

Richard A Neher

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

10,511
citations

76326

40
h-index

71685

76
g-index

135
all docs

135
docs citations

135
times ranked

15195
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution, geographic spreading, and demographic distribution of Enterovirus D68. <i>PLoS Pathogens</i> , 2022, 18, e1010515.	4.7	19
2	Augur: a bioinformatics toolkit for phylogenetic analyses of human pathogens. <i>Journal of Open Source Software</i> , 2021, 6, 2906.	4.6	129
3	Limited Predictability of Amino Acid Substitutions in Seasonal Influenza Viruses. <i>Molecular Biology and Evolution</i> , 2021, 38, 2767-2777.	8.9	12
4	Interactions between seasonal human coronaviruses and implications for the SARS-CoV-2 pandemic: A retrospective study in Stockholm, Sweden, 2009-2020. <i>Journal of Clinical Virology</i> , 2021, 136, 104754.	3.1	25
5	SARS-CoV-2 N501Y Introductions and Transmissions in Switzerland from Beginning of October 2020 to February 2021—Implementation of Swiss-Wide Diagnostic Screening and Whole Genome Sequencing. <i>Microorganisms</i> , 2021, 9, 677.	3.6	32
6	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , 2021, 19, e3001236.	5.6	200
7	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021, 6, 821-823.	13.3	221
8	Molecular Epidemiology and Evolutionary Trajectory of Emerging Echovirus 30, Europe. <i>Emerging Infectious Diseases</i> , 2021, 27, 1616-1626.	4.3	18
9	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712.	27.8	363
10	Nextclade: clade assignment, mutation calling and quality control for viral genomes. <i>Journal of Open Source Software</i> , 2021, 6, 3773.	4.6	496
11	Efficient inference, potential, and limitations of site-specific substitution models. <i>Virus Evolution</i> , 2020, 6, veaa066.	4.9	3
12	Cryptic transmission of SARS-CoV-2 in Washington state. <i>Science</i> , 2020, 370, 571-575.	12.6	217
13	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. <i>Cell</i> , 2020, 181, 990-996.e5.	28.9	321
14	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.1	68
15	Characterising the epidemic spread of influenza A/H3N2 within a city through phylogenetics. <i>PLoS Pathogens</i> , 2020, 16, e1008984.	4.7	17
16	Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. <i>Eurosurveillance</i> , 2020, 25, .	7.0	186
17	2019-novel Coronavirus (2019-nCoV): estimating the case fatality rate — a word of caution. <i>Swiss Medical Weekly</i> , 2020, 150, w20203.	1.6	135
18	Potential impact of seasonal forcing on a SARS-CoV-2 pandemic. <i>Swiss Medical Weekly</i> , 2020, 150, w20224.	1.6	223

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19	COVID-19 epidemic in Switzerland: on the importance of testing, contact tracing and isolation. <i>Swiss Medical Weekly</i> , 2020, 150, w20225.	1.6	367
20	Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution. <i>ELife</i> , 2020, 9, .	6.0	35
21	Asynchrony between virus diversity and antibody selection limits influenza virus evolution. <i>ELife</i> , 2020, 9, .	6.0	25
22	Evaluation of two workflows for whole genome sequencing-based typing of influenza A viruses. <i>Journal of Virological Methods</i> , 2019, 266, 30-33.	2.1	9
23	Intra- and interpatient evolution of enterovirus D68 analyzed by whole-genome deep sequencing. <i>Virus Evolution</i> , 2019, 5, vez007.	4.9	20
24	Quantitative contribution of efflux to multi-drug resistance of clinical <i>Escherichia coli</i> and <i>Pseudomonas aeruginosa</i> strains. <i>EBioMedicine</i> , 2019, 41, 479-487.	6.1	37
25	Evolution and rapid spread of a reassortant A(H3N2) virus that predominated the 2017â€“2018 influenza season. <i>Virus Evolution</i> , 2019, 5, vez046.	4.9	19
26	Phylogenetic theory of persistence, extinction and speciation of rapidly adapting pathogens. <i>ELife</i> , 2019, 8, .	6.0	30
27	TreeTime: Maximum-likelihood phylogenetic analysis. <i>Virus Evolution</i> , 2018, 4, vex042.	4.9	883
28	Predictive Modeling of Influenza Shows the Promise of Applied Evolutionary Biology. <i>Trends in Microbiology</i> , 2018, 26, 102-118.	7.7	95
29	panX: pan-genome analysis and exploration. <i>Nucleic Acids Research</i> , 2018, 46, e5-e5.	14.5	241
30	Nextstrain: real-time tracking of pathogen evolution. <i>Bioinformatics</i> , 2018, 34, 4121-4123.	4.1	2,287
31	Incomplete inhibition of HIV infection results in more HIV infected lymph node cells by reducing cell death. <i>ELife</i> , 2018, 7, .	6.0	12
32	<i>Arabidopsis thaliana</i> and <i>Pseudomonas</i> Pathogens Exhibit Stable Associations over Evolutionary Timescales. <i>Cell Host and Microbe</i> , 2018, 24, 168-179.e4.	11.0	145
33	Colistin susceptibility test evaluation of multiple-resistance-level <i>Pseudomonas aeruginosa</i> isolates generated in a morbidostat device. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 3368-3374.	3.0	10
34	Real-Time Analysis and Visualization of Pathogen Sequence Data. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	25
35	Improving the quality and workflow of bacterial genome sequencing and analysis: paving the way for a Switzerland-wide molecular epidemiological surveillance platform. <i>Swiss Medical Weekly</i> , 2018, 148, w14693.	1.6	28
36	Temporal dynamics of gene expression and histone marks at the <i>Arabidopsis</i> shoot meristem during flowering. <i>Nature Communications</i> , 2017, 8, 15120.	12.8	96

