

# Yael Steuerman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11759868/publications.pdf>

Version: 2024-02-01

12  
papers

510  
citations

1163117

8  
h-index

1199594

12  
g-index

12  
all docs

12  
docs citations

12  
times ranked

1302  
citing authors

#	ARTICLE	IF	CITATIONS
1	Leveraging the cell lineage to predict cell-type specificity of regulatory variation from bulk genomics. <i>Genetics</i> , 2021, 217, .	2.9	1
2	Predicting brain metastasis in early stage non-small cell lung cancer patients by gene expression profiling. <i>Translational Lung Cancer Research</i> , 2020, 9, 682-692.	2.8	14
3	Anemia measurements to distinguish between viral and bacterial infections in the emergency department. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2019, 38, 2331-2339.	2.9	4
4	Linking Cell Dynamics With Gene Coexpression Networks to Characterize Key Events in Chronic Virus Infections. <i>Frontiers in Immunology</i> , 2019, 10, 1002.	4.8	7
5	Cell composition analysis of bulk genomics using single-cell data. <i>Nature Methods</i> , 2019, 16, 327-332.	19.0	94
6	Dissection of Influenza Infection In Vivo by Single-Cell RNA Sequencing. <i>Cell Systems</i> , 2018, 6, 679-691.e4.	6.2	165
7	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. <i>Frontiers in Genetics</i> , 2016, 7, 172.	2.3	12
8	ImmQuant: a user-friendly tool for inferring immune cell-type composition from gene-expression data. <i>Bioinformatics</i> , 2016, 32, 3842-3843.	4.1	51
9	Exploiting Gene-Expression Deconvolution to Probe the Genetics of the Immune System. <i>PLoS Computational Biology</i> , 2016, 12, e1004856.	3.2	8
10	CoD: inferring immune-cell quantities related to disease states. <i>Bioinformatics</i> , 2015, 31, 3961-3969.	4.1	10
11	Digital cell quantification identifies global immune cell dynamics during influenza infection. <i>Molecular Systems Biology</i> , 2014, 10, 720.	7.2	103
12	Deciphering molecular circuits from genetic variation underlying transcriptional responsiveness to stimuli. <i>Nature Biotechnology</i> , 2013, 31, 342-349.	17.5	41