Thomas B Kepler

List of Publications by Year in descending order

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		19657	22832
148	14,211	61	112
papers	citations	h-index	g-index
155 all docs	155 docs citations	155 times ranked	13892 citing authors

THOMAS R KEDIED

#	Article	IF	CITATIONS
1	Co-evolution of a broadly neutralizing HIV-1 antibody and founder virus. Nature, 2013, 496, 469-476.	27.8	961
2	Invertebrate immune systems – not homogeneous, not simple, not well understood. Immunological Reviews, 2004, 198, 10-24.	6.0	589
3	B-cell–lineage immunogen design in vaccine development with HIV-1 as a case study. Nature Biotechnology, 2012, 30, 423-433.	17.5	432
4	Broadly neutralizing human antibody that recognizes the receptor-binding pocket of influenza virus hemagglutinin. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14216-14221.	7.1	402
5	Analysis of a Clonal Lineage of HIV-1 Envelope V2/V3 Conformational Epitope-Specific Broadly Neutralizing Antibodies and Their Inferred Unmutated Common Ancestors. Journal of Virology, 2011, 85, 9998-10009.	3.4	393
6	Vaccine Induction of Antibodies against a Structurally Heterogeneous Site of Immune Pressure within HIV-1 Envelope Protein Variable Regions 1 and 2. Immunity, 2013, 38, 176-186.	14.3	374
7	Diversification of Ig Superfamily Genes in an Invertebrate. Science, 2004, 305, 251-254.	12.6	366
8	Pathway level analysis of gene expression using singular value decomposition. BMC Bioinformatics, 2005, 6, 225.	2.6	332
9	Classification of osteoarthritis biomarkers: a proposed approach. Osteoarthritis and Cartilage, 2006, 14, 723-727.	1.3	330
10	Advantage of rare HLA supertype in HIV disease progression. Nature Medicine, 2003, 9, 928-935.	30.7	311
11	Maturation Pathway from Germline to Broad HIV-1 Neutralizer of a CD4-Mimic Antibody. Cell, 2016, 165, 449-463.	28.9	305
12	The T helper type 2 response to cysteine proteases requires dendritic cell–basophil cooperation via ROS-mediated signaling. Nature Immunology, 2010, 11, 608-617.	14.5	287
13	Complex Antigens Drive Permissive Clonal Selection in Germinal Centers. Immunity, 2016, 44, 542-552.	14.3	278
14	Cooperation of B Cell Lineages in Induction of HIV-1-Broadly Neutralizing Antibodies. Cell, 2014, 158, 481-491.	28.9	266
15	Cyclic re-entry of germinal center B cells and the efficiency of affinity maturation. Trends in Immunology, 1993, 14, 412-415.	7.5	258
16	Drug concentration heterogeneity facilitates the evolution of drug resistance. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 11514-11519.	7.1	240
17	High-throughput isolation of immunoglobulin genes from single human B cells and expression as monoclonal antibodies. Journal of Virological Methods, 2009, 158, 171-179.	2.1	235
18	Preconfiguration of the antigen-binding site during affinity maturation of a broadly neutralizing influenza virus antibody. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 264-269.	7.1	227

