

# Steven H Kleinstein

## List of Publications by Year in descending order

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Version: 2024-02-01

122  
papers

12,144  
citations

28190

55  
h-index

32761

100  
g-index

137  
all docs

137  
docs citations

137  
times ranked

17909  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. <i>Nature Communications</i> , 2022, 13, 440.	5.8	100
2	Phylogenetic analysis of migration, differentiation, and class switching in B cells. <i>PLoS Computational Biology</i> , 2022, 18, e1009885.	1.5	40
3	Alignment free identification of clones in B cell receptor repertoires. <i>Nucleic Acids Research</i> , 2021, 49, e21-e21.	6.5	15
4	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.	6.6	164
5	Divergent and self-reactive immune responses in the CNS of COVID-19 patients with neurological symptoms. <i>Cell Reports Medicine</i> , 2021, 2, 100288.	3.3	121
6	Cutting Edge: Distinct B Cell Repertoires Characterize Patients with Mild and Severe COVID-19. <i>Journal of Immunology</i> , 2021, 206, 2785-2790.	0.4	31
7	Single-cell immunophenotyping of the skin lesion erythema migrans identifies IgM memory B cells. <i>JCI Insight</i> , 2021, 6, .	2.3	10
8	Heterogeneity of meningeal B cells reveals a lymphopoietic niche at the CNS borders. <i>Science</i> , 2021, 373, .	6.0	218
9	Comparing Host Module Activation Patterns and Temporal Dynamics in Infection by Influenza H1N1 Viruses. <i>Frontiers in Immunology</i> , 2021, 12, 691758.	2.2	0
10	LinkedImm: a linked data graph database for integrating immunological data. <i>BMC Bioinformatics</i> , 2021, 22, 105.	1.2	4
11	Mind the gap from research laboratory to clinic: Challenges and opportunities for next-generation assays in human diseases. <i>Vaccine</i> , 2021, 39, 5233-5239.	1.7	0
12	Elevated N-Linked Glycosylation of IgG V Regions in Myasthenia Gravis Disease Subtypes. <i>Journal of Immunology</i> , 2021, 207, 2005-2014.	0.4	14
13	CD4+ follicular regulatory T cells optimize the influenza virus-specific B cell response. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	30
14	B Cell Mobilization, Dissemination, Fine Tuning of Local Antigen Specificity and Isotype Selection in Asthma. <i>Frontiers in Immunology</i> , 2021, 12, 702074.	2.2	4
15	Sex-Biased Aging Effects on Ig Somatic Hypermutation Targeting. <i>Journal of Immunology</i> , 2021, 206, 101-108.	0.4	2
16	Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. <i>ELife</i> , 2021, 10, .	2.8	28
17	Intranasal priming induces local lung-resident B cell populations that secrete protective mucosal antiviral IgA. <i>Science Immunology</i> , 2021, 6, eabj5129.	5.6	76
18	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.	3.3	33

