Jason A Greenbaum

List of Publications by Year
in descending order

49 papers	12,562 citations	201385 27 h-index	243296 44 g-index
54 all docs	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. Cell, 2020, 181, 1489-1501.e15.	13.5	3,220
2	Antigen-Specific Adaptive Immunity to SARS-CoV-2 in Acute COVID-19 and Associations with Age and Disease Severity. Cell, 2020, 183, 996-1012.e19.	13.5	1,494
3	Selective and cross-reactive SARS-CoV-2 T cell epitopes in unexposed humans. Science, 2020, 370, 89-94.	6.0	1,036
4	The immune epitope database (IEDB) 3.0. Nucleic Acids Research, 2015, 43, D405-D412.	6.5	1,014
5	Properties of MHC Class I Presented Peptides That Enhance Immunogenicity. PLoS Computational Biology, 2013, 9, e1003266.	1.5	636
6	Improved methods for predicting peptide binding affinity to MHC class II molecules. Immunology, 2018, 154, 394-406.	2.0	629
7	Impact of Genetic Polymorphisms on Human Immune Cell Gene Expression. Cell, 2018, 175, 1701-1715.e16.	13.5	588
8	Comprehensive analysis of dengue virus-specific responses supports an HLA-linked protective role for CD8 $^{+}$ T cells. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2046-53.	3.3	524
9	Immune epitope database analysis resource. Nucleic Acids Research, 2012, 40, W525-W530.	6.5	446
10	Comprehensive analysis of T cell immunodominance and immunoprevalence of SARS-CoV-2 epitopes in COVID-19 cases. Cell Reports Medicine, 2021, 2, 100204.	3.3	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. Immunogenetics, 2011, 63, 325-335.	1.2	351
12	Pre-existing immunity against swine-origin H1N1 influenza viruses in the general human population. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20365-20370.	3.3	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. PLoS Pathogens, 2013, 9, e1003130.	2.1	258
14	IEDB-AR: immune epitope database—analysis resource in 2019. Nucleic Acids Research, 2019, 47, W502-W506.	6.5	247
15	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. Journal of Molecular Recognition, 2007, 20, 75-82.	1.1	209
16	Unique phenotypes and clonal expansions of human CD4 effector memory T cells re-expressing CD45RA. Nature Communications, 2017, 8, 1473.	5.8	208
17	Automated benchmarking of peptide-MHC class I binding predictions. Bioinformatics, 2015, 31, 2174-2181.	1.8	127
18	IL-10-producing intestinal macrophages prevent excessive antibacterial innate immunity by limiting IL-23 synthesis. Nature Communications, 2015, 6, 7055.	5.8	103

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19	Predicting T cell recognition of MHC class I restricted neoepitopes. OncoImmunology, 2018, 7, e1492508.	2.1	82
20	Immunological consequences of intragenus conservation of *Mycobacterium tuberculosis* T-cell epitopes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E147-55.	3.3	69
21	Circulating T cell-monocyte complexes are markers of immune perturbations. ELife, 2019, 8, .	2.8	67
22	TCRMatch: Predicting T-Cell Receptor Specificity Based on Sequence Similarity to Previously Characterized Receptors. Frontiers in Immunology, 2021, 12, 640725.	2.2	64
23	Dengue Virus Evolution under a Host-Targeted Antiviral. Journal of Virology, 2015, 89, 5592-5601.	1.5	49
24	YAP and MRTF-A, transcriptional co-activators of RhoA-mediated gene expression, are critical for glioblastoma tumorigenicity. Oncogene, 2018, 37, 5492-5507.	2.6	49
25	Transcriptomic Analysis of CD4+ T Cells Reveals Novel Immune Signatures of Latent Tuberculosis. Journal of Immunology, 2018, 200, 3283-3290.	0.4	43
26	T-cell epitope conservation across allergen species is a major determinant of immunogenicity. Journal of Allergy and Clinical Immunology, 2016, 138, 571-578.e7.	1.5	40
27	Development of Asthma in Inner-City Children: Possible Roles of MAIT Cells and Variation in the Home Environment. Journal of Immunology, 2018, 200, 1995-2003.	0.4	38
28	Single-cell eQTL analysis of activated T cell subsets reveals activation and cell type–dependent effects of disease-risk variants. Science Immunology, 2022, 7, eabm2508.	5.6	32
29	T-cell recognition is shaped by epitope sequence conservation in the host proteome and microbiome. Immunology, 2016, 148, 34-39.	2.0	31
30	Immunoproteomic analysis of house dust mite antigens reveals distinct classes of dominant T cell antigens according to function and serological reactivity. Clinical and Experimental Allergy, 2017, 47, 577-592.	1.4	26
31	Transcriptome and chromatin landscape of iNKT cells are shaped by subset differentiation and antigen exposure. Nature Communications, 2021, 12, 1446.	5.8	21
32	Immunodominance in allergic T-cell reactivity to Japanese cedar in different geographic cohorts. Annals of Allergy, Asthma and Immunology, 2016, 117, 680-689.e1.	0.5	14
33	Combined assessment of MHC binding and antigen abundance improves T cell epitope predictions. IScience, 2022, 25, 103850.	1.9	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. Human Immunology, 2015, 76, 917-922.	1.2	11
36	Identifying inaccuracies in gene expression estimates from unstranded RNA-seq data. Scientific Reports, 2019, 9, 16342.	1.6	9

#	ARTICLE	IF	CITATIONS
37	TLR9 Sensing of Self-DNA Controls Cell-Mediated Immunity to Listeria Infection via Rapid Conversion of Conventional CD4+ T Cells to Treg. Cell Reports, 2020, 31, 107249.	2.9	9
38	Overcoming the Ontology Enrichment Bottleneck with Quick Term Templates. Nature Precedings, 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. Immunology, 2020, 161, 139-147.	2.0	6
40	Predicting the Success of Fmoc-Based Peptide Synthesis. ACS Omega, 2022, 7, 23771-23781.	1.6	6
41	Reply to Satheshkumar and Moss: Poxvirus transcriptome analysis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, E63-E64.	3.3	4
42	A phase 1b study of personalized neoantigen vaccine plus pembrolizumab in adults with advanced cancer.. Journal of Clinical Oncology, 2021, 39, 2615-2615.	0.8	4
43	Developmentally distinct CD4$^+$T$_{reg}$lineages shape the CD8$^+$T cell response to acute *Listeria* infection. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2113329119.	3.3	4
44	Response to Comment on "Development of Asthma in Inner-City Children: Possible Roles of MAIT Cells and Variation in the Home Environment" Journal of Immunology, 2018, 200, 3317-3318.	0.4	3
45	Towards the prediction of non-peptidic epitopes. PLoS Computational Biology, 2022, 18, e1009151.	1.5	2
46	A comprehensive analysis of the IEDB MHC class-I automated benchmark. Briefings in Bioinformatics, 2022, 23, .	3.2	2
47	TiArA: A Virtual Appliance for the Analysis of Tiling Array Data. PLoS ONE, 2010, 5, e9993.	1.1	0
48	Kinetic Analysis of a Complete Poxvirus Transcriptome Reveals a Novel Class of Genes. FASEB Journal, 2008, 22, .	0.2	0
49	Distinguishing cell–cell complexes from dual lineage cells using single‐cell transcriptomics is not trivial. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2022, 101, 547-551.	1.1	0