

# Jason A Greenbaum

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

12,562  
citations

201674

27  
h-index

243625

44  
g-index

54  
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54  
docs citations

54  
times ranked

21126  
citing authors

#	ARTICLE	IF	CITATIONS
1	Targets of T Cell Responses to SARS-CoV-2 Coronavirus in Humans with COVID-19 Disease and Unexposed Individuals. <i>Cell</i> , 2020, 181, 1489-1501.e15.	28.9	3,220
2	Antigen-Specific Adaptive Immunity to SARS-CoV-2 in Acute COVID-19 and Associations with Age and Disease Severity. <i>Cell</i> , 2020, 183, 996-1012.e19.	28.9	1,494
3	Selective and cross-reactive SARS-CoV-2 T cell epitopes in unexposed humans. <i>Science</i> , 2020, 370, 89-94.	12.6	1,036
4	The immune epitope database (IEDB) 3.0. <i>Nucleic Acids Research</i> , 2015, 43, D405-D412.	14.5	1,014
5	Properties of MHC Class I Presented Peptides That Enhance Immunogenicity. <i>PLoS Computational Biology</i> , 2013, 9, e1003266.	3.2	636
6	Improved methods for predicting peptide binding affinity to MHC class II molecules. <i>Immunology</i> , 2018, 154, 394-406.	4.4	629
7	Impact of Genetic Polymorphisms on Human Immune Cell Gene Expression. <i>Cell</i> , 2018, 175, 1701-1715.e16.	28.9	588
8	Comprehensive analysis of dengue virus-specific responses supports an HLA-linked protective role for CD8 <sup>+</sup> T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2046-53.	7.1	524
9	Immune epitope database analysis resource. <i>Nucleic Acids Research</i> , 2012, 40, W525-W530.	14.5	446
10	Comprehensive analysis of T cell immunodominance and immunoprevalence of SARS-CoV-2 epitopes in COVID-19 cases. <i>Cell Reports Medicine</i> , 2021, 2, 100204.	6.5	437
11	Functional classification of class II human leukocyte antigen (HLA) molecules reveals seven different supertypes and a surprising degree of repertoire sharing across supertypes. <i>Immunogenetics</i> , 2011, 63, 325-335.	2.4	351
12	Pre-existing immunity against swine-origin H1N1 influenza viruses in the general human population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20365-20370.	7.1	298
13	Memory T Cells in Latent Mycobacterium tuberculosis Infection Are Directed against Three Antigenic Islands and Largely Contained in a CXCR3+CCR6+ Th1 Subset. <i>PLoS Pathogens</i> , 2013, 9, e1003130.	4.7	258
14	IEDB-AR: immune epitope database analysis resource in 2019. <i>Nucleic Acids Research</i> , 2019, 47, W502-W506.	14.5	247
15	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. <i>Journal of Molecular Recognition</i> , 2007, 20, 75-82.	2.1	209
16	Unique phenotypes and clonal expansions of human CD4 effector memory T cells re-expressing CD45RA. <i>Nature Communications</i> , 2017, 8, 1473.	12.8	208
17	Automated benchmarking of peptide-MHC class I binding predictions. <i>Bioinformatics</i> , 2015, 31, 2174-2181.	4.1	127
18	IL-10-producing intestinal macrophages prevent excessive antibacterial innate immunity by limiting IL-23 synthesis. <i>Nature Communications</i> , 2015, 6, 7055.	12.8	103