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19	Position-Dependent Differential Targeting of Somatic Hypermutation. <i>Journal of Immunology</i> , 2020, 205, 3468-3479.	0.4	9
20	Human germinal centres engage memory and naive B cells after influenza vaccination. <i>Nature</i> , 2020, 586, 127-132.	13.7	194
21	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. <i>Cancer Cell</i> , 2020, 37, 655-673.e11.	7.7	93
22	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.	1.3	20
23	Somatic hypermutation analysis for improved identification of B cell clonal families from next-generation sequencing data. <i>PLoS Computational Biology</i> , 2020, 16, e1007977.	1.5	25
24	A Potently Neutralizing Antibody Protects Mice against SARS-CoV-2 Infection. <i>Journal of Immunology</i> , 2020, 205, 915-922.	0.4	186
25	A structured model for immune exposures. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	2
26	Seasonal Variability and Shared Molecular Signatures of Inactivated Influenza Vaccination in Young and Older Adults. <i>Journal of Immunology</i> , 2020, 204, 1661-1673.	0.4	28
27	Single-cell repertoire tracing identifies rituximab-resistant B cells during myasthenia gravis relapses. <i>JCI Insight</i> , 2020, 5, .	2.3	37
28	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.	0.4	42
29	Reporting and connecting cell type names and gating definitions through ontologies. <i>BMC Bioinformatics</i> , 2019, 20, 182.	1.2	9
30	Migrant memory B cells secrete luminal antibody in the vagina. <i>Nature</i> , 2019, 571, 122-126.	13.7	77
31	Early B cell tolerance defects in neuromyelitis optica favour anti-AQP4 autoantibody production. <i>Brain</i> , 2019, 142, 1598-1615.	3.7	62
32	Identification of Subject-Specific Immunoglobulin Alleles From Expressed Repertoire Sequencing Data. <i>Frontiers in Immunology</i> , 2019, 10, 129.	2.2	67
33	Inferred Allelic Variants of Immunoglobulin Receptor Genes: A System for Their Evaluation, Documentation, and Naming. <i>Frontiers in Immunology</i> , 2019, 10, 435.	2.2	63
34	Gene set meta-analysis with Quantitative Set Analysis for Gene Expression (QuSAGE). <i>PLoS Computational Biology</i> , 2019, 15, e1006899.	1.5	14
35	Cutting Edge: Ig H Chains Are Sufficient to Determine Most B Cell Clonal Relationships. <i>Journal of Immunology</i> , 2019, 203, 1687-1692.	0.4	48
36	A linked data graph approach to integration of immunological data. , 2019, 2019, 1742-1749.		0

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37	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, .	5.8	65
38	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.	3.3	71
39	Spatiotemporal segregation of human marginal zone and memory B cell populations in lymphoid tissue. <i>Nature Communications</i> , 2018, 9, 3857.	5.8	78
40	CEDAR OnDemand: a browser extension to generate ontology-based scientific metadata. <i>BMC Bioinformatics</i> , 2018, 19, 268.	1.2	10
41	Affinity Maturation Is Impaired by Natural Killer Cell Suppression of Germinal Centers. <i>Cell Reports</i> , 2018, 24, 3367-3373.e4.	2.9	59
42	AIRR Community Standardized Representations for Annotated Immune Repertoires. <i>Frontiers in Immunology</i> , 2018, 9, 2206.	2.2	71
43	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.	2.2	15
44	A spectral clustering-based method for identifying clones from high-throughput B cell repertoire sequencing data. <i>Bioinformatics</i> , 2018, 34, i341-i349.	1.8	55
45	Local Clonal Diversification and Dissemination of B Lymphocytes in the Human Bronchial Mucosa. <i>Frontiers in Immunology</i> , 2018, 9, 1976.	2.2	15
46	Optimized Threshold Inference for Partitioning of Clones From High-Throughput B Cell Repertoire Sequencing Data. <i>Frontiers in Immunology</i> , 2018, 9, 1687.	2.2	20
47	Dysregulation of B Cell Repertoire Formation in Myasthenia Gravis Patients Revealed through Deep Sequencing. <i>Journal of Immunology</i> , 2017, 198, 1460-1473.	0.4	92
48	Hierarchical Clustering Can Identify B Cell Clones with High Confidence in Ig Repertoire Sequencing Data. <i>Journal of Immunology</i> , 2017, 198, 2489-2499.	0.4	137
49	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.	6.6	202
50	Comment on "A Database of Human Immune Receptor Alleles Recovered from Population Sequencing Data". <i>Journal of Immunology</i> , 2017, 198, 3371-3373.	0.4	46
51	Solving Immunology?. <i>Trends in Immunology</i> , 2017, 38, 116-127.	2.9	45
52	Interleukin-10 from CD4 <sup>+</sup> follicular regulatory T cells promotes the germinal center response. <i>Science Immunology</i> , 2017, 2, .	5.6	139
53	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. <i>Science Immunology</i> , 2017, 2, .	5.6	122
54	Adaptive Immune Receptor Repertoire Community recommendations for sharing immune-repertoire sequencing data. <i>Nature Immunology</i> , 2017, 18, 1274-1278.	7.0	163

