Steven H Kleinstein

List of Publications by Year
in descending order

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	Phosphoenolpyruvate Is a Metabolic Checkpoint of Anti-tumor T Cell Responses. Cell, 2015, 162, 1217-1228.	13.5	1,044
2	Change-O: a toolkit for analyzing large-scale B cell immunoglobulin repertoire sequencing data. Bioinformatics, 2015, 31, 3356-3358.	1.8	643
3	Two levels of protection for the B cell genome during somatic hypermutation. Nature, 2008, 451, 841-845.	13.7	524
4	pRESTO: a toolkit for processing high-throughput sequencing raw reads of lymphocyte receptor repertoires. Bioinformatics, 2014, 30, 1930-1932.	1.8	417
5	Germinal Center B Cell and T Follicular Helper Cell Development Initiates in the Interfollicular Zone. Immunity, 2011, 34, 947-960.	6.6	406
6	B cells populating the multiple sclerosis brain mature in the draining cervical lymph nodes. Science Translational Medicine, 2014, 6, 248ra107.	5.8	394
7	CD80 and PD-L2 define functionally distinct memory B cell subsets that are independent of antibody isotype. Nature Immunology, 2014, 15, 631-637.	7.0	348
8	Definition of Germinal-Center B Cell Migration InÂVivo Reveals Predominant IntrazonalÂCirculationÂPatterns. Immunity, 2007, 26, 655-667.	6.6	274
9	Differential Expression of Ly6C and T-bet Distinguish Effector and Memory Th1 CD4+ Cell Properties during Viral Infection. Immunity, 2011, 35, 633-646.	6.6	265
10	The transcription factors ZEB2 and T-bet cooperate to program cytotoxic T cell terminal differentiation in response to LCMV viral infection. Journal of Experimental Medicine, 2015, 212, 2041-2056.	4.2	238
11	Heterogeneity of meningeal B cells reveals a lymphopoietic niche at the CNS borders. Science, 2021, 373, .	6.0	218
12	Automated analysis of high-throughput B-cell sequencing data reveals a high frequency of novel immunoglobulin V gene segment alleles. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E862-70.	3.3	215
13	Practical guidelines for B-cell receptor repertoire sequencing analysis. Genome Medicine, 2015, 7, 121.	3.6	215
14	Polycomb Repressive Complex 2-Mediated Chromatin Repression Guides Effector CD8 + T Cell Terminal Differentiation and Loss of Multipotency. Immunity, 2017, 46, 596-608.	6.6	202
15	Models of Somatic Hypermutation Targeting and Substitution Based on Synonymous Mutations from High-Throughput Immunoglobulin Sequencing Data. Frontiers in Immunology, 2013, 4, 358.	2.2	197
16	Human germinal centres engage memory and naive B cells after influenza vaccination. Nature, 2020, 586, 127-132.	13.7	194
17	High-resolution antibody dynamics of vaccine-induced immune responses. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4928-4933.	3.3	186
18	Salmonella Infection Drives Promiscuous B Cell Activation Followed by Extrafollicular Affinity Maturation. Immunity, 2015, 43, 120-131.	6.6	186

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19	A Potently Neutralizing Antibody Protects Mice against SARS-CoV-2 Infection. Journal of Immunology, 2020, 205, 915-922.	0.4	186
20	Quantifying selection in high-throughput Immunoglobulin sequencing data sets. Nucleic Acids Research, 2012, 40, e134-e134.	6.5	179
21	Salmonella Typhimurium Type III Secretion Effectors Stimulate Innate Immune Responses in Cultured Epithelial Cells. PLoS Pathogens, 2009, 5, e1000538.	2.1	177
22	Quantitative set analysis for gene expression: a method to quantify gene set differential expression including gene-gene correlations. Nucleic Acids Research, 2013, 41, e170-e170.	6.5	171
23	Dynamic expression profiling of type I and type III interferon-stimulated hepatocytes reveals a stable hierarchy of gene expression. Hepatology, 2014, 59, 1262-1272.	3.6	169