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19	The Egyptian Rousette Genome Reveals Unexpected Features of Bat Antiviral Immunity. Cell, 2018, 173, 1098-1110.e18.	28.9	220
20	Staged induction of HIV-1 glycan–dependent broadly neutralizing antibodies. Science Translational Medicine, 2017, 9, .	12.4	212
21	Initial antibodies binding to HIV-1 gp41 in acutely infected subjects are polyreactive and highly mutated. Journal of Experimental Medicine, 2011, 208, 2237-2249.	8.5	198
22	Review of 54 patients with complete DiGeorge anomaly enrolled in protocols for thymus transplantation: outcome of 44 consecutive transplants. Blood, 2007, 109, 4539-4547.	1.4	195
23	Diversion of HIV-1 vaccine–induced immunity by gp41-microbiota cross-reactive antibodies. Science, 2015, 349, aab1253.	12.6	191
24	Identification of autoantigens recognized by the 2F5 and 4E10 broadly neutralizing HIV-1 antibodies. Journal of Experimental Medicine, 2013, 210, 241-256.	8.5	171
25	Two Distinct Broadly Neutralizing Antibody Specificities of Different Clonal Lineages in a Single HIV-1-Infected Donor: Implications for Vaccine Design. Journal of Virology, 2012, 86, 4688-4692.	3.4	159
26	H3N2 Influenza Infection Elicits More Cross-Reactive and Less Clonally Expanded Anti-Hemagglutinin Antibodies Than Influenza Vaccination. PLoS ONE, 2011, 6, e25797.	2.5	158
27	Viral Receptor-Binding Site Antibodies with Diverse Germline Origins. Cell, 2015, 161, 1026-1034.	28.9	151
28	Reconstructing a B-cell clonal lineage. I. Statistical inference of unobserved ancestors. F1000Research, 2013, 2, 103.	1.6	150
29	Measurement of Cell Migration on Surface-Bound Fibronectin Gradients. Langmuir, 2004, 20, 8279-8286.	3.5	142
30	Somatic Hypermutation in B Cells: An Optimal Control Treatment. Journal of Theoretical Biology, 1993, 164, 37-64.	1.7	141
31	Antibodies to a Conserved Influenza Head Interface Epitope Protect by an IgG Subtype-Dependent Mechanism. Cell, 2019, 177, 1124-1135.e16.	28.9	141
32	Immunoglobulin Gene Insertions and Deletions in the Affinity Maturation of HIV-1 Broadly Reactive Neutralizing Antibodies. Cell Host and Microbe, 2014, 16, 304-313.	11.0	137
33	Pentavalent HIV-1 vaccine protects against simian-human immunodeficiency virus challenge. Nature Communications, 2017, 8, 15711.	12.8	137
34	Isolation of a Human Anti-HIV gp41 Membrane Proximal Region Neutralizing Antibody by Antigen-Specific Single B Cell Sorting. PLoS ONE, 2011, 6, e23532.	2.5	137
35	Sequence-Intrinsic Mechanisms that Target AID Mutational Outcomes on Antibody Genes. Cell, 2015, 163, 1124-1137.	28.9	136
36	Reduction of conductance-based neuron models. Biological Cybernetics, 1992, 66, 381-387.	1.3	128

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37	Memory B Cells that Cross-React with Group 1 and Group 2 Influenza A Viruses Are Abundant in Adult Human Repertoires. Immunity, 2018, 48, 174-184.e9.	14.3	124
38	Human Immunodeficiency Virus Type 1-Specific Cytotoxic T Lymphocyte Activity Is Inversely Correlated with HIV Type 1 Viral Load in HIV Type 1-Infected Long-Term Survivors. AIDS Research and Human Retroviruses, 1999, 15, 1219-1228.	1.1	120
39	Potent and broad HIV-neutralizing antibodies in memory B cells and plasma. Science Immunology, 2017, 2, .	11.9	119
40	SoDA: implementation of a 3D alignment algorithm for inference of antigen receptor recombinations. Bioinformatics, 2006, 22, 438-444.	4.1	117
41	HIV-1 Envelope gp41 Antibodies Can Originate from Terminal Ileum B Cells that Share Cross-Reactivity with Commensal Bacteria. Cell Host and Microbe, 2014, 16, 215-226.	11.0	105
42	Reconstructing a B-Cell Clonal Lineage. II. Mutation, Selection, and Affinity Maturation. Frontiers in Immunology, 2014, 5, 170.	4.8	104
43	Influenza immunization elicits antibodies specific for an egg-adapted vaccine strain. Nature Medicine, 2016, 22, 1465-1469.	30.7	104
44	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. Frontiers in Immunology, 2017, 8, 1418.	4.8	102
45	Normalization and analysis of DNA microarray data by self-consistency and local regression. Genome Biology, 2002, 3, research0037.1.	9.6	99
46	Functional Relevance of Improbable Antibody Mutations for HIV Broadly Neutralizing Antibody Development. Cell Host and Microbe, 2018, 23, 759-765.e6.	11.0	98
47	Patient Socioeconomic Status Is an Independent Predictor of Operative Mortality. Annals of Surgery, 2010, 252, 552-558.	4.2	97
48	Th17 cytokines differentiate obesity from obesityâ€associated type 2 diabetes and promote <scp>TNF</scp> α production. Obesity, 2016, 24, 102-112.	3.0	96
49	An autoreactive antibody from an SLE/HIV-1 individual broadly neutralizes HIV-1. Journal of Clinical Investigation, 2014, 124, 1835-1843.	8.2	93
50	Initiation of immune tolerance–controlled HIV gp41 neutralizing B cell lineages. Science Translational Medicine, 2016, 8, 336ra62.	12.4	86
51	Statistical mixture modeling for cell subtype identification in flow cytometry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2008, 73A, 693-701.	1.5	84
52	Envelope Deglycosylation Enhances Antigenicity of HIV-1 gp41 Epitopes for Both Broad Neutralizing Antibodies and Their Unmutated Ancestor Antibodies. PLoS Pathogens, 2011, 7, e1002200.	4.7	82
53	Virus-like Particles Identify an HIV V1V2 Apex-Binding Neutralizing Antibody that Lacks a Protruding Loop. Immunity, 2017, 46, 777-791.e10.	14.3	81
54	Mimicry of an HIV broadly neutralizing antibody epitope with a synthetic glycopeptide. Science Translational Medicine, 2017, 9, .	12.4	81