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55	Multiple network-constrained regressions expand insights into influenza vaccination responses. <i>Bioinformatics</i> , 2017, 33, i208-i216.	1.8	9
56	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. <i>Frontiers in Immunology</i> , 2017, 8, 1418.	2.2	102
57	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.	1.5	20
58	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.	6.5	19
59	Characterization of Diabetogenic CD8+ T Cells. <i>Journal of Biological Chemistry</i> , 2016, 291, 11230-11240.	1.6	25
60	A Model of Somatic Hypermutation Targeting in Mice Based on High-Throughput Ig Sequencing Data. <i>Journal of Immunology</i> , 2016, 197, 3566-3574.	0.4	63
61	Age-associated vascular inflammation promotes monocytois during atherogenesis. <i>Aging Cell</i> , 2016, 15, 766-777.	3.0	41
62	VDJML: a file format with tools for capturing the results of inferring immune receptor rearrangements. <i>BMC Bioinformatics</i> , 2016, 17, 333.	1.2	16
63	Long-lived antigen-induced IgM plasma cells demonstrate somatic mutations and contribute to long-term protection. <i>Nature Communications</i> , 2016, 7, 11826.	5.8	84
64	Recurrent genetic defects in classical Hodgkin lymphoma cell lines. <i>Leukemia and Lymphoma</i> , 2016, 57, 2890-2900.	0.6	13
65	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.	0.4	66
66	Individual heritable differences result in unique cell lymphocyte receptor repertoires of naive and antigen-experienced cells. <i>Nature Communications</i> , 2016, 7, 11112.	5.8	123
67	Systems Immunology Reveals Markers of Susceptibility to West Nile Virus Infection. <i>Vaccine Journal</i> , 2015, 22, 6-16.	3.2	35
68	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.	3.3	215
69	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.	3.3	77
70	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.	1.9	62
71	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.	1.8	49
72	Human Dendritic Cell Response Signatures Distinguish 1918, Pandemic, and Seasonal H1N1 Influenza Viruses. <i>Journal of Virology</i> , 2015, 89, 10190-10205.	1.5	27

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73	Production of IL-10 by CD4+ regulatory T cells during the resolution of infection promotes the maturation of memory CD8+ T cells. <i>Nature Immunology</i> , 2015, 16, 871-879.	7.0	159
74	Salmonella Infection Drives Promiscuous B Cell Activation Followed by Extrafollicular Affinity Maturation. <i>Immunity</i> , 2015, 43, 120-131.	6.6	186
75	Change-O: a toolkit for analyzing large-scale B cell immunoglobulin repertoire sequencing data. <i>Bioinformatics</i> , 2015, 31, 3356-3358.	1.8	643
76	The center for expanded data annotation and retrieval. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1148-1152.	2.2	74
77	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.	0.6	80
78	Comparative analysis of anti-viral transcriptomics reveals novel effects of influenza immune antagonism. <i>BMC Immunology</i> , 2015, 16, 46.	0.9	19
79	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.	4.2	238
80	Phosphoenolpyruvate Is a Metabolic Checkpoint of Anti-tumor T Cell Responses. <i>Cell</i> , 2015, 162, 1217-1228.	13.5	1,044
81	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. <i>Immunity</i> , 2015, 43, 605-614.	6.6	49
82	Practical guidelines for B-cell receptor repertoire sequencing analysis. <i>Genome Medicine</i> , 2015, 7, 121.	3.6	215
83	Ageing-dependent alterations in gene expression and a mitochondrial signature of responsiveness to human influenza vaccination. <i>Aging</i> , 2015, 7, 38-52.	1.4	72
84	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.	3.3	186
85	B cells populating the multiple sclerosis brain mature in the draining cervical lymph nodes. <i>Science Translational Medicine</i> , 2014, 6, 248ra107.	5.8	394
86	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.	3.6	169
87	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.	0.4	53
88	Computational resources for high-dimensional immune analysis from the Human Immunology Project Consortium. <i>Nature Biotechnology</i> , 2014, 32, 146-148.	9.4	65
89	pRESTO: a toolkit for processing high-throughput sequencing raw reads of lymphocyte receptor repertoires. <i>Bioinformatics</i> , 2014, 30, 1930-1932.	1.8	417
90	Immune Markers Associated with Host Susceptibility to Infection with West Nile Virus. <i>Viral Immunology</i> , 2014, 27, 39-47.	0.6	31

