissue. This helps compare the expression of the gene between conditions and sequencing platforms to avoid biased conclusions.

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	Bu	Average	seq data rpm	1336	Data ta	ble											Cove	rage C				
	OTEX																-	0%	100%			
	TCGA															0	•	0	0			
	'	spleen	peripheral blood	thymus	lung	intestine	lymph node	stomach	bladder	prostate		kidney	breast	adipose	tonsil	uterus	skin	esophagus	liver			
	GTEx	•	۰	•	0	0		•	•													
	TCGA		\bigcirc	٥	0		٥	0														
		blood vessel	pancreas	adrenal gland	ovary	heart	eye	brain	muscle	abdomen	bone marrow	diaphragm	gingiva	nasal cavity	nasopharynx	nose	placenta	spinal column	ureter			

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	Bulk RNAseq data	Data tab	le					
	Tissue	GTEx Coverage ↑	GTEx Average TPM	GTEx Number of samples	TCGA Coverage	TCGA Average TPM	TCGA Number of samples	
	lung	100%	299.96	576 / 578	92%	36.58	1061 / 1155	
	stomach	86%	131.88	308 / 359	83%	28.44	237 / 286	
	prostate	86%	100.56	210 / 245	67%	14.03	335 / 502	
	thymus	87%	132.96	567 / 653	63%	288.44	384 / 605	
	intestine	65%	305.59	624 / 966	83%	24.25	438 / 527	
	breast	71%	72.01	327 / 459	74%	29.59	827 / 1118	
	uterus	61%	38.29	103 / 170	77%	36.43	352 / 459	
	bladder	57%	118.67	12 / 21	72%	23.99	364 / 504	

2.4. Literature review

Other literature information about the gene, retrieved from UniProt, is also presented to support conclusions and provide explanations for observed gene expression patterns.

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	III. Literature review	[sour	rce]			
	Gene name	CD3D				
	Protein name	T-cell surface glycoprotein CD3 delta chain (T-cell receptor T3 delta chain) (CD antigen CD3d) CD3 delta T-cell surface glycoprotein CD3 delta chain (T-cell receptor T3 delta chain)				
	Synonyms	T3D hCG_40222				
	Description	FUNCTION: Part of the TCR-CD3 complex present on T-lymphocyte cell surface that plays an essential role in adaptive immune response. When antigen presenting cells (APCs) activate T-cell receptor (TCR), TCR-mediated signals are transmitted across the cell membrane by the CD3 chains CD3D, CD3E, CD3G and CD3Z. All CD3 chains contain immunoreceptor tyrosine-based activation motifs (ITAMs) in their cytoplasmic domain. Upon TCR engagement, these motifs become phosphorylated by Src family protein tyrosine kinases LCK and FVN, resulting in the activation of downstream signaling pathways . In addition of this role of signal transduction in T-cell activation, CD3D plays an essential role in thymocyte differentiation. Indeed, participates in correct intracellular TCR-CD3 complex, assembly and surface expression. In absence of a functional TCR-CD3 complex, thymocytes are unable to differentiate properly. Interacts with CD4 and CD8 and thus serves to establish a functional link between the TCR and coreceptors CD4 and CD8, which is needed for activation and positive selection of CD4 or CD8 T-cells.				
	Accessions	B0YIY4				

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.