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55	Analysis of immunoglobulin transcripts and hypermutation following SHIVAD8 infection and protein-plus-adjuvant immunization. Nature Communications, 2015, 6, 6565.	12.8	77
56	Initiation of HIV neutralizing B cell lineages with sequential envelope immunizations. Nature Communications, 2017, 8, 1732.	12.8	76
57	Recognition of synthetic glycopeptides by HIV-1 broadly neutralizing antibodies and their unmutated ancestors. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18214-18219.	7.1	73
58	Affinity maturation in an HIV broadly neutralizing B-cell lineage through reorientation of variable domains. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10275-10280.	7.1	73
59	Selective and site-specific mobilization of dermal dendritic cells and Langerhans cells by Th1- and Th2-polarizing adjuvants. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8334-8339.	7.1	70
60	Vaccine Elicitation of High Mannose-Dependent Neutralizing Antibodies against the V3-Glycan Broadly Neutralizing Epitope in Nonhuman Primates. Cell Reports, 2017, 18, 2175-2188.	6.4	69
61	First Qualification Study of Serum Biomarkers as Indicators of Total Body Burden of Osteoarthritis. PLoS ONE, 2010, 5, e9739.	2.5	68
62	Immunogenic Stimulus for Germline Precursors of Antibodies that Engage the Influenza Hemagglutinin Receptor-Binding Site. Cell Reports, 2015, 13, 2842-2850.	6.4	67
63	Morphologic Analysis Correlates with Gene Expression Changes in Cultured F344 Rat Mesothelial Cells. Toxicology and Applied Pharmacology, 2000, 169, 205-221.	2.8	66
64	Unselected Mutations in the Human Immunodeficiency Virus Type 1 Genome Are Mostly Nonsynonymous and Often Deleterious. Journal of Virology, 2004, 78, 2426-2433.	3.4	66
65	Structure and Diversity of the Rhesus Macaque Immunoglobulin Loci through Multiple De Novo Genome Assemblies. Frontiers in Immunology, 2017, 8, 1407.	4.8	66
66	Identifying differential expression in multiple SAGE libraries: an overdispersed log-linear model approach. BMC Bioinformatics, 2005, 6, 165.	2.6	65
67	SoDA2: a Hidden Markov Model approach for identification of immunoglobulin rearrangements. Bioinformatics, 2010, 26, 867-872.	4.1	65
68	Antibody Light-Chain-Restricted Recognition of the Site of Immune Pressure in the RV144 HIV-1 Vaccine Trial Is Phylogenetically Conserved. Immunity, 2014, 41, 909-918.	14.3	65
69	Similar CD19 Dysregulation in Two Autoantibody-Associated Autoimmune Diseases Suggests a Shared Mechanism of B-Cell Tolerance Loss. Journal of Clinical Immunology, 2007, 27, 53-68.	3.8	61
70	Inference of the HIV-1 VRC01 Antibody Lineage Unmutated Common Ancestor Reveals Alternative Pathways to Overcome a Key Glycan Barrier. Immunity, 2018, 49, 1162-1174.e8.	14.3	61
71	Modeling and optimization of populations subject to time-dependent mutation Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 8219-8223.	7.1	59
72	Prospective Estimation of Recombination Signal Efficiency and Identification of Functional Cryptic Signals in the Genome by Statistical Modeling. Journal of Experimental Medicine, 2003, 197, 207-220.	8.5	59