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37	Rapid and Consistent Evolution of Colistin Resistance in Extensively Drug-Resistant <i>Pseudomonas aeruginosa</i> during Morbidostat Culture. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	57
38	Error rates, PCR recombination, and sampling depth in HIV-1 whole genome deep sequencing. <i>Virus Research</i> , 2017, 239, 106-114.	2.2	42
39	<i>In vivo</i> mutation rates and the landscape of fitness costs of HIV-1. <i>Virus Evolution</i> , 2017, 3, vex003.	4.9	85
40	Estimating time of HIV-1 infection from next-generation sequence diversity. <i>PLoS Computational Biology</i> , 2017, 13, e1005775.	3.2	45
41	HIV Cell-to-Cell Spread Results in Earlier Onset of Viral Gene Expression by Multiple Infections per Cell. <i>PLoS Pathogens</i> , 2016, 12, e1005964.	4.7	62
42	Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1701-9.	7.1	165
43	Establishment and stability of the latent HIV-1 DNA reservoir. <i>ELife</i> , 2016, 5, .	6.0	119
44	Challenges with Using Primer IDs to Improve Accuracy of Next Generation Sequencing. <i>PLoS ONE</i> , 2015, 10, e0119123.	2.5	27
45	nextflu: real-time tracking of seasonal influenza virus evolution in humans. <i>Bioinformatics</i> , 2015, 31, 3546-3548.	4.1	153
46	Population genomics of inpatient HIV-1 evolution. <i>ELife</i> , 2015, 4, .	6.0	206
47	Predicting evolution from the shape of genealogical trees. <i>ELife</i> , 2014, 3, .	6.0	159
48	Genetic Diversity in the Interference Selection Limit. <i>PLoS Genetics</i> , 2014, 10, e1004222.	3.5	96
49	Characterization of Genetic Diversity in the Nematode <i>Pristionchus pacificus</i> from Population-Scale Resequencing Data. <i>Genetics</i> , 2014, 196, 1153-1165.	2.9	79
50	Genetic Draft, Selective Interference, and Population Genetics of Rapid Adaptation. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2013, 44, 195-215.	8.3	161
51	Mathematical modeling of escape of HIV from cytotoxic T lymphocyte responses. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2013, 2013, P01010.	2.3	38
52	Quantifying Selection against Synonymous Mutations in HIV-1 env Evolution. <i>Journal of Virology</i> , 2013, 87, 11843-11850.	3.4	45
53	Quantifying the range of a lipid phosphate signal in vivo. <i>Journal of Cell Science</i> , 2013, 126, 5453-64.	2.0	9
54	Inferring HIV Escape Rates from Multi-Locus Genotype Data. <i>Frontiers in Immunology</i> , 2013, 4, 252.	4.8	35

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55	Coalescence and genetic diversity in sexual populations under selection. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15836-15841.	7.1	60
56	Genealogies of rapidly adapting populations. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 437-442.	7.1	203
57	Emergence of clones in sexual populations. Journal of Statistical Mechanics: Theory and Experiment, 2013, 2013, P01008.	2.3	16
58	FFPopSim: an efficient forward simulation package for the evolution of large populations. Bioinformatics, 2012, 28, 3332-3333.	4.1	52
59	Fluctuations of Fitness Distributions and the Rate of Muller's Ratchet. Genetics, 2012, 191, 1283-1293.	2.9	63
60	Estimating the Strength of Selective Sweeps from Deep Population Diversity Data. Genetics, 2012, 191, 593-605.	2.9	46
61	Dynamic Mutation—Selection Balance as an Evolutionary Attractor. Genetics, 2012, 191, 1309-1319.	2.9	96
62	Statistical genetics and evolution of quantitative traits. Reviews of Modern Physics, 2011, 83, 1283-1300.	45.6	87
63	Target search on a dynamic DNA molecule. Physical Review E, 2011, 84, 051911.	2.1	14
64	Genetic Draft and Quasi-Neutrality in Large Facultatively Sexual Populations. Genetics, 2011, 188, 975-996.	2.9	78
65	Correlated Evolution of Nearby Residues in Drosophilid Proteins. PLoS Genetics, 2011, 7, e1001315.	3.5	48
66	Recombination Rate and Selection Strength in HIV Intra-patient Evolution. PLoS Computational Biology, 2010, 6, e1000660.	3.2	154
67	Competition between recombination and epistasis can cause a transition from allele to genotype selection. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6866-6871.	7.1	99
68	Blind Source Separation Techniques for the Decomposition of Multiply Labeled Fluorescence Images. Biophysical Journal, 2009, 96, 3791-3800.	0.5	113
69	Topological estimation of percolation thresholds. Journal of Statistical Mechanics: Theory and Experiment, 2008, 2008, P01011.	2.3	50
70	Optimal Flexibility for Conformational Transitions in Macromolecules. Physical Review Letters, 2007, 99, 178101.	7.8	1
71	Force-Induced DNA Slippage. Biophysical Journal, 2007, 92, 2491-2497.	0.5	44
72	Intermediate phase in DNA melting. Physical Review E, 2006, 73, 030902.	2.1	19

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73	Kinetic Accessibility of Buried DNA Sites in Nucleosomes. <i>Physical Review Letters</i> , 2006, 97, 208102.	7.8	33
74	DNA as a Programmable Viscoelastic Nanoelement. <i>Biophysical Journal</i> , 2005, 89, 3846-3855.	0.5	10
75	Dynamics of Force-Induced DNA Slippage. <i>Physical Review Letters</i> , 2004, 93, 198102.	7.8	18
76	Applying spectral fingerprinting to the analysis of FRET images. <i>Microscopy Research and Technique</i> , 2004, 64, 185-195.	2.2	64