

# Steven H Kleinstein

## List of Publications by Year in descending order

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122  
papers

12,144  
citations

28274

55  
h-index

32842

100  
g-index

137  
all docs

137  
docs citations

137  
times ranked

17909  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phosphoenolpyruvate Is a Metabolic Checkpoint of Anti-tumor T Cell Responses. <i>Cell</i> , 2015, 162, 1217-1228.	28.9	1,044
2	Change-O: a toolkit for analyzing large-scale B cell immunoglobulin repertoire sequencing data. <i>Bioinformatics</i> , 2015, 31, 3356-3358.	4.1	643
3	Two levels of protection for the B cell genome during somatic hypermutation. <i>Nature</i> , 2008, 451, 841-845.	27.8	524
4	pRESTO: a toolkit for processing high-throughput sequencing raw reads of lymphocyte receptor repertoires. <i>Bioinformatics</i> , 2014, 30, 1930-1932.	4.1	417
5	Germinal Center B Cell and T Follicular Helper Cell Development Initiates in the Interfollicular Zone. <i>Immunity</i> , 2011, 34, 947-960.	14.3	406
6	B cells populating the multiple sclerosis brain mature in the draining cervical lymph nodes. <i>Science Translational Medicine</i> , 2014, 6, 248ra107.	12.4	394
7	CD80 and PD-L2 define functionally distinct memory B cell subsets that are independent of antibody isotype. <i>Nature Immunology</i> , 2014, 15, 631-637.	14.5	348
8	Definition of Germinal-Center B Cell Migration In Vivo Reveals Predominant Intrazonal Circulation Patterns. <i>Immunity</i> , 2007, 26, 655-667.	14.3	274
9	Differential Expression of Ly6C and T-bet Distinguish Effector and Memory Th1 CD4+ Cell Properties during Viral Infection. <i>Immunity</i> , 2011, 35, 633-646.	14.3	265
10	The transcription factors ZEB2 and T-bet cooperate to program cytotoxic T cell terminal differentiation in response to LCMV viral infection. <i>Journal of Experimental Medicine</i> , 2015, 212, 2041-2056.	8.5	238
11	Heterogeneity of meningeal B cells reveals a lymphopoietic niche at the CNS borders. <i>Science</i> , 2021, 373, .	12.6	218
12	Automated analysis of high-throughput B-cell sequencing data reveals a high frequency of novel immunoglobulin V gene segment alleles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E862-70.	7.1	215
13	Practical guidelines for B-cell receptor repertoire sequencing analysis. <i>Genome Medicine</i> , 2015, 7, 121.	8.2	215
14	Polycomb Repressive Complex 2-Mediated Chromatin Repression Guides Effector CD8 + T Cell Terminal Differentiation and Loss of Multipotency. <i>Immunity</i> , 2017, 46, 596-608.	14.3	202
15	Models of Somatic Hypermutation Targeting and Substitution Based on Synonymous Mutations from High-Throughput Immunoglobulin Sequencing Data. <i>Frontiers in Immunology</i> , 2013, 4, 358.	4.8	197
16	Human germinal centres engage memory and naive B cells after influenza vaccination. <i>Nature</i> , 2020, 586, 127-132.	27.8	194
17	High-resolution antibody dynamics of vaccine-induced immune responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4928-4933.	7.1	186
18	Salmonella Infection Drives Promiscuous B Cell Activation Followed by Extrafollicular Affinity Maturation. <i>Immunity</i> , 2015, 43, 120-131.	14.3	186