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73	Differential Reactivity of Germ Line Allelic Variants of a Broadly Neutralizing HIV-1 Antibody to a gp41 Fusion Intermediate Conformation. Journal of Virology, 2011, 85, 11725-11731.	3.4	56
74	Neutralization-guided design of HIV-1 envelope trimers with high affinity for the unmutated common ancestor of CH235 lineage CD4bs broadly neutralizing antibodies. PLoS Pathogens, 2019, 15, e1008026.	4.7	56
75	Toxin-Coupled MHC Class I Tetramers Can Specifically Ablate Autoreactive CD8+ T Cells and Delay Diabetes in Nonobese Diabetic Mice. Journal of Immunology, 2010, 184, 4196-4204.	0.8	55
76	Predicted and inferred waiting times for key mutations in the germinal centre reaction: Evidence for stochasticity in selection. Immunology and Cell Biology, 1998, 76, 373-381.	2.3	54
77	Identification and utilization of arbitrary correlations in models of recombination signal sequences. Genome Biology, 2002, 3, research0072.1.	9.6	54
78	A two-tiered model for simulating the ecological and evolutionary dynamics of rapidly evolving viruses, with an application to influenza. Journal of the Royal Society Interface, 2010, 7, 1257-1274.	3.4	54
79	Recapitulation of HIV-1 Env-antibody coevolution in macaques leading to neutralization breadth. Science, 2021, 371, .	12.6	49
80	Comparison of multiple vaccine vectors in a single heterologous prime-boost trial. Vaccine, 2008, 26, 6108-6118.	3.8	45
81	Structural Constraints of Vaccine-Induced Tier-2 Autologous HIV Neutralizing Antibodies Targeting the Receptor-Binding Site. Cell Reports, 2016, 14, 43-54.	6.4	45
82	The Distribution of Variation in Regulatory Gene Segments, as Present in MHC Class II Promoters. Genome Research, 1998, 8, 124-134.	5.5	43
83	The Nucleotide-Replacement Spectrum Under Somatic Hypermutation Exhibits Microsequence Dependence That Is Strand-Symmetric and Distinct from That Under Germline Mutation. Journal of Immunology, 2000, 164, 1971-1976.	0.8	43
84	Chiropteran types I and II interferon genes inferred from genome sequencing traces by a statistical gene-family assembler. BMC Genomics, 2010, 11, 444.	2.8	43
85	Sequence intrinsic somatic mutation mechanisms contribute to affinity maturation of VRC01-class HIV-1 broadly neutralizing antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8614-8619.	7.1	42
86	Belowground factors mediating changes in methane consumption in a forest soil under elevated CO2. Global Biogeochemical Cycles, 2002, 16, 23-1-23-14.	4.9	41
87	Large-scale analysis of human heavy chain V(D)J recombination patterns. Immunome Research, 2008, 4, 3.	0.1	41
88	Boosting of HIV envelope CD4 binding site antibodies with long variable heavy third complementarity determining region in the randomized double blind RV305 HIV-1 vaccine trial. PLoS Pathogens, 2017, 13, e1006182.	4.7	38
89	The 185/333 Gene Family Is a Rapidly Diversifying Host-Defense Gene Cluster in the Purple Sea Urchin Strongylocentrotus purpuratus. Journal of Molecular Biology, 2008, 379, 912-928.	4.2	36
90	Surface plasmon resonance measurements of plasma antibody avidity during primary and secondary responses to anthrax protective antigen. Journal of Immunological Methods, 2014, 404, 1-12.	1.4	35