24	Immune dysregulation and autoreactivity correlate with disease severity in SARS-CoV-2-associated multisystem inflammatory syndrome in children. Immunity, 2021, 54, 1083-1095.e7.	6.6	164
25	Adaptive Immune Receptor Repertoire Community recommendations for sharing immune-repertoire sequencing data. Nature Immunology, 2017, 18, 1274-1278.	7.0	163
26	Production of IL-10 by CD4+ regulatory T cells during the resolution of infection promotes the maturation of memory CD8+ T cells. Nature Immunology, 2015, 16, 871-879.	7.0	159
27	Interleukin-10 from CD4+ follicular regulatory T cells promotes the germinal center response. Science Immunology, 2017, 2, .	5.6	139
28	Hierarchical Clustering Can Identify B Cell Clones with High Confidence in Ig Repertoire Sequencing Data. Journal of Immunology, 2017, 198, 2489-2499.	0.4	137
29	NLRP10 is a NOD-like receptor essential to initiate adaptive immunity by dendritic cells. Nature, 2012, 484, 510-513.	13.7	126
30	Individual heritable differences result in unique cell lymphocyte receptor repertoires of naÃ¯ve and antigen-experienced cells. Nature Communications, 2016, 7, 11112.	5.8	123
31	Multicohort analysis reveals baseline transcriptional predictors of influenza vaccination responses. Science Immunology, 2017, 2, .	5.6	122
32	Divergent and self-reactive immune responses in the CNS of COVID-19 patients with neurological symptoms. Cell Reports Medicine, 2021, 2, 100288.	3.3	121
33	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. Frontiers in Immunology, 2017, 8, 1418.	2.2	102
34	Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19. Nature Communications, 2022, 13, 440.	5.8	100
35	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. Cancer Cell, 2020, 37, 655-673.e11.	7.7	93
36	Dysregulation of B Cell Repertoire Formation in Myasthenia Gravis Patients Revealed through Deep Sequencing. Journal of Immunology, 2017, 198, 1460-1473.	0.4	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. Journal of Immunology, 2009, 183, 7314-7325.	0.4	86
38	Estimating Hypermutation Rates from Clonal Tree Data. Journal of Immunology, 2003, 171, 4639-4649.	0.4	85
39	Long-lived antigen-induced IgM plasma cells demonstrate somatic mutations and contribute to long-term protection. Nature Communications, 2016, 7, 11826.	5.8	84
40	Detecting selection in immunoglobulin sequences. Nucleic Acids Research, 2011, 39, W499-W504.	6.5	83
41	Interleukin-29 Functions Cooperatively with Interferon to Induce Antiviral Gene Expression and Inhibit Hepatitis C Virus Replication. Journal of Biological Chemistry, 2008, 283, 30079-30089.	1.6	81
42	Neutralizing antibodies against West Nile virus identified directly from human B cells by single-cell analysis and next generation sequencing. Integrative Biology (United Kingdom), 2015, 7, 1587-1597.	0.6	80
43	Spatiotemporal segregation of human marginal zone and memory B cell populations in lymphoid tissue. Nature Communications, 2018, 9, 3857.	5.8	78
44	Analysis of gene–environment interactions in postnatal development of the mammalian intestine. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1929-1936.	3.3	77
45	Migrant memory B cells secrete luminal antibody in the vagina. Nature, 2019, 571, 122-126.	13.7	77
46	Intranasal priming induces local lung-resident B cell populations that secrete protective mucosal antiviral IgA. Science Immunology, 2021, 6, eabj5129.	5.6	76
47	Improved methods for detecting selection by mutation analysis of Ig V region sequences. International Immunology, 2008, 20, 683-694.	1.8	75