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19	A Potently Neutralizing Antibody Protects Mice against SARS-CoV-2 Infection. <i>Journal of Immunology</i> , 2020, 205, 915-922.	0.8	186
20	Quantifying selection in high-throughput Immunoglobulin sequencing data sets. <i>Nucleic Acids Research</i> , 2012, 40, e134-e134.	14.5	179
21	Salmonella Typhimurium Type III Secretion Effectors Stimulate Innate Immune Responses in Cultured Epithelial Cells. <i>PLoS Pathogens</i> , 2009, 5, e1000538.	4.7	177
22	Quantitative set analysis for gene expression: a method to quantify gene set differential expression including gene-gene correlations. <i>Nucleic Acids Research</i> , 2013, 41, e170-e170.	14.5	171
23	Dynamic expression profiling of type I and type III interferon-stimulated hepatocytes reveals a stable hierarchy of gene expression. <i>Hepatology</i> , 2014, 59, 1262-1272.	7.3	169
24	Immune dysregulation and autoreactivity correlate with disease severity in SARS-CoV-2-associated multisystem inflammatory syndrome in children. <i>Immunity</i> , 2021, 54, 1083-1095.e7.	14.3	164
25	Adaptive Immune Receptor Repertoire Community recommendations for sharing immune-repertoire sequencing data. <i>Nature Immunology</i> , 2017, 18, 1274-1278.	14.5	163
26	Production of IL-10 by CD4 <sup>+</sup> regulatory T cells during the resolution of infection promotes the maturation of memory CD8 <sup>+</sup> T cells. <i>Nature Immunology</i> , 2015, 16, 871-879.	14.5	159
27	Interleukin-10 from CD4 <sup>+</sup> follicular regulatory T cells promotes the germinal center response. <i>Science Immunology</i> , 2017, 2, .	11.9	139
28	Hierarchical Clustering Can Identify B Cell Clones with High Confidence in Ig Repertoire Sequencing Data. <i>Journal of Immunology</i> , 2017, 198, 2489-2499.	0.8	137
29	NLRP10 is a NOD-like receptor essential to initiate adaptive immunity by dendritic cells. <i>Nature</i> , 2012, 484, 510-513.	27.8	126
30	Individual heritable differences result in unique cell lymphocyte receptor repertoires of naïve and antigen-experienced cells. <i>Nature Communications</i> , 2016, 7, 11112.	12.8	123
31	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. <i>Science Immunology</i> , 2017, 2, .	11.9	122
32	Divergent and self-reactive immune responses in the CNS of COVID-19 patients with neurological symptoms. <i>Cell Reports Medicine</i> , 2021, 2, 100288.	6.5	121
33	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. <i>Frontiers in Immunology</i> , 2017, 8, 1418.	4.8	102
34	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. <i>Nature Communications</i> , 2022, 13, 440.	12.8	100
35	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. <i>Cancer Cell</i> , 2020, 37, 655-673.e11.	16.8	93
36	Dysregulation of B Cell Repertoire Formation in Myasthenia Gravis Patients Revealed through Deep Sequencing. <i>Journal of Immunology</i> , 2017, 198, 1460-1473.	0.8	92

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37	Taking Advantage: High-Affinity B Cells in the Germinal Center Have Lower Death Rates, but Similar Rates of Division, Compared to Low-Affinity Cells. <i>Journal of Immunology</i> , 2009, 183, 7314-7325.	0.8	86
38	Estimating Hypermutation Rates from Clonal Tree Data. <i>Journal of Immunology</i> , 2003, 171, 4639-4649.	0.8	85
39	Long-lived antigen-induced IgM plasma cells demonstrate somatic mutations and contribute to long-term protection. <i>Nature Communications</i> , 2016, 7, 11826.	12.8	84
40	Detecting selection in immunoglobulin sequences. <i>Nucleic Acids Research</i> , 2011, 39, W499-W504.	14.5	83
41	Interleukin-29 Functions Cooperatively with Interferon to Induce Antiviral Gene Expression and Inhibit Hepatitis C Virus Replication. <i>Journal of Biological Chemistry</i> , 2008, 283, 30079-30089.	3.4	81
42	Neutralizing antibodies against West Nile virus identified directly from human B cells by single-cell analysis and next generation sequencing. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 1587-1597.	1.3	80
43	Spatiotemporal segregation of human marginal zone and memory B cell populations in lymphoid tissue. <i>Nature Communications</i> , 2018, 9, 3857.	12.8	78
44	Analysis of gene-environment interactions in postnatal development of the mammalian intestine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1929-1936.	7.1	77
45	Migrant memory B cells secrete luminal antibody in the vagina. <i>Nature</i> , 2019, 571, 122-126.	27.8	77
46	Intranasal priming induces local lung-resident B cell populations that secrete protective mucosal antiviral IgA. <i>Science Immunology</i> , 2021, 6, eabj5129.	11.9	76
47	Improved methods for detecting selection by mutation analysis of Ig V region sequences. <i>International Immunology</i> , 2008, 20, 683-694.	4.0	75
48	The center for expanded data annotation and retrieval. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1148-1152.	4.4	74
49	The immune cell infiltrate populating meningiomas is composed of mature, antigen-experienced T and B cells. <i>Neuro-Oncology</i> , 2013, 15, 1479-1490.	1.2	72
50	Ageing-dependent alterations in gene expression and a mitochondrial signature of responsiveness to human influenza vaccination. <i>Aging</i> , 2015, 7, 38-52.	3.1	72
51	AIRR Community Standardized Representations for Annotated Immune Repertoires. <i>Frontiers in Immunology</i> , 2018, 9, 2206.	4.8	71
52	Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22664-22672.	7.1	71
53	Identification of Subject-Specific Immunoglobulin Alleles From Expressed Repertoire Sequencing Data. <i>Frontiers in Immunology</i> , 2019, 10, 129.	4.8	67
54	Autoreactive T Cells from Patients with Myasthenia Gravis Are Characterized by Elevated IL-17, IFN- $\gamma$ , and GM-CSF and Diminished IL-10 Production. <i>Journal of Immunology</i> , 2016, 196, 2075-2084.	0.8	66