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91	Key mutations stabilize antigenâ€binding conformation during affinity maturation of a broadly neutralizing influenza antibody lineage. Proteins: Structure, Function and Bioinformatics, 2015, 83, 771-780.	2.6	34
92	Amino Acid Changes in the HIV-1 gp41 Membrane Proximal Region Control Virus Neutralization Sensitivity. EBioMedicine, 2016, 12, 196-207.	6.1	34
93	Geometric phase shifts under adiabatic parameter changes in classical dissipative systems. Physical Review Letters, 1991, 66, 847-849.	7.8	32
94	Enhanced Evolvability in Immunoglobulin V Genes Under Somatic Hypermutation. Journal of Molecular Evolution, 1999, 49, 23-26.	1.8	30
95	The Targeting of Somatic Hypermutation Closely Resembles That of Meiotic Mutation. Journal of Immunology, 2001, 166, 892-899.	0.8	29
96	Longitudinal Analysis of T-Cell Receptor Variable β Chain Repertoire in Patients with Acute Graft-versus-Host Disease after Allogeneic Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2006, 12, 335-345.	2.0	29
97	β Cell-Specific CD4+ T Cell Clonotypes in Peripheral Blood and the Pancreatic Islets Are Distinct. Journal of Immunology, 2009, 183, 7585-7591.	0.8	29
98	Secretion of MIP-1Î ² and MIP-1Î [±] by CD8+ T-lymphocytes correlates with HIV-1 inhibition independent of coreceptor usage. Cellular Immunology, 2011, 266, 154-164.	3.0	28
99	Statistical analysis of antigen receptor spectratype data. Bioinformatics, 2005, 21, 3394-3400.	4.1	26
100	Statistical inference of sequence-dependent mutation rates. Current Opinion in Genetics and Development, 2001, 11, 612-615.	3.3	25
101	Spatial mixture modelling for unobserved point processes: examples in immunofluorescence histology. Bayesian Analysis, 2009, 4, 297-316.	3.0	25
102	Improved Inference of Mutation Rates: I. An Integral Representation for the Luria–Delbrück Distribution. Theoretical Population Biology, 2001, 59, 41-48.	1.1	23
103	Combined HIV-1 Envelope Systemic and Mucosal Immunization of Lactating Rhesus Monkeys Induces a Robust Immunoglobulin A Isotype B Cell Response in Breast Milk. Journal of Virology, 2016, 90, 4951-4965.	3.4	23
104	The Dynamics of T-Cell Receptor Repertoire Diversity Following Thymus Transplantation for DiGeorge Anomaly. PLoS Computational Biology, 2009, 5, e1000396.	3.2	22
105	Geometric phase shifts in chemical oscillators. Nature, 1991, 349, 506-508.	27.8	21
106	Open Source Research — the Power of Us. Australian Journal of Chemistry, 2006, 59, 291.	0.9	21
107	Quantification of total T-cell receptor diversity by flow cytometry and spectratyping. BMC Immunology, 2013, 14, 35.	2.2	21
108	The Multiscale Systems Immunology project: software for cell-based immunological simulation. Source Code for Biology and Medicine, 2008, 3, 6.	1.7	20

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109	HIV DNA-Adenovirus Multiclade Envelope Vaccine Induces gp41 Antibody Immunodominance in Rhesus Macaques. Journal of Virology, 2017, 91, .	3.4	20
110	Neonate-primed CD8+ memory cells rival adult-primed memory cells in antigen-driven expansion and anti-viral protection. International Immunology, 2006, 18, 249-257.	4.0	19
111	Boosting with AIDSVAX B/E Enhances Env Constant Region 1 and 2 Antibody-Dependent Cellular Cytotoxicity Breadth and Potency. Journal of Virology, 2020, 94, .	3.4	19
112	Genetic Plasticity of V Genes Under Somatic Hypermutation: Statistical Analyses Using a New Resampling-Based Methodology. Genome Research, 1999, 9, 1294-1304.	5.5	17
113	Genetic and structural analyses of affinity maturation in the humoral response to <scp>HIV</scp> â€1. Immunological Reviews, 2017, 275, 129-144.	6.0	17
114	Spike initiation and propagation on axons with slow inward currents. Biological Cybernetics, 1993, 68, 209-214.	1.3	16
115	Improved Inference of Mutation Rates: II. Generalization of the Luria–Delbrück Distribution for Realistic Cell-Cycle Time Distributions. Theoretical Population Biology, 2001, 59, 49-59.	1.1	16
116	Terminal deoxynucleotidyl transferases from elasmobranchs reveal structural conservation within vertebrates. Immunogenetics, 2003, 55, 594-604.	2.4	16
117	Spatiotemporal programming of a simple inflammatory process. Immunological Reviews, 2007, 216, 153-163.	6.0	16
118	Metastasizing patent claims on BRCA1. Genomics, 2010, 95, 312-314.	2.9	16
119	Physiological Insights from Cellular and Network Models of the Stomatogastric Nervous System of Lobsters and Crabs. American Zoologist, 1993, 33, 29-39.	0.7	15
120	Egyptian Rousette IFN-ω Subtypes Elicit Distinct Antiviral Effects and Transcriptional Responses in Conspecific Cells. Frontiers in Immunology, 2020, 11, 435.	4.8	15
121	SpA: web-accessible spectratype analysis: data management, statistical analysis and visualization. Bioinformatics, 2005, 21, 3697-3699.	4.1	14
122	A Bayesian approach for estimating calibration curves and unknown concentrations in immunoassays. Bioinformatics, 2011, 27, 707-712.	4.1	14
123	A Model for Migratory B Cell Oscillations from Receptor Down-Regulation Induced by External Chemokine Fields. Bulletin of Mathematical Biology, 2013, 75, 185-205.	1.9	14
124	Paradoxical suppression of poly-specific broadly neutralizing antibodies in the presence of strain-specific neutralizing antibodies following HIV infection. Journal of Theoretical Biology, 2011, 277, 55-66.	1.7	13
125	Structural analysis of the unmutated ancestor of the HIV-1 envelope V2 region antibody CH58 isolated from an RV144 vaccine efficacy trial vaccinee. EBioMedicine, 2015, 2, 713-722.	6.1	13
126	Isolation and Structure of an Antibody that Fully Neutralizes Isolate SIVmac239 Reveals Functional Similarity of SIV and HIV Glycan Shields. Immunity, 2019, 51, 724-734.e4.	14.3	13