48	The center for expanded data annotation and retrieval. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1148-1152.	2.2	74
49	The immune cell infiltrate populating meningiomas is composed of mature, antigen-experienced T and B cells. Neuro-Oncology, 2013, 15, 1479-1490.	0.6	72
50	Aging-dependent alterations in gene expression and a mitochondrial signature of responsiveness to human influenza vaccination. Aging, 2015, 7, 38-52.	1.4	72
51	AIRR Community Standardized Representations for Annotated Immune Repertoires. Frontiers in Immunology, 2018, 9, 2206.	2.2	71
52	Repertoire-wide phylogenetic models of B cell molecular evolution reveal evolutionary signatures of aging and vaccination. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22664-22672.	3.3	71
53	Identification of Subject-Specific Immunoglobulin Alleles From Expressed Repertoire Sequencing Data. Frontiers in Immunology, 2019, 10, 129.	2.2	67
54	Autoreactive T Cells from Patients with Myasthenia Gravis Are Characterized by Elevated IL-17, IFN-Î³, and GM-CSF and Diminished IL-10 Production. Journal of Immunology, 2016, 196, 2075-2084.	0.4	66

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55	Computational resources for high-dimensional immune analysis from the Human Immunology Project Consortium. Nature Biotechnology, 2014, 32, 146-148.	9.4	65
56	Overexpression of T-bet in HIV infection is associated with accumulation of B cells outside germinal centers and poor affinity maturation. Science Translational Medicine, 2019, 11, .	5.8	65
57	Shared VH1-46 gene usage by pemphigus vulgaris autoantibodies indicates common humoral immune responses among patients. Nature Communications, 2014, 5, 4167.	5.8	63
58	A Model of Somatic Hypermutation Targeting in Mice Based on High-Throughput Ig Sequencing Data. Journal of Immunology, 2016, 197, 3566-3574.	0.4	63
59	Inferred Allelic Variants of Immunoglobulin Receptor Genes: A System for Their Evaluation, Documentation, and Naming. Frontiers in Immunology, 2019, 10, 435.	2.2	63
60	Prolonged Proinflammatory Cytokine Production in Monocytes Modulated by Interleukin 10 After Influenza Vaccination in Older Adults. Journal of Infectious Diseases, 2015, 211, 1174-1184.	1.9	62
61	Early B cell tolerance defects in neuromyelitis optica favour anti-AQP4 autoantibody production. Brain, 2019, 142, 1598-1615.	3.7	62
62	Affinity Maturation Is Impaired by Natural Killer Cell Suppression of Germinal Centers. Cell Reports, 2018, 24, 3367-3373.e4.	2.9	59
63	Influence of seasonal exposure to grass pollen on local and peripheral blood IgE repertoires in patients with allergic rhinitis. Journal of Allergy and Clinical Immunology, 2014, 134, 604-612.	1.5	55
64	A spectral clustering-based method for identifying clones from high-throughput B cell repertoire sequencing data. Bioinformatics, 2018, 34, i341-i349.	1.8	55
65	TLR4 Ligands Lipopolysaccharide and Monophosphoryl Lipid A Differentially Regulate Effector and Memory CD8+ T Cell Differentiation. Journal of Immunology, 2014, 192, 4221-4232.	0.4	53
66	The mutation patterns in B-cell immunoglobulin receptors reflect the influence of selection acting at multiple time-scales. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140242.	1.8	49
67	Interactive Big Data Resource to Elucidate Human Immune Pathways and Diseases. Immunity, 2015, 43, 605-614.	6.6	49
68	Cutting Edge: Ig H Chains Are Sufficient to Determine Most B Cell Clonal Relationships. Journal of Immunology, 2019, 203, 1687-1692.	0.4	48
69	Antiviral Response Dictated by Choreographed Cascade of Transcription Factors. Journal of Immunology, 2010, 184, 2908-2917.	0.4	46