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55	Computational resources for high-dimensional immune analysis from the Human Immunology Project Consortium. <i>Nature Biotechnology</i> , 2014, 32, 146-148.	17.5	65
56	Overexpression of T-bet in HIV infection is associated with accumulation of B cells outside germinal centers and poor affinity maturation. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	65
57	Shared VH1-46 gene usage by pemphigus vulgaris autoantibodies indicates common humoral immune responses among patients. <i>Nature Communications</i> , 2014, 5, 4167.	12.8	63
58	A Model of Somatic Hypermutation Targeting in Mice Based on High-Throughput Ig Sequencing Data. <i>Journal of Immunology</i> , 2016, 197, 3566-3574.	0.8	63
59	Inferred Allelic Variants of Immunoglobulin Receptor Genes: A System for Their Evaluation, Documentation, and Naming. <i>Frontiers in Immunology</i> , 2019, 10, 435.	4.8	63
60	Prolonged Proinflammatory Cytokine Production in Monocytes Modulated by Interleukin 10 After Influenza Vaccination in Older Adults. <i>Journal of Infectious Diseases</i> , 2015, 211, 1174-1184.	4.0	62
61	Early B cell tolerance defects in neuromyelitis optica favour anti-AQP4 autoantibody production. <i>Brain</i> , 2019, 142, 1598-1615.	7.6	62
62	Affinity Maturation Is Impaired by Natural Killer Cell Suppression of Germinal Centers. <i>Cell Reports</i> , 2018, 24, 3367-3373.e4.	6.4	59
63	Influence of seasonal exposure to grass pollen on local and peripheral blood IgE repertoires in patients with allergic rhinitis. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 134, 604-612.	2.9	55
64	A spectral clustering-based method for identifying clones from high-throughput B cell repertoire sequencing data. <i>Bioinformatics</i> , 2018, 34, i341-i349.	4.1	55
65	TLR4 Ligands Lipopolysaccharide and Monophosphoryl Lipid A Differentially Regulate Effector and Memory CD8+ T Cell Differentiation. <i>Journal of Immunology</i> , 2014, 192, 4221-4232.	0.8	53
66	The mutation patterns in B-cell immunoglobulin receptors reflect the influence of selection acting at multiple time-scales. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140242.	4.0	49
67	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. <i>Immunity</i> , 2015, 43, 605-614.	14.3	49
68	Cutting Edge: Ig H Chains Are Sufficient to Determine Most B Cell Clonal Relationships. <i>Journal of Immunology</i> , 2019, 203, 1687-1692.	0.8	48
69	Antiviral Response Dictated by Choreographed Cascade of Transcription Factors. <i>Journal of Immunology</i> , 2010, 184, 2908-2917.	0.8	46
70	Comment on "A Database of Human Immune Receptor Alleles Recovered from Population Sequencing Data". <i>Journal of Immunology</i> , 2017, 198, 3371-3373.	0.8	46
71	Solving Immunology?. <i>Trends in Immunology</i> , 2017, 38, 116-127.	6.8	45
72	Phenotypic and Ig Repertoire Analyses Indicate a Common Origin of IgD <sup>hi</sup> CD27 <sup>hi</sup> Double Negative B Cells in Healthy Individuals and Multiple Sclerosis Patients. <i>Journal of Immunology</i> , 2019, 203, 1650-1664.	0.8	42