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127	Geometric phases in dissipative systems. Chaos, 1991, 1, 455-461.	2.5	10
128	Flow: Statistics, visualization and informatics for flow cytometry. Source Code for Biology and Medicine, 2008, 3, 10.	1.7	10
129	Density-dependent Prenatal Androgen Exposure as an Endogenous Mechanism for the Generation of Cycles in Small Mammal Populations. Journal of Theoretical Biology, 1998, 190, 93-106.	1.7	9
130	Amino acid biophysical properties in the statistical prediction of peptide-MHC class I binding. Immunome Research, 2007, 3, 9.	0.1	9
131	Improving peptide-MHC class I binding prediction for unbalanced datasets. BMC Bioinformatics, 2008, 9, 385.	2.6	8
132	Rescue of cytotoxic function in the CD8α knockout mouse by removal of MHC class II. European Journal of Immunology, 2008, 38, 1511-1521.	2.9	7
133	Genetic correlates of autoreactivity and autoreactive potential in human Ig heavy chains. Immunome Research, 2009, 5, 1.	0.1	7
134	Bayesian Spatio-Dynamic Modeling in Cell Motility Studies: Learning Nonlinear Taxic Fields Guiding the Immune Response. Journal of the American Statistical Association, 2012, 107, 855-865.	3.1	7
135	High-throughput identification and dendritic cell-based functional validation of MHC class I-restricted Mycobacterium tuberculosis epitopes. Scientific Reports, 2014, 4, 4632.	3.3	7
136	HIV-1 Envelope Mimicry of Host Enzyme Kynureninase Does Not Disrupt Tryptophan Metabolism. Journal of Immunology, 2016, 197, 4663-4673.	0.8	6
137	Intra-seasonal antibody repertoire analysis of a subject immunized with an MF59®-adjuvanted pandemic 2009 H1N1 vaccine. Vaccine, 2018, 36, 5325-5332.	3.8	4
138	Hypermutation in T cells questioned. Nature, 1995, 375, 286-286.	27.8	3
139	Mixtures of Gaussian wells: Theory, computation, and application. Computational Statistics and Data Analysis, 2012, 56, 3809-3820.	1.2	3
140	Microsimulation of Inducible Reorganization in Immunity. , 2006, , 437-450.		3
141	Bayesian Estimation of the Active Concentration and Affinity Constants Using Surface Plasmon Resonance Technology. PLoS ONE, 2015, 10, e0130812.	2.5	3
142	Development of Neutralization Breadth against Diverse HIVâ€1 by Increasing Ab–Ag Interface on V2. Advanced Science, 2022, , 2200063.	11.2	3
143	Waiting times to appearance and dominance of advantageous mutants: estimation based on the likelihood. Mathematical Biosciences, 2001, 170, 59-77.	1.9	2
144	A linear two-state model with complex dynamics. Physics Letters, Section A: General, Atomic and Solid State Physics, 2001, 280, 204-208.	2.1	2

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145	An Information-Theoretic Method for the Treatment of Plural Ancestry in Phylogenetics. Molecular Biology and Evolution, 2008, 25, 1199-1208.	8.9	2
146	Unconventional Interrogation Yields HIV's Escape Plan. Cell Host and Microbe, 2017, 21, 659-660.	11.0	1
147	Gain-Scanning for Protein Microarray Assays. Journal of Proteome Research, 2020, 19, 2664-2675.	3.7	1
148	HLA and HIV Infection Progression: Application of the Minimum Description Length Principle to Statistical Genetics. Lecture Notes in Computer Science, 2006, , 1-12.	1.3	0