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19	Predicting T cell recognition of MHC class I restricted neopeptides. <i>Oncolmunology</i> , 2018, 7, e1492508.	4.6	82
20	Immunological consequences of intragenus conservation of <i>Mycobacterium tuberculosis</i> T-cell epitopes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E147-55.	7.1	69
21	Circulating T cell-monocyte complexes are markers of immune perturbations. <i>ELife</i> , 2019, 8, .	6.0	67
22	TCRMatch: Predicting T-Cell Receptor Specificity Based on Sequence Similarity to Previously Characterized Receptors. <i>Frontiers in Immunology</i> , 2021, 12, 640725.	4.8	64
23	Dengue Virus Evolution under a Host-Targeted Antiviral. <i>Journal of Virology</i> , 2015, 89, 5592-5601.	3.4	49
24	YAP and MRTF-A, transcriptional co-activators of RhoA-mediated gene expression, are critical for glioblastoma tumorigenicity. <i>Oncogene</i> , 2018, 37, 5492-5507.	5.9	49
25	Transcriptomic Analysis of CD4+ T Cells Reveals Novel Immune Signatures of Latent Tuberculosis. <i>Journal of Immunology</i> , 2018, 200, 3283-3290.	0.8	43
26	T-cell epitope conservation across allergen species is a major determinant of immunogenicity. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 571-578.e7.	2.9	40
27	Development of Asthma in Inner-City Children: Possible Roles of MAIT Cells and Variation in the Home Environment. <i>Journal of Immunology</i> , 2018, 200, 1995-2003.	0.8	38
28	Single-cell eQTL analysis of activated T cell subsets reveals activation and cell type-dependent effects of disease-risk variants. <i>Science Immunology</i> , 2022, 7, eabm2508.	11.9	32
29	T-cell recognition is shaped by epitope sequence conservation in the host proteome and microbiome. <i>Immunology</i> , 2016, 148, 34-39.	4.4	31
30	Immunoproteomic analysis of house dust mite antigens reveals distinct classes of dominant T cell antigens according to function and serological reactivity. <i>Clinical and Experimental Allergy</i> , 2017, 47, 577-592.	2.9	26
31	Transcriptome and chromatin landscape of iNKT cells are shaped by subset differentiation and antigen exposure. <i>Nature Communications</i> , 2021, 12, 1446.	12.8	21
32	Immunodominance in allergic T-cell reactivity to Japanese cedar in different geographic cohorts. <i>Annals of Allergy, Asthma and Immunology</i> , 2016, 117, 680-689.e1.	1.0	14
33	Combined assessment of MHC binding and antigen abundance improves T cell epitope predictions. <i>IScience</i> , 2022, 25, 103850.	4.1	13
34	Targeting the tumor mutanome for personalized vaccination in a TMB low non-small cell lung cancer. , 2022, 10, e003821.		12
35	Development and validation of a sample sparing strategy for HLA typing utilizing next generation sequencing. <i>Human Immunology</i> , 2015, 76, 917-922.	2.4	11
36	Identifying inaccuracies in gene expression estimates from unstranded RNA-seq data. <i>Scientific Reports</i> , 2019, 9, 16342.	3.3	9

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37	TLR9 Sensing of Self-DNA Controls Cell-Mediated Immunity to <i>Listeria</i> Infection via Rapid Conversion of Conventional CD4 <sup>+</sup> T Cells to Treg. <i>Cell Reports</i> , 2020, 31, 107249.	6.4	9
38	Overcoming the Ontology Enrichment Bottleneck with Quick Term Templates. <i>Nature Precedings</i> , 0, , .	0.1	6
39	A behind-the-scenes tour of the IEDB curation process: an optimized process empirically integrating automation and human curation efforts. <i>Immunology</i> , 2020, 161, 139-147.	4.4	6
40	Predicting the Success of Fmoc-Based Peptide Synthesis. <i>ACS Omega</i> , 2022, 7, 23771-23781.	3.5	6
41	Reply to Satheshkumar and Moss: Poxvirus transcriptome analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, E63-E64.	7.1	4
42	A phase 1b study of personalized neoantigen vaccine plus pembrolizumab in adults with advanced cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, 2615-2615.	1.6	4
43	Developmentally distinct CD4 <sup>+</sup> T <sub>reg</sub> lineages shape the CD8 <sup>+</sup> T cell response to acute <i>Listeria</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2113329119.	7.1	4
44	Response to Comment on "Development of Asthma in Inner-City Children: Possible Roles of MAIT Cells and Variation in the Home Environment". <i>Journal of Immunology</i> , 2018, 200, 3317-3318.	0.8	3
45	Towards the prediction of non-peptidic epitopes. <i>PLoS Computational Biology</i> , 2022, 18, e1009151.	3.2	2
46	A comprehensive analysis of the IEDB MHC class-I automated benchmark. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	2
47	TiArA: A Virtual Appliance for the Analysis of Tiling Array Data. <i>PLoS ONE</i> , 2010, 5, e9993.	2.5	0
48	Kinetic Analysis of a Complete Poxvirus Transcriptome Reveals a Novel Class of Genes. <i>FASEB Journal</i> , 2008, 22, .	0.5	0
49	Distinguishing cell-cell complexes from dual lineage cells using single-cell transcriptomics is not trivial. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2022, 101, 547-551.	1.5	0