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73	Altered Folate Availability Modifies the Molecular Environment of the Human Colorectum: Implications for Colorectal Carcinogenesis. <i>Cancer Prevention Research</i> , 2011, 4, 530-543.	1.5	41
74	Age-associated vascular inflammation promotes monocytosis during atherogenesis. <i>Aging Cell</i> , 2016, 15, 766-777.	6.7	41
75	Phylogenetic analysis of migration, differentiation, and class switching in B cells. <i>PLoS Computational Biology</i> , 2022, 18, e1009885.	3.2	40
76	Single-cell repertoire tracing identifies rituximab-resistant B cells during myasthenia gravis relapses. <i>JCI Insight</i> , 2020, 5, .	5.0	37
77	Systems Immunology Reveals Markers of Susceptibility to West Nile Virus Infection. <i>Vaccine Journal</i> , 2015, 22, 6-16.	3.1	35
78	Thymus-derived B cell clones persist in the circulation after thymectomy in myasthenia gravis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30649-30660.	7.1	33
79	Toward Quantitative Simulation of Germinal Center Dynamics: Biological and Modeling Insights from Experimental Validation. <i>Journal of Theoretical Biology</i> , 2001, 211, 253-275.	1.7	32
80	Multiple Transcription Factor Binding Sites Predict AID Targeting in Non-Ig Genes. <i>Journal of Immunology</i> , 2013, 190, 3878-3888.	0.8	32
81	Integrating B Cell Lineage Information into Statistical Tests for Detecting Selection in Ig Sequences. <i>Journal of Immunology</i> , 2014, 192, 867-874.	0.8	32
82	Immune Markers Associated with Host Susceptibility to Infection with West Nile Virus. <i>Viral Immunology</i> , 2014, 27, 39-47.	1.3	31
83	Mantle cell lymphoma in cyclin D1 transgenic mice with Bim-deficient B cells. <i>Blood</i> , 2014, 123, 884-893.	1.4	31
84	Cutting Edge: Distinct B Cell Repertoires Characterize Patients with Mild and Severe COVID-19. <i>Journal of Immunology</i> , 2021, 206, 2785-2790.	0.8	31
85	CD4+ follicular regulatory T cells optimize the influenza virus-specific B cell response. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	30
86	Gene Expression Gradients along the Tonotopic Axis of the Chicken Auditory Epithelium. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2011, 12, 423-435.	1.8	29
87	Seasonal Variability and Shared Molecular Signatures of Inactivated Influenza Vaccination in Young and Older Adults. <i>Journal of Immunology</i> , 2020, 204, 1661-1673.	0.8	28
88	Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. <i>ELife</i> , 2021, 10, .	6.0	28
89	Human Dendritic Cell Response Signatures Distinguish 1918, Pandemic, and Seasonal H1N1 Influenza Viruses. <i>Journal of Virology</i> , 2015, 89, 10190-10205.	3.4	27
90	Identification of Core DNA Elements That Target Somatic Hypermutation. <i>Journal of Immunology</i> , 2012, 189, 5314-5326.	0.8	26

