

# Lira Mamanova

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7881567/publications.pdf>

Version: 2024-02-01

16  
papers

2,888  
citations

623734

14  
h-index

996975

15  
g-index

23  
all docs

23  
docs citations

23  
times ranked

5580  
citing authors

#	ARTICLE	IF	CITATIONS
1	Local and systemic responses to SARS-CoV-2 infection in children and adults. <i>Nature</i> , 2022, 602, 321-327.	27.8	179
2	Cross-tissue immune cell analysis reveals tissue-specific features in humans. <i>Science</i> , 2022, 376, eabl5197.	12.6	265
3	Tumor to normal single-cell mRNA comparisons reveal a pan-neuroblastoma cancer cell. <i>Science Advances</i> , 2021, 7, .	10.3	78
4	Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. <i>Nature Medicine</i> , 2021, 27, 546-559.	30.7	261
5	Somatic mutations and single-cell transcriptomes reveal the root of malignant rhabdoid tumours. <i>Nature Communications</i> , 2021, 12, 1407.	12.8	41
6	High-throughput full-length single-cell RNA-seq automation. <i>Nature Protocols</i> , 2021, 16, 2886-2915.	12.0	13
7	Single cell derived mRNA signals across human kidney tumors. <i>Nature Communications</i> , 2021, 12, 3896.	12.8	27
8	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , 2021, 597, 250-255.	27.8	266
9	MultiMAP: dimensionality reduction and integration of multimodal data. <i>Genome Biology</i> , 2021, 22, 346.	8.8	27
10	A cell atlas of human thymic development defines T cell repertoire formation. <i>Science</i> , 2020, 367, .	12.6	368
11	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019, 574, 365-371.	27.8	392
12	Spatiotemporal immune zonation of the human kidney. <i>Science</i> , 2019, 365, 1461-1466.	12.6	281
13	Setting Up a Single-Cell Genomic Laboratory. <i>Methods in Molecular Biology</i> , 2019, 1979, 3-8.	0.9	0
14	Single-cell transcriptomes from human kidneys reveal the cellular identity of renal tumors. <i>Science</i> , 2018, 361, 594-599.	12.6	511
15	Low-bias, strand-specific transcriptome Illumina sequencing by on-flowcell reverse transcription (FRT-seq). <i>Nature Protocols</i> , 2011, 6, 1736-1747.	12.0	22
16	FRT-seq: amplification-free, strand-specific transcriptome sequencing. <i>Nature Methods</i> , 2010, 7, 130-132.	19.0	122