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91	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.	1.5	55
92	Integrating B Cell Lineage Information into Statistical Tests for Detecting Selection in Ig Sequences. <i>Journal of Immunology</i> , 2014, 192, 867-874.	0.4	32
93	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.	7.0	348
94	Shared VH1-46 gene usage by pemphigus vulgaris autoantibodies indicates common humoral immune responses among patients. <i>Nature Communications</i> , 2014, 5, 4167.	5.8	63
95	Mantle cell lymphoma in cyclin D1 transgenic mice with Bim-deficient B cells. <i>Blood</i> , 2014, 123, 884-893.	0.6	31
96	Multiple Transcription Factor Binding Sites Predict AID Targeting in Non-Ig Genes. <i>Journal of Immunology</i> , 2013, 190, 3878-3888.	0.4	32
97	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.	2.2	197
98	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.	6.5	171
99	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.	3.2	22
100	The immune cell infiltrate populating meningiomas is composed of mature, antigen-experienced T and B cells. <i>Neuro-Oncology</i> , 2013, 15, 1479-1490.	0.6	72
101	Quantifying selection in high-throughput Immunoglobulin sequencing data sets. <i>Nucleic Acids Research</i> , 2012, 40, e134-e134.	6.5	179
102	Identification of Core DNA Elements That Target Somatic Hypermutation. <i>Journal of Immunology</i> , 2012, 189, 5314-5326.	0.4	26
103	NLRP10 is a NOD-like receptor essential to initiate adaptive immunity by dendritic cells. <i>Nature</i> , 2012, 484, 510-513.	13.7	126
104	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.	6.6	265
105	Somatic hypermutation targeting is influenced by location within the immunoglobulin V region. <i>Molecular Immunology</i> , 2011, 48, 1477-1483.	1.0	22
106	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.	0.9	29
107	Germinal Center B Cell and T Follicular Helper Cell Development Initiates in the Interfollicular Zone. <i>Immunity</i> , 2011, 34, 947-960.	6.6	406
108	Detecting selection in immunoglobulin sequences. <i>Nucleic Acids Research</i> , 2011, 39, W499-W504.	6.5	83

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109	Altered Folate Availability Modifies the Molecular Environment of the Human Colorectum: Implications for Colorectal Carcinogenesis. <i>Cancer Prevention Research</i> , 2011, 4, 530-543.	0.7	41
110	Gene Expression Analysis of Forskolin Treated Basilar Papillae Identifies MicroRNA181a as a Mediator of Proliferation. <i>PLoS ONE</i> , 2010, 5, e11502.	1.1	18
111	Antiviral Response Dictated by Choreographed Cascade of Transcription Factors. <i>Journal of Immunology</i> , 2010, 184, 2908-2917.	0.4	46
112	Coregulation mapping based on individual phenotypic variation in response to virus infection. <i>Immunome Research</i> , 2010, 6, 2.	0.1	4
113	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.	0.4	86
114	Salmonella Typhimurium Type III Secretion Effectors Stimulate Innate Immune Responses in Cultured Epithelial Cells. <i>PLoS Pathogens</i> , 2009, 5, e1000538.	2.1	177
115	Two levels of protection for the B cell genome during somatic hypermutation. <i>Nature</i> , 2008, 451, 841-845.	13.7	524
116	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.	1.6	81
117	Getting Started in Computational Immunology. <i>PLoS Computational Biology</i> , 2008, 4, e1000128.	1.5	10
118	Improved methods for detecting selection by mutation analysis of Ig V region sequences. <i>International Immunology</i> , 2008, 20, 683-694.	1.8	75
119	Definition of Germinal-Center B Cell Migration In Vivo Reveals Predominant Intrazonal Circulation Patterns. <i>Immunity</i> , 2007, 26, 655-667.	6.6	274
120	Estimating Hypermutation Rates from Clonal Tree Data. <i>Journal of Immunology</i> , 2003, 171, 4639-4649.	0.4	85
121	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.	1.8	23
122	Toward Quantitative Simulation of Germinal Center Dynamics: Biological and Modeling Insights from Experimental Validation. <i>Journal of Theoretical Biology</i> , 2001, 211, 253-275.	0.8	32