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91	Characterization of Diabetogenic CD8+ T Cells. <i>Journal of Biological Chemistry</i> , 2016, 291, 11230-11240.	3.4	25
92	Somatic hypermutation analysis for improved identification of B cell clonal families from next-generation sequencing data. <i>PLoS Computational Biology</i> , 2020, 16, e1007977.	3.2	25
93	Why are there so few key mutant clones? The influence of stochastic selection and blocking on affinity maturation in the germinal center. <i>International Immunology</i> , 2003, 15, 871-884.	4.0	23
94	Somatic hypermutation targeting is influenced by location within the immunoglobulin V region. <i>Molecular Immunology</i> , 2011, 48, 1477-1483.	2.2	22
95	Impaired Toll-Like Receptor 3-Mediated Immune Responses from Macrophages of Patients Chronically Infected with Hepatitis C Virus. <i>Vaccine Journal</i> , 2013, 20, 146-155.	3.1	22
96	Generation of Long-Lived Bone Marrow Plasma Cells Secreting Antibodies Specific for the HIV-1 gp41 Membrane-Proximal External Region in the Absence of Polyreactivity. <i>Journal of Virology</i> , 2016, 90, 8875-8890.	3.4	20
97	Optimized Threshold Inference for Partitioning of Clones From High-Throughput B Cell Repertoire Sequencing Data. <i>Frontiers in Immunology</i> , 2018, 9, 1687.	4.8	20
98	Single cell immune profiling of dengue virus patients reveals intact immune responses to Zika virus with enrichment of innate immune signatures. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008112.	3.0	20
99	Comparative analysis of anti-viral transcriptomics reveals novel effects of influenza immune antagonism. <i>BMC Immunology</i> , 2015, 16, 46.	2.2	19
100	RAG1 targeting in the genome is dominated by chromatin interactions mediated by the non-core regions of RAG1 and RAG2. <i>Nucleic Acids Research</i> , 2016, 44, gkw633.	14.5	19
101	Gene Expression Analysis of Forskolin Treated Basilar Papillae Identifies MicroRNA181a as a Mediator of Proliferation. <i>PLoS ONE</i> , 2010, 5, e11502.	2.5	18
102	VDJML: a file format with tools for capturing the results of inferring immune receptor rearrangements. <i>BMC Bioinformatics</i> , 2016, 17, 333.	2.6	16
103	The CAIRR Pipeline for Submitting Standards-Compliant B and T Cell Receptor Repertoire Sequencing Studies to the National Center for Biotechnology Information Repositories. <i>Frontiers in Immunology</i> , 2018, 9, 1877.	4.8	15
104	Local Clonal Diversification and Dissemination of B Lymphocytes in the Human Bronchial Mucosa. <i>Frontiers in Immunology</i> , 2018, 9, 1976.	4.8	15
105	Alignment free identification of clones in B cell receptor repertoires. <i>Nucleic Acids Research</i> , 2021, 49, e21-e21.	14.5	15
106	Gene set meta-analysis with Quantitative Set Analysis for Gene Expression (QuSAGE). <i>PLoS Computational Biology</i> , 2019, 15, e1006899.	3.2	14
107	Elevated N-Linked Glycosylation of IgG V Regions in Myasthenia Gravis Disease Subtypes. <i>Journal of Immunology</i> , 2021, 207, 2005-2014.	0.8	14
108	Recurrent genetic defects in classical Hodgkin lymphoma cell lines. <i>Leukemia and Lymphoma</i> , 2016, 57, 2890-2900.	1.3	13

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109	Getting Started in Computational Immunology. PLoS Computational Biology, 2008, 4, e1000128.	3.2	10
110	CEDAR OnDemand: a browser extension to generate ontology-based scientific metadata. BMC Bioinformatics, 2018, 19, 268.	2.6	10
111	Single-cell immunophenotyping of the skin lesion erythema migrans identifies IgM memory B cells. JCI Insight, 2021, 6, .	5.0	10
112	Multiple network-constrained regressions expand insights into influenza vaccination responses. Bioinformatics, 2017, 33, i208-i216.	4.1	9
113	Reporting and connecting cell type names and gating definitions through ontologies. BMC Bioinformatics, 2019, 20, 182.	2.6	9
114	Position-Dependent Differential Targeting of Somatic Hypermutation. Journal of Immunology, 2020, 205, 3468-3479.	0.8	9
115	Coregulation mapping based on individual phenotypic variation in response to virus infection. Immunome Research, 2010, 6, 2.	0.1	4
116	LinkedImm: a linked data graph database for integrating immunological data. BMC Bioinformatics, 2021, 22, 105.	2.6	4
117	B Cell Mobilization, Dissemination, Fine Tuning of Local Antigen Specificity and Isotype Selection in Asthma. Frontiers in Immunology, 2021, 12, 702074.	4.8	4
118	A structured model for immune exposures. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	2
119	Sex-Biased Aging Effects on Ig Somatic Hypermutation Targeting. Journal of Immunology, 2021, 206, 101-108.	0.8	2
120	A linked data graph approach to integration of immunological data. , 2019, 2019, 1742-1749.		0
121	Comparing Host Module Activation Patterns and Temporal Dynamics in Infection by Influenza H1N1 Viruses. Frontiers in Immunology, 2021, 12, 691758.	4.8	0
122	Mind the gap from research laboratory to clinic: Challenges and opportunities for next-generation assays in human diseases. Vaccine, 2021, 39, 5233-5239.	3.8	0