70	Comment on â€œA Database of Human Immune Receptor Alleles Recovered from Population Sequencing Dataâ€. Journal of Immunology, 2017, 198, 3371-3373.	0.4	46
71	Solving Immunology?. Trends in Immunology, 2017, 38, 116-127.	2.9	45
72	Phenotypic and Ig Repertoire Analyses Indicate a Common Origin of IgDˉCD27ˉ Double Negative B Cells in Healthy Individuals and Multiple Sclerosis Patients. Journal of Immunology, 2019, 203, 1650-1664.	0.4	42

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73	Altered Folate Availability Modifies the Molecular Environment of the Human Colorectum: Implications for Colorectal Carcinogenesis. Cancer Prevention Research, 2011, 4, 530-543.	0.7	41
74	Ageâ€associated vascular inflammation promotes monocytosis during atherogenesis. Aging Cell, 2016, 15, 766-777.	3.0	41
75	Phylogenetic analysis of migration, differentiation, and class switching in B cells. PLoS Computational Biology, 2022, 18, e1009885.	1.5	40
76	Single-cell repertoire tracing identifies rituximab-resistant B cells during myasthenia gravis relapses. JCI Insight, 2020, 5, .	2.3	37
77	Systems Immunology Reveals Markers of Susceptibility to West Nile Virus Infection. Vaccine Journal, 2015, 22, 6-16.	3.2	35
78	Thymus-derived B cell clones persist in the circulation after thymectomy in myasthenia gravis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30649-30660.	3.3	33
79	Toward Quantitative Simulation of Germinal Center Dynamics: Biological and Modeling Insights from Experimental Validation. Journal of Theoretical Biology, 2001, 211, 253-275.	0.8	32
80	Multiple Transcription Factor Binding Sites Predict AID Targeting in Non-Ig Genes. Journal of Immunology, 2013, 190, 3878-3888.	0.4	32
81	Integrating B Cell Lineage Information into Statistical Tests for Detecting Selection in Ig Sequences. Journal of Immunology, 2014, 192, 867-874.	0.4	32
82	Immune Markers Associated with Host Susceptibility to Infection with West Nile Virus. Viral Immunology, 2014, 27, 39-47.	0.6	31
83	Mantle cell lymphoma in cyclin D1 transgenic mice with Bim-deficient B cells. Blood, 2014, 123, 884-893.	0.6	31
84	Cutting Edge: Distinct B Cell Repertoires Characterize Patients with Mild and Severe COVID-19. Journal of Immunology, 2021, 206, 2785-2790.	0.4	31
85	CD4+ follicular regulatory T cells optimize the influenza virusâ€"specific B cell response. Journal of Experimental Medicine, 2021, 218, .	4.2	30
86	Gene Expression Gradients along the Tonotopic Axis of the Chicken Auditory Epithelium. JARO - Journal of the Association for Research in Otolaryngology, 2011, 12, 423-435.	0.9	29
87	Seasonal Variability and Shared Molecular Signatures of Inactivated Influenza Vaccination in Young and Older Adults. Journal of Immunology, 2020, 204, 1661-1673.	0.4	28
88	Human B cell lineages associated with germinal centers following influenza vaccination are measurably evolving. ELife, 2021, 10, .	2.8	28
89	Human Dendritic Cell Response Signatures Distinguish 1918, Pandemic, and Seasonal H1N1 Influenza Viruses. Journal of Virology, 2015, 89, 10190-10205.	1.5	27
90	Identification of Core DNA Elements That Target Somatic Hypermutation. Journal of Immunology, 2012, 189, 5314-5326.	0.4	26

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91	Characterization of Diabetogenic CD8+ T Cells. Journal of Biological Chemistry, 2016, 291, 11230-11240.	1.6	25
92	Somatic hypermutation analysis for improved identification of B cell clonal families from next-generation sequencing data. PLoS Computational Biology, 2020, 16, e1007977.	1.5	25
93	Why are there so few key mutant clones? The influence of stochastic selection and blocking on affinity maturation in the germinal center. International Immunology, 2003, 15, 871-884.	1.8	23
94	Somatic hypermutation targeting is influenced by location within the immunoglobulin V region. Molecular Immunology, 2011, 48, 1477-1483.	1.0	22
95	Impaired Toll-Like Receptor 3-Mediated Immune Responses from Macrophages of Patients Chronically Infected with Hepatitis C Virus. Vaccine Journal, 2013, 20, 146-155.	3.2	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. Journal of Virology, 2016, 90, 8875-8890.	1.5	20
97	Optimized Threshold Inference for Partitioning of Clones From High-Throughput B Cell Repertoire Sequencing Data. Frontiers in Immunology, 2018, 9, 1687.	2.2	20
98	Single cell immune profiling of dengue virus patients reveals intact immune responses to Zika virus with enrichment of innate immune signatures. PLoS Neglected Tropical Diseases, 2020, 14, e0008112.	1.3	20
99	Comparative analysis of anti-viral transcriptomics reveals novel effects of influenza immune antagonism. BMC Immunology, 2015, 16, 46.	0.9	19
100	RAG1 targeting in the genome is dominated by chromatin interactions mediated by the non-core regions of RAG1 and RAG2. Nucleic Acids Research, 2016, 44, gkw633.	6.5	19
101	Gene Expression Analysis of Forskolin Treated Basilar Papillae Identifies MicroRNA181a as a Mediator of Proliferation. PLoS ONE, 2010, 5, e11502.	1.1	18
102	VDJML: a file format with tools for capturing the results of inferring immune receptor rearrangements. BMC Bioinformatics, 2016, 17, 333.	1.2	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. Frontiers in Immunology, 2018, 9, 1877.	2.2	15
104	Local Clonal Diversification and Dissemination of B Lymphocytes in the Human Bronchial Mucosa. Frontiers in Immunology, 2018, 9, 1976.	2.2	15
105	Alignment free identification of clones in B cell receptor repertoires. Nucleic Acids Research, 2021, 49, e21-e21.	6.5	15
106	Gene set meta-analysis with Quantitative Set Analysis for Gene Expression (QuSAGE). PLoS Computational Biology, 2019, 15, e1006899.	1.5	14
107	Elevated N-Linked Glycosylation of IgG V Regions in Myasthenia Gravis Disease Subtypes. Journal of Immunology, 2021, 207, 2005-2014.	0.4	14
108	Recurrent genetic defects in classical Hodgkin lymphoma cell lines. Leukemia and Lymphoma, 2016, 57, 2890-2900.	0.6	13

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109	Getting Started in Computational Immunology. PLoS Computational Biology, 2008, 4, e1000128.	1.5	10
110	CEDAR OnDemand: a browser extension to generate ontology-based scientific metadata. BMC Bioinformatics, 2018, 19, 268.	1.2	10
111	Single-cell immunophenotyping of the skin lesion erythema migrans identifies IgM memory B cells. JCI Insight, 2021, 6, .	2.3	10
112	Multiple network-constrained regressions expand insights into influenza vaccination responses. Bioinformatics, 2017, 33, i208-i216.	1.8	9
113	Reporting and connecting cell type names and gating definitions through ontologies. BMC Bioinformatics, 2019, 20, 182.	1.2	9
114	Position-Dependent Differential Targeting of Somatic Hypermutation. Journal of Immunology, 2020, 205, 3468-3479.	0.4	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.	1.2	4
117	B Cell Mobilization, Dissemination, Fine Tuning of Local Antigen Specificity and Isotype Selection in Asthma. Frontiers in Immunology, 2021, 12, 702074.	2.2	4
118	A structured model for immune exposures. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	2
119	Sex-Biased Aging Effects on Ig Somatic Hypermutation Targeting. Journal of Immunology, 2021, 206, 101-108.	0.4	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.	2.2	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.